2007 SACNAS NATIONAL CONFERENCE

Society for Advancement of Chicanos and Native Americans in Science

SACNAS NATIONAL CONFERENCE ABSTRACTS 2007

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2007 SACNAS National Conference
Kansas City, Missouri
October 11-14, 2007

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SACNAS is pleased to present the fourth annual volume of the SACNAS National Conference Abstracts, featuring the research conducted by undergraduate and graduate students under the guidance of a dedicated cadre of SACNAS mentors.

ORAL PRESENTATIONS

Graduate student oral research presentations take place on Friday, October 12, from 1:15 to 2:45 p.m.

ORAL PRESENTERS CHECK-IN

All oral presenters are required to check in and receive their presentation ribbons during the registration process at the Registration and Information Area in Lobby 2300 of the Kansas City Convention Center.

ORAL PRESENTATION SET UP

Graduate oral presenters must arrive between 12:30 to 1 p.m. on Friday, October 12, to their assigned presentation room. Bring all PowerPoint materials at this time to be loaded onto presentation equipment.

POSTER PRESENTATIONS

All graduate and undergraduate student poster research presentations take place in Exhibit Hall E. Friday poster presentations take place on Friday, October 12, from 3 to 6 p.m. Saturday poster presentations take place on Saturday, October 13, from 9 a.m. to 12 p.m.

POSTER PRESENTERS CHECK-IN

All poster presenters are required to check in and receive their presentation ribbons during the registration process at the Registration and Information Area in Lobby 2300 of the Kansas City Convention Center. Ribbons are required for entry into Exhibit Hall E for poster setup.

POSTER PRESENTATION SET UP

All poster presentations are designated by poster board number and date of presentation. Presenters may set up poster materials in Exhibit Hall E **only** during the set up times corresponding to their presentation day.

FRIDAY PRESENTERS SET UP
Friday, October 12: 7:30–8 a.m.

SATURDAY PRESENTERS SET UP
Saturday, October 13: 7:30–8 a.m.

POSTER PRESENTATION TAKE DOWN

All Friday posters must be taken down at 6 p.m. on Friday, October 12. Saturday posters must be taken down at 12 p.m. on Saturday, October 13. SACNAS cannot be responsible for posters that have not been taken down at designated time; unclaimed posters will be discarded.

ORAL AND POSTER PRESENTATIONS INDEX

For a complete index of all oral and poster presenters (listed in alphabetical order by presenter's last name), see pages 179-184.

2008 ORAL AND POSTER RESEARCH PRESENTATIONS

For information on submitting an oral or poster abstract for the 2008 SACNAS National Conference, which will take place October 9–12 in Salt Lake City, Utah, email info@sacnas.org.

FLOOR PLANS

Please refer to the exhibit hall floor plan on the inside back cover of this publication, and to the floor plans on pages 81–84 of the conference program to help you navigate the conference.

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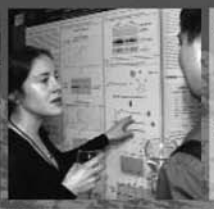

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REVIEW PROCESS

The SACNAS Presentations Committee organizes activities related to the student scientific sessions. These sessions advance the organization's strategic efforts to support students' preparation for their professional science careers and, more specifically, the demanding rigors of discipline-focused professional conferences. Our goal is to provide fair and positive abstract review, presentation mentoring/judging, and awards selection processes that promote growth and experience for emerging scientists, mathematicians, and engineers. Accordingly, we focus our abstract selection and scientific presentation evaluation process on constructive student-professional engagement and mentoring.

Students and mentors alike have responded positively to our efforts. This year, over 500 abstracts were submitted for the 2007 SACNAS National Conference. We actively recruited over 140 professionals from our membership who enthusiastically volunteered their time and energy to function as abstract evaluators. We instructed each abstract reviewer to give each student constructive feedback, while giving a fair and unbiased appraisal of the abstract quality in the overall score. Each abstract was reviewed by two experts in a manner similar to evaluations in traditional scientific societies. Student abstracts were scored with criteria using a numerical scoring system for:

- Rationale (purpose, objective, and/or hypothesis)
- Approach (methods and/or materials)
- Findings (data and analysis)
- Presentation (discipline-appropriate style and substance)

As part of our effort to continually improve the quality of student presentations, we asked the reviewers to incorporate a high standard for accepted submissions. Abstracts that scored 60 percent or higher were unconditionally accepted. Students who received lower scores have been required to revise their abstract using reviewer comments to guide the modification of their resubmissions. We believe that this process has led to excellent quality abstracts, and we are proud to publish them in this fourth volume.

At the conference, all poster and oral presentations will be evaluated using a similar process. We believe this will provide for a learning and rewarding experience for both students and mentor-judges.

In keeping with our mission, the SACNAS Presentations Committee strives to continually make improvements to the student scientific sessions, and we welcome all input regarding the process. Finally, we warmly thank the SACNAS members and other reviewers who generously contributed their time and energy to our task.

Sincerely,
2007 SACNAS Student Presentations Committee

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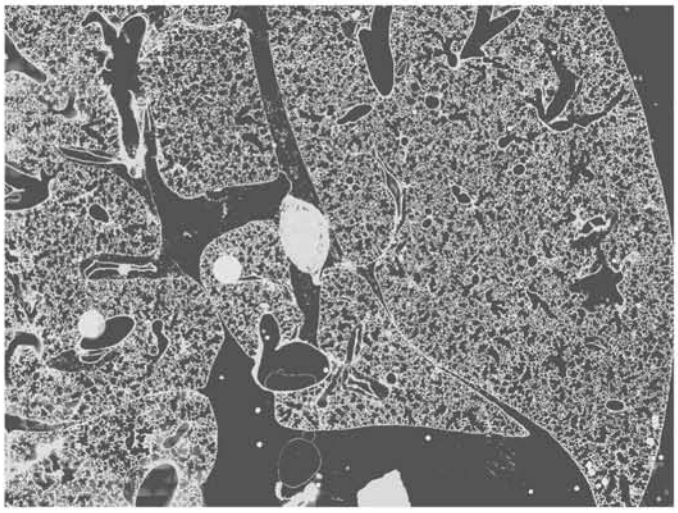

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GRADUATE STUDENT ORAL ABSTRACTS 2007

BIOLOGICAL SCIENCES

BIOCHEMISTRY

CC 2215C

EFFECTS OF PROLINE MUTATIONS ON THE STRUCTURE AND FUNCTION OF HIV 1 FUSION PEPTIDE

Maximiliano Vallejos, Patrick Mobley. *California State Polytechnic University, Pomona, Pomona, Calif.*

Infection of HIV-1 is choreographed by the transmembrane glycoprotein gp41. The insertion of the N-terminus fusion peptide (FP) of gp41 is the first step in HIV-1 infection. Synthetic FP (23 residue peptide) inserts into the target cell membrane in alpha-helical form from residues 3-15, while residues 16-23 remain unstructured or retain some beta-sheet structure. Proline is known to disrupt alpha-helices and beta-sheets. FP with mutations G5P, G10P, A15P, and G20P were synthesized in to determine whether the helix or sheet is required at these positions for fusion activity. Membrane perturbing studies were done by measuring erythrocyte hemolysis, while secondary structure analyses were performed with a Fourier-transform infrared spectrometer (FT-IR). A structure/function correlation was then assessed with the information obtained from both experimental procedures. Mutants G5P, G10P, and A15P were found to have lower hemolytic activity than wildtype FP, while G20P showed greater hemoglobin leakage. At 60 micro-molar concentration of FP, hemolysis was 62.2%, while mutants G5P, G10P, A15P, and G20P were 14.6%, 5.7%, 27.2%, and 83.4%, respectively. For FT-IR studies, FP and mutants were dried from 1,1,1,3,3,3-hexafluoroisopropanol (HFIP) and deuterium oxide (D2O) to mimic a membrane-like environment and an aqueous environment, correspondingly. When dried from HFIP, mutations did not have a significant effect in the helical content, while beta-sheet concentration was affected for G5P (30%) and G10P (23%), compared to ~40% in FP, A15P, and G20P. D2O results showed a correlation in beta-sheet increase which increased hemolysis results. Beta-sheet structure in the fusion peptide is then necessary for HIV-1 infection.

CANCER BIOLOGY

CC 2203

MECHANISMS OF EPIGENETIC GENE MODIFICATION FOLLOWING NEONATAL EXPOSURE TO DIETHYLSTILBESTROL (DES) AND ITS RELATIONSHIP TO HORMONAL CARCINOGENESIS

Karla Michelle Hernandez-Cruz[1,3], Wendy Jefferson[3], Harriet Kinyamu[3], Retha Newbold[2], Trevor Archer[3]. [1]*Universidad Metropolitana, San Juan, P.R.,* [2]*Laboratory of Molecular Toxicology, National Institute of Environmental Health Sciences, Research Triangle Park, N.C.,* [3]*Laboratory of Molecular Carcinogenesis, National Institute of Environmental Health Sciences, Research Triangle Park, N.C.*

CD-1 mice treated neonatally with the synthetic estrogen DES develop high prevalence of uterine adenocarcinoma by 18 months of age. To further characterize the molecular mechanisms underlying the development of uterine cancer, we utilized microarray analysis to monitor changes in gene expression in the uterus of DES treated mice. Estrogen regulated genes like lactoferrin are changed during the time of treatment and long after the initial exposure. DES exposure alters methylation patterns in the promoter region of lactoferrin and other estrogen regulated genes. These data suggest that epigenetic events permanently alter gene expression after DES treatment, but whether these gene alterations lead to cancer is still unknown. The goal of this project is to identify epigenetic mechanisms by which these alterations occur and which ones are involved in either the initiation or promotion of cancer. Chromatin (DNA and histones) is an ultimate template for epigenetic regulation. DNA methyltransferases establish methylation patterns on DNA that are heritable. We have determined the levels of DNA methyltransferases and chromatin modifying proteins known to facilitate epigenetic regulation using real time RT-PCR and Western blot analysis. We are currently developing an *in vivo* chromatin immunoprecipitation (ChIP) assay to identify proteins associated with hypomethylated DNA sequences in the promoter region of estrogen regulated genes. This will allow us to evaluate chromatin modifying proteins involved in epigenetic regulation during development, the mechanism by which estrogen interferes with this process and how these changes ultimately contribute to cancer.

CC 2203

INTRACELLULAR TRAFFICKING OF SEQUESTERED AMINE-CONTAINING MOLECULES FROM THE LYSOSOME: A FUNCTIONAL ROLE FOR THE NPC1 PROTEIN

Allyn Kaufmann, Muralikrishna Duvvuri, Jeffrey Krise. *University of Kansas, Lawrence, Kans.*

Niemann-Pick C1 (NPC1) is a lysosome-associated membrane protein which for several decades has been implicated in cholesterol homeostasis. Mutations in NPC1 results in Niemann-Pick Type-C (NP-C) disease, which is characterized by neurodegeneration and death of individuals in early childhood. Recent research has challenged the notion that cholesterol homeostasis is the sole cause of the disease, and is, perhaps, secondary to another unknown defective role. Our research has shown that NPC1 facilitates the fusion between lysosomes and late-endosomes creating an organelle that can expand in the presence of high amine concentrations. This event does not occur in cells with defective NPC1. Specifically, we propose that NPC1 is able to sense increasing concentrations of amines, which leads to the formation of a hybrid-organelle capable of facilitating secretion to the extracellular space. To further understand this trafficking step a pulse-chase technique was employed to localize radiolabeled dextran to lysosomes and secretion to the extracellular space was monitored as a function of time. Many compounds, including amines, were investigated for their influence on total dextran secretion from the cell. NPC1-mediated secretion of lysosomal cargo can be significantly stimulated when certain lysosomotropic amines are administered. The same treatments showed no influence on secretion in cells with non-functional NPC1. Furthermore, stimulation is concentration dependent and exclusive to amines that accumulate excessively into lysosomes. Future studies are aimed at supporting this functional role for NPC1, which may provide clues towards new therapeutic strategies that have been severely lacking since the discovery of NP-C disease.

CC 2203

ENHANCED C-MYB PROTEIN EXPRESSION AT THE G1/S TRANSITION IN THE HUMAN JURKAT CELL LINE

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c-Myb is the cellular homolog of v-Myb, an oncoprotein encoded by Avian Myeloblastosis virus, which causes leukemia in animals. v-Myb is truncated at the N and C termini and contains numerous mutations that enhance its oncogenic potential. The c-*myb* gene is known to control the proliferation of hematopoietic cells and has been implicated in the control of the cell cycle. The c-Myb protein interacts with cyclin D1 and CDK6, which regulate the cell cycle at the G1/S transition. It is hypothesized that c-Myb differentially regulates gene expression at various stages of the cell cycle. In order to determine c-Myb's role in the cell cycle, Jurkat cells, a human T-cell leukemia cell line, were blocked at various stages of the cell cycle with chemical agents such as hydroxyurea, double thymidine block, and nocodozole. Examination of treated cells revealed an accumulation of the c-Myb protein in cells blocked at the G1/S transition, while mRNA levels remained relatively constant. A possible mechanism for the increased stability of c-Myb protein may be post-translational modifications. This mechanism is supported by the previously published data indicating c-Myb is highly modified. Furthermore, an anti-acetyl c-Myb antibody developed in our laboratory highly enriched for acetylated c-Myb at the G1/S transition. These results suggest that post-translational modifications of c-Myb may enhance its stability at the G1/S transition of the cell cycle.

GENERAL BIOLOGY

CC 2206

THE SECONDARY STRUCTURE OF RESILIN

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Little information exists concerning the secondary and tertiary structures of elastic proteins due to complicated intrinsic properties that make it nearly impossible to use conventional methods, such as x-ray crystallography, for determining structures. The highly resilient protein resilin is no exception. Resilin is a common elastic protein in arthropods and has possible biomedical applications. It stores large amounts of strain energy needed to power flight, jumping, and striking mechanisms. It is also possible that resilin is responsible for the strain energy storage capabilities of the mantis shrimp appendage. Previous researchers have shown that under high entropy conditions, the protein consists of random coils interspersed between di- and tri-tyrosine cross-links and that resilin's ability to store energy is due to a secondary structure that becomes more ordered under stress. There is, however, a lack of information regarding its low entropy structure. Using secondary structure prediction servers, the possible local structures present in the low-entropy form have been predicted. Due to high proline and glycine content, the amino acid sequence suggests that the protein could consist of consecutive beta-turns that form a spring-like beta-spiral. The servers suggest that the protein does not contain beta structures, but could consist of four to five short alpha helices interspersed between random coils. To expand upon the information obtained from the prediction servers, experiments employing circular dichroism are being used to detect conformational changes in the secondary structure of resilin. In addition, the thermodynamic properties of the structural changes in the protein are under investigation.

CC 2206

TOWARDS REVEALING THE RELATIONSHIPS BETWEEN ECOPHYSIOLOGICAL AND METABOLIC CHARACTERISTICS OF *SHEWANELLA* STRAINS

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Shewanella is an important model microorganism for bioremediation studies. This genus is composed of several ecologically diverse microorganisms capable of reducing a wide variety of compounds under anaerobic conditions including toxic and mutagenic metals such as chromium. The overall goal of this study is to better understand the relationships between metabolic capabilities and ecophysiological characteristics of respiratory-versatile members of this important genus. Such understanding is critical for developing and implementing bioremediation strategies. Metabolic pathways of the bacteria were automatically reconstructed by analyzing the genome annotations of 11 sequenced *Shewanella* species using the PathoLocic Pathway Predictor software. To relate metabolic capabilities with ecophysiological characteristics, enzyme enrichment of each metabolic pathway for each species was used for creating a hierarchical clustering of the species and hierarchical clustering of the identified metabolic pathways with subsequent comparative analysis of these hierarchies. Preliminary analysis of the results suggest identified clusters of *Shewanella* species may correspond to ecophysiologically similar *Shewanella* species characterized by enriched metabolic pathways. Although these results are preliminary, they are promising and may provide further understanding of the metabolic strategies for survival in different ecophysiological habitats.

CC 2206

SCHISTOSOME GENETIC DIVERSITY AND STRUCTURING IN A BRAZILIAN VILLAGE

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Digenean trematodes of the genus *Schistosoma* are responsible for chronic schistosomiasis in over 200 million people worldwide. Debilitating hepatic, intestinal, and urinary pathology make schistosomiasis a parasitic disease of global socioeconomic and public health concern. In Brazil alone, an estimated 35 million people live at continual risk of infection by the species *Schistosoma mansoni*. In order to evaluate epidemiological patterns of infection among human definitive hosts, we assessed the genetic diversity and population subdivision of *S. mansoni* infrapopulations in patients from a highly endemic village in the state of Minas Gerais, Brazil. Parasite eggs were isolated from fecal samples collected from 30 patients and passaged through lab-strain *Biomphalaria glabrata* snails, followed by BALB/c mice to acquire adult worms. Five hundred eighty-five male and female worms were genotyped at 9 microsatellite loci. Genetic diversity of parasites was relatively high (H_S 0.632) and standard measures of inbreeding indicated that the parasite population is panmictic (F_{IS} -0.008). Furthermore, measures of population subdivision indicated significant but low levels of population partitioning (F_{ST} 0.052; F'_{ST} 0.15). We conclude that patients within this village are sampling a broad range of schistosome genetic diversity and are effectively acting as "genetic mixing bowls" for the parasites. These results contrast with those previously observed in another Brazilian village, and thus provide a unique opportunity for comparisons of environmental and epidemiological differences that are likely to influence host-parasite coevolution, parasite transmission, and the evolution and rate of spread of novel traits such as drug resistance within the parasite population.

GENOMICS AND BIOINFORMATICS

CC 2210

RAPID EVOLUTION AT GENES INVOLVED IN THE CONTROL OF *DROSOPHILA* GERMLINE STEM CELL MAINTENANCE AND DIFFERENTIATION

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Drosophila germline stem cell (GSC) maintenance and differentiation is a carefully controlled process. GSCs are present in a niche environment, and close proximity to the niche allows for multiple, local signals to repress stem cell differentiation. In addition, genes expressed within the GSCs also help these cells to maintain their stem cell identity. GSCs undergo asymmetric division and the daughter cell that is moved out of the niche begins to differentiate. Given the intricate control exhibited in this pathway, one might expect that the genes involved would be under extreme functional constraint. However, we have recently shown that two of these genes, *bag of marbles* (*bam*) and *benign gonial cell neoplasm* (*bgcn*), are rapidly evolving in *Drosophila melanogaster* and the closely related *D. simulans*. With the goal of better understanding the selective forces acting on this pathway, we have surveyed DNA sequence variation from population samples of *D. melanogaster* and *D. simulans* at several other genes involved in the control of GSC maintenance and differentiation. Analyses of polymorphism and divergence have

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revealed evidence of recurrent and recent adaptive fixations in additional genes in this pathway. The data also suggest that there are multiple evolutionary forces acting to cause the adaptive evolution that we see. We hope to use a "selection map" coupled with functional analyses to test alternative hypotheses as to what intrinsic or extrinsic factors are shaping the molecular evolution of this critical differentiation pathway.

CC 2210

GENOMIC ANALYSIS OF DENGUE-2 VIRUS STRAINS INVOLVED IN DISEASE

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Dengue Virus belongs to the genus *Flavivirus* within the family *Flaviviridae*. This arbovirus is transmitted by *Aedes aegypti* mosquito causing dengue fever (DF) and dengue hemorrhagic fever (DHF). Dengue virus has 4 serotypes (DEN-1, 2, 3, 4), each providing specific lifetime immunity, and short-term cross-immunity. Infection with dengue viruses results in a spectrum of disease ranging from a fever (dengue fever), hemorrhage (dengue hemorrhagic fever) and hypovolemic shock (dengue shock syndrome). Currently dengue epidemic activity is found in large portions of Central and South America, the Caribbean, Africa, Southeast Asia, and even parts of Australia and New Zealand. Dengue and dengue hemorrhagic fever continues to be a global problem mainly in the tropical and sub tropical areas of the world. Tens of millions of cases of dengue fever and up to hundreds of thousands of cases of dengue hemorrhagic fever occur each year. No dengue vaccine is available. Although a few host factors involved in flavivirus replication have been identified, it is still not completely understood the molecular interactions between virus and host components that influence virulence of these viruses. The aim of this research is to compare virulent and avirulent strains of Dengue in a bid to identify key amino acids among nonstructural proteins that are important in virus-host interaction. We have identified some amino acids changes among the virulent hemorrhagic strains of Dengue for NS3 and NS5 non-structural proteins. The selection the most interesting residues to study was based on their conservation within other flaviviruses and their locations on the available structures. Interestingly these are surface exposed residues, which presumably are interacting with other host proteins. We will incorporate some of these mutations on a replicon system that contains a reporter gene, which allow us to monitor viral replication. In addition the replication efficiency will be tested by studying the plaque phenotype of these mutations on the full-length cDNA. As a starting point, we have initiated to incorporate mutations located on NS3 protein on the dengue replicon. Further, the mutants will be characterized with respected to replication efficiencies.

CC 2203

BAYESIAN NETWORKS FOR GENE EXPRESSION REGULATORY PATHWAY ANALYSIS OF HUMAN PLACENTAL MICROARRAY DATA

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Bayesian statistical thinking is considered by many as a revolutionary force within genetics and bioinformatics. A Bayesian network is a graphical model that encodes statistical relationships among a set of variables. In this way it can be used as an exploratory *in silico* biological tool to infer novel gene expression regulatory pathways in a given genome. Our hypothesis is to confirm and predict new gene expression regulatory pathways in human placenta. Human placenta gene expression time series Affymetrix data is obtained from standard molecular genetic techniques. Using a 2 Gigabyte, 2 Gigahertz computer, we employed a variety of learning algorithms, including K2, hill-climbing, and simulated annealing to create a final gene expression network of 40 gene expression profiles for human placenta. Our results confirmed and inferred a number of novel gene expression regulatory pathways in the human placenta. This network will be confirmed by molecular genetic methods. We expect to explore the pathways as a dynamical Bayesian network and plan to program new visualization software that will allow for analysis of the network as a three-dimensional surface. To summarize, we performed exploratory analysis of gene regulatory pathways of the human placenta (maternal-fetal interface) during normal pregnancy using Bayesian network methodology. The results obtained are consistent with known regulatory pathways in the human placenta, and predict interesting connections not previously discerned by standard bioinformatics analyses.

HEALTH AND MEDICINE

CC 2201

DEVELOPMENT OF GUIDELINES FOR RESEARCH AMONG NATIVE AMERICAN COMMUNITIES

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Native American communities face many challenges as they strive to combat health disparities among their people. Past experiences with research organizations and with federal and state governments have resulted in misunderstandings, mistrust and tight constraints on outside research projects among many tribes. For researchers who hope to work with Native populations, one challenge becomes how to best partner with communities to combat health disparities. The purpose of this research project was to develop community-based participatory research (CBPR) guidelines for successful partnerships between Native American communities and academic research institutions. For this project, I conducted an extensive literature review of CBPR principles and best practice suggestions for working with Native American populations. I then reviewed procedures used in a successful implementation of CBPR principles through participation in a research project developed in partnership with a Northern Plains tribe. The goal of the project is to increase cervical cancer awareness and screening among that population. From this information, we compiled a set of guidelines for developing successful partnerships between research institutions and Native American communities. Community-based participatory research has emerged in recent years as an important method to help combat health disparities among various racial, ethnic, and socioeconomic groups. However, the use of a CBPR approach alone does not ensure successful partnership with Native American communities. Guidelines such as those presented here may help future researchers engage in successful research partnerships with Native American communities.

IMMUNOLOGY

CC 2201

TRANSCRIPTIONAL REPRESSOR ATF3 BINDS TO THE IFN-β PROMOTER IN MACROPHAGES

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The cytokine Interferon-beta (IFN-β) promotes beneficial immune responses to infection and exacerbates or prevents adverse immune responses that contributes to autoimmunity and allergy. Macrophages are a major source of IFN-β. Under stress-free conditions, macrophages secrete very low levels of IFN-β. However, following exposure to stimuli associated with microbial infection such as lipopolysaccharide (LPS), macrophages rapidly increase transcription of this cytokine. Recently, our lab found that macrophages deficient in Activating Transcription Factor 3 (ATF3) produce significantly higher amounts of IFN-β mRNA than wild type macrophages, suggesting that ATF3 is a transcriptional repressor of the IFN-β gene. Thus, ATF3 may function to limit production of this cytokine, thereby preventing host pathology associated with IFN-β over abundance. To determine whether ATF3-mediated repression of IFN-β occurs via direct interaction between ATF3 and the IFN-β promoter, chromatin immunoprecipitation (ChIP) assays were performed. ChIP results indicate that ATF3 is not bound to the IFN-β promoter in unstimulated macrophages, but it is bound in macrophages stimulated with LPS for 4 hours. We are currently investigating the kinetics of ATF3 binding to the IFN-β promoter as well as the binding of other regulatory proteins known to bind this promoter. These experiments will generate a more comprehensive view of IFN-β transcriptional regulation. Nonetheless, our data are the first indication that ATF3 binds to the IFN-β promoter in macrophages in an inducible manner and this event is likely to mediate the repressive effect of ATF3 on IFN-β transcription.

CC 2201

MECHANISM AND SIGNIFICANCE OF TOLL-LIKE RECEPTOR 9 RETENTION IN THE ENDOPLASMIC RETICULUM

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Toll-like receptors (TLRs) have evolved to recognize conserved features of microbial pathogens. Several TLR family members recognize nucleic acids as signatures of viral infection. For example, TLR9 recognizes unmethylated CpG DNA motifs present in many DNA viruses. While ensuring the detection of pathogens, this specificity for nucleic acids also exposes the host to potential autoimmunity due to inappropriate recognition of self nucleic acid. Thus, mechanisms must exist that prevent self recognition while still allowing detection of foreign nucleic acid. In this context, it is striking that all the TLRs involved in nucleic acid sensing are retained intracellularly, while other TLRs are expressed at the cell surface. We hypothesize that the intracellular compartmentalization of TLR9 prevents the recognition of self DNA. To test this hypothesis, we are defining the motif within TLR9 that is responsible for its intracellular retention. Using this information, we will test whether TLR9 mutants with altered localization have enhanced reactivity to self nucleic acid. Chimeric receptors will be created by swapping domains of TLR9 and other TLRs, mainly TLR4. To assess localization of chimeric receptors, surface biotinylation, endoglycosidase H digestion and

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immunofluorescence will be used. Lastly, to evaluate the effect of TLR9 mislocalization *in vivo*, knock-in mice will be made expressing mislocalized receptors and analyzed for autoimmune phenotypes. These experiments will allow us to demonstrate the importance of TLR9's intracellular localization in self versus non-self nucleic acid recognition.

MARINE BIOLOGY

CC 2202

EFFECTS OF LIGHT AND COLUMN HEIGHT ON DIEL VERTICAL MIGRATION OF THE MARINE GASTROPOD *KELLETIA KELLETII*

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Marine veliger *Kelletia kelletii* larvae exhibit diel vertical migratory (DVM) behavior; larvae ascend at night and are demersal during the day. We investigated how light and vessel height influenced DVM behavior and whether DVM patterns in the lab were similar to those in the field. We hypothesized that DVM behavior would be light-initiated and would not be affected by column height, and that field surface densities of *K. kelletii* larvae would be higher at 2400 h than at 1200 h. We placed 100 larvae in replicate cultures (n=4) under two different light treatments, natural (16:8) and a dark-only photoperiod (0:24), and two different column heights (15 or 125 cm). Vertical positions in the column were recorded every 4 h for 24 h. Surface plankton tows (n=3) were conducted at 1200 h and 2400 h off the coast of Palos Verdes, CA. Column height and the interaction between photoperiod and time were significant (3-way full-factorial ANOVA for photoperiod, column height and time). Cultures in shorter columns had significantly greater proportions of demersal larvae. During daytime, natural photoperiod treatments had higher proportions of demersal larvae than dark-only treatments; at night there was no significant difference between light and dark treatments. Plankton tows revealed significantly higher densities of total veliger (2-sided F-test, n=3, $p<0.05$) and similar trends for *K. kelletii* (T-test, n=3, $p>0.05$) at the surface at 2400 h compared to 1200 h. Unraveling DVM behavior in *K. kelletii* larvae can aid in understanding distributional patterns of adults.

CC 2202

INTERACTION OF TURBULENCE AND FOOD AVAILABILITY ON FEEDING OF SEA URCHIN LARVAE

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Length of the larval period depends upon environmental factors such as food availability, which has important implications for development and dispersal of marine invertebrates. This study investigates whether turbulence also affects food availability to sea urchin larvae. Theoretically, turbulence should help larvae overcome food limitation by increasing the rate of predator-prey encounters and, consequently, ingestion. Larvae of the white sea urchin *Lytechinus pictus* maintained at limiting food concentrations were exposed to steady laminar shear generated in simple Couette flow. Grazing and ingestion rates of larvae were determined based on changes in cell concentration of the prey *Rhodomonas lens*. Grazing and ingestion rates were greater in larvae exposed to shear compared to still controls. These results support encounter rate theory and suggest that turbulence may be another environmental factor that affects larval development time.

MICROBIOLOGY

CC 2215A

CHARACTERIZATION OF *PHRB* IN *NEISSERIA GONORRHOEAE*

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The human pathogen *Neisseria gonorrhoeae* is the causative agent of the sexually transmitted disease gonorrhea. *N. gonorrhoeae* is a gram negative bacterium, and as an obligate human pathogen that resides in the genital tract the organism does not normally experience UV or visible light. Surprisingly, *N. gonorrhoeae* carries a functional copy of the *phrB* gene, which in other organisms encodes a DNA photolyase that repairs UV induced pyrimidine dimers with energy provided by visible light. We considered whether *phrB* is a pseudogene, encodes a photolyase, or expresses an alternate function. qPCR analysis showed that *phrB* mRNA is expressed, suggesting that it is a functional gene. A null mutant and a functional complement inserted at an irrelevant second site in the genome were constructed to test for roles of the *phrB* gene. The null mutant has a small colony phenotype that is rescued by complementation. This small colony morphology may be related to the altered cellular morphology and cell division problems visualized by thin section electron microscopy. In contrast to other organisms, *N. gonorrhoeae phrB* does not function in UV repair. We hypothesize that *phrB* plays a role in the normal physiology of this bacterium and we are exploring the function of *phrB* in the biology of this important human pathogen.

CC 2215A

ELUCIDATING THE ROLE OF THE YELLOW FEVER NS3 HELICASE DOMAIN III

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Flaviviruses, yellow fever (YF) being the prototype member, affects people in over 100 countries worldwide. Though a vaccine is available, effective anti-viral therapeutics have not been developed. One target for anti-viral drugs is the helicase. The helicase is located in the C-terminal 440 amino acids of non-structural protein 3 (NS3). The helicase is thought to unwind a RNA duplex important for genome replication, but its precise function is unknown. The crystal structures of several flavivirus helicases have been solved. These structures have three domains with a groove running between domains I and II and a cleft running between domains II and III. All seven helicase motifs necessary for helicase activity are located in the groove between domains I and II. We want to determine the role of domain III. Based on the YF helicase structure and sequence alignments we targeted helix 10 for mutagenesis. Helix 10 is an amphipathic helix located on the surface of domain III. Sequence alignments reveal a net charge difference on the solvent exposed residues across the flavivirus helix 10's. To determine the role of this helix a chimera was constructed by replacing the YF helix 10 sequence with that of Dengue2. This chimera had a lethal plaque phenotype, a 12 hour lag in replication and a defect in release of infectious virus. Whether the lag in replication is responsible for the complete deficiency of virus release is unknown, but these results imply that domain III is involved early in replication and possibly viral particle production.

CC 2215A

IDENTIFICATION OF FLGO AND FLGP: TWO NOVEL PROTEINS INVOLVED IN *VIBRIO CHOLERAE* MOTILITY

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The organism *Vibrio cholerae* is the causative agent of the disease cholera. Our research focuses on novel factors contributing to the directional movement of the *V. cholerae* polar flagellum. It has previously been demonstrated that the direction of flagellar rotation can alter the infectivity of the bacterium, thus indicating that motility is an important virulence factor of this pathogenic organism. Under wild type (WT) conditions, the flagellum rotates in two directions, counter-clockwise and clockwise. If the flagellum rotates counter-clockwise, the bacterium swims in a linear fashion. However, if the flagellum turns clockwise, the bacterium makes random "tumbles" to change direction. Two genes, which we named *flgO* and *flgP*, were identified as activated by RpoN (an alternate transcription factor) via microarray analysis comparing wild type *V. cholerae* and *ΔrpoN* strains. Null mutations were constructed for both the *flgO* and *flgP* genes and both strains demonstrated a decrease in intestinal colonization. Further investigation of the *ΔflgO*and *ΔflgP* strains demonstrated defects in motility, believed to be a result of the inability of the bacterium to control the direction of rotation of its flagellum. We hypothesize that the loss of the ability to control motility is responsible for the reduction in colonization. Our studies show that the *flgO* and *flgP* mutants are highly motile, but display an increased rate of tumbles or reversals as compared to WT. We plan to examine these phenotypes further in order to understand how *FlgO* and *FlgP*, which have not previously been described, are involved in motility.

MOLECULAR/CELLULAR BIOLOGY

CC 2215A

THE NEUROSECRETORY VESICLE PROTEIN PHOGRIN IS A PHOSPHATIDYLINOSITOL PHOSPHATASE WHOSE ACTIVITY REGULATES INSULIN SECRETION

Leslie Ann Caromile, Anush Oganesian, Scott Coats, Ron Seifert, Dan Bowen-Pope. *University of Washington School of Medicine, Seattle, Wash.*

Phogrin (NE-6, IA-2β) is a 64KD protein present on insulin-containing secretory granules in pancreatic beta cells. Auto-antibodies against Phogrin are common in pre-diabetics and are used clinically to diagnose a pre-diabetic state. Although Phogrin has sequence homology to tyrosine phosphatases, no enzymatic activity has been reported. We therefore tested Phogrin for enzymatic activity, determined its preferred substrates and investigated a possible role for Phogrin in the insulin secretion pathway. We found that Phogrin dephosphorylates inositol phospholipids, including phosphatidylinositol-4,5-bisphospate, $PI(4,5)P_2$, which is known to regulate membrane vesicle dynamics during insulin secretion. Additionally, PKA-dependent phosphorylation of Phogrin decreases its phosphatidylinositol phosphatase activity by 80%. Phogrin overexpression in pancreatic rat beta cells reduced plasma membrane levels of $PI(4,5)P_2$ by 50% and decreased glucose stimulated insulin secretion by 80%. Our results suggest that Phogrin is a phosphatidylinositol phosphatase that contributes to differential expression of $PI(4,5)P_2$ in secretory vesicles and the plasma membrane and thereby helps regulate insulin secretion. These results identify steps at which the secretory pathway for insulin release may be mis-regulated in diabetes and/or manipulated therapeutically. (Funded by JDRF 1-2006-841, NIH T32 HL07312.)

CC 2208

MAPPING FUNCTIONAL DOMAINS IN THE HIV INTEGRATION COFACTOR LEDGF/P75

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LEDGF/p75 is an important cofactor for HIV DNA integration therefore HIV infection is severely impaired in cells lacking this protein. LEDGF/p75 strongly interacts with the host chromatin through its chromatin binding domain, located at the N-terminus of the protein, and with HIV integrase through its integrase binding domain in the C-terminal region. Both domains are required for the virological role of LEDGF/p75 and it has been proposed that LEDGF/p75 acts as a molecular tether that links the HIV preintegration complex (PIC) to the host chromatin allowing viral DNA integration. The implication of other cellular proteins in this process, however, is still unknown and it is possible to speculate that other factors implicated in HIV integration could be recruited by LEDGF/p75 to the HIV PIC-LEDGF/p75-chromatin complex. In order to evaluate this hypothesis we have analyzed the role in HIV infection of six different regions within LEDGF/p75 that are rich in charged amino acids since charged segments of the proteins are often implicated in protein-protein interactions. Mutants lacking each of these regions were generated by site directed mutagenesis, verified by DNA sequencing and stably expressed in a human T cell line stably deficient for LEDGF/p75. An HIV reporter virus expressing firefly luciferase was used to evaluate the susceptibility to HIV infection of T cells lacking LEDGF/p75 expression or engineered to re-express LEDGF/p75 wild-type or mutants. The interaction of each of these LEDGF/p75 mutants with HIV integrase and with the host chromatin was also evaluated using immunoblotting and cellular fractionation techniques.

CC 2208

REGULATION OF MYC AT THE TRANSLATIONAL LEVEL

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Deregulation of Myc family proto-oncogenes has long been associated with human cancers. Myc proteins are transcription factors that control a broad range of cellular activities including cell growth, proliferation, differentiation, apoptosis, and cell motility. Given the diversity of their functions, Myc expression and protein function is tightly regulated at multiple levels throughout the cell cycle. Regulation at the transcriptional and post-translational (i.e., protein stability) level has been well characterized. Recently, work in our laboratory has suggested that regulation of Myc at the translational level is a major control point. Using a mouse mesenchymal cell line, CH3 10T1/2, we have developed an assay system in which we stimulate cell cycle entry through stimulation with fibroblast growth factor 2. During cell cycle entry, Myc RNA levels are induced by 1 hour and high levels of Myc RNA are present through 24 hours. In contrast to the RNA expression profile, Myc protein levels are only transiently increased and only very low levels of Myc protein are observed even when Myc RNA levels are very high. Use of ribosome and proteasome inhibitors were used to show that Myc protein stability is not significantly altered, suggesting Myc is regulated at the translational level. Elucidating the mechanism underlying translation control of Myc mRNA will be crucial in understanding the normal and oncogenic functions of Myc family proteins and may provide new avenues for therapeutic advances in cancer treatment.

CC 2215A

ROLE OF THE FLAVIVIRUS ENVELOPE PROTEIN IN VIRUS MATURATION AND ENTRY

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Flaviviruses are responsible for a number of serious human diseases. Critical events in the viral life cycle include viral maturation and host cell entry. During the course of the life cycle, the envelope protein (E) undergoes a number of conformational changes critical in viral maturation and entry. This work focuses on elucidating residues critical in mediating the various conformations E assumes during the life cycle and what roles they play. Firstly, we are looking at two transmembrane helices within the stem linker region of E, linking ectodomains and transmembrane domains of the protein. Previous mutational and structural data suggest that the helices play several roles in mediating the various conformations E assumes during the life cycle. Several deletions were made within conserved regions of E to investigate this. Secondly, we are interested in determining which residues within E are critical in stabilizing the mature particle. In the mature particle, E is arranged into sets of antiparallel homodimers known as "rafts." Based on a pseudo atomic map, regions of potential contact between rafts were identified and conserved residues within those regions selected for mutational analysis. Both sets of mutants have been tested for infectivity, protein expression and virus release. None of the mutants produced infectious virus, but all express some level of protein and all have been found to release viral RNA into transfected supernatants at levels 10-fold or less reduced from wild type. We are currently in the process of determining the nature of the defect.

CC 2208

THE CLATHRIN ADAPTOR-ENDOCYTIC SCAFFOLD INTERACTION MODULATES THE TEMPORAL REGULATION OF ENDOCYTIC INTERNALIZATION

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The internalization process of clathrin-mediated endocytosis involves over fifty cytosolic proteins acting in a highly coordinated fashion to form a cargo-containing clathrin-coated vesicle. Current studies in many labs focus on elucidating the regulation of spatiotemporal coupling of endocytic proteins, beginning with the selection of cargo proteins at the plasma membrane by clathrin adaptors. However, the mechanisms mediating the spatiotemporal regulation of these interactions are still poorly understood. In this study, we are exploring the requirements of the clathrin adaptor proteins Ent1/2 and Yap1801/2 (homologues of epsin and AP180/CALM proteins) for the spatiotemporal regulation of endocytosis. We have identified the NPF-motif/EH-domain interaction between adaptors and endocytic scaffold proteins as critical for the successful progression of endocytosis in *S. cerevisiae*. Quadruple deletion mutant cells lacking these four adaptors and carrying a plasmid encoding mutations in adaptor NPF motif have defects in endocytosis, organization of the actin cytoskeleton, and growth at 37˚C. Real-time fluorescence microscopy experiments revealed that the spatiotemporal dynamics of the early- and late-acting scaffold proteins Ede1 and Pan1, respectively, are altered when the NPF-motif/EH-domain interaction is compromised. Moreover, the absence of adaptors resulted in a decreased recruitment to endocytic sites of the invagination/scission factor Myo5. The spatiotemporal alterations in the dynamics and functions of the endocytic scaffolds, and the myosin Myo5, in adaptor mutant cells, indicate that the NPF-motif/EH-domain interaction regulates the transition from early (cargo-gathering) to late (scission) events, and suggest that the interaction between adaptors and scaffold proteins is essential for the spatiotemporal regulation of endocytosis.

CC 2208

I4898T MUTATION IN THE RYANODINE RECEPTOR AS A POSSIBLE MOUSE MODEL OF CENTRAL CORE DISEASE

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Ryanodine receptor (RYR1) is a calcium-release channel located in the sarcoplasmic reticulum membrane of skeletal muscle. The RYR1 mutation of isoleucine 4898 to threonine (I4898T) has been identified in patients with central core disease (CCD). CCD is a congenital myopathy in human characterized by central cores in muscle biopsy, muscle weakness, delay motor development, and etc. The purpose of this study is to create a mouse model of CCD and explore mechanisms by which the I4898T mutations in RYR1 affect calcium homeostasis and excitation-contraction coupling in skeletal muscle. We hypothesizes that the I4898T mouse model will mimic the phenotype (central core, muscles weakness, leaky RYR1) associated with the human CCD. The mice were generated using the transgenic mouse technology. Soleus and extensor digitorum longus muscles from first generation mice were used to establish the presence of central cores and muscle weakness. Cross-sections were obtained from muscle and stained with Hematoxylin and Eosin and NADH-tetrazolium reductase (for core presentation). We also perform contractile studies as a measurement of muscle weakness. Finally, total glutathione (GSH) and GSH/GSSH (glutathione disulfide) ratio levels were measured using skeletal muscle homogenates as a measurement of oxidative stress levels, which may be secondary to leaky RYR1 caused by the mutation. Preliminary data suggest that there is a difference in contractile studies and in oxidative stress levels between the wildtype and heterozygous mice. Core presentation has not been confirmed. Additional experiments will be conducted with second and third generation mice.

CC 2208

TEM8, A GENE IMPLICATED IN NEO-ANGIOGENESIS, SHOWS DRAMATIC TISSUE-SPECIFIC AND DEVELOPMENTAL EXPRESSION

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Tumor endothelial marker 8 (TEM8), a type-1 integral membrane protein, was originally identified by virtue of enhanced expression in the endothelium of colon carcinomas. It has therefore been implicated in neo-angiogenesis, a crucial requirement for the development of cancerous tumors and metastasis. However, the exact mechanism remains unclear. The native ligand of TEM8 is also unknown. The only definitive known function of TEM8 is that it serves as a receptor for anthrax toxin. TEM8 has five splice variants, three reported before (var1-3) and two that we found (var4-5). TEM8 transcripts exist at very low levels in normal tissues. We have carried out extensive semi-quantitative nested PCR to assess TEM8 expression in a large number of human fetal and adult tissues. Var3, a secreted form, showed the broadest and greatest expression. Whereas var4, a membrane bound form, showed highly selective expression in digestive tissues, var2, the smallest membrane bound form, showed broader expression. Surprisingly, var1, another membrane bound form and the largest of the variants, was only in prostate. Var5, the

... continues on next page

second secreted form, was also only in prostate. All variants show differential expression, and overall the gene shows remarkable tissue-specific and developmental expression. However, it remains unknown which variants or expression patterns are important for neo-angiogenesis, whether in tumors or other pathological conditions. Our extensive expression analysis of TEM8 has revealed the expression patterns of all five variants in normal human tissues. This would help define any expression patterns that correlate with the formation of tumor vasculature, or other forms of neo-angiogenesis.

NEUROSCIENCE

CC 2201

PROGESTERONE RECEPTORS IN THE ANTEROVENTRAL PERIVENTRICULAR NUCLEUS OF THE HYPOTHALAMUS

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Progesterone (P_4) is required for the appropriate timing and amplification of the luteinizing hormone surge that precedes ovulation, but it is unknown whether these actions are mediated by the nuclear P_4 receptor (PR) alone or if a membrane receptor is also involved. Many nongenomic actions of P_4 have been described, including a proposed role in GnRH release, and several membrane PRs, including 25Dx, have been identified. The anteroventral periventricular nucleus (AVPV) is critical for the neural regulation of ovulation, and the dual phenotype GABAergic/Glutamatergic neurons in this region contain 25Dx. In granulosa cells of the ovary, 25Dx has been reported to interact with SERBp1, a membrane protein necessary for the antiapoptotic action of P_4; however; the expression of SERBp1 has never been reported in the brain. We used dual-label *in situ* hybridization to determine if 25Dx is colocalized with SERBp1 in the brain. We now report the novel finding that SERBp1 is expressed in the brain, and is colocalized with 25Dx. Additionally, the nuclear PR, SERBp1 and 25Dx mRNA are coexpressed in these dual-phenotype neurons of the AVPV. Furthermore, the expression pattern of these genes is particularly abundant in this nucleus. Our findings suggest a multiplicity of receptors within the same critical neurons. Studies in progress are investigating the roles of these putative PRs in the regulation of GABA/Glutamate neurons and the neural control of ovulation.

CC 2201

CHARACTERIZATION OF ETHANOL-RELATED BEHAVIORS IN B6XFVB AND B6XNZB F1 HYBRID MICE: RELATION TO CONTROL OF ETHANOL INTAKE

Angela Ozburn, Adron Harris, Yuri Blednov. *University of Texas at Austin, Austin, Tex.*

When comparing EtOH intake of inbred and F1 hybrid mice, we found that changes in EtOH experience result in sustained preference in C57Bl/6JxFVB/NJ (B6xFVB) mice and reduced preference in C57Bl/6JxNZB/B1NJ (B6xNZB) mice, thus providing models of high and moderate EtOH consumption. To define differences in EtOH responses which can predict these differences in preference, we characterized behaviors for B6xNZB and B6xFVB mice by determining their responses to tests of conditioned place preference (CPP), conditioned taste aversion (CTA), duration of loss of righting reflex (LORR), and acute withdrawal. Both hybrids demonstrated a CPP for EtOH, spending 69±3% time in EtOH paired compartments. EtOH induced a CTA for 0.15% saccharin for both hybrids. However, after 5 conditioning trials, B6xFVB consumed 49±9% of saccharin (% of pre-conditioning consumption), while B6xNZB showed a significantly more severe CTA by consuming only 25±5%. The duration of LORR produced by 3.2 and 3.4g/kg EtOH was shorter for B6xFVB (27±1 and 34±3 min, respectively) than for B6xNZB (74±10 and 88±9 min, respectively). To test EtOH induced withdrawal severity EtOH was administered, suppressing basal handling induced convulsions (HIC) for 4 to 7 hours followed by increased HIC for 3 to 6 hours. B6xFVB showed greater withdrawal severity than B6xNZB. In summary, both hybrids have similar sensitivities to the rewarding effects of EtOH, but B6xNZB are more sensitive than B6xFVB to the aversive and sedative properties of EtOH. These results offer insights about factors that determine high (B6xFVB) and moderate (B6xNZB) EtOH consumption in these new genetic models. (Supported by AA16424 & AA13520.)

ZOOLOGY

CC 2202

SPATIAL PATTERNS OF RELATEDNESS IN AN OBLIGATE ARMY-ANT-FOLLOWING BIRD DO NOT SUPPORT FAMILY LIVING DESPITE SOCIALITY

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The spatial distribution of relatives among social animals can help illuminate the ultimate causes of group living while simultaneously shaping conservation issues. We studied patterns of relatedness in ocellated antbirds, obligate army-ant-following birds that form daily feeding aggregations at swarms of nomadic army ants. A study in a recently isolated forest in Panama

concluded that these birds live in family groups that maintain large communal areas. Unfortunately, the Panamanian population declined to extinction during the study. Thus, it is possible that observed family living could have been the result of inbreeding rather than the natural organization of the population. We tested family living in this species within continuous forest in Costa Rica using radio telemetry and microsatellite markers. We tested several hypotheses associated with family living: group roosting, high genetic relatedness between roosting neighbors, and high relatedness within foraging aggregations. Our molecular genetic data indicate the study population was not inbred and mated pairs held semi-exclusive roosting areas. Relatedness between nearest neighbors was not significantly different from zero, but males within foraging aggregations showed non-zero (although very low) levels of relatedness. This apparent contradiction can be explained because a bird must travel across two roosting areas (on average) to find ants, and that marginal genetic structure was detected for males whose roosting areas are separated by that distance. Overall, we found no support for family living in ocellated antbirds, and speculate that family living in Panama was caused by a rapidly declining population that was inbred.

CC 2202
MITOCHONDRIAL DNA AND KARYOTYPIC DIFFERENTIATION OF A GEOGRAPHICALLY ISOLATED PENINSULAR POPULATION OF MAZAMA POCKET GOPHERS (*THOMOMYS MAZAMA*) IN WASHINGTON
Corey Welch. *University of Washington, Seattle, Wash.*

The level of divergence of contemporary populations across the geographic range of a species can be used to understand the historical biogeography of a species. Pleistocene glacial cycles have strongly shaped the current distributions of species in the Pacific Northwest. The Olympic Peninsula and its mountaintops have promoted isolation and provided refugia that have resulted in local endemism. Due to their fossorial lifestyle and well documented high degree of localized genetic structuring, pocket gophers are an ideal organism to address historical patterns of colonization and divergence. In Washington the Mazama pocket gopher, *Thomomys mazama*, occurs in alpine meadows of the Olympic National Park and lowland prairie remnants of the south Puget Sound and southern Washington. All Washington subspecies are listed as 'threatened,' and recovery plans are being implemented based on the genetic uniqueness of local populations. Using maximum likelihood analyses of 408 base pairs of the mitochondrial control region, we have identified four haplotype groups within Washington, three associated with the lowland prairies and the fourth, which is highly divergent, in the alpine Olympic National Park population. This alpine population diverged while being isolated within an ice-free mountaintop refugium during glacial cycling. The southernmost lowland population was originally mistakenly identified as *T. talpoides douglasii,* based on bacular measurements, but our skull and mtDNA data demonstrate it to be synonymous with *T. mazama oregonus* populations from northwest Oregon. Because this southern population represents the earliest description of any *T. mazama*, we suggest that the renaming of *T. mazama* to *T. douglasii*.

CHEMISTRY

ANALYTICAL CHEMISTRY

CC 2209
POSSIBLE ENVIRONMENTAL EXPOSURES OF URANIUM FROM SHEEP
Lydia Edgewater, Jani Ingram. *Northern Arizona University, Flagstaff, Ariz.*

During the 1940s to 1970s, uranium mining took place on the Navajo Reservation, resulting in hundreds of abandoned mines and areas of mine waste. The issue with past mine activities continues to be a problem for the people who live near the abandoned mines on the Navajo Reservation. A suspected pathway of uranium exposure to the Navajo is through their food supply, specifically from mutton, a traditional food eaten by the Navajo people. In the summer of 2006, we worked with a Navajo family who provided our research group with aged sheep which had grazed on the abandoned mines near Cameron, Ariz. for most of its life. We are working with this family to analyze the organs and tissues of the sheep to determine if uranium accumulation is present. A focus of the recent work on this project has been to develop extraction procedures for uranium analysis. These extracts are then analyzed for elemental uranium using inductively coupled plasma mass spectrometry. We are interested in determining accumulation of uranium in specific organs and tissues of the sheep because the Navajo people eat and utilize much of the sheep for their daily lives. The information learned from these studies will be reported back to the affected Chapters.

CC 2209

CHARACTERIZATION OF THE DNA-MEDIATED PURIFICATION AND ASSEMBLY OF SINGLE-WALLED CARBON NANOTUBES

Germarie Sanchez-Pomales, Lenibel Santiago-Rodriguez, Nelson E. Rivera-Velez, Carlos R. Cabrera. *University of Puerto Rico, San Juan, P.R.*

Carbon nanotubes (CNTs) possess outstanding structural, mechanical, and electronic properties. Nevertheless, to achieve the full potential of the CNTs, many problems still need to be solved, including the development of an easy purification procedure, the design of functionalization chemistries that result in increased solubility of the CNTs without altering their properties, and the development of a straightforward methodology for the attachment of aligned CNTs on solid substrates. DNA offers a solution to all of the previous challenges. Recently, the dispersion of CNTs in aqueous solvents by the non-covalent functionalization of the tubes with DNA molecules was reported. On the other hand, the self-assembling technique has been previously used by our group to attach aligned DNA-CNT complexes on gold. During our functionalization experiments, we found out that the methodology used leads to the DNA-assisted purification of CNTs. The results obtained by Raman spectroscopy, transmission electron microscopy, scanning electron microscopy and energy dispersive spectroscopy showed a decrease in the CNTs impurities after functionalization with DNA and demonstrated that the method used is a straightforward and time-effective route for the purification of CNTs at room temperature. The purified CNTs were subsequently immobilized on gold via the formation of self-assembled monolayers, and we determined that the CNTs were attached in a perpendicular fashion to the gold electrodes. These results suggest that the non-covalent functionalization of CNTs by DNA might find applications in the development of novel purification procedures and in the design of new nanodevices.

CC 2209

CARBON NANOTUBES COVALENTLY ATTACHED ON GOLD AS SUBSTRATE FOR DNA SENSING USING METHYLENE BLUE

Lenibel Santiago-Rodriguez, Nella M. Vargas-Barbosa, Germarie Sanchez-Pomales, Carlos R. Cabrera. *University of Puerto Rico, Rio Piedras Campus, San Juan, P.R.*

Deoxyribonucleic acid (DNA) detection is an area of intensive research. The most widely used method for DNA detection is optical technique, which offers sensitivity but is expensive, tedious and requires high power. Electrochemical techniques are advantageous because they are inexpensive, require less energy, and at the same time offer high sensitivity and selectivity. DNA detection using electrochemical techniques could be used in a future for disease diagnosis, food safety, and environmental monitoring. Here we report the preparation and characterization of a gold substrate modified with 11-amino-1-undecanethiol (AUT) which amine group was used for the covalent attachment of single-walled carbon nanotubes (SWNT). The as-described substrate was used for the DNA immobilization and detection. Cyclic voltammograms using a solution of 1 mM $[Fe(CN)_6]^{-3}$/$[Fe(CN)_6]^{-4}$ in phosphate buffer at pH 7 demonstrate that SWNT covalently attached to gold presents a nanoelectrode array behavior which is characterized by a sigmoidal shape, low capacitive current and scan-rate independent limiting current. Our nanoelecrode array is capable of detecting the DNA hybridization using cyclic voltammetry. As an alternative, we used methylene blue (MB) which is an electroactive organic dye widely used to detect DNA hybridization due to its high affinity for guanine bases. Square wave voltammetry was used to monitored MB responses. We found that the MB response diminishes with hybridization which was reported before. In summary, our results demonstrate that the modification of gold with SWNT forming a nanoelectrode array can be used for the DNA hybridization detection.

BIOCHEMISTRY

CC 2209

DESIGNED METALLO-LIPIDS FOR DNA-DELIVERY INTO EUKARYOTIC CELLS

Alejandro Arzola, Itzia Cruz-Campa, Hugo Alarcon, Araceli Jimenez, Juan C. Noveron. *University of Texas at El Paso, El Paso, Tex.*

Synthetic vehicles for the delivery of DNA plasmids into eukaryotic cells provide for safe and cost-effective tools for gene-based therapies. Here, we report the synthesis and characterization of mononuclear and dinuclear metallo-lipids containing Cu(II) and Zn(II) ions that condense and deliver long DNA strands into mammalian cells. Variations in alkyl chain length, metal type, DNA plasmid length, and cell target established structure-function relationships. Atomic force microscopy (AFM) in the liquid phase and X-ray spectroscopy of DNA condensates will be presented. Cells of COS-1, mouse and human macrophages, and HeLa cells are transfected with plasmids of PVAX containing 3kb, PEGSP-N1 (4.1 kb) and PVAX-BT (6.1kb). Dependence of DNA release on gluthathione (GSH) and other natural metal-chelator molecules will be discussed with respect to controlled-release methods.

CC 2209
SYNTHESIS AND CHARACTERIZATION OF AMPHIPHILIC PLATINUM COMPLEXES WITH TUMOR-SUPPRESSOR PROPERTIES
Fabiola A. Cruz-Sanchez, Ernesto Nakayasu, Joanne Ellzey, Armando Varela, Renato Aguilera, Juan C. Noveron. *University of Texas at El Paso, El Paso, Tex.*

Cancer afflicts people of all ages and races. Therapeutic protocols for the treatment of cancer involve radiation therapy, chemotherapy, and surgery. Cisplatin is one of the three most widely utilized antitumor drugs worldwide. Cisplatin effectiveness towards cancer cells is attributable to its ability to interfere with DNA at the nucleus of the tumor cells. However, cisplatin compounds have many side effects that arise from their systemic bio-distribution in the body, which affect healthy tissues far from the affected area. We present the synthesis and characterization of a new family of cisplatin analogues with lyotropic properties that incorporate amphiphilic components to cisplatin moieties to modulate their bio-distribution via pre-programmed intra-cellular reactions. The synthesis of amphiphilic metal-binding molecules were carried out with bidentate coordination moieties and lipid groups ([2,2']Bipyridinyl-5,5'-dicarbonyl dichloride with R-Nuc (R=$C_{12}H_{25}$, Nuc=OH)). The compounds vary systematically in terms of Mononuclear and polynuclear Platinum complexes with the substitution of the chlorides for other pyridine ligands, and in the use of ester (-COOC-) linkage that bridge the metal-binding group and hydrophobic components. Lipid-Pt complexes were characterized with ^{1}H nuclear magnetic and electrospray mass spectrometry. As expected, the lipocomplex exhibited an isotopic distribution characteristic of Pt complexes. They were characterized with atomic force microscopy and transmission electron microscopy. The ligands as well as the corresponding Pt complexes self-assemble into micelles in water. This research presents the critical micelle concentration of these ligands. Currently, we are working on the LD_{50} (dose required to kill half the members of a tested population) of these compounds.

GENERAL CHEMISTRY

CC 2215C
TEACHING CHEMISTRY USING FIELD-BASED LEARNING
Beatriz Estrada, Jani Ingram. *Northern Arizona University, Flagstaff, Ariz.*

The goal is to provide a foundational chemistry course to explore real-world problems viewing two approaches. The first approach was to involve undergraduate students in a small group, field research experience in a spring 2007 course. As a graduate student, I designed the project for the undergraduate students in the class. The study focused on investigating water chemistry of snow pack near mining areas in Silverton, Colorado during a week. Data reported are metal concentrations, using atomic absorption, ion chromatography, and pH in the areas where water samples were collected, as well as what the students gained from this experience. The second approach is a modification of general (freshmen) chemistry curriculum in an investigation of issues important to their communities utilizing water field samples as the venue for learning. Students will be assessed according to what they learned from the course by writing a formal report and presentation of material gathered. The student reaction to this experience will be compared to the students taking the traditional freshman laboratory course (control group). A pre- and post- survey will be administered to both the pilot and control groups to assess the educational gains of the module. Data reported will be metal concentrations and pH in the areas where water samples were collected, using atomic absorption and ion chromatography, as well as what the students gained from this experience. The results of both approaches are the key to restructure the lower division laboratory curriculum toward innovative, relevant learning.

CC 2215C
ASSESSING THE LEARNING OBJECTIVES AND CONCEPTUAL UNDERSTANDING IN A CHEMISTRY-BASED GAME
Kermin Martinez-Hernandez, Gabriela C. Weaver, Carlos R. Morales, Kellen Maicher. *Purdue University, West Lafayette, Ind.*

A chemistry-based video game was developed to verify their educational potential in a classroom setting. Previous findings of our project suggested that males and females have stronger preference for first person shooter, strategy, and role playing games. Therefore, we incorporated characteristics of those genres in our game. Students played our chemistry game and four commercial video games from different genres (first person shooter, strategy, adventure/puzzle, and educational) that were popular in the past. We wanted to verify if students achieve the learning objectives of the task in the game, verify if students' level of conceptual understanding changed after game intervention, and to obtain students perceptions of our game design elements versus other commercial games. Students were able to assess game design elements, game development, and goals accomplishment through different quantitative and qualitative methods, including pre-post open ended chemistry content surveys, Likert scale surveys, focus group interviews, and individual interviews. This presentation will discuss the results of our study and further educational implications.

INORGANIC CHEMISTRY

CC 2215C

MOLECULAR MAGNETS BASED ON LANTHANIDE IONS AND THE $TCNQF_4$ RADICAL

Nazario Lopez, Hanhua Zhao, Andrey V. Prosvirin, Abdellatif Chouai, Kim R. Dunbar. *Texas A&M University, College Station, Tex.*

The field of molecular magnetism has experienced fast growth over the last decade due to the discovery of high-temperature molecule-based magnets, multifunctional magnetic materials, and single-molecule magnets. Although molecular magnets based on mixed transition metals are quite common, analogous 4f-nd magnets are relatively rare. In principle, the incorporation of lanthanide ions with strong magnetic anisotropy and large magnetic moments into such materials is an excellent idea, but, due to the shielding of the 4f electrons, coupling between 4f and d orbital bearing spins is quite weak. A more promising avenue is the combination of 4f ions with organic radicals as evidenced by results found for materials based on lanthanides and nitronyl nitroxide radicals as well as organocyanides such as $TCNE^{-\bullet}$ (tetracyanoethylene) and $TCNQ^{-\bullet}$ (7,7,8,8-tetracyanoquinodimethane). Recently, we have extended our work with TCNQ to include chemistry of 4f elements with 2,3,5,6-tetrafluoro-7,7,8,8-tetracyanoquinodimethane ($TCNQF_4$) and prepared a homologous series of $Ln(TCNQF_4)$ complexes. X-ray crystallography was used to structurally characterize these materials. Their magnetic properties were determined using a superconducting quantum interference device (SQUID) magnetometer. Bulk magnetic ordering was observed in compounds with Ln = Sm, Dy, Gd; while the Tb analogue displays behavior characteristic of single-molecule magnets. To the best of our knowledge, the Tb analogue is the first example of a single-molecule magnet based on lanthanide ions and organic radicals. These results along with the syntheses and characterization of these new f-block/$TCNQF_4$ materials will be presented.

ECOLOGY

CC 2206

FAILURE OF DIVERSITY TO MAINTAIN NITROGEN FIXATION IN A COASTAL WETLAND FACING SEDIMENTATION AND THE TRIPLE BORDER FENCE

Serena Moseman. *Scripps Institution of Oceanography, San Diego, Calif.*

Sedimentation is a growing and complex threat to coastal ecosystems worldwide. Deforestation as well as coastal (urban and agricultural) developments destabilize and unleash polluted sediments into aquatic habitats. In Tijuana Estuary (Calif.), major winter rains can carry both sediment from denuded hillsides and untreated, nitrogen-rich sewage into salt marshes that are critical habitat for several endangered species. The effects of this complex disturbance on wetland biota are not well understood but are expected to be exacerbated by construction of the controversial Triple Border Fence. A manipulative field experiment was performed to determine the independent and combined effects of sediment and nitrogen-loading on nitrogen-fixing microbes in the cordgrass (*S. foliosa*) zone of the restored Friendship Marsh of Tijuana Estuary. Impacts on the activity of nitrogen-fixing microbes, key indicators of salt marsh ecosystem health, were determined by acetylene reduction assays. Effects of the disturbance on the composition and diversity of nitrogen-fixing microbes was determined via the genetic fingerprinting technique, T-RFLP (terminal restriction length polymorphism). The combination of sediment and nitrogen inputs was found to cause significant declines in nitrogen fixation rates after 2 and 17 days. However, preliminary results suggest that neither diversity nor composition of nitrogen fixing microbes were significantly affected. Together, these results reveal that, despite expectations of functional redundancy among diverse microbial assemblages, sedimentation can diminish microbially-dependent functions of wetland ecosystems, with negative implications for the Triple Border Fence construction at Tijuana Estuary.

CC 2206

MOLECULAR EVOLUTION OF THE FUNGAL AVIRULENCE GENE *AVR-PITA* IN THE RICE BLAST FUNGUS *PYRICULARIA ORYZAE* (TELOMORPH *MAGNAPORTHE GRISEA*)

Mariah Veit, Morris Levy, Maria Levy. *Purdue University, West Lafayette, Ind.*

Pyricularia oryzae is the ascomycete fungus responsible for rice blast disease and, globally, is the most important pathogen of rice. Understanding the allelic diversity of the avirulence gene *Avr-Pita*, which determines the specificity of cultivar infection, will provide a new insight into the rapid evolution of virulence shifts that make the rice blast fungus so difficult to manage. This research was conducted to determine the sequence and copy number diversity of *Avr-Pita* alleles in Colombia. The sequencing and copy number data was used to address the relative frequency of mutational mechanisms displayed at the locus, i.e., duplication, deletion, interruption by transposon insertion, and point mutations, both missense and nonsense. The future

direction of this research includes analyzing isolates from around the world, looking at the distribution of genes in isolates with more than one copy of the gene, and construction of the *Avr-Pita* gene tree and determining its implications for the history of pathogen migration (phylogeography). The data to date indicate a strong representation of isolates with one or more copies of the gene, and strong conservation of *Avr-Pita* RFLP profiles among 15 clonal lineages identified by DNA fingerprinting. All mechanisms of mutation have been identified but the evolutionary balance appears to favor virulence shifts due to gene modification and duplication rather than gene loss or disruption.

ENGINEERING

BIOMEDICAL ENGINEERING AND BIOTECHNOLOGY

CC 2210

MULTI-CHANNEL CONTROL BASED ON SINGLE MUSCLE CONTRACTIONS

Claudia Perez Maldonado, Sanjay Joshi, Anthony Wexler. *University of California, Davis, Davis, Calif.*

The high number of spinal cord injured (SCI) individuals and the detriment of their quality of life show their need for interfaces with assistive technologies. This work presents the research performed to develop an interface that uses the contractions of a facial muscle to generate two control signals that are used to move a computer cursor. To demonstrate the feasibility of using electrical signals generated during muscle contractions (EMG) to develop two independent control signals to move the computer cursor two approaches were used: a computer simulation and a case study on a single subject. An EMG signal was simulated and processed to obtain its frequency content by the use of a Fourier transform (FT). The spectral powers developed within two different regions of frequency were analyzed and it was found that they could be used to generate the two control signals required. The surface EMG signals of the *Auricularis Superior* muscle of one subject were then acquired and the spectral powers within the frequency regions determined by the simulation were used to generate the X or Y position of the computer cursor. The person kept visual contact with the cursor and significantly improved the control over its position for different cursor-to-target activities. The results show that humans may be capable of controlling single muscle contractions to generate electrical signals with specific power levels within two regions of frequency and that such information can be used to develop a non-invasive and accessible interface for subjects with all levels of SCIs.

CC 2214

INCREASING THE FREQUENCY RESPONSE OF ACOUSTIC REFLECTOMETRY

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Acoustic reflectometry technique (ART) is a non invasive technique which is used to estimate the cross sectional area as function of the distance of a cylindrical cavity. In other words, ART is used to estimate the shape of a cavity by using acoustic waves in the audible frequency range. The technique consists of driving an incident acoustic wave through a pipeline and forcing it to make impact into the cavity to be analyzed. In order to estimate the area profile, both incident and reflected acoustic waves need to be recorded and identified. ART has been used by biomedical engineers to estimate a human upper airway area profile, but the technique has some limits because the environment involved in this application is particularly affected by acoustical losses, and it is impossible to generate an ideal acoustic pulse. Our objective consists of substituting that acoustic impulse instead of pure tones to improve the accuracy of those previous results. Our hypothesis, based on a simulation called steady state acoustic reflectometry technique (SSART), has shown excellent accuracy when the incident acoustic wave covers the entire audible spectrum. Two important advantages of SSART lie in the fact that we do not need to identify those initial points on both incident and reflected acoustic waves, and it could be less sensitive to acquisition noise. In spite of SSART is long in time when applied, it is possible to decrease the number of pure tones by using an interpolation technique on the impulse response obtained from SSART.

GENERAL ENGINEERING

CC 2210

AN INNOVATIVE DATA ACQUISITION APPROACH TO DETERMINE FATIGUE DURING SURGERIES

Andrew Blackman, Delia Valles-Rosales. *New Mexico State University, Las Cruces, N.Mex.*

Human fatigue is an important factor that affects job performance, health, and safety. For medical doctors patient safety is of up most importance, but there are few studies focused on ergonomic assessments in plastic surgeries. There have been some methods proposed in surgeries such as laparoscopic based on manual recording as well as automated recording system. However, these approaches are expensive and take tremendous amount of time to record data. We are proposing an inexpensive method to make postural measurements based on the rapid upper limb assessment (RULA) definition of the most ergonomic position. Our approach consists of using MiniDV camcorders to track the doctor's movements during a surgery, and using the doctor's movements to drive a 3D solid polygon model. Light emitting diodes (LEDs) will be placed in key pivot points on the medical doctor for a reference point for motion tracking. We also plan to deliver a survey to a medical doctor while he is performing surgery. The survey consists of an eight questions about his levels of fatigue based on different muscle groups. The selection of time to deliver the survey will be randomly chosen to statistically analyzing it later. The questionnaire will provide data to be compared with the scores obtained from the recording data to identify the possible subjective causes of high stress scores in addition to the assumed various postures.

ENVIRONMENTAL SCIENCE

CC 2211

EFFECT OF ARSENITE ON THE ACTIVITY OF OXIDATIVE STRESS ENZYMES AND DNA INTEGRITY IN THE ROOT ZONE OF PEA PLANTS

Hiram Castillo-Michel[1], Kenneth Dokken[1], Alejandro Martinez-Martinez[2], Jose Peralta-Videa[1], Jorge Gardea-Torresdey[1]. *[1]University of Texas at El Paso, El Paso, Tex., [2]Universidad Autonoma de Ciudad Juarez, Cd. Juarez, Chihuahua, Mexico.*

Arsenic is a metalloid element found in the environment as organic and inorganic complexes. Inorganic forms of arsenic are the most detrimental for all living organisms including plants. Inorganic arsenic is known to be a human carcinogen. Moreover, arsenic in the 3 + oxidation state is reported to be the most toxic of all inorganic arsenic forms. In this study, 12 day old pea plants will be exposed to As(III) at different concentrations for 7 days in hydroponics. The effect of arsenic exposure over the DNA material in the root zone will be assessed using the polymerase chain reaction based method called random amplified polymorphic DNA (RAPD). Results will provide insight about possible mutations and damage to DNA caused by As(III). In addition to this the specific activity of the important oxidative stress enzymes catalase and ascorbate peroxidase will be assessed using microplate assays. In summary, the results obtained from these experiments will determine the potential effect of As(III) on the increase of reactive oxygen species and their implication on DNA damage.

CC 2214

RELATION BETWEEN USERS IN BEACHES OF BARCELONA AND THE AMOUNT OF WASTES COLLECTED IN THE SAME ONES: DATA COLLECTED BY ARGUS VIDEO-MONITORING SYSTEM AND THE COLLECTED WASTE SYSTEM OF THE CITY COUNCIL

Viviam Charriez-Serrano[1], Jorge Gillén[2]. *[1]Metropolitan University of Puerto Rico, San Juan, P.R., [2]Marine Sciences Institute, Barcelona, Spain.*

The solid wastes in the European coasts have increase and it has become a great problem not only for the coasts of the Mediterranean, but for the entire world. To identify the problem of the waste increase in this coast, the Institute of Marine Science (ICM) in Barcelona, has carried out a study on the amount of users in beaches of Nova Icaria and Somorrostro using a video-monitoring system called *Argus*, which belongs to the Coastal Station of Barcelona. The city council of Barcelona, which is working hand to hand, provides the data of waste harvesting during the summer season (June to September) for 2004, 2005, and 2006. A total of 1,717 kg of collected wastes has been obtained and around 2,085 users have visited the beaches mentioned during the period of study. The purpose of this research is to relate the amount of users who visit the beaches Nova Icaria and Somorrostro in Barcelona, using the collected data provide by the *Argus* system and the amount of generated wastes obtained by the city council data. Besides, it pretends to determine if there's a relation between the number of users and the amount of sweepings generated in the mentioned beaches. The collected data of the *Argus* system had not been used previously to establish a comparison of this nature. Preceding studies had shown a relation between the beaches users and the collected sweepings, but those were not considering as precise.

CC 2211

METHOD DEVELOPMENT FOR THE ANALYSIS OF WASTEWATER ORGANIC CONTAMINANTS

Roberto De La Torre Roche, Wen-Yee Lee. *University of Texas at El Paso, El Paso, Tex.*

The continuous exponential growth in human population has increased the demand for the Earth's limited supply of freshwater, especially in semiarid/arid areas where water is too valuable to use only once. Thus, protecting the integrity of our water resources is one of the most essential environmental issues. One of the major concerns is the potential adverse human and ecological health effects resulting from wastewater organic contaminants (WWCs) such as household chemicals, pharmaceuticals, and other consumables as well as biogenic hormones. These chemicals have the ability to disrupt the endocrine system by interfering with the mechanisms that govern the biosynthesis, transport or availability, and metabolism of hormones. These chemicals can be released directly to the environment after passing through wastewater treatment processes, which often are not designed to remove them from the effluent. In addition, they can affect the ecosystem even at very low concentrations, i.e., ng/L range. Therefore, analytical method development is an important key element for the detection of WWCs at low concentration level. This project is aimed to develop methods to analyze WWCs in wastewater and surface water at parts per trillion levels using a green technique called stir bar sorptive extraction (SBSE) with thermal desorption coupled with gas chromatography and mass spectroscopy. Derivatization process is used to increase the recovery of WWCs from water samples. Selected WWCs for analysis are: Bisphenol A, 17β-estradiol, estrone, and 17α-ethynylestradiol. Method optimization using extraction time, sample volume, derivatization agents, detection limits will be reported.

CC 2211

SCREENING THE PHYTOREMEDIATION POTENTIAL OF DESERT BROOM (*BACCHARIS SAROTHROIDES* GRAY) GROWING ON MINE TAILINGS IN ARIZONA, USA

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This research was conducted at a copper mine tailings reclamation project (CMTRP) located in the Globe-Miami mining district near Claypool, Ariz. Desert broom (*Baccharis sarothroides*) an environmentally friendly and available plant that might have phytoremediation potential, grows at the CMTRP. Therefore, in this research metal concentrations both in the tailings and plants were investigated. Triplicate samples of soil cover, tailings and plants of desert broom were collected. The metal concentrations in the soil cover and tailings were determined using ICP-OES. Based on the concentration, the elements were classified as major elements: (K > Al > Fe > Ca > Mg > Na > Cu > P) and minor elements: (Mn > Pb > Mo > Cr > Zn > As > Ni > Co). The concentration of Cu, Pb, Mo, Cr, Zn, As, Ni, and Co in tailings was 454.9, 209.7, 89.32, 85.6, 51.2, 49.2, 39.3, and 36.3 mg/kg, respectively. The concentration for major and minor elements in the soil cover was 10% to 15% higher than that of the tailings except for Cu and Mo. The concentration of Cu, Pb, Cr, Zn, As, Ni, and Co in desert broom was 819.3, 152.7, 56.7, 39.9, 43.1, 97.3, and 26.3 mg/kg for roots and 1212.7, 102.2, 104.4, 56.12, 34.3, 31.2, and 10.1 mg/kg for shoots, respectively. Considering the translocation factor, enrichment coefficient, and accumulation factor, desert broom could be a potential hyperaccumulator of Cu, Pb, Cr, Zn, As, and Ni for application in phytoremediation of copper mine tailings in Arizona.

CC 2211

PROTEIN BOUND ORGANELLES COMPARTMENTALIZE THE METABOLISM OF FUCOSE IN THE CELLULOLYTIC BACTERIUM *CLOSTRIDIUM PHYTOFERMENTANS*

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Clostridium phytofermentans is a nutritionally versatile cellulolytic bacterium capable of growth on a variety of biomass-derived substrates including cellulose, cellobiose, glucose, xylan, xylose, arabinose, fucose and rhamnose. The major non-gaseous products of its fermentation include ethanol, acetate, formate and lactate. A genome-enabled analysis targeting specialized fermentation pathways implicated a putative operon of fifteen genes for fucose metabolism. In addition to enzymes involved with fucose metabolism this operon also encodes seven genes with strong sequence homology to the shell proteins of the cyanobacterial carboxysomes. This genomic analysis suggests fucose metabolism involves compartmentalization of enzymatic reactions within the lumen of a proteinaceous organelle analogous to the carboxysomes. Using a reverse transcriptase PCR shell protein expression was confirmed to be up regulated during growth on fucose. Proteinaceous organelles were visualized in thin sections of cells by means of transmission electron microscopy when cells were grown on fucose but not on cellobiose. A highly purified preparation of organelles was prepared and denaturing SDS-PAGE revealed that the organelles consisted of approximately twelve polypeptides. Using combined evidence from genomic and protein analyses as well as electron microscopy, fermentation product analysis and biochemical assays, a model has been proposed. This model predicts that the organelle enhances the efficiency of an enzymatic reaction central to fucose metabolism by concentrating the enzyme, activase, co-factor and substrate to the lumen of the organelle, which results in enhanced enzymatic efficiency, and cellular protection from toxic intermediates.

CC 2214

INFLUENCE OF DIFFERENT LAND USES ON CARBON STOCK AND SOIL ORGANIC CARBON DYNAMICS IN A SEMIARID AREA OF SE SPAIN

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Conversion of forest to cropland influences a number of soil properties. One of the most pronounced and widespread changes that occur is the decline in soil C, which is attributed to different factors. Three land uses were selected: forest, a non irrigated olive cropland, and an abandoned area which was cultivated with pasture 25 years ago. These areas are located in the northeast of Murcia region (SE Spain). The objective of this study was to establish the change in the soil carbon pool (CP) for different aggregate sizes with land use change. The CP (particulated organic matter and mineral-associated organic matter) at two soil depths (0 to 5 cm and 5 to 20 cm) in three soil fractions (>2000μ, 2000 to 250μ, and 250 to 50μ) were analyzed. The soils in the study areas are a Typic Petrocalcid, Typic Haplocalcid, and Calcaric Reosol for forest, olive, and abandoned area, respectively. All of them have a loam texture. After 100 years of cultivation a reduction in the soil carbon stock (at the top 5 cm) of about 51% was observed when the total OC in the cultivated area was compared to the natural non-disturbed one. Mineral-associated organic carbon (MAC) represented the higher percentage (between 50% and 68%) of the total soil OC for all the aggregate sizes studied with an increase of this percentage as aggregate size increases. Particulate organic carbon (POC) was the CP most affected by cultivation at 5 cm depth. Overall, for the aggregate class between 250 to 50μm, the POC in the olive cropland was reduced from about 46% to 27.8%.

CC 2211

THE PRESENCE OF DIALKYLPHOSPHATES IN DUST FROM URBAN AND FARMWORKER HOMES: COULD THEIR PRESENCE ALTER THE WAY WE ASSESS PESTICIDE EXPOSURES?

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Dialkylphosphates are metabolites and breakdown products of many organophosphate pesticides commonly used as nonspecific urinary biomarkers of exposure to parent organophosphate pesticides. These urinary metabolites are used to estimate exposure to organophosphates in epidemiological and exposure assessment studies. Recent evidence suggests that urinary dialkylphosphates may also result from exposure to preformed dialkylphosphates in foods and in the environment. This possibility could result in overestimation of exposure to parent organophosphate compounds and misclassification of exposure in epidemiology studies. To establish the presence of dialkylphosphates in the environment, we collected dust samples from urban and agricultural homes (n=80 dust samples). Samples were analyzed for six dialkylphosphates (diethylphosphate, diethylthiophosphate, diethyldithiophosphate, dimethylphosphate, dimethylthiophosphate, and dimethyldithiophosphate) using a newly-validated laboratory method developed with the Centers for Disease Control and Prevention. Median dust levels for urban homes were 55, 12, and 72 nmol/g for total diethyls, total dimethyls and total dialkylphosphates, respectively; while levels in agricultural homes were 44, 14, and 60 nmol/g for total diethyls, total dimethyls and total dialkylphosphates, respectively. Total dialkylphosphates in dust ranged from 28-1712 nmol/g in urban homes and from 28-919 nmol/g in agricultural homes. This is the first study to report the presence of dialkylphosphates in dust. Their presence suggests a need for multimedia assessment studies and measurement of both parent organophosphates and their degradation products when using nonspecific urinary biomarkers of exposure to assess pesticide exposure. Multimedia assessments will help determine the potential contribution from all sources, aid interpretation of urinary dialkylphosphates, and minimize exposure misclassification in epidemiology studies.

CC 2214

THE USE OF ORGANIC AND MODIFIED CLAY TO PREVENT ENVIRONMENTAL CONTAMINATION BY PESTICIDE

Carlos Rivera, Juan Cornejo, Lucia Cox, Rafael Celis. *Instituto de Recursos Naturales y Agrobiologicos de Sevilla, Sevilla, Spain.*

The use of pesticides in the production of better and more abundant agriculture products is imminent when we talk about of the future in that nature. Pesticide use supposes to ensure the quality of the harvest, free of every organism that damages it. However, 80% of that pesticide doesn't fulfill the intention. This percentage becomes a problem in the contamination of the underground water and can affect the environment of other organism that are important in the quality of the soil. For this study we are using the pesticide MCPA, an acid type pesticide that has an elevated risk of percolation through the soil and can affect underground water and living organisms. Through the use of clay for decontamination and prevention we sought to determine the adsorption capacity of the organic and modified clay on pesticides of polar or acid type, with the purpose of using it for the

decontamination of a limited soil area and to be employed as an agent of pesticide percolation controller. To determine the adsorption capacity of the clay, we used a chromatograph to show us the presence of the pesticide. We conducted a column leaching experiment to compare the vertical movement of a standard commercial formulation of MCPA with that of different formulation in which the herbicide was pre-adsorbed on modified clays. Every day, for approximately two weeks, we added 15 ml of distillate water and the next day took samples from twelve leaching column that were hand-packed with soil and treated with a different formulation of MCPA. To each one of those columns we added an equivalent quantity of 2 Kg/ha of MCPA. We observed that the concentration of MCPA in leaches is reduced by the application of the by-based formulation of the herbicide. In addition, for some of the formulation the leaching of MCPA is retarded. Leaching of MCPA decreased in the following order: commercial > Sa-hexadim > Sw.-hdtma600 > Sa-hdtma200. Concluding with the experiment we can say that the clay with the organic cation Sa-hdtma200 reacted much better with the pesticide MCPA when we talk about preventing the percolation and extending the life of the pesticide in the soil.

GEOSCIENCES

CC 2204

USING GIS AND LIDAR FOR MODELING AND VISUALIZATION OF LOCALIZED SEA LEVEL RISE

Kalonie Hulbutta, Dave McDermott. *Haskell Indian Nations University, Lawrence, Kans.*

The availability of Light Detecting and Ranging (LiDAR) data and high-resolution imagery aids in the analysis of the impact of sea level rise on individual coastal communities. Local studies can consider specific environmental factors including tides, storm surges, and coastal development that cannot be effectively modeled at a national or global scale. Two sites in Maine were selected for inundation: the Biddeford Pool area and Orchard Beach. Using LiDAR data with submeter vertical resolution and one-foot resolution orthophotos, we were able to model the impact of sea level rise on the natural and built environments at a level of precision not typically available in coastal impact studies. Our model also included the contribution of low tide and high tide for the selected sites. ESRI's raster calculator was used to adjust elevation values and simulate changes in sea level. A raster grid was created for each half-meter increment of inundation. High-resolution orthophotos help illustrate residential and commercial impact as well as fluctuations in tidal zones as the sea level rises. Further analyses will be conducted to estimate the population affected and total area of the newly inundated regions. Animated visualizations of the flood event can be created using Visual Nature Studio or Macromedia Flash.

CC 2204

AN ACOUSTIC LENS SYSTEM: DESIGN AND ITS APPLICATIONS IN GEOPHYSICAL METHODS

Angel Acosta-Colon, Laura Pyrak-Nolte. *Purdue University, West Lafayette, Ind.*

The interpretation of fractures geophysical response, using seismic measurements will change depending of the scale of the seismic observation due of the intrinsic length scales within the fracture. These length scales include those associated with the geometry of the fracture, the wavelength of the seismic signal, and the size of the region probed by the seismic beam. The main objective of the acoustic lens system was to understand how the scale of observation (probe size) influences measured changes in the fracture seismic response caused by reactive flow in a fracture in carbonate rocks (Limestone). The lens was designed based on the geometrical properties of an ellipse. An elliptical lens will eliminate on-axis aberration and also had been used since the 1950s for focusing ultrasonic field in liquid media. Most of the acoustic lens designs used in geophysics are to focus energy at a particular point in space. In our study, we created a pseudo-collimated wave (parallel waves) as output of the lens, in which the collimated width determined the probe size. The resulted width was 3 mm, 20 mm, and 60 mm. The use of the acoustic lens system to obtain seismic measurement in fractured Limestone sample are analyzed to understand if the seismic properties of the fractures are scalable (the ability to scale up to large scales, i.e., from 3 mm to 60 mm). In this study, an acoustic lens system is presented as a new technique to understand the seismic properties of fractures at different scales.

CC 2204

VISITOR CONCEPTIONS AND MEANING MAKING AT PETRIFIED FOREST NATIONAL PARK

Nievita Bueno Watts, Steven Semken, Monica Pineda, Cheryl Alvarado. *Arizona State University, Tempe, Ariz.*

When observing the spectacular natural landscapes of our National Parks, how do visitors make meaning of the geology? Deeper understanding of visitor conceptions can inform the design and implementation of more effective geoscience displays and interpretative programs. The researcher investigated visitors' ideas about geological processes, features, and history at Petrified Forest National Park in northern Arizona, a place renowned for its colorful badlands and fossil wealth. Data were

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collected from semi-structured interviews of 80 visitor groups (n = 235) encountered at Blue Mesa, a popular viewpoint locality. Volunteer subjects were asked to explain the formation of the landscape, describe the depositional environments coded in the rocks (including the origin of fossil logs) and account for the present high elevation of the Colorado Plateau. These results were analyzed using the Verbal Analysis methodology of Chi (1997). In the absence of accurate geological understanding of the landscape, visitors frequently used familiar-place knowledge based on specific places with which the visitor has had prior experience. Qualitative analyses indicate that visitors variously make meaning by (1) relating landscapes to familiar places; (2) building on religious explanations; (3) superimposing past landscapes on modern ones; and (4) patching together bits of information from media sources. Visitors were found to have difficulty in visualizing past landscapes. It is recommended that future exhibits and interpretative programs use visitor reliance on familiar-place knowledge to help visitors build normative conceptions about PEFO landscape formation through the inclusion of modern-day analogs.

CC 2204

OXYGEN ISOTOPIC STUDY OF CARBONATE MINERALS FROM THE MID-CRETACEOUS LOW LATITUDES: INSIGHTS INTO THE CRETACEOUS GLOBAL HYDROLOGIC CYCLE

Marina Suarez[1], Luis Gonzalez[1], Gregory Ludvigson[2], David Ufnar[3]. *[1]University of Kansas, Lawrence, Kans., [2]Kansas Geological Survey, Lawrence, Kans., [3]University of Southern Mississippi, Hattiesburg, Miss.*

Oxygen isotopic studies of pedogenic carbonate minerals (calcite and siderite) from the mid-Cretaceous of North America (Alaska to Texas) suggests the hydrologic cycle was important in regulating global temperatures during greenhouse periods. This study adds pedogenic mineral oxygen isotope data from southern Mexico and Colombia that completes a northern hemisphere latitudinal transect through the Americas (Alaska to Colombia). The southern Mexico carbonate mineral samples are from a sequence of highly fossiliferous laminated limestone deposited in a freshwater influenced coastal lagoon. The Colombia samples are fluvial to estuarine deposit and show extensive pedogenic development. Carbonate mineral isotopic data are used to estimate the oxygen isotopic composition of paleogroundwaters and thus precipitation. The Cretaceous precipitation oxygen isotope latitudinal gradient is slightly more depleted than the modern precipitation oxygen isotope gradient, but much more depleted than the expected Cretaceous groundwater composition based on simple temperature relationships (e.g., Dansgaard's 1964). The new data are consistent with earlier calculations based on mid to high latitude data (Kansas to Alaska) that suggested that both precipitation and evaporation were much more intense during the mid-Cretaceous resulting in intense isotopic depletion of the airmasses as they transferred moisture from the tropics to the poles.

MATHEMATICS

CC 2205

CONDUCTION VELOCITY AND INTERSPIKE INTERVAL IN MODELS OF ACTION POTENTIALS IN MYELINATED NERVE FIBERS

Eric Benavidez. *University of Kansas, Lawrence, Kans.*

Several models explore the characteristics of the action potentials and associated currents used to transmit information across myelinated nerve fibers (Frankenhaeuser & Huxley, 1963; Goldman & Albus, 1968; McIntyre, Richardson & Grill, 2001; Naundorf, Wolf & Volgushev, 2006). Additionally, the models of Goldman and Albus (1968) and McIntyre, Richardson, and Grill (2001) explore aspects of the conduction velocity and the interspike interval of sequences of these currents. Miller and Rinzel (1981) have found a relation between conduction velocity and interspike interval or firing frequency in the classical Hodgkin and Huxley model. In this presentation, the conduction velocity and interspike interval of these classical and current models are compared with experimentally observed velocities and interspike intervals.

CC 2205

EXPLICIT STOCHASTIC MODELS FOR THE POPULATION DYNAMICS OF *TRIBOLIUM*

Alberto Izarraraz, Robert Desharnais. *California State University, Los Angeles, Los Angeles, Calif.*

Models that incorporate random chance are useful tools to study the dynamics of ecological populations. Most stochastic models are phenomenological deterministic equations with an added random term representing "noise." However, noise does not explain the mechanistic nature of random processes within the population. An explicit stochastic model provides insight on the mechanisms leading to randomness. I propose to develop explicit demographic stochastic models for insects of the genus *Tribolium*, estimate parameters for the model using data from laboratory populations, and compare the predictive ability of the

models using time series population data. The models will take into account a variety of potential sources of demographic stochasticity, such as a deviations in the sex ratio, different birth and survival rates among individuals, and different rates of development. This project can serve as a paradigm for the way one can model stochasticity explicitly and connect it to experimental data.

CC 2205

VISUALIZING INVARIANT MANIFOLDS FOR THE PLANAR RESTRICTED THREE BODY PROBLEM

Claudia Santiago, Caroline Furman, Alexander Lorz, Aalok Shah. [1]*University of Chicago, Chicago, Ill.,* [2]*University of Cambridge, Cambridge, Mass.,* [3]*Duke University, Durham, N.C.,* [4]*University of Texas at El Paso, El Paso, Tex.*

Our Solar System is connected by a large system of tube-like conduits called invariant manifolds. These manifolds are propagated from periodic orbits surrounding the fixed points of the planar circular restricted three body problem. They provide low energy transport throughout the Solar System, and as a result, the means to construct new energy-efficient spacecraft trajectories. In our research, we investigate the geometric structure of these manifolds. Specifically, we are interested in visualizing the invariant manifolds as 2D surfaces in a 3D space. Currently, manifolds in Matlab are generated by the propagation of individual trajectories and are represented as a set of unorganized points. Consequently, it is difficult to analyze these manifolds as structures as well as to portray their intersections. In this project we plan to reconstruct the surface from a discrete set of points. We are investigating two different methods for representing the invariant manifolds. The first is the Delaunay triangulation method, which has superior approximation properties in comparison to rectangular meshes. The latter is the level set method in which a surface is reconstructed from the set of points using partial differential equations. Using our surface representation we will examine different properties of the invariant manifolds such as their curvature and the rate at which trajectories separate.

CC 2205

A MATHEMATICAL MODEL OF THE *DROSOPHILA* HEART

Genevieve Toutain[1], Pamela Reitsma[2], Irina Kareva[3], Odalys Colon-Rentas[1]. [1]*Arizona State University, Tempe, Ariz.,* [2]*University of Maine, Orno, Maine,* [3]*University of Maryland, College Park, Md.*

The heart of *Drosophila melanogaster* is a tubular organ that contains two types of excitable cells which work together to pump hemolymph through the body. At the cellular level, specific ion channels involved in the heartbeat of *Drosophila* have been identified and studied using genetic mutations and pharmacological agents. In this work the *Drosophila* heart is modeled as a network of excitable cells in order to explore the biophysical mechanisms underlying the generation of the heartbeat. The model cells are arranged in a tubular shape to form a network connected by gap junctions. Pacemaker cells with an intrinsic rhythm are added at one end of the network model and generate a wave of contraction down the heart. Using the model, channel kinetics are manipulated to explore the effects of different channels on *Drosophila* heartbeat. Model results are compared to experimental data.

CC 2205

DYNAMICS OF A GENE EXPRESSION MODEL WITH TIME DELAY

Anael Verdugo, Richard Rand. *Cornell University, Ithaca, N.Y.*

The mathematical study of biological systems has become an important research field in science. In particular, the study of time lags or delays has played a significant role in the dynamics of gene transcription and protein synthesis models. In principle, the influence of such delays can result in oscillatory mRNA and protein expressions. I will describe a gene expression model and its dynamical behavior close to a Hopf bifurcation. This will be accomplished by using Lindstedt's perturbation method and a center manifold reduction on the system. The final outcome results in closed form expressions for the limit cycle amplitude and frequency of oscillation. These results provide analytical evidence that delays can drive oscillations in gene activity.

PHYSICS

CC 2207

DETECTION OF SPECIAL NUCLEAR MATERIALS

Steven Kane, David Koltick. *Purdue University, West Lafayette, Ind.*

With millions of cargo containers delivered yearly to U.S. ports, the U.S. Customs and Border Protection Bureau is in dire need of non-invasive scanners which can detect and image radiation emitted by illicit special nuclear materials. Special nuclear materials, such as uranium-235, are the main ingredients in nuclear weapons because they can achieve a self-sustaining fission reaction. This work will discuss a scanner, which utilizes a neutron-probing beam. Within an associated particle neutron generator, deuterium ions are accelerated onto a tritiated target, leading to a fusion reaction that produces correlated beams of neutrons and alpha particles that escape back-to-back. A built-in alpha detector with a ZnO(Ga) phosphor detects alpha-induced scintillations. The neutron that is correlated to a detected alpha particle penetrates effortlessly through the cargo. In the presence of a special nuclear material, the neutron is absorbed by a nucleus in the sample. The nucleus undergoes fission, splitting into two fission products while releasing energetic prompt gamma rays and prompt neutrons. Shortly after, the fission products beta-decay, emitting delayed gamma rays and delayed neutrons. The released gamma rays and neutrons form a unique signature of special nuclear materials. A detector registers gamma rays that coincide with a correlated alpha particle. An improved signal-to-background ratio is achieved over conventional neutron generators that lack an alpha detector. A fast data acquisition system collects timing and energy data, which is feed into an algorithm displaying a threat/no threat status and an image. Preliminary results will be available in October.

CC 2207

ESTIMATING POLAR CAP ELECTRON DENSITY PROFILES USING IMAGE RPI SOUNDINGS

Aramis Martinez, Patricia Reiff. *Rice University, Houston, Tex.*

We are developing a novel approach to determining electron number density profiles using polar cap IMAGE RPI soundings. We extract the virtual reflection distances for the right-hand extraordinary-mode polarized component of a set of sounding pulses ducted earthward by field-aligned density depletions. The virtual distances are used to estimate of the real distance height of the reflection points along the field line, and the density at each reflection is determined from the extraordinary-mode cutoff relation. Statistical studies of in situ density measurements have established the suitability of a power law to describe density as a function of altitude, so we generate and iteratively adjust a power law in terms of geocentric height along the field line. The power law includes a constant term, which represents density at large distances and will allow us to account for elevated densities observed at the satellite in recent studies of geomagnetically active times.

CC 2207

THE TELESCOPE ARRAY PROJECT: DEPLOYMENT AND FIRST DATA OF A NEW HYBRID COSMIC RAY DETECTOR

Douglas Rodriguez. *University of Utah, Salt Lake City, Utah.*

Extensive air showers produced by cosmic rays have been studied since their first discovery by Pierre Auger in 1939. Since that time many techniques have been developed to observe and understand these air showers and the primary particles producing them. Surface detectors, like those found in the AGASA experiment, measure the charged components of the showers when the "pancake" of the shower reaches the surface of the Earth. Fluorescence detectors, like those of the HiRes experiment, are able to observe the shower itself as it traverses the atmosphere. Fluorescence telescopes measure the ultraviolet light emitted during the interaction between the charged particles contained in the shower and air molecules. The Telescope Array (TA) experiment combines these two forms of cosmic ray detection systems into a single hybrid detector located in Millard County, Utah. Initially intended to resolve the differences at the GZK cut-off (E = 10^19.5 eV) between the AGASA and HiRes spectra, TA/TALE (Telescope Array Low Energy Extension) will also provide new evidence concerning the galactic/extragalactic origins of high energy cosmic rays shown recently in the HiRes data. The information obtained by this experiment will also help answer many of the additional questions concerning cosmic rays' composition, anisotropy and energy spectrum. This presentation will discuss the background of the experiment as well as the first data collected.

CC 2207
FABRICATION OF A PLASTIC MICROFLUIDIC DEVICE FOR DIAGNOSTIC APPLICATION
Chetan Sood, David Koltick. *Purdue University, West Lafayette, Ind.*

The fabrication of plastic microfluidic devices is an intricate matter dealing with temperature, pressure, and time all of which must be optimized before a microfluidic device is produced efficiently. Using a programmable hydraulic press to maintain constant pressure and variable temperature for specified times, devices were made using poly(methyl methacrylate) (PMMA). PMMA is a clear, disposable plastic that was used as a shatterproof replacement for the more expensive glass; the device fabrication is also comparatively simple. Initially holes were drilled in the PMMA, and a channel template consisting of polycarbonate strips was placed on top of the holes. This whole ensemble was placed between aluminum blocks in the press at 15,000 lbs and 102˚C to create the channel. The other challenge encountered was to create a cover for the channel. This was done by initiating a bond with a second piece of PMMA on top of the channel, using a bonding solution and a new recipe in the press. Essentially these recipes are found in literature but need minor modification before producing robust results. A bond was created without significantly deforming the channel as seen with fluorescent imaging. Ultimately these devices will be used for immunoassays using electrophoretic separation of proteins and protein complexes. For this application, it is important to minimize non-specific adsorption of proteins to channel walls. To this end, a fluorescently labeled protein was added to the channel and washed through with varying concentrations of detergent to determine the extent of protein adhesion to channels.

SOCIAL AND BEHAVIORAL SCIENCE

CC 2215B
HEALTH AND WATER AFFECTS IN A NATIVE COMMUNITY
Tommy Rock, Ronda Francis, Jani Ingram. *Northern Arizona University, Flagstaff, Ariz.*

The purpose of this study is to find out how the communities surrounding the abandoned uranium mines are impacted. A pathway of exposure from these abandon uranium mines includes their water resources, which they depend on for consumption, livestock, and irrigation. In many areas the residents have no running water and must haul water from unregulated wells. The isolated communities are impacted by the water situation. Our research lab has collected water samples from nine water sources in various places in the region. One well has been found to have uranium concentrations approximately four times the E.P.A. drinking water standard. Another is almost two times the drinking standard and a third is at the standard. The other wells are below the standard. We are surveying the communities to determine where they get their water, how they use it, and the frequency that they haul. Before asking any survey questions, we ask for the community members consent to participate in our study. If they agree to participate, we not only administer the survey, but we also collect G.P.S data to determine the location of their house with respect to the wells. The purpose of collecting location information is so we can plot the area from high impact to the least impact. We are using Garmin Legend Cx G.P.S to get their coordinates when we get consent from the household. Once we get the coordinates, we plot them on the map using ArcGIS 9.1. The results will be shared with Navajo Nation.

CC 2215B
FACTORS ASSOCIATED WITH ADHERENCE TO RECOMMENDATIONS FOR CANCER SCREENING AMONG AMERICAN INDIANS IN CALIFORNIA
Vanessa Watts, Graham Colditz. *Harvard School of Public Health, Boston, Mass.*

American Indians (AI) use health preventive services less often than other populations in the US. This disparity underscores the need for further understanding the determinants of screening behavior among AI. Even though most AI in California (CA) live in urban areas, research examining their health status is lacking. This purpose of this study is to compare adherence to recommendations for obtaining Pap tests, mammograms, and colorectal cancer (CRC) screenings among rural and urban AI in CA. We used the California Health Interview Surveys from 2001, 2003, and 2005 (n=2266). The data set was restricted based on national guidelines for each screening test. Multivariate logistic regression was performed to determine the association of demographic and health care access with adherence to screening guidelines. Almost 78% of AI adults in CA live in urban areas. Significant differences for education, poverty, comorbid condition, insurance, IHS access, smoking, and tribal affiliation were found between urban and rural AI. For all three tests, the association between access to care and screening adherence was significant ($p<0.05$). Higher educational attainment [OR 1.61 (1.09, 2.37)], a comorbid condition [OR 1.54 (1.15, 2.06)] and being a non-smoker [OR 1.57 (1.12, 2.20)] increased likelihood for CRC screening. Experiencing discrimination decreased the likelihood for obtaining a Mammogram [OR 2.40 (1.13, 5.11)]. Adherence rates did not differ by rural/urban residence. These results expand previous research examining urban/rural residence effects on health behaviors. Our study supports the finding that health care access is the most important factor associated with adherence.

CC 2215B

THE ROLE OF PARENTHOOD IN THE SELF-CONCEPT OF COLLEGE STUDENTS: WHEN EXPLICIT AND IMPLICIT ASSESSMENTS TELL DIFFERENT STORIES

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The present research examined the extent to which parenthood is incorporated into the self-concept of college students. A sample of undergraduate students (90 men and 87 women) completed three Implicit Association Tests (IATs) assessing the extent to which they identified with the concepts "parenthood" and "college education" (Self-Concept IAT), the extent to which these two concepts were linked to gender categories (Gender Roles IAT), and the extent to which they identified with gender categories (Gender Identity IAT). They also completed explicit self-report measures of the same constructs. Explicitly, both men and women strongly and equally identified with college education rather than with parenthood. Implicitly, women identified equally with parenthood and college education, whereas men showed a stronger identification with college education than with parenthood. In addition, implicit measures revealed that traditional gender roles accounted for a stronger identification with parenthood for participants who displayed a female identity and a stronger identification with college education for participants who displayed a male identity. These findings suggest that parenthood plays a more important role in the self-concept of college students than self-reports would indicate. Implicit measures are particularly suited to reveal the pervasive influences of conventional gender roles on the self-concept of college students.

CC 2215B

I'M WHITE YOU'RE BLACK, BUT WE'RE ALL WOMEN: EMPHASIZING COMMON IDENTITY IMPROVES INTERGROUP RELATIONS FOR WHITE WOMEN

Francine Segovia, Denise Sekaquaptewa. *University of Michigan, Ann Arbor, Mich.*

Although racial stereotypes are most often examined in regards to racial minorities, a strong stereotype exists about European Americans, i.e., that they are likely to be prejudiced against African Americans (Goff, 2005; Shelton, 2003). In a laboratory experiment we tested the hypothesis that when White women discuss a race-related topic in front of Black women, they would show speech disfluencies and concern about being stereotyped. Second, we tested an intervention designed to reduce this effect, based on social identity theory. Intervention group participants were instructed to reflect on something they had in common with the others: gender. 71 White female undergraduates were randomly assigned to speak about a race-related topic (slavery in colonial America) in front of either a group of Black or White women. Orthogonal to this manipulation, half the participants received the intervention designed to emphasize their shared gender identity. Results confirmed predictions regarding stereotyping concern [$F(1,67)=4.03$, $p<.05$], speech disfluencies [$F(1,52)=5.61$, $p<.05$], and a measure of feeling comfortable in the group [$F(1,67)=4.67$, $p<.05$]. In the non-intervention condition, White women showed more speech errors and greater concern about stereotyping when talking about race to the Black than the White group. However, in the intervention condition, participants showed fewer speech errors, less concern about stereotyping, and reported feeling more comfortable in the Black group. This research showed that Whites have diminished communication when talking to Blacks about race, but that this effect can be reduced when Whites think about what they have in common with Black people.

STUDENT POSTER ABSTRACTS 2007

ASTRONOMY

A2-FRI

ABNORMAL CLUSTERS OF STARS AND THE FORMATION OF GALAXIES

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Theorists' predict that galaxies like our Milky Way are formed when smaller galaxies merge into larger galaxies. As those smaller galaxies merge with larger galaxies, they are stretched apart until they are absorbed into the larger galaxy, yet their stars retain similar Doppler velocities which make them distinct from the rest of the larger galaxy. Our project aims to test this possible explanation by looking at the velocities of stars in our galaxy. Our method will be to fit a smooth model to the Doppler velocities and look for clumps of stars that deviate from the model. In order to do this, we retrieved the Doppler velocities and magnitudes of stars from the Sloan Digital Sky Survey (SDSS)/SkyServer database. We created two velocity histograms, one for bright stars and one for fainter stars, in three regions of sky. Then we observed discrepancies in the distribution between the two graphs and created a best fit curve for the histograms. Through simulations, we independently determined at what bin count and at what bin width the deviations from the curve are statistically significant. These limitations will act as guidelines for finding further clusters throughout our galaxy as well as in other spiral galaxies. The detection of these clusters within the galaxies can help astronomers understand how large galaxies have formed through the process of mergers and interactions with smaller galaxies.

A3-SAT

HOUSING CONSTRUCTION FOR ASHRA DETECTORS

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The ASHRA experiment (All-Sky Survey High Resolution Air-Shower Detectors) is a collaboration between the University of Hawai'i-Hilo and the University of Tokyo-Japan. The experiment implements 28 detectors on the 11,000 ft. level of Mauna Loa in Hawai'i, to detect air showers, Cherenkov radiation and Nitrogen fluorescence created by collisions between particles in Earth's atmosphere and high-energy particles. Next to Mauna Loa is Mauna Kea, an inactive volcano that is being used by ASHRA detectors as a filter to observe air showers created from tau neutrinos. My involvement with the experiment has been to construct housings for the detectors. This included leveling the land, assembling the walls and roofs, installing the steel frames for the detectors, and putting in shutter doors and insulation. Housings are important for the detectors because they provide a constant temperature which is required for the electronic equipment, they provide protection from the elements and they prevent dust and other particles from interfering with the optics. By the end of the internship I had completed 20 detector housings. My assistance facilitated rapid construction of the housings which benefited the ASHRA project tremendously by allowing them to meet their construction deadline earlier than expected. ASHRA will begin to observe the night sky for air showers in October. The information gained from the future observations made by the ASHRA experiment will help us to understand high energy particles and their origins.

A3-FRI

SERENDIPITY IN THE DEEP SURVEY

Heather Kaluna[1,2], Puragra GuhaThakurta[2], David Rosario[2]. *[1]University of Hawai'i at Hilo, Hilo, Hawaii, [2]University of California, Santa Cruz, Santa Cruz, Calif.*

Galaxy formation and evolution constitutes one of the largest inquiries in astronomy today. Some of the faintest and most distant dwarf galaxies are found accidentally as spatially super-imposed or offset emission lines on a main target galaxy's spectrum. These serendipitously detected galaxies are referred to as serendips, some of which are dwarf galaxies. By measuring a galaxy's redshift, the degree that its light has moved towards the red end of the electromagnetic spectrum, we are able to determine its distance. The goal of this project is to gain insight into galaxy evolution by studying these serendips, which cover a distance that corresponds to a look-back time of half the age of the universe. To search for these serendipitous galaxies and find their redshifts, we used an IDL program called ZSPEC, which looks at galaxy spectra taken with the Keck telescopes for the Deep Extragalactic Evolutionary Probe (DEEP) survey. By studying the same serendips in a Hubble Space Telescope image of a DEEP sub-region, we were able to look at dwarf galaxy building blocks and compare them to more luminous, fully assembled

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galaxies. The results of this work will be discussed. Our studies should provide insight into the evolution of galaxy luminosities, morphologies and star formation processes.

A1-SAT

SOLAR FLARES: DO THEY AFFECT THE TOTAL BRIGHTNESS OF THE SUN?

Geovani Mejia Salazar, Gibor Basri. *University of California, Berkeley, Berkeley, Calif.*

In 2008, NASA will launch a telescope that will monitor the change of radiance of 100,000 stars in the Milky Way galaxy. The primary objective of this mission, known as the Kepler Mission, is to search for terrestrial and large planets in the habitable zone. The NASA scientists will utilize the transit method to detect these extrasolar planets. This method involves the precise monitoring of the radiance of the star, and looking for small dips caused by the planet crossing in front of it. However, the radiance of the stars is not constant since the stars will show the effects of magnetic activity (active regions and starspots). The goal of this study is to test whether the Sun's total radiance also shows the effects of solar flares. These effects are noticeable in low-mass stars, but with stars like our Sun, scientists are not sure. We analyzed the strongest solar flares of 2001 (an active year for the Sun) and made a preliminary determination that flares do not affect the total brightness of the Sun.

A1-FRI

SPECTROSCOPIC ANALYSIS OF ALPHA CENTAURI A AND ALPHA CENTAURI B DETERMINING SURFACE GRAVITY, MICROTURBULENCE, AND EFFECTIVE TEMPERATURE

John Olgin[1], Verne Smith[2]. [1]*University of Texas at El Paso, El Paso, Tex.,* [2]*National Optical Astronomy Observatory, Tucson, Ariz.*

I improve upon the existing spectral analysis techniques by introducing a more precise and accurate, semi-empirical method for determining stellar atmospheric parameters. This procedure provides improved stellar metal abundances, effective temperatures, surface gravities and microturbulences for Alpha Centauri A and B, the Sun, and Arcturus by deriving a new model atmosphere for each star in question. This process is compared with results from other empirical and semi-empirical methods. Spectra of Alpha Centauri A and B are obtained form the Spectroscopic Survey of Stars in the Solar neighborhood project (S^4N) by Allende et al. (2004). Spectra of the Sun and Arcturus were obtained from Smith, V.V, 2004 via private communication. Spectra were analyzed using software packages, IRAF and MOOG, and solutions were obtained using an iterative approach to fit model atmospheres of Kurucz (1980) to the spectra yielding the atmospheric stellar parameters in question. This method is an improvement on past methods as it uses measurements of both Fe I and Fe II lines to constrain the model atmospheres.

A2-SAT

INVESTIGATION OF THE PRESENCE OF MOLECULAR HYDROGEN IN SUNSPOTS

Jessi Willstrop. *Maui Community College, Kuhului, Hawaii.*

The penumbra of a sunspot is a light region that surrounds the much cooler umbra at the center. The goal of this project is to determine the intensity of molecular hydrogen in the umbra and penumbra to gain a better understanding of the formation of sunspots. Penumbral growth was observed by viewing images of active regions of the Sun where sunspots were forming. To measure the intensity of molecular hydrogen, a spectrometer that detects in the infrared must be used. The Varian 7000 FT-IR, a Fourier transform infrared spectrometer, is the instrument being used to take spectra of the sunspots. We learned to install and operate the FT-IR. The instrument was then tested and calibrated in the laboratory environment with an infrared source to verify the proper operation. After calibration the instrument was connected to the Institute for Astronomy's Solar-C telescope on Haleakala with an infrared fiber light feed. Infrared spectra of the sun will be presented.

BIOLOGICAL SCIENCES

BIOCHEMISTRY

F10-SAT

STRUCTURAL BASIS OF TOLL-LIKE RECEPTOR SIGNALING THROUGH TOLL-LIKE RECEPTER ADAPTER PROTEIN

Damien Abreu, Kaury Eisenman, Yorgo Modis. *Yale University, New Haven, Conn.*

The innate immune system utilizes germline-encoded Toll-like receptors (TLRs) to recognize unique pathogen molecules including viral DNA, RNA, and bacterial cell wall components. Upon binding molecular fragments from pathogens on the cell surface or in cellular compartment, TLRs initiate the innate immune response via their intracellular Toll/interleukin-1 receptor (TIR) domain. Adapter proteins such as toll-like receptor adapter protein (TIRAP) and myeloid differentiation protein 88 (MyD88) interact with TIR domains of specific TLRs in signaling. Little is known, however, about how these proteins interact on the molecular level. We aim to use X-ray crystallography to determine the structure of TIRAP in complex with the TIR domains of TLR4, and of MyD88. I will first form a complex of TLR4 TIR domains with TIRAP by mixing purified protein or by coexpression in *E. coli*, and then form the complex with MyD88. Currently, I have cloned a TLR4 TIR domain truncation with a C-terminal histidine tag into a pET21a vector, and I have expressed protein. A point mutation of S180L in TIRAP has been shown to provide resistance against four infectious diseases: infectious pneumococcal disease (IPD), bacteremia, malaria, and tuberculosis. The atomic structure of TIRAP bound to the TIR domain of TLR4 and MyD88 will help us understand how such a point mutation protects against disease. My work has the potential to lead to the design of therapeutic drugs that could act by changing TIRAP structure or inhibiting or strengthening protein complex formation.

F14-FRI

TARGETING OF A FOLATE-CONJUGATED TRINITROPHENYL HAPTEN SHOWS ANTI-INFLAMMATORY ACTIVITY IN RATS WITH ADJUVANT-INDUCED ARTHRITIS AFTER HAPTEN IMMUNIZATION

Wilfredo Ayala-López, Young Su Yi, Sumith Kularatne, Philip S. Low. *Purdue University, West Lafayette, Ind.*

Activated macrophages play a central role in the pathogenesis of rheumatoid arthritis. They are responsible for the initiation and maintenance of the symptoms of the disease. Synovial macrophages from arthritic joints overexpress the folate receptor β, allowing for the targeting of folate conjugated compounds for the diagnosis and treatment of rheumatoid arthritis. We have shown therapeutic efficacy by targeting a folate-conjugated hapten (FITC) to FITC-immunized rodents with experimentally induced arthritis. Here, we have synthesized a folate conjugate of another class of hapten and compared its binding affinity for the folate receptor *in vitro* and its anti-inflammatory activity with that of folate-FITC in rats with adjuvant-induced arthritis. For binding affinity studies, human cell lines expressing the folate receptor were incubated with [^{3}H]-folate and different concentrations of the folate-TNP conjugate, to assess the competitive binding of the drug to the folate receptor. For animal studies, female Lewis rats were immunized three times before the induction of arthritis with heat-killed *Mycobacterium butyricum* in mineral oil. Rats were treated five times a week with folate-FITC or folate-TNP for a period of 35 days. Assessment of therapeutic efficacy included the analysis of arthritis score, paw volumes, bone erosion, splenomegaly, among other therapeutic endpoints. Folate-TNP had a similar efficacy as that of folate-FITC in the reduction of arthritis score, paw volumes, bone erosion, and splenomegaly. The data presented herein supports the concept that folate-hapten targeted immunotherapy can effectively treat experimental models of rheumatoid arthritis.

F10-FRI

ANTIBIOTIC EFFECTS ON THE RATE OF GROWTH OF *ANAPLASMA MARGINALE* IN ENDOTHELIAL CELL

Xochil Galeano Ubeda, Anthony F. Barbet, Liliam Corby. *University of Florida, Gainesville, Fla.*

Anaplasma marginale is an obligate intracellular bacteria that targets erythrocytes in cattle. It invades them and multiplies inside causing anemia, fever, weight loss, abortion, respiratory distress, and often death. The disease is most commonly transmitted by ticks. The objective of our experiment is to observe the effects of Spectinomycin and Chloramphenicol on the rate of growth of *Anaplasma marginale*. Recent studies have proved that *Anaplasma marginale* can also infect endothelial cells *in vitro* which it can suggest that vascular endothelium can be involved in symptoms caused by the bacteria. Due to this, the host cells lines used in this study were endothelial rhesus monkey cells (RF6A). 20 uninfected T-25 flasks were grown, infected with the bacteria, and subsequently the following concentrations were added: Spectinomycin 100 μg/ml to 4 flasks, Spectinomycin 200 μg/ml to 4 flasks, Chloramphenicol 10 μg/ml to 4 flasks, Chloramphenicol 50 μg/ml to 4 flasks, and no antibiotics to (negative control) 4 flasks. The variations in concentrations derive from previous studies where these concentrations proved to be effective. In order to follow the effects of the antibiotics, cytospin, cell counting, and DNA extraction will be performed every 8 days after adding antibiotics from 5 randomly picked flasks. Once all the flasks have been processed, Real Time PCR will be done to obtain a quantitative analysis of the rate of growth of the organism. The results of this study will be of importance in the development of new treatments for anaplasmosis.

F9-FRI

CHARACTERIZATION OF *THERMUS THERMOPHILUS* ADPGLUCOSE PYROPHOSPHORYLASE

Jacob Gonzalez, Go Watanabe, Christopher R. Meyer. *California State University, Fullerton, Fullerton, Calif.*

ADPGlucose Pyrophosphorylase (ADPG PPase) catalyzes a key reaction in glucan synthesis and is regulated by allosteric metabolites. Little is known about thermophilic forms of this enzyme. Our lab has successfully expressed and purified the recombinant enzyme from *Thermus thermophilus* HB 27 and collected kinetic data at 75˚C. The present study extends the kinetic data set to include 37˚C and alternative nucleotide specificity. Also, three unique prolines in the sequence were identified compared to other ADPG PPase, which may provide structural rigidity and account for heat stability. Kinetics studies were carried out by initiating the reaction in the ADPG synthesis direction and monitoring the formation of [^{14}C] ADPG from [^{14}C] G1P. Unexpectedly, the V_{max} at 37˚C was ~1-fold lower then measured at 75˚C, holding ~70% of its catalytic activity. The $S_{0.5}$ for ATP and Mg^{2+} in the absence of activators (G6P, FBP, and F6P) were in fair agreement with the results obtained at 75˚C. The $S_{0.5}$ for G1P in the absence of activators decreased ~5-fold, which may account for the unusual catalytic efficiency. The specific activity for CTP, GTP, UTP, and TTP were determined to be 0.6%, 0.3%, 0.15%, and 0.001%, respectively, of the activity with ATP as a substrate. Interestingly, the fold-activation increased dramatically for CTP and UTP, to ~9 and ~30-fold by FBP, respectively. The P100A, P122A, and P195A mutations were successfully generated by site-directed mutagenesis. Detailed heat stability tests as well as probing the effects of double and triple proline substitutions are in progress.

F12-FRI

A COMPARATIVE STUDY OF TWO pLDH MALARIA TESTS

Amelia Hilgart, Jessica Bryant. *University of New Mexico, Albuquerque, N.Mex.*

The high prevalence of malaria in sub-Saharan West Africa is one of the causes of morbidity and mortality in pregnant women of the area. Although microscopy is the gold standard for the diagnosis of malaria, the malaria parasite has a tendency to sequester in the placental tissue making detection by standard microscopic methods difficult. Microscopy also requires a trained pathologist to read the blood film slides. Other methods based on the detection of *Plasmodium* LDH(pLDH) have been developed and are suitable for use in the field. This study was conducted to compare two different pLDH methods, the FluoroMal Falciparum/Pan Malaria Test and the *CareStart*™ Malaria pLDH test. One-hundred sixty three pregnant women in Nigeria were recruited for the study from Jos University Teaching Hospital (JUTH) antenatal clinic in Jos, Nigeria. The malaria parasite was detected in 13 women (8.1%) by the FluoroMal Falciparum/ Pan Malaria Test and 6 (3.7%) by the *CareStart*™ Malaria pLDH test. The data suggests that the FluoroMal Falciparum/ Pan Malaria Test assay is more sensitive and can determine the malaria parasite at a lower parasite load than the *CareStart*™ Malaria pLDH assay. PCR analysis will be used to determine which test was, in fact, more accurate.

F9-SAT

SMOKING AND PARKINSON'S DISEASE: DOES NICOTINE AFFECT α-SYNUCLEIN FIBRILLATION

Monica Muniz, Anthony Fink. *University of California, Santa Cruz, Santa Cruz, Calif.*

Alpha-synuclein is a presynaptic protein that is abundantly distributed in the brain. It is a natively unfolded protein but in patients with Parkinson's disease, it adopts a polymerized conformation known as amyloid fibrils. The exact mechanism of Parkinson's disease pathogenesis is not understood but fibrillation of α-synuclein in dopaminergic neurons in the substantia nigra is believed to play a major role. Epidemiological studies have shown that smoking can lessen the incidence of Parkinson's disease, indicating that smoke may contain chemicals that are neuro-protective. The kinetics of α-synuclein fibrillation have been studied in relation to five different compounds found in cigarette smoke: anabasine, cotinine, hydroquinone, nicotine, and nornicotine. An *in vitro* assay based on the fluorescence of the dye Thioflavin T when it binds to fibrils was used to monitor the rate and extent of fibril formation. Our results will show if these compounds affect the rate of fibrillation: if they decrease fibrillation it could explain the positive effects of smoking on Parkinson's disease.

F8-SAT

CASPASE ACTIVATION INDUCED BY AN IMMUNOTOXIN TARGETING THE HUMAN TRANSFERRIN RECEPTOR IN MALIGNANT B-CELLS

Isabel I. Neacato, Tracy R. Daniels, Manuel L. Penichet. *University of California, Los Angeles, Los Angeles, Calif.*

We previously developed a mouse/human chimeric antibody fusion protein composed of avidin genetically fused to a human IgG3 specific for the human transferrin receptor (hTfR) as a universal delivery system for cancer therapy. We unexpectedly discovered that anti-hTfR IgG3-Av alone possesses a strong intrinsic anti-proliferative/pro-apoptotic activity against certain hematopoietic malignant cell lines. Importantly, this cytotoxicity can potentially be enhanced by conjugation to biotinylated therapeutic agents. In fact, we have recently demonstrated that the antibody fusion protein conjugated to biotinylated saporin (b-SO6), a toxin derived from the *Saponaria officinalis* plant, increases the apoptotic activity in sensitive cells (IM-9) and sensitizes cells that previously showed resistance to the antibody fusion protein alone (U266). The goal of this study was to evaluate the activation of multiple caspases in the malignant B-cell lines IM-9 and U266 in order to elucidate the pathway by which anti-hTfR IgG3-Av/b-SO6 induces cell death. Using a fluorogenic caspase assay to measure caspase activation, we found that anti-hTfR IgG3-Av/b-SO6 enhances the cytotoxicity in IM-9 cells and sensitizes U266 resistant cells by inducing apoptosis through activation of caspases 2, 3, 4, 8, and 9. More importantly our studies show, for the first time, that apoptosis is induced through a non-classical pathway that involves the early activation of caspases 2, 3, and 4. These studies are important in our understanding of the cytotoxicity of anti-hTfR IgG3-Av/b-SO6, an immunotoxin that can be potentially used in the treatment of B-cell malignancies such as multiple myeloma.

F13-FRI

DEPHOSPHORYLATION OF THE RETINOBLASTOMA PROTEIN

Busola Oluwole, Rachel Steinhardt, Seth Rubin. *University of California, Santa Cruz, Santa Cruz, Calif.*

The Rubin lab deals with understanding biochemical mechanisms that control the cell cycle. Specifically, we deal with the proteins that control entry into the S Phase. E2F is a family of transcription factors that activate genes necessary for DNA synthesis. Retinoblastoma (Rb) and related "pocket proteins" bind to E2F to inhibit transcription until the cell is ready to begin S phase. The activity of Rb, specifically its ability to regulate E2F, is controlled by a chemical modification known as phosphorylation. In the active state, Rb contains no phosphate groups and can bind and inhibit E2F. Immediately preceding S phase, phosphate groups are added to the protein such that its interaction with E2F is disrupted. Following cell division, Rb is returned to an unphosphorylated state so it can bind and inhibit E2F until the cell is ready to begin another round of replication. Dephosphorylation is achieved by removal of phosphate groups on Rb by an enzyme known as protein phosphotase 1 (PP1). A focus of our lab is to further explore the Rb-PP1 interaction to understand how PP1 recognizes and binds to Rb. Inactivation of the retinoblastoma gene is implicated in several types of cancers such as retinoblastoma, a tumor of retina. Our lab uses X-ray crystallography to acquire atomic resolution structures of protein complexes and nuclear magnetic resonance (NMR) to study protein structure and protein-protein interactions.

F11-SAT

DEVELOPING A CELL-ADHESION MICROARRAY ASSAY TO IDENTIFY NOVEL T CELL INTERACTIONS USING A PROTEIN LIBRARY

Peter Ramirez[1], Irene Tom[2], Lino Gonzalez[2]. *[1]University of California, Santa Barbara, Santa Barbara, Calif., [2]Genetech, Inc., South San Francisco, Calif.*

T cell activation is primarily mediated by the T cell antigen receptor, but many other proteins on the T cell surface are necessary to regulate T cell activity. Though many of these interactions have been described, there are potentially unidentified proteins on T cells that modulate their activity. Protein microarrays have been successfully used to detect specific interaction and adhesion of intact cells to panels of peptides, proteins and glycans. Protein microarrays offer a high-throughput method for evaluating many interactions simultaneously while requiring only small sample quantities. In this study, a protein microarray cell-adhesion assay will be developed to look for new ligand/receptor interactions that may be involved in T cell activation. A microarray of an extracellular protein library which contains ~1100 unique proteins will be generated. This array will then be probed with Jurkats, a leukemic T cell line, to identify proteins that bind to these cells at different stages of activation. To develop this high-throughput cell-adhesion assay, we will be evaluating microarray surfaces for reproducible immobilization of SPDI proteins, optimizing conditions for cell adhesion with minimal background and verifying hits for binding specificity. This cell-adhesion microarray assay will be useful for cell profiling studies to identify novel interactions with other cell lines.

F11-FRI

CHARACTERIZATION OF THE INTERACTION OF THE YEAST PROTEINS DAP1 AND ERG11

Amber Smith, Theodore Holamn, Nadine Gassner, Alisha Thompson. *University of California, Santa Cruz, Santa Cruz, Calif.*

Previous research has strongly suggested that there is an interaction between the damage resistant heme binding protein Dap1 and the cytochrome P450 protein Erg11. Previous studies have hypothesized that Dap1p could be an initiator to Erg11p[1]. This interaction is important because it has been demonstrated that Dap1p mutants are sensitive to antifungal agents which are direct inhibitors of the Erg11 enzyme by an unknown mechanism. These findings suggest that Dap1p maybe a good target for both antifungal drug recovery and may serve as a model for drug resistance in mammalian cells. The focus of our research will be to express and purify both Dap1p and Erg11p. We have successfully expressed Dap1p with a pET28a vector and purified it to high homogeneity. Initial expression trails for Erg11p in a pET28a vector did not yield soluble protein. Next we will express Erg11p with a vector traditionally used for P450 expression. Once expressed a NiNTA column will be used for initial purification. The binding conditions of Dap1p to Erg11p will be identified using Western blots and size exclusion chromatography. We will measure binding affinities with isothermal titration calorimetry. These results will inform the design of future experiments to identify novel chemotherapeutic agents and models.

F8-FRI

IDENTIFYING EGG WHITE PROTEINS USING COUNTERCURRENT CHROMATOGRAPHY AND MATRIX-ASSISTED LASER DESORPTION/IONIZATION TIME-OF-FLIGHT MASS SPECTROMETRY

Jamie Thomas[1], Yoichiro Ito[2], Henry Fales[2], Leticia Cano[2]. *[1]Oklahoma City University, Oklahoma City, Okla., [2]Center for Biochemistry and Biophysics, National Heart, Lung, and Blood Institute, National Institutes of Health, Bethesda, Md.*

To illustrate the utility of countercurrent chromatography (CCC) with matrix-assisted laser desorption/ionization time-of- flight mass spectrometry (MALDI-TOF MS) in the separation and identification of proteins in biological samples. CCC is a separation technique that uses centrifugal force and a two phase solvent system to separate compounds. The procedure was tested for protein separations by using a set of protein standards (cytochrome C, human serum albumin (HSA), beta lactoglobulin, alpha chymotrypsin, and trypsinogen). The standards were separated using polyethylene glycol (PEG) 1000 and potassium phosphate as the two phase solvent system. After removing the PEG using a 10 kDa MWCO filter, the standards were analyzed using MALDI-TOF MS. The molecular weights were compared to those found in the NCBI database. A complex biological sample, egg white, was separated using CCC in the same manner as the protein standards. The protein standards were separated in the order: cytochrome C, alpha chymotrypsin, beta lactoglobulin, and trypsinogen. The egg whites were separated in this order: lysozyme, ovalbumin, and lysozyme C. The NCBI database confirms that these proteins are in egg whites. This is the first time that MALDI-TOF MS has been used with CCC. These experiments show that CCC can be used to separate proteins in biological research.

F13-SAT
INHIBITION OFHIV-1 REVERSE TRANSCRIPTASE BY RNA APTAMERS
Angela Whatley, Donald Burke, Rebecca Chitima-Matsinga, Judy Gohndrone, Frankie Rose, Robin Cutler, Dayal Saran, Dan Held. *University of Missouri, Columbia, Columbia, Mo.*

Forty million people are living with HIV world-wide. The current standard of care is the use of highly active antiretroviral treatment (HAART), a multi-drug combination therapy. The implementation of HAART has greatly increased the life expectancy of HIV infected individuals. However, HAART can lead to many problems associated with the toxicity of the drugs. Additionally, HIV has a high mutation rate which can lead to drug resistance over time. These issues highlight the pressing need for alternative therapies for the treatment of HIV. Short RNAs such as aptamers have shown great promise as a new class of therapeutics. RNA aptamers are short RNAs selected for their ability to bind to a specific target. An *in vitro* enzymatic assay was used to identify the most potent aptamers that inhibit reverse transcriptase (RT) from subtype B virus. The most potent aptamers were further investigated for their ability to inhibit RT from subtype A virus. In this study we screened 19 aptamers for their ability to inhibit the enzymatic activity of RT from HIV-1 subtype A virus. Nine of the nineteen aptamers tested were able to inhibit RT from subtype A virus (with IC50 values less than 60 nM). The ability of these nine aptamers to inhibit RT from both subtype A and B virus suggest that they may be good inhibitors of other evolutionarily distinct HIV viruses. This broad-spectrum inhibition suggests the potential of combating rapidly evolving drug resistant HIV. In conclusion cross-clade aptamers may have great potential as possible RNA therapeutics against HIV-1.

CANCER BIOLOGY

F2-SAT
ROLES OF XRCC2 AND XRCC3 ATPASES IN HOMOLOGOUS RECOMBINATION REPAIR OF DNA DOUBLE-STRAND BREAKS
Antonio Abeyta, Leyma De Haro, Jac Nickoloff. *University of New Mexico School of Medicine–Cancer Research Center, Albuquerque, N.Mex.*

DNA double-strand breaks (DSBs) are common types of DNA damage in humans that can be caused by radiation and metabolic processes, including DNA replication. Incorrect repair of DSBs destabilizes the genome, ultimately leading to cancer. Two main repair pathways are non-homologous end joining (NHEJ) and homologous recombination (HR). Defects in two HR proteins, BRCA1 and BRCA2, predispose to breast cancer. It is likely that all HR proteins contribute to genome stabilization and tumor suppression. Two other HR proteins, XRCC2 and XRCC3, are related to the RAD51 recombinase and are implicated in HR initiation; XRCC3 also has late roles in HR. Both XRCC2 and XRCC3 are ATPases. We hypothesize that ATP hydrolysis is important for early and late HR functions. We are constructing an HR substrate that will be integrated into the genome of Chinese hamster ovary cells that lack either XRCC2 or XRCC3. The HR substrate has a DSB target site that is cleaved on expression of the restriction enzyme I-SceI; which will enable us to measure HR efficiency, and HR outcomes such as gene conversion and crossing-over, to assess both initiation and late-stage functions of XRCC2 and XRCC3. The cells will be co-transfected with the I-SceI vector and expression vectors to complement the XRCC2/3 defects with wild-type or ATPase-defective versions of each protein. HR products will be selected and analyzed by genetic and molecular methods. These studies will provide new insight into HR mechanisms and may reveal new targets to enhance tumor cell killing during radio- and chemotherapy.

F1-SAT
IMMUNOHISTOCHEMISTRY IN CRYOSECTIONED MOUSE INTESTINES
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Colorectal cancer is the third most common form of cancer in the U.S. Mutation of the tumor suppressor gene adenomatous polyposis coli (*Apc*) is an early, if not initiating, event in over 80% of all colorectal cancers. There are over 800 *Apc* mutations that have been identified, most of them causing a protein truncation and at least partial loss of function. Inherited mutations in *Apc* lead to development of colon polyps, some of which will eventually form malignant tumors. However, much remains unknown about the cellular function(s) of APC and how loss of functional APC results in tumorigenesis. APC binds microtubule plus ends, is found at cell junctions and can shuttle in and out of the nucleus. One of APC's best characterized functions is to down regulate cytoplasmic β-catenin. Other functions, including the role of nuclear APC, remain less clear. My research has focused on analysis of the nuclear function of APC in mouse intestines. For these studies, I use a mouse model recently developed in the Neufeld lab in which mutations were introduced to inactivate the two major nuclear localization signals (NLS) of APC, rendering APC unable to enter the nucleus. I use cryosectioning followed by confocal microscopy to observe changes in localization of β-catenin, APC and other proteins, as well as changes in the physiology of mouse intestines. Use of this model will allow elucidation of the role of nuclear APC in tumor suppression under physiological conditions.

F6-SAT

MITOCHONDRIAL PERMEABILITY AND CASPASES 3 AND 7 ACTIVATION ON A431 CELLS TREATED WITH BENZAZOLO QUINOLINIUM SALTS

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In this study we are evaluating the apoptotic induction capacity of Benzazolo[3,2-*a*]quinolinium salts (BQs) in A431 tumor cell lines. Previous studies indicated the citotoxic and mutagenic capacity of BQs in A431 proving cell-drug interaction. In this investigation the main objectives were to determine mitochondrial membrane permeabilization and activation of caspases 3 and 7, pivotal biochemical indicators of apoptosis. Membrane permeability and caspases activation were determined by fluorescent analysis with MITO PT™ and Magic Red™ fluorescent dyes respectively. For both assays A431 tumor cells were treated with NBQ38, ABQ38, NBQ95, and ABQ95 at 24, 48, and 72 hours. A valinomycin positive control was included for membrane permeabilization and recombinant human caspase 3 with a C-terminal histidine tag as positive control for caspases activation analysis. Fluorescence microscopy analysis showed that mitochondrial membrane was permeabilized with all four BQs drugs at 72 hours. The MITO PT™ fluorescence analysis results indicated that in comparison with none exposed, BQs induced from 25% to 60% membrane permeabilization on exposed cultures. Preliminary treatments with NBQ38 presented the strongest mitochondrial damage. Results on the Magic Red™ fluorescence emission for active caspases 3 and 7 revealed that treated cells have no significant difference on caspases activation when compared to the control group. This preliminary study suggests that the main apoptotic route involves permeabilization of the mitochondrial membrane without activation of caspases 3 and 7. Future assays will include analysis of caspases 8 and 9 to determine if the apoptotic route is via the extrinsic or intrinsic pathway.

F4-SAT

ALTERATIONS IN C-MYB LEVELS CHANGE HEMATOPOIESIS

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Hematopoiesis depends on distinct threshold levels of the transcription factor c-Myb. This has been shown in c-myb knock out mice, which die during embryogenesis due to insufficient hematopoiesis. However, little is known about how hematopoiesis may change in humans due to decreased levels of c-Myb. In this study, short hairpin RNAs were used to decrease the amount of c-Myb in K562 cells, an erythroleukemia cell line. Electroporation was used to introduce the short hairpin constructs, and then mRNA levels were analyzed by using real time PCR (RT-PCR). The c-Myb mRNA levels were decreased in the cells transfected with the shRNA constructs, as a consequence levels of cyclin B1, a c-Myb regulated gene, mRNA levels were also decreased. The c-Myb protein levels were also examined and showed a decrease in the amount of c-Myb protein levels from shRNA transfected cells when compared to control K562 cells. These results have shown that the c-Myb protein and mRNA levels can be decreased by using shRNA. Gene expression analysis of human hematopietic cells due to decreased c-Myb levels is the next major aim of this study and will be examined to determine how the gene expression may change and what biologically does this mean for hematopoiesis.

F1-FRI

ROR RECEPTORS INVOLVEMENT IN MUSCLE DEVELOPMENT

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Wnt signaling via beta-catenin independent pathways plays a major role in embryonic development. Experiments using different animal model systems show that this signaling pathway controls tissue polarity and movement. Wnt-5a and Wnt-5b are Wnt family members that are typically thought to signal via beta-catenin independent pathways and are linked to myogenesis. Recently, Ror2 was shown to be a receptor for Wnt-5a. Wnt-5a signals via Ror2 to activate a beta-catenin independent pathway in 293T cells. In somites, Wnt5b, which generally signals via a beta-independent pathway, is expressed in the dorsalmedial lip(DML) of the dermomyotome. Thus, we hypothesize that Ror receptors are involve in muscle development. To test this hypothesis, we first performed RT-PCR of RNA isolated from somites of stage I-III somites in HH stage 10 chick embryos. Using this approach, we identified transcription of both Ror1 and Ror2. We also performed RT-PCR of RNA isolated from C2C12 myoblast cell line. These experiments also showed the presence of Ror1 and Ror2 in myogenesis. At the present time, we are performing section *in situ* hybridization with probes for Ror 1, Ror2, and Wnt-5 in order to locate specific expression in somites in chick embryos.

F4-FRI

ANTI-TUMOR AND ANTI-ANGIOGENIC EFFECTS OF TISSUE INHIBITOR OF METALLOPROTEINASE (TIMP)-2

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The extracellular matrix (ECM) plays a central role in the maintaining the structure and function of normal tissue. In pathological conditions such as cancer, the turnover of the ECM is essential for tumor progression and angiogenesis, the formation of new blood vessels, and to further the metastatic process. Thus, inhibition of ECM-proteolysis is pivotal in controlling the growth of tumors. The tissue inhibitors of matrix metalloproteases (TIMPs) are the endogenous inhibitors of Matrix metalloproteases (MMP), the main proteases involved in the ECM-turnover. TIMP-2 is one of the four members of the TIMP-family. In this study, the effects of TIMP-2 on the growth of melanoma tumor cells *in vitro*, and on an *in vivo* xenograft model of human-lung carcinoma were determined. TIMP-2 had a direct effect on tumor cells, inducing their differentiation, as well as promoting cell death by apoptosis as determined by microscopy and immunoflourescence techniques. TIMP-2 significantly reduced tumor-cell proliferation in a concentration-dependent fashion. In mice, overexpression of TIMP-2 in lung-tumor cells significantly reduced tumor size and extended survival of mice as compared with mice xenotransplanted with tumor-cell controls. These results support TIMP-2 as a regulator of ECM-proteolysis and their potential agent for cancer treatment.

F3-FRI

IN SITU PROFILING OF ASTROCYTOMA SIGNALING PATHWAYS

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Cancer is an acquired disease of somatic genetic/epigenetic alterations, the end result of which is dysregulated expression or function of key signaling pathway proteins. Astrocytomas, the most common intracranial malignancies, are a diverse group of brain tumors with potentially dismal patient outcomes for which few effective drugs are available. Genetically-engineered mouse (GEM) models of astrocytoma represent a powerful technique for defining the molecular genetic abnormalities involved in tumor initiation and progression and for preclinical evaluation of targeted chemotherapeutic agents. GEM astrocytoma models have been generated based on the recurrent aberrations observed in the human tumors, including cell cycle (RB), mitogenic (RTK-RAS-MAPK), and motogenic (PI3K-PTEN-AKT) pathways. GEM astrocytomas appear morphologically similar to their human counterparts, but the similarities in signaling pathway abnormalities are currently unknown. To validate their usefulness in preclinical studies, we are performing high-throughput in-situ protein pathway profiling using tissue microarrays and quantitative fluorescence immunohistochemistry to: (1) examine the signaling pathway abnormalities caused by defined genetic lesions in GEM astrocytomas and (2) identify protein biomarkers that can identify human astrocytomas that most closely resemble their GEM counterparts. Integrated "cross-species" molecular characterization of both GEM and human astrocytomas and cultured cells will provide a direct link between preclinical drug development in cell culture and GEM astrocytoma models and rational design of human clinical trials involving only those astrocytoma patients with similar signaling pathway abnormalities.

F3-SAT

ISOFORM SELECTIVE PI3-KINASE INHIBITORS IN BREAST CANCER CELL LINES

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The phosphoinositide 3-kinase (PI3-kinase) signaling pathway is an important regulator of many normal cellular functions, and is deregulated in many different diseases including cancer. PTEN, Ras and PIK3CA mutations are some of the genetic alterations in this pathway. We hypothesize that these genetic alterations cause different biochemical and biological effects induced by PI3-kinase inhibitors in human tumors. To test this, we analyzed breast cancer cell lines with different genetic alterations and treated them with PI-103 and PIK-108 (PI3-kinase inhibitors), U0126 (MEK1/2 inhibitor), Rapamycin (mTOR inhibitor), and FMK (p90RSK inhibitor). PI-103 was able to inhibit the phosphorylation of pS6 and pPKB causing a G1 arrest in most cell lines examined. In contrast, a cell line expressing activated KRas (MDA-MB-231) showed resistance against PI-103, since it was not able to inhibit pS6 and pPKB phosphorylation or cause a G1 arrest. To determine if the *ras* oncogene provided the resistance of the KRas mutant cell line to PI-103, the *ras* oncogene was transfected into the PIK3CA mutant cell line BT20. In the parental and empty-vector cell lines, PI-103 was able to inhibit pS6 and pPKB phosphorylation. In contrast, in the KRasG12D transfected cell line, PI-103 was not able to completely abolish pS6 and pPKB phosphorylation, and the G1 arrest was reduced. Thus, these results indicate that genetic alterations in the PI3-kinase signaling pathway have the ability to be differently inhibited by PI3-kinase inhibitors in breast cancer cell lines. (Supported by NIH BRIDGE 5-R25-GM48972-08 and UCSF Breast SPORE.)

F2-FRI

DOES REDUCTION OF GLUT1 IN MAMMARY TUMOR CELLS SUPPRESS PROLIFERATION AND ALTER CELL METABOLISM?

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Glucose is essential for energy production and is transported to all the cells of the body to meet their energy needs. Glucose is metabolized to form ATP, the main source of chemical energy for cellular processes. Tumor cells show increased glucose uptake and glucose metabolism compared to normal cells. GLUT1 is a member of the family of proteins that facilitate transport of glucose across cellular membranes; it is the major glucose transporter expressed in tumor cells. Studies of human tumors have shown that there is a significant association between the expression of GLUT1 and clinical outcome. Patients with higher levels of GLUT1 in their tumors have lower survival rates than patients whose tumors express low levels of GLUT1. We transfected two mouse mammary tumor cell lines established from mammary tumors that appeared in MMTV-c-Neu transgenic mice, with five short hairpin RNA (shRNA) vectors directed against GLUT1, in addition to control vectors, to knockdown the expression of GLUT1. Cell lysates were harvested 24, 48, 72, and 96 hours following transfection and the level of GLUT1 quantitated by immunoblotting. One shRNA was best at eliminating expression of GLUT1 in both cell lines. We will determine the effect that loss of GLUT1 has upon glucose uptake, cell proliferation, and apoptosis (programmed cell death). We hypothesize eliminating GLUT1 expression will reduce glucose transport, cellular proliferation, and glucose metabolism in tumor cells. This change may also stimulate apoptosis of tumor cells. These studies will provide evidence whether targeting GLUT1 is an effective anti-cancer therapy.

F5-FRI

BIOLOGICAL TESTING OF COMPOUNDS WITH MEDICINAL POTENTIAL

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A set of newly synthesized indenopyridines have been analyzed for anticancer activity. The compounds were tested for biological activity on Jurkat T-cell leukemia, and HeLa cervical cancer cell lines for apoptosis, cell viability, and cell cycle analysis. These analyses involved the use of flow cytometry and spectrophotometery; through these methods, the compounds were shown to have antiproliferative activity. Specifically, the percent of apoptotic cell death rate was found to be greatly increased after various exposure times to low micromolar concentrations. Exposure of normal peripheral blood lymphocytes to these compounds at the same concentrations result in minimal induction of apoptosis. Through apoptotic effect on cancer cells, these compounds can be considered as a potential anti-cancer drug due to their selective inhibition of transformed cell line proliferation. It is possible that these compounds work as topoisomerase I inhibitors because their polycyclic planar structure may permit them to intercalate into the DNA. The structure-function relationship for indenopyridines will be defined further on a variety of transformed and normal cell lines.

F5-SAT

A PATHWAY SCREEN: IDENTIFYING NATURAL PRODUCT EXTRACTS THAT TARGET THE RHO PATHWAY

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Rho GTPases regulate diverse cellular processes, including cytokinesis, the final step in cell division. The underlying mechanisms by which Rho GTPases coordinate cleavage furrow formation, ingression and cytokinesis completion remain poorly characterized. To address this question, a phenotypic screen was developed that uses automated microscopy to identify natural product extracts that target the Rho pathway using chemical genetics and partial inhibition of Rho in HeLa cells. During the development of the phenotypic screen, an intermediate Rho inhibitor phenotype that gives both the enhancement of binucleate cells and an actin phenotype that is desired. Through a series of parameter analysis performed on the HeLa cells, the screening assay was optimized. Subsequently, the automated microscopy images were analyzed using automated imaging analysis with *CellProfiler*. Natural product extracts that enhanced binucleate cells were identified. Rho pathway-specific small molecules will then be used to dissect the role of Rho signaling during cytokinesis. Misregulation of the Rho pathway has been implicated in many types of cancers. Therefore, Rho pathway-specific small molecules have promising therapeutic potential.

ENDOCRINOLOGY

F7-SAT

IDENTIFICATION, STABILITY AND ISOLATION OF AN EXTRAORDINARY STABLE 46-KDA DISULFIDE-LINKED DIMER OF BOVINE PROLACTIN

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Bovine prolactin (bPRL) is a heterogeneous mixture of protein isoforms that vary in charge and molecular weight. The purpose of this research was to determine if a stable disulfide-dimer of bPRL exists and if so to isolate it for the later assessment of its biological significance. The hypothesis is that the 46-kDa bPRL is a stable disulfide-linked dimer of the 23-kDa monomer of bPRL. The methods used consisted of an analytical SDS-PAGE to separate bPRL isoforms. Next, western blotting was used to determine if the separated proteins were bPRL isoforms. Once identification was complete, samples of the 46-kDa bPRL were separated via preparative SDS-PAGE and then electroeluted. Fractions of these 46-kDa bPRL samples were then incubated at 95°C for 3 minutes, 30 minutes, 1 hour, 3 hours, and 5 hours in 2-mercaptoethanol to break the presumed dimer into monomers. The reaction products were then separated by analytical SDS-PAGE to detect relative amounts of the 46-kDa bPRL and monomeric PRL in the samples over time. Analytical Native Urea-polyacrylamide gels and Analytical SDS-PAGE were used to isolate and identify the 46-kDa bPRL. Results indicated that as incubation time in the 2-mercaptoethanol increased, the amounts of the 46-kDa bPRL decreased and the amount of the 23-kDa bPRL increased. The schism of the dimer was contingent on time and temperature and the 46-kDa bPRL was purified in native form as shown by analytical SDS-PAGE of excised bands of Native UREA-PAGE bPRL extracts. In conclusion, the 46-kDa bPRL is a stable disulfide-linked dimer that can be broken into 23-kDa monomers by extended incubation in SDS Sample Buffer at elevated temperature. Also, the 46-kDa bPRL can be isolated by native preparative UREA-PAGE.

F6-FRI

GLYCOSYLATED HUMAN GROWTH HORMONE ISOFORM BLOCKS GROWTH OF HUMAN BREAST CANCER CELLS

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Breast cancer incidence among women increased in the 1990s and it continues as a major public health problem manifesting racial and ethnic disparities in mortality. Hormones play a vital role in breast cancer as they stimulate cellular growth. Steroid hormones, such as estrogen have long been associated with increased breast cancer incidence, on the other hand, human growth hormone (hGH) is also correlated with increased incidence of human breast cancer, pointing to a need for development of hGH antagonists to block hGH-dependent breast cancers. Recently, a novel glycosylated 24-kDa-hGH has been isolated, which has potential as a hGH antagonist because the site of glycosylation lies in the receptor-binding site. The objective of this research was to investigate the new untested concept that glycosylated 24-kDa-hGH would impede proliferation of human breast cancer cells. The hypothesis tested was that glycosylated 24-kDa-hGH would produce growth-inhibitory effects in MCF-7 human breast cancer cells. To test this hypothesis, the number of viable breast cancer cells were quantified following a 72 hr incubation in nutrient-rich media at 37°C, in a humidified atmosphere of 95% air, 5% CO2, in the absence of GHs (vehicle control) or in the presence of either 22-kDa hGH or glycosylated 24-kDa-hGH. One-Way ANOVA followed by Student-Neuman-Keuls post-hoc test assessed differences in breast cancer cell proliferation among the treatments. Results demonstrated that glycosylated 24-kDa-hGH significantly decreased the growth of human breast cancer cells compared to the 22-kDa hGH and to the control group, whereas 22-kDa hGH stimulated their proliferation. The importance of this work is that it demonstrates that glycosylated 24-kDa-hGH possesses therapeutic potential as an anti-neoplastic agent for combating human breast cancer growth *in vivo*. Additionally, a new avenue for research regarding breast cancer therapy has emerged. Future research will reveal the signal transduction mechanisms triggered when inhibiting breast cancer cell growth and *in vivo* efficacy of the hormone's ability to reduce tumor size and number in nude mice.

GENERAL BIOLOGY

F46-SAT

TARGETED IDENTIFICATION OF PROTEINS WITH CHANGES IN OXIDATION STATUS

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Oxidative stress plays a role in the process of aging and related diseases. We postulate that identifying proteins with changes in oxidation status will aid in understanding aging and pathways involved in age-related disease. This work involves optimization of a method utilizing immunoprecipation and mass spectrometry to selectively identify proteins that have been oxidized, with

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application to a mouse model of diabetes.The OxyBlot system is used to assess levels of protein carbonyl oxidation by antibody binding and Western blot detection. However, the oxidized proteins are generally not identified, unless by re-probing, restricting the amount of information obtained from the experiment. We took an alternative approach and used the Oxyblot reagents to immunoprecipitate carbonyl-oxidized proteins. We homogenized mouse kidneys and hearts in an EDTA-containing buffer to maintain oxidation status. Samples were derivatized with 2,4-Dinitrophenylhydrazine, then incubated with anti-DNPH antibody and protein A beads overnight. Proteins from washed beads were eluted by boiling in Laemmli buffer and separated by 1D SDS-PAGE. Protein bands were visualized with a stain, then excised, digested, and identified by tandem mass spectrometry and database searching. Optimization was accomplished by investigating parameters such as antibody incubation time and temperature, and volume of protein A beads. BSA oxidized with iron chloride served as a positive control. Oxidation status was verified by western blot. Preliminary experiments in mouse hearts revealed 8 bands with significant changes in oxidation status between NOD and FVB mice. The 40 proteins identified with strong scores were mitochondrial proteins, suggesting that our method is selective.

F26-FRI

THE ANTIMICROBIAL ACTIVITIES OF THE TRADITIONAL HERBAL MEDICINE PU GANG YING

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The purpose of the experiment was to look for antimicrobial activity of a dandelion plant known as Pu Gang Ying (*Taraxcacun officinale)* against gram-negative and gram-positive bacteria. Pu Gang Ying has long been used by Arab, European, and Chinese physicians as a laxative and diuretic. With the ever-growing antibiotic resistance in bacteria, scientists are in a race to find new sources for antibiotics. Thus after extensive research on antibiotics produced by soil bacteria, researchers are turning toward potential antibiotics produced by plants. Aqueous, methanolic, ethanolic, acetone, and methylene chloride extracts of *T. officinale* were prepared. The extracts were filtered, dried, and reconstituted from their respective solvents. The bacteria chosen for the inhibition tests were *Escherichia coli* and *Pseudomonas aeruginosa* (gram-negative), *Staphylococcus aureus* (gram-positive), and *Mycobacterium smegmatis* (acid-fast). A well-diffusion assay was used to test for antimicrobial activity and to determine the minimum inhibitory concentration (MIC). The ethanolic and methanolic extracts inhibited the growth of *S. aureus*, *E. coli*, and *P.aeruginosa* bacteria, in all concentrations; however, the aqueous, acetone, and methylene chloride extracts did not inhibit the growth of any of these bacteria. Antimycobacterial effectiveness will be reported. The MIC for the alcoholic extracts was 2.2 g/mL. These results indicate that dandelion could be useful as antibiotic against gram-positive and gram-negative bacteria.

F49-SAT

DETERMINING EFFECTS OF THE *DINB* GENE ON SPONTANEOUS MUTAGENESIS IN *ESCHERICHIA COLI* USING A TRYPTOPHAN REVERSION ASSAY

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The *dinB* gene in *E.coli* encodes DNA Polymerase IV, a member of a family of polymerases that has been characterized to lack 3' to 5' exonuclease activity and to function in translesion synthesis in prokaryotes and eukaryotes. Expression of *dinB* is induced during SOS repair, but also occurs in moderate concentrations at basal levels. Increased expression of *dinB* was found to promote mutagenesis at undamaged λ phage DNA and plasmid DNA, affecting both base-pair substitution and frameshift mutations. The purpose of this study was to investigate the role of *dinB* in spontaneous mutagenesis at chromosomal sequences. We hypothesized that the frequency of spontaneous mutation in the *trpA* chromosomal marker will decrease in *dinB* mutant strains. Using the *trpA23* and *trpA46* alleles we measured the frequency of mutation in $dinB^+$ and $dinB^-$ strains over a 12 day incubation period on minimal media. Revertants were then qualitatively categorized according to mutation classes using the indole glycerol phosphate accumulation test. To further differentiate among basepair substitutions within the same phenotypic class the *trpA* gene was sequenced. The results showed that spontaneous mutation frequencies decreased in *dinB* double mutants 5-fold for *trpA46* and 2-fold for *trpA23*. The decrease is expected to be represented by A:T to G:C transitions and by A:T to T:A transversions, which will be confirmed in three weeks by sequence analysis. The results indicated that the *dinB* gene contributes to spontaneous mutagenesis at certain chromosomal sequences by preferential mutagenesis of A:T base-pairs. (Supported by NSF–REU grant #DBI-0647160.)

F53-SAT

KUPFFER CELL DEPLETION BY LIPOSOMAL CLODRONATE PREVENTS HEPATIC MRP4 INDUCTION FOLLOWING ACETAMINOPHEN EXPOSURE

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Increased expression of efflux transporters has been documented with hepatic damage of varying etiologies. The multidrug resistance-associated protein 4 (Mrp4) is the most significantly up-regulated transporter in mouse liver after toxic administration of acetaminophen (APAP). Mrp4 levels are also increased in human liver following APAP overdose. While expression profiles of transporters following APAP hepatotoxicity are well-characterized, the signaling pathways contributing to these changes remain unknown. We hypothesized that Kupffer cell (KC)-derived mediators participate in the regulation of hepatic transporters. To investigate this, C57BL/6J mice were pretreated with liposomal clodronate (0.1 ml i.v.) to deplete KCs and then challenged with APAP (500 mg/kg i.p.). Hepatic Mrp4 protein expression was determined by western blot and immunohistochemistry. At 72 hours after APAP dosing Mrp4 levels were increased by 33-fold in mice receiving empty liposomes. Immunohistochemistry showed that Mrp4 staining was confined to centrilobular hepatocytes. Depletion of KCs by liposomal clodronate increased susceptibility to APAP hepatotoxicity. Remarkably, KC depletion completely prevented Mrp4 induction by APAP. These findings show that KCs protect the liver from APAP toxicity and that KC mediators released in response to APAP are responsible for Mrp4 induction. Enhanced Mrp4 expression may represent a compensatory response to enhance the elimination of mediators of tissue injury and bile constituents from an injured liver. Alternatively, Mrp4 induction might augment the secretion of signaling molecules for tissue repair from injured hepatocytes.

F45-SAT

CALCIUM PROPIONATE ADDITION DOES INFLUENCE *IN VITRO* FIBER DISAPPEARANCE OF GAS PRODUCTION

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Improving nutritional status of range cattle while grazing dormant forage can improve animal productivity. The inclusion of calcium propionate has been shown to improve reproductive performance in young range cows. The objective of this study was to determine if dietary supplement containing calcium propionate improved neutral detergent disappearance (NDF) from diet samples *in vitro*. We hypothesized that calcium propionate will enhance the microbe's metabolism and will increase gas production. Treatments were applied to triplicate *in vitro* tubes in two separate trials. Treatment mimicked feeding 0, 40, or 80 g of calcium propionate to 500 kg range cows. Diet samples of dormant vegetation were collected via ruminal evacuation and incubated in the presence of buffered ruminal fluid that approximated saliva. *In vitro* tubes were incubated in a 39 C shaker for 48 hours. After incubation, samples were dried, weighed and analyzed for NDF. Disappearance was 36.2%, 36.9%, and 37.2% for 0, 40, and 80 g, respectively. Gas production was 300, 320, and 317 mL. These results indicate that the inclusion of calcium propionate has little influence on NDF disappearance or gas production. Therefore improvement in animal performance when fed calcium propionate occurs from a mechanism other than influencing the activity of the ruminal micro flora. (Supported by NIH Bridge grant R25 GM R25 GM48998.)

F27-FRI

DO ALDEHYDES IN DIATOMS AFFECT GROWTH AND SURVIVAL OF SEA URCHIN LARVAE?

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Marine diatoms contain a variety of chemicals, some of which may reduce predation by planktonic grazers. The objective of my study was to determine whether aldehydes in diatoms affect the ingestion rate and growth of green sea urchin larvae (*Strongylocentrotus droebachiensis)*. I fed the larvae one of three diets: (1) *Dunaliella tertiolecta* (a non-toxic green phytoplankton species), (2) *Skelotonema costatum* 2092 (a diatom with low aldehydde content), or (3) *S. costatum* 1332 (a diatom with high aldehyde content). To measure effects of the aldehydes on ingestion rate, I added polystyrene beads to cultures of *S. droebachiensis* larvae with one of the three diets treatments and counted the number ingested by larvae in that treatment. To determine the effects of aldehydes on growth, I measured lengths of the anterolateral arms, postoral arms, preoral arms and midbody of larvae in each diet treatment. Diet did not affect rates of ingestion; larvae in all treatments ate similar numbers of beads. I saw, however, differences in morphology of larvae based on their diet. Larvae were largest in the *Dunaliella tertiolecta* treatment as expected, but there was no difference in the two *Skeletonema costatum* treatments. I concluded that the aldehydes present in *Skeletonema costatum* are probably not effective defenses against grazing by larvae of sea urchins.

F54-FRI

THE ASSOCIATION OF CRB1 AND CRB2 MUTATIONS WITH RETINAL DISEASES AND THE COMPARE OF THE MUTATIONS WITH OTHER ORGANISMS

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Some diseases are the result of mutations of amino acids in genes. Retinitis pigmentosa (RP) and Leber congenital amaurosis (LCA) are the product of mutations in the crumbs homolog 1 (CBR1) gene. RP causes retinal degeneration and people experience a gradual decline in their vision because photoreceptor cells die. LCA is a degenerative disease that appears at birth or in early months of life that results in a severe loss of vision. The crumbs homolog 2 (CRB2) gene is expressed in kidney, fetal eye, ARPE-19, RPE/choroids, retina, and brain. We used the translation of amino acid of CRB1 and CRB2 to located mutations mentioned in the literature. Then we used the Sorting Intolerant From Tolerant (SIFT) program, and observed its predictions whether mutations are tolerated or not tolerated and a score for each prediction. We determined the categories of amino acids, determined the amino acids at sites homologous to the disease sites using the sequences of human, macaque, mouse, opossum, zebra fish, and fruit flies. Then we found the Grantham distance between the original amino acids and the mutations. When we use SIFT, some mutations appear to be tolerant. In my opinion, if they all are disease-associated mutations then they all should be intolerant. We compared the organism's original amino acid with CRB1 and CRB2 and found that some organisms like macaque, mouse opossum, zebra fish and fruit flies possess some CRB 2 mutations that human have. This could be used to make studies and compare diseases of the retina.

F55-SAT

CORRELATION BETWEEN LDL-DELIVERY SYSTEM, SUBCELLULAR DISTRIBUTION AND PDT EFFICIENCY OF HYPERICIN IN U-87MG CELLS

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Low-density lipoproteins (LDL) play a key role in the delivery of hydrophobic photosensitizer to tumor cells in photodynamic therapy (PDT). Hypericin (Hyp) is a natural photosensitizing pigment, which displays an antiproliferative and cytotoxic effect on tumor cells. The dependence of the uptake of Hyp by human glioma U-87MG cells on the level of expression of LDL receptors has been studied. The results show that the intracellular concentration of Hyp in U-87MG cells in the presence of LDL is proportional to the Hyp/LDL molar ratio. A special role of the LDL receptor pathway for Hyp delivery to U-87MG cells was confirmed by the increase of Hyp uptake and in the situation when number of LDL receptors on the cell surface was elevated. To be able to investigate this behaviour we used methods like flow cytometry, fluorescence spectroscopy and confocal microscopy. Moreover, the co-localization experiments showed the lysosomal localization of Hyp following the uptake and that the concentration of Hyp in these organelles was enhanced in the cells with elevated number of LDL receptors. Finally a correlation between PDT effectiveness, Hyp delivery into the cells (different incubation media, activated and non-activated LDL receptors) and Hyp sub-cellular localization has been investigated.

F49-FRI

EXPLORING MICROBIAL DIFFERENCES IN ORGANIC AND CONVENTIONAL FOODS

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Consumers did not anticipate cancer-causing agents, early maturing of their preteen daughters, and contaminated food recalls when preservatives, additives, and antibiotics were introduced into the agricultural world. Dilemmas of conventional foods have individuals returning to the organic manufacturing of food. Researchers disagree on the benefits of organic products. Therefore, supplementary research needs to be conducted to establish objective facts on the benefits and detriments of organic and conventional productions. This research will compare and contrast the shelf-life, microbial growth, and possible microbial resistance to antibiotics in organic and conventional produce. Subsequently information developed will be connected to the cost of health of the consumer. I hypothesize; organic foods will support the growth of a microbial population more effectively. That there will be a difference in the presence of microbial population between conventional and organic foods and the microbes found on conventional produces will be resistant to selected antibiotics. Selected produce were sampled nine times over three weeks for microbial contamination and streaked onto TSA plates. The plates were examined and quantified for microbial growth. Shelf-life of the products was measured through the increase microbe population. Distinct colonies were isolated and identified to genus through biochemical testing. Identical genra with in each grouping were subjected to antibiotic resistance testing. The anticipated shelf-life results will be connected to the cost of food. The microbial and antibiotic resistance will be correlated to the health of the consumer. In conclusion, the advantage and disadvantage of conventional and organic produce will be examined.

F47-FRI

MEIOTIC RECOMBINATION IN FISSION YEAST

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In the fission yeast *Schizosaccharomyces pombe,* the formation of DNA double strand breaks (DSB) by Rec12 is necessary to initiate meiotic recombination. In this study we look at two factors that can affect the formation of DSBs. In the first experiment, we nullified Rec12, belonging to the Spo11/Top6A topoisomerase family, to abolish DSBs and recombination. A mutation in *rad2*, encoding a homolog of the FEN-1 flap endonuclease, suppresses the *rec12* mutation and restores recombination levels without the formation of observable DSBs, indicating a novel pathway. We have created a genetic screen using *S. pombe* and a mutant *rad2* library to isolate temperature-sensitive alleles of *rad2*. These conditional *rad2* alleles will help us identify other factors that may be involved in initiating recombination when it does not follow the *rec12* pathway. In the second experiment, two palindromic sequences of DNA, one in each chromosome and 160 bp long, can recombine together at a high frequency. An 80 bp single insertion in one chromosome and the palindrome in the other produced a very low frequency of recombinants. Here we have created an 80 bp single insertion, positioned in the opposite orientation, to determine the frequency of recombination. We expect to see high levels of recombination if DNA homology is required for recombination. More interestingly, if we see low levels of recombination, there may be other factors such as nonhomologous end-joining involved. In the event that this happens, further investigation will be needed to determine the factors required for recombination.

F52-SAT

Resolution of Phylogenetic Patterns Within Monocots

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Monocotyledons, or monocots, are one of two groups of angiosperms that comprise approximately 60,000 species, 92 families, and 12 orders. Exemplary monocots include agaves, grasses, palms, gingers, orchids, irises, and aroids. Most comprehensive evolutionary phylogenetic studies leave numerous relationships unresolved and inadequately supported. Various questions remain for monocots regarding their origin, patterns of morphological divergence, geographic diversification, and ecological radiation. By creating new nuclear monocot multigene phylogenies I can then compare to established chloroplast/mitochondrial multigene phylogenies. Nuclear and plastid genes have different patterns of inheritance; we will analyze conflicts and sources for incongruence before combining all data into a consensus phylogeny. After tissue collections, DNA/RNA extractions, and synthesizing cDNA from taxa across 39 families, I will utilize conserved low copy nuclear genes generated by our lab to construct a nuclear multigene phylogeny. In previous analyses, we identified 13 challenging nodes in a phylogeny of 125 monocots based on several chloroplast /mitochondrial plastid genes chloroplasts. Our primary experimental approach is to generate nuclear multigene phylogenies from sequence data to resolve these 13 ambiguous nodes; with over 100 nuclear gene primers available to screen to find phylogenetic informative variation. After independently constructing gene tree phylogenies for each nuclear gene, conduct incongruence tests, and if appropriate combine all the nuclear genes into a single analysis. I will construct a resolved, strongly supported higher-level phylogeny for the monocots using data from all three genomic compartments (ncDNA, cpDNA, mtDNA). This phylogeny will be used to interpret morphological evolution and ecological/biogeographical patterns among monocot lineages.

F46-FRI

STUDIES ON THE ROLE OF P-BODY FORMATION IN THE DEVELOPMENT OF *SACCHAROMYCES CEREVISIAE* QUIESCENT CELLS

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Quiescence is a poorly understood but universal state of dormant cells that play an important role in the survival of all species, including unculturable microbes, disease-causing microbes like *M. tuberculosis*, and stem cells. When yeast colonies exhaust glucose and other carbon sources, cells divide, leading to the production of quiescent daughter cells and non-quiescent mother cells. Quiescent daughter cells can be isolated because they are denser than non-quiescent cells. Because quiescent cells did not form in mutants lacking some p-body proteins, I hypothesized that p-bodies are important for increased density of quiescent cells. To determine the timing and extent of p-body formation in quiescent and non-quiescent cells, green fluorescent protein fused p-body proteins will be detected microscopically and quantified by flow cytometry. Additional analyses of p-body accumulation in cells of different density, to determine whether there is a correlation between p-body accumulation and density, will be presented.

F53-FRI

WHAT IS THE ROLE OF RAP1 IN CELL ADHESION DURING *DROSOPHILA* EYE DEVELOPMENT?

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Rap1 is a small guanosine triphosphatase (GTPase) known to regulate cell adhesion during development. Cell adhesion is important during development because cells need to be in specific positions in order for tissues and organs to develop and function properly. Because the *Drosophila* eye is genetically flexible, highly organized and, in the early stages, develops in a manner very similar to the mammalian eye, it is a good model system for understanding how Rap1 regulates cell adhesion. We generated marked loss- and gain-of-function Rap1 mutant clones (patches of Rap1 mutant cells surrounded by wild type tissue) in the precursors of the adult *Drosophila* eye. To determine if Rap1 loss-of-function mutant cells lose cell adhesion we measured clone roundness (an indirect effect of differences in intercellular adhesion) by determining the ratio of the clones' area to perimeter. When we compared the average roundness of Rap1 loss-of-function clones to control clones we found no statistically significant difference, which indicates that Rap1 does not modify cell adhesion in this context. For gain-of-function Rap1 clones we used antibody staining to assess expression of various protein markers for processes important for eye development, including photoreceptor cluster spacing, cluster rotation, and photoreceptor and accessory cell recruitment. Even though changes in the normal patterns of expression of the different markers are seen, further data analysis needs to be performed in order to fully conclude in which of these events Rap1 may play a role.

F44-SAT

HUMAN β-DEFENSIN-2 AS CHEMOKINE: POTENTIAL AVENUES TOWARD DEFENSIN-BASED ANTI-CANCER DRUGS

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Broadly defined, β-defensins are small (~40AA) positively charged peptides with well defined structure and broad spectrum antimicrobial properties. Given the high structural homology between chemokines and defensins, it is not surprising that a number of defensins have now been found to act as chemokines. Human β-defensin-2 (hBD-2) has been shown to act as a chemokine for the chemokine receptor, CCR6, which was previously thought to be activated only via the chemokine, CCL20. Incidentally, high CCR6 expression levels are a prognostic for aggressively metastatic hepatic carcinoma and correlate well with short survival times. If the CCR6 binding epitope on hBD-2 can be determined, small molecule analogs bearing this pattern might function well as anti-metastatic chemotherapeutics. The project described here aims to determine this molecular pattern using a structure-activity relationship (SAR) with alanine mutants of hBD-2 and a high information content lab-on-a-chip (LOC) chemotaxis assay. The hBD-2 mutant library was constructed using a novel gene construction method in conjunction with a glutathione S-transferase fusion protein expression system. CCR6-expressing HEK293 cells are utilized in the LOC assay which employs a gradient generator and real-time monitoring of cell migration. In concert with the SAR, quantitative single-cell measurements using fluorescence-assisted cell sorting (FACS) and LOC methods are being used to elicit quantitative data that accurately describes CCR6-mediated chemotaxis.

F44-FRI

LDH GENOTYPES AND FITNESS IN THE LYNX SPIDER *PEUCETIA VIRIDANS* (ARANEAE, OXYOPIDAE)

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We analyzed the relationship between Ldh genotypes and fitness characteristics for the lynx spider, *Peucetia viridans*. We collected 103 female *P. viridans* and their egg sacs from southern California in 2006 and recorded their fitness correlates (carapace width; weight; body condition; egg sac weight; egg number; average egg weight). Ldh genotypes were determined using electrophoresis and the performance of each genotype with respect to the six fitness correlates was analyzed using ANOVA. ANOVA indicated that Ldh^{BB} genotypes produced significantly heavier eggs than Ldh^{AA} genotypes, with Ldh^{AB} genotypes producing eggs of intermediate weight. These results contrast with those for Ldh based on the analysis of *P. viridans* females and their egg sacs collected during 2004 (n=80) and 2005 (n=331). In 2004, Ldh^{AA} genotypes were larger, heavier and produced more eggs than Ldh^{AB} and Ldh^{BB} genotypes, suggesting the influence of selection on the Ldh locus, while in 2005, there were no significant fitness differences among the genotypes. These contrasting results for Ldh over a three year period may reflect the influence of rainfall variation. Specifically, 2003 to 2004 was a below normal rainfall year; the 2004 to 2005 season was the second wettest on record; and the 2005 to 2006 season was near the long-term average. Thus, prey for *P. viridans* were probably harder to find in 2004 and 2006 than in 2005. Since genetic variability-fitness relationships are likely to be more significant and detectable during stressful years, this may have caused the performance differences between Ldh genotypes in 2004 and 2006 (drier years) versus 2005 (wetter year).

F50-FRI
SPECIES RICHNESS AND BIOGEOGRAPHY OF INSECTS IN FORESTS ESTABLISHED ON SILICA SANDS
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Insects constitute one of the most important groups of organisms with an extensive distribution and great diversity. They affect the ecosystems by having important roles in litter decomposition and food webs. However, little is known of species richness and biogeography of insects in an ecosystem established on silica sands. The Reserva Natural de la Laguna Tortuguero, located in the northern area of Puerto Rico, is a protected area that is characterized by soils composed primarily of silica sands. This kind of soil and habitat fragmentation has caused the flora to be limited to those species adapted to a deficiency of nutrients and stress. We selected two study sites that correspond to a gradient of plant species richness, diversity, and abundance, consequently, there is a light and litter gradient. The first site is composed of shrubs and other small plants while the other one has a higher complexity where the trees dominate. We collected the specimens using nets. The insects were preserved, treated according to the specifications of an entomological collection and identified to family. As expected, we found that the open area had more richness of Orthoptera, Coleoptera, and Hymenoptera than the more complex one.

F56-FRI
ADP-RIBOSYLATION FACTOR 1 IS NECESSARY FOR SPINDLE ASSEMBLY IN *XENOPUS LAEVIS* EXTRACT
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The mitotic spindle is crucial for the proper segregation of chromosomes, which is essential for the production of healthy cells. However, the mechanisms involved in the formation of the mitotic spindle are poorly understood. Recent research suggests that membranes may play a role. Microtubule associated proteins (MAPs), which are necessary for normal spindle function, have also recently been found to be membrane associated. Furthermore, high speed *Xenopus laevis* egg extract, which lacks membranes, is unable to form a bipolar spindle. Our hypothesis was that Golgi-derived membrane is directly involved in spindle assembly and function. To test this we used the *Xenopus laevis* extract system, which reconstitutes mitotic spindle assembly and dynamics *in vitro*. Brefeldin A (BFA), a small molecule inhibitor of Golgi-derived membrane, was added to the extract prior to spindle assembly and the results examined using fluorescence microscopy. BFA treatment disrupted proper spindle formation and chromosome segregation. To further test our hypothesis, a dominantly active form of Arf1, the purported target of BFA, was added to the extract and its effects on spindle assembly were also measured. Arf1(Q69L) treatment caused severe defects in spindle assembly and there was a dramatic reduction in the amount of spindles formed. Based upon the available data, we conclude that Golgi-derived membrane is necessary for proper spindle assembly and function.

F50-SAT
HIV ENVELOPE EPITOPE IMMUNIZATION
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In the development of the HIV vaccine we are currently unable to elicit by immunization, antibodies capable of neutralizing a wide variety of HIV strands. Neutralizing antibodies have been found which bind to various epitopes on the HIV envelope. These epitopes vary in prevalence among HIV strands. 4E10 and 447D are two envelope epitopes with high prevalence. The goal is to develop a protein scaffold which holds and presents the 4E10 or 447D epitope in such way that elicits a neutralizing immune response to that epitope. *E. coli* plasmids, which were encoded for specific epitope carrying scaffolds, were brought in from an outside lab. This plasmid was transformed via heat shock into *E. coli* and grown in medium. The *E. coli* was then induced to over express the scaffold sequence of the plasmid. The resulting scaffold was purified and concentrated. If the scaffold expressed in a soluble form is was tested in guinea pigs to check for an immune response. Out of the 52 scaffolds attempted, 25 were expressed and soluble of which 8 were tested for an immune response. Of the 8 tested 2 bound sufficiently to antibodies however this binding did not occur at the epitope region of the scaffold. Thus far none of the scaffolds have elicited an immune response.

F45-FRI
TITRATION OF THE SPINDLE ASSEMBLY CHECKPOINT IN EMBRYONIC CELLS
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During mitosis, the spindle assembly checkpoint (SAC) monitors chromosome attachment to the mitotic spindle, and prevents mitotic progression if even a single chromatid is improperly attached. This checkpoint is vital for proper development, yet in the eggs and early embryos of many animals spindle disruption results in only a moderate delay in mitotic progression. This poor

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response may be due either to a lack of SAC gene expression, or a disproportionately low kinetochore: cytoplasmic ratio that weakens the ability of the SAC to arrest mitosis. To study checkpoint responses during early embryogenesis, we are using eggs and early embryos of the sea urchins *Strongylocentrous purpuratus* and *Lytechinus pictus*. RT-PCR analyses reveal that mRNAs for the SAC proteins are present in the egg and early embryo, but their expression is not uniform in the earliest stages of development. To test the hypothesis that the efficacy of the SAC is a function of the ratio of kinetochores to cell volume, we measured the length of mitotic arrest of control diploid or polyspermic eggs treated with microtubule poisons. Measurements of cells with varying degrees of polyspermy revealed that increased numbers of sperm (i.e., chromosomes and kinetochores) linearly lengthened the time in mitosis. Together, these results suggest that embryonic cells do have a mitotic checkpoint, and efforts are underway to confirm this using dominant-negative mutants of Mad2 to ablate the checkpoint response. (Supported by NIH grants SO6-GM08136 and GM07667.)

F48-FRI

FERTILIZATION TRIGGERS THE PHOSPHORYLATION AND RECRUITMENT OF THE ACTIN-BINDING PROTEIN MOESIN IN SEA URCHIN EGGS

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The binding of sperm and egg sets into motion a series of events that reinitiates the cell cycle and the developmental program. One immediate downstream effect of fertilization is the reorganization of the actin cytoskeleton. In the unfertilized sea urchin egg, the cortical actin cytoskeleton is comprised of a thin layer of actin filaments and short microvilli, which undergo a dramatic elongation following sperm binding. In an effort to better understand how fertilization triggers remodeling of the actin cytoskeleton during development, we examined the localization dynamics and post-translational modifications of the actin-binding protein moesin. Using antibodies raised against the actin-binding domain, moesin was found only on microvilli, but not on microvillar rootlets, consistent with its role as a membrane-cytoskeletal linker. However, moesin was not recruited to microvilli until fifteen to twenty minutes following fertilization, well after microvillar elongation had occurred. In contrast, phosphorylation at threonine 553, which activates actin-binding activity, could be detected as early as five minutes post-fertilization. These preliminary results suggest that while ERM proteins may not be required for the initial elongation of microvilli following fertilization, they might play a significant role in the stabilization and maturation of these actin-based structures. (Supported by NIH Bridge Program grant no. R25 GM R25 GM48998.)

F25-FRI

ANTIMICROBIAL ACTIVITY OF THE CHINESE HERB *OLDENLANDIA DIFFUSA* (BAI HUA SHE SHE CAO)

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The antibiotics available today are widely used, resulting in increased antibiotic resistant bacteria. New sources of antibiotics are needed because the rate of discovery of antimicrobials from microbial sources has declined. Plants have been used as effective remedies in many cultures for centuries, thus these plants are possible sources of antimicrobials. In this study, the Chinese herb *Oldenlandia diffusa* (Bai Hua She She Cao, 白花蛇舌草) was screened for antimicrobial compounds because it has long been used in Asia to treat skin sores, fever, sore throat, appendicitis, and urinary tract infections. An ethanolic extract was prepared with 90 mL 50% ethanol and 25 g ground plant. We screened the extract for antimicrobial activity against eight bacteria and yeast using the well diffusion assay. We determined the minimum inhibitory concentration (MIC) using serial dilutions and compared lysozyme activity of the extract to egg-white lysozyme. The extract was analyzed for sugars, lipids, and amino acids. The carbohydrate-amino acid extract inhibited *Micrococcus luteus*, *Salmonella enterica*, and *Bacillus subtilis.* The MIC against *M. luteus* and *B. subtilis* is 44 mg/mL, and 97 mg/mL against *S. enterica.* It is unlikely that *O. diffusa* possesses lysozyme. The extract was also tested as a possible food preservative and the data are presented. In conclusion, we believe that *O. diffusa* has the potential to serve a role in preventing growth of foodborne pathogens *in vivo* or in foods.

F28-FRI

HIGH-THROUGHPUT SCREENING OF 4,159 YEAST GFP-FUSION STRAINS UNDER DIFFERENT GROWTH CONDITIONS

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Systems biology is based on the comprehensive, quantitative analysis of the components of a biological system as they interact, functionally, over time. This requires integration of data from several levels of cellular organization. Our laboratory studies quiescent (Q) and non-quiescent (NQ) cells from the eukaryotic unicellular organism *Saccharomyces cerevisiae*. We use density-gradient centrifugation to separate cells from stationary-phase cultures into two fractions, which we identify as Q and NQ cells.

Q cells are dense, thermotolerant, unbudded, bright by phase contrast microscopy, contain few mitochondria and contain high concentrations of glycogen. In contrast, NQ cells are less dense, less thermotolerant, are darker by phase contrast microscopy, can be budded, contain mitochondrial and Golgi profiles, and contain little glycogen. Previously we conducted extensive microarray analyses to characterize RNA abundance of these cells in and exiting stationary-phase. This study utilizes the yeast-GFP clone collection from UCSF (Invitrogen) and high-throughput flow cytometry to begin characterizing changes in protein abundance under diverse growth conditions. Each GFP-fusion strain carries a tagged ORF with the coding sequence of *Aequorea Victoria* GFP (S65T). Each distinct GFP-fusion protein has been characterized during exponential growth but not under starvation conditions. Data will be presented on flow cytometry measurements of the GFP-fusion strains under several conditions including characterization of the fusion library under starvation conditions. This represents the first high-throughput analysis (20 to 40 samples/min.) of these strains under a variety of growth conditions and the data will be integrated with other high-throughput data to discover condition-specific pathways. (Supported by NIH MARC Program.)

F51-SAT
ASC DEPLETION IN HELA CELLS BY SIRNA
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Cells respond to pathogens by producing proinflammatory molecules in an attempt to alter the course of infection. One example is the formation of an inflammasome, a multi-protein complex that can activate Caspase-1 which in turn processes the proinflammatory cytokines IL-1B and IL-18. Part of the NALP3 inflammasome which activates caspase-1 is ASC, an adaptor protein necessary for inflammasome function. To study the role of the NALP3 inflammasome during infection of host cells, we would like to produce cells cultures which are unable to produce a functional inflammasome. One technique that can be used is to introduce short interference RNA to reduce host cell ASC, an integral part of the NALP3 inflammasome. Hela cells were grown in a 12 well plates to 70% confluence before treatment with a transfection reagent and ASC siRNA and incubated at 37c for 24 hours. After 24 hours, RNA extraction was performed by using a QIAGEN RNeasy kit, and the RNA measured using a spectrophotometer. The RNA was then converted to cDNA by reverse transcription for use in quantitative PCR, which would allow for checking the relative levels of ASC mRNA. Three independent experiments averaged an ASC mRNA reduction of 75% (compared to treatment with transfection reagent alone). Further experiments can now be carried out in ASC siRNA transfected HeLa to investigate differences in the inflammatory response.

F26-SAT
TESTING PERSIAN HERBAL REMEDIES FOR ANTIBACTERIAL PROPERTIES
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Fighting bacterial infections has always been a challenge for healthcare providers. Since the 1940s, antibiotics provided a formidable weapon against these infections. However, antibiotic usage is selecting for antibiotic-resistance bacteria. Traditional herbal remedies may provide sources for new antibacterial drugs. We tested the antibacterial properties of two Persian herbal treatments: (1) a mixture of *Valeriana officinalis* roots and *Borago officinalis* petals which is used to treat colds and sore throat and (2) quince (*Cydonia oblonga*) seeds which are used to treat sore throat. We prepared aqueous, methanolic, and methylene chloride plant extracts. We tested the extracts against *Staphylococcus aureus* (gram-positive) and *Escherichia coli* (gram-negative) bacteria using the disk-diffusion assay. The diffusion assay determined that the antibacterial agent is best extracted using methanol in both cases. We measured the effect of the methanolic extracts on bacterial growth spectrophotometrically. *E. coli* is inhibited by both *Valeriana-Borago* and quince and *S. aureus* is inhibited by quince. We believe these plants may provide a new antibiotic.

F54-SAT
HUMAN INJURED AIRWAY EPITHELIUM PHENOTYPE STIMULATES HUMAN MESENCHYMAL STEM CELLS TRANSFORMATION
Edna Judith Santillan, Nikita Malavia, Steven C. George. *University of California, Irvine, Irvine, Calif.*

According to the Annual U.S. Prevalence Statistics for Chronic Diseases, "1 of every 4 Americans suffers from asthma and allergies." Important aspects of chronic asthma include airway remodeling and airway epithelial injury/shedding. A hallmark feature of airway remodeling is increased amounts of myofibroblasts and airway smooth muscle (HASM) leading to airway narrowing. Our hypothesis is that the injured epithelial transforms mesenchymal stem cells (HMSC) to a fibroblast or smooth muscle phenotype, which adds to the subepithelial fibrosis or HASM hyperplasia. The normal human bronchial epithelial cells (NHBE) are seeded on 12 well Transwell® inserts and grown at an air-liquid interface for a period of 14 to 21 days to attain muco-ciliary differentiation. HMSC are seeded on 12 well plates at 25,000 cells per well for 24 hours then serum free media is added for 48 hours. After this, the NHBE transwells are co-cultured with the HMSC in NHBE media. The NHBE are then

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injured with a pipet tip every other day for a period of 8 days. The HMSC RNA, protein, and media are collected at days 2 and 8. Western blots and RT-PCR analysis for fibroblast and smooth muscle phenotypes are performed. α-smooth muscle actin protein and smoothelin are expressed in HMSC co-cultured with NHBE. If HMSC do transform to smooth muscle cell phenotype, this will help in developing therapies targeting prevention of the transformation of the HMSC, thereby preventing narrowing of the human airway by HASM deposition.

F51-FRI

THE IMPORTANCE OF E-CADHERIN IN EMBRYONIC STEM CELL HEMATOPOIESIS

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Embryonic stem cells (ESC) have the ability to proliferate and to differentiate into any type of cell found in the body; therefore, they can differentiate into hematopoietic cells which are blood cells. E-cadherin (Cdh1) is an adherens junction protein expressed in ESC that has been shown to be involved in cell differentiation. The role of E-cadherin in murine ESC (mESC) differentiation into cells of the hematopoietic lineage is not well understood, which is the reason for this research. RNA interference (RNAi) was used to silence E-cadherin. Under this condition, β-catenin goes into the nucleus and results in the expression of genes that are associated with differentiation. The green fluorescent protein (GFP) was the marker that was transfected into our RNAi to identify when Cdh1 was being silenced (GFP+) or not (GFP-). Growing embryoid bodies (clusters of differentiating stem cells) for five days results in two cell populations: GFP+ and GFP-. Analysis was done on morphology, Cdh1 gene expression, and differentiation of these cell populations using microscopy, quantitative reverse transcription polymerase chain reaction (RT-PCR) and cell culture techniques, respectively. The purpose of analyzing these populations is to better understand the commitment of ESC to hematopoietic cells. Our results showed that there was no significant difference in morphology or gene expression among the GFP populations giving way for further experimenting while our colony forming assays to determine hematopoietic potential were contaminated preventing further analysis.

F47-SAT

REGULATION OF REPRODUCTION & AGING IN QUIESCENT CELLS FROM *SACCHAROMYCES CEREVISIAE* STATIONARY-PHASE CULTURES

Phillip Tapia, Jr., Ray Joe, Margaret Werner-Washburne. *University of New Mexico, Albuquerque, N.Mex.*

Most cells on earth are in a quiescent or G_0 state. Maintenance of cells in this state, including eggs, neurons, and stem cells, is critical for species survival. For a variety of reasons, quiescence is poorly studied and, thus, it is not yet known what genes are essential for survival in and exit from the quiescent state. We are studying quiescent cells of the yeast *Saccharomyces cerevisiae.* Quiescent cells are daughter cells, formed after glucose exhaustion. They are unbudded, bright by phase-contrast microscopy, dense, and completely synchronous when re-entering the mitotic cell cycle. We examined the role of *sic1* mutants in quiescent and non-quiescent cells because Sic1p is a homolog of p27kip1, which is required for the $G_0 \rightarrow S$ transition in mammalian stem cells. Sic1p regulates replication initiation and is required for rapamycin-induced (TOR-mediated) cell-cycle arrest in yeast. We determined that quiescent cells lacking Sic1p are viable but show a small increase in budding compared with parental cells and 50% decrease in the ability to reproduce at day 7, post-inoculation. Only 2 other mutants have been found that decrease reproduction in quiescent yeast cells, and one of these is thought to be a negative regulator of the TOR pathway. The specific role of TOR in maintenance of reproductive capacity in quiescent cells is extremely interesting because TOR also plays an important role in chronological aging. Further work to examine the role of TOR and the Sic1p complex in quiescent cell reproduction and, potentially, to aging will be presented. (Supported by NIH-IMSD.)

F43-FRI

GENETIC AND PATHOGENIC DIVERSITY OF THE RICE BLAST FUNGUS, *PYRICULARIA ORYZAE*, IN BRAZIL

Dawn Taylor, Morris Levy, Maria Levy. *Purdue University, West Lafayette, Ind.*

The rice blast fungus, *Pyricularia oryza*e, is the most significant pathogen of domestic rice worldwide. Historically, the pathogen has been difficult to manage because of its broad pathogenic variability. However, recent studies have shown that rice blast populations typically are composed of distinct, clonal lineages and that each lineage is incompatible with at least one known resistance gene of rice. We are characterizing the population structure of rice blast in Brazil with the expectation of finding resistance gene combinations that would be most effective in that country. Brazil is the largest producer of rice in the Americas and is suspected of having the most variable population of the rice blast fungus as well. The genetic diversity will be characterized first by DNA fingerprinting (repetitive-probe RFLP profiles) and then with other molecular markers. Lineage arrangements are then determined by phylogenetic cluster analysis. The pathogenic diversity will be determined using inoculation assays of rice lines with known resistance genes, identifying any lineage-specific incompatibilities. Currently, we are studying a sample of 265 isolates that were collected from 1986 to 2003 from throughout Brazilian rice growing regions. Tentatively, we have identified 31 DNA-fingerprint lineages in this sampling. Lineage A, the most common in southern Brazil, is

incompatible with the blast resistance gene, *Pi-ta*. The complete distribution of pathogenic variation among Brazilian lineages will provide more insight into their evolution on the rice germplasm used in Brazil and how best to manage the pathogen genetically through host resistance gene combinations.

F48-SAT

FATTY ACID UTILIZATION BY THE FUNGAL PLANT PATHOGEN *CRYPHONETIA PARASITICA*

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The utilization of fatty acids is important for the development of fungi. Genes encoding enzymes for fatty acid metabolism have been shown to be up-regulated during the infection processes of fungal pathogens of animals and plants. In this study we have examined the capacity of the filamentous fungal plant pathogen, *Cryphonectria parasitic,* to grow on various fatty acids as sole carbon source. In *C. parasitica,* reduced virulence can be obtained by infection with dsRNA viruses of the family *Hypoviridae*. Therefore, we have examined the hypothesis that the capacity to metabolize fatty acids is compromised as part of the virus-infected phenotype. Tested compounds included lauric acid, myristic acid, elaidic acid, erucic acid, and stearic acid. Growth on all substrates was observed except for stearic acid. However, virus infection did not appear to significantly alter the capacity to utilize these compounds. Previous evidence has also shown that G-protein function was partially compromised in hypovirus-infected mycelium. Therefore we have further assessed the growth of *C. parasitica* strains that have been deleted for one or more of the G-protein subunits. Results of growth patterns indicate these pathways are important for fatty acid metabolism. These data indicate that defective fatty acid metabolism is not a major contributor to reduced virulence of hypovirus-infected mycelium, but that G-protein signaling pathways are. (Supported by NIH Bridge grant R25 GM48998.)

F43-SAT

BIOMAGNIFICATION OF WETLAND CONTAMINANTS IN GARDEN SPIDERS

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The purpose of this study was to examine spatial heterogeneity in the heavy metal accumulation in garden spiders, *Argiope trifasciata,* and to assess the impact of heavy metal loads on spider fitness. During October 2006, adult females were collected from three sites at the Ballona Wetlands, a highly degraded urban wetland in Los Angeles. Spiders were measured (carapace width, mm) and weighed (mg) prior to analysis with atomic absorption spectroscopy to yield whole-body metal concentrations (Cd, Cr, Cu, Pb, Zn). Size and weight values were natural logarithm transformed and the procedures of Jakob et al. (1996) were used to generate the residual index (RI, the residuals of body mass on body size), a non-destructive measure of body condition, for each spider. ANOVA tests were used to assess spatial heterogeneity in whole-body metal concentrations among the three sites. Of the five metals, cadmium and chromium were homogeneous among sites, whereas copper, lead, and zinc varied significantly by site with different patterns in each case. Regression analysis for each metal using various groupings of the samples showed significantly negative relationships between dry metal concentrations and spider bodily parameters in four cases (Cd: size, weight; Cd, Cu: residual index). As major invertebrate predators, spiders may bioaccumulate materials from the bodies of their prey. Our results are consistent with such a possibility and suggest that web-building spiders residing in polluted areas may be compromised in terms of fitness.

F28-SAT

FROM LACTONASE TO LACTAMASE: PROMISCUITY AND CHEMISTRY PROMOTING ENZYME CATALYTIC EVOLUTION

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Mechanisms by which genome and proteome complexity have evolved are fundamental questions in evolutionary biology. While the mechanisms by which enzymes evolve and take on new catalytic roles is still unclear, some evidence points to the role of previous catalytic function in promoting the evolution of enzymes to fill new catalytic niches. One classic example is the evolution of beta-lactamases from peptidases and lactonases, which have similar catalytic functions. We asked if one of the 'ancestral' proteins, peptidases and lactonases, could hydrolyze beta-lactams to some degree, however slight. N-acyl-homoserine lactone hydrolase (AHL-lactonase) was chosen because it's a member of the metallo-beta-lactamase superfamily and it contains a fairly large active site that may accommodate new substrates. AHL-lactonase was purified from recombinant *E. coli* and a pH-sensitive colorimetric assay was used to investigate possible beta-lactamase activity of AHL-lactonase. Results show that AHL-lactonase can hydrolyze penicillin. With gene duplication and natural selection driving gene divergence, AHL-lactonase can easily fill this new catalytic niche because its previous catalytic function is so similar. As we further understand the mechanisms governing enzyme evolution, the evolution of proteome complexity may be more predictable than previously understood. Based on these results, future studies can focus on directed and random evolution experiments to improve the lactamase activity of AHL-lactonase.

F27-SAT
WILL YOUR RETINA BURN?
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The retinal pigment epithelium provides a foundation and nutrition for the photoreceptors. However, the retinal pigment epithelial cells naturally develop a substance called lipofuscin which tends to autofluoresce when the retina is exposed to certain intensities of light damaging the retina. If *ex vivo*, or non-living, cells are exposed to various light intensities produced by a commercial ophthalmoscope for time periods at 2.5, 5, 10, and 15 minutes, we hypothesized that the photoreceptors will dim and eventually rejuvenate to appear normal in all cases. In order to investigate our hypothesis light intensities of various commercial ophthalmoscopes were calculated and these instruments were then used to expose various locations of *ex vivo* retinal epithelial cells for the durations of the time specified above. The cells were observed 1 hour, 24 hours, and 48 hours after the exposure to determine whether any dimming has occurred and if any present, how long the dimming lasts. The results of this work and conclusion will be discussed and will hopefully be helpful in determining how intense commercial ophthalmoscopes should be in order to avoid damaging a patient's retina.

GENOMICS AND BIOINFORMATICS

F18-SAT
BIOINFORMATIC AUTOMATION APPROACH TO QUALITY ASSESSMENT OF HIGH THROUGHPUT DNA SEQUENCING DATA
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Systematic management and assessment of the exponential increase of DNA sequence data is a major burden experienced by high throughput genomics research laboratories. The Arizona Genomics Institute produces ~6 Mbp of sequence data per day from a multitude of species and sources. It was proposed to create an automated check system for quality and contamination of the data produced; a pipeline that automatically retrieves sequence code on a daily basis, performs some assessment and reports a summary. This pipeline is a collection of computer codes which automatically: (1) extracts a random portion (10%) of each DNA sequence project produced daily, (2) sends the data to a super computer to perform similarity searches, (3) retrieves outputs from the super computer and extracts and sorts the desired information, and (4) displays summary reports in an easily readable form. Since this pipeline will be used daily, a set of efficient and straightforward tools were needed. We utilized the programming language Perl and BioPerl modules to write the pipeline. These are object-oriented modules designed for the most common bioinformatics needs. The University of Arizona super computer "Aura" was used to perform BLAST analyses on the sequences. The "Aura" computer is used because of its speed and because it maintains updated genbank deposited data sets for which the AGI DNA sequences are compared. We adopted the outputs to confirm species, check for contaminations, and report success. (Funded by NSF Plant Genome Program, Project Number 501877.)

F23-SAT
AMINO ACID SUBSTITUTIONS IN IL2RG IN *HOMO SAPIENS*, *SUS SCROFA*, *RATTUS NORVEGICUS*, AND *CANIS LUPUS FAMILIARIS*
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There are over 30 disease-causing amino acid substitutions linked to IL2RG. Substitutions in IL2RG, interleukin 2 receptor gamma, may cause SCID, severe combined immunodeficiency. SCID is characterized by a fault or defect in a protein that constructs a receptor whose job is to establish communication between immune cells, T cells and B cells. This type of disease is often fatal to humans; yet humans are not the only species that can get this disease. It was found that several other species, including *Canis lupus familiaris*, *Rattus norvegicus*, and *Sus scrofa* can suffer from SCID. All four species have identical amino acids in positions where substitutions were found, with exception of certain positions. *Rattus norvegicus* has different amino acids in positions 98, 230, and 278; while *Sus scrofa* and *Canis lupus familiaris* have only one different amino acid, in position 227. Most of the positions where disease-associated amino acid substitutions were found are in conserved sites. Conserved sites are positions in the gene where amino acids tend to stay the same throughout evolution, meaning that if certain sites have not changed throughout time, they are very important for the protein function in all species. We evaluated each substitution for biochemical severity using Grantham distance. Grantham distance is the distance between the original amino acid and the mutated amino acid. To predict the severity of each substitution, we used a program called SIFT, Sorting Intolerant From Tolerant. SIFT calculates the effect of a substitution by comparing the conserved sites with the mutation.

F22-FRI

FUNCTIONAL GENOMIC ANALYSIS OF SEXUAL DEVELOPMENT IN *NEUROSPORA CRASSA*

Christine Chee, Joseph Kunkel, Charles Sanchez, Mary Anne Nelson. *University of New Mexico, Albuquerque, N.Mex.*

Knockouts (KOs) of each of the ~10,000 genes of the filamentous fungus *Neurospora crassa* are being constructed by the NIH-supported Program Project, Functional Analysis of a Model Filamentous Fungus, Jay Dunlap, PI. One of the goals of this project is to characterize phenotypes for each of the genes in N. crassa. Though *N. crassa* is a model filamentous fungus, little is known about the genes associated with its sexual cycle. The NIH P01 award supports limited vegetative and sexual phenotypic analyses. In a pilot project, we have extended those analyses to include self or homozygous crosses of the KO strains, in order to identify strains with recessive sexual defects. In this pilot project, we have conducted genetic analysis of over 100 KO strains for dominant and recessive sexual development defects, as well as male-specific defects. Initial results showed that about 5% of the KO strains fail to form protoperithecia or female sexual structures, while 3% form protoperithecia but no perithecia (mature fruiting bodies). One KO strain forms perithecia but no sexual progeny (ascospores). Computational and cytological analyses of selected sexual development mutants will be presented, as will models for the roles of the corresponding proteins in normal sexual development. (Supported by the NIH MARC award to CC and the NIH Program Project (P01) award to MAN (Jay Dunlap, PI).)

F20-FRI

IDENTIFYING GENES IN THE RETINAL DIFFERENTIATION PATHWAY OF *DROSOPHILA*

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The retinal differentiation (RD) pathway is responsible for the development of the retina in *Drosophila melanogaster*. This pathway involves a gene called *eyeless* at the top of the pathway, followed by three downstream genes. My project is to identify other genes in the pathway that are downstream of *eyeless*. First, 100 novel genes were found to be induced by *eyeless*. These genes were therefore characterized to possibly be involved in the RD pathway. Second, using piggyBac transposing elements, stocks were generated to contain deletions of each gene. Third, PCR was use to verify the gene deletions in each stock. Next, a series of crosses was done to generate mutant eye cells. These cells express the development of the retina when a particular gene is deleted. If the mutant flies survive to third instar larvae, then antibody staining is done to compare the protein structure to the normal eye. Mutant adult flies are embedded and sectioned to analyze the internal structure of the retina. Five of the gene deletions gave normal eye phenotype; therefore, these genes are not sufficient for retinal differentiation. Furthermore, eight genes when deleted from the *D. melanogaster* genome caused an abnormal eye phenotype, such as rough eyes or no lens formation. Further research on these genes includes, rescuing the gene that was deleted to see if flies with the rescued gene express a normal eye. If so, these genes can be concluded to be sufficient and necessary for RD.

F19-FRI

GENERATION OF THE BEST DELETION LIBRARY: CHLORAMBUCIL VS. GAMMA RADIATION

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By comparing the deletions in mouse and human cancers, to build deletion libraries, critical regions in cancer development may be uncovered, in hopes of isolating genes involved in development. Two means of inducing deletion mutations, chemical and radiation, have allowed for efficient building of deletion libraries, which has sparked novel ways of developing and viewing these genetic deletions and subsequent phenotypic variations. Comparative genomic hybridization (CGH) was used to delineate whether CHL or ionizing gamma radiation, produced a better genomic deletion, for building a library. By crossing 129S1/SvImJ (J129) mice with B6(Cg)- *Tyr^{c-2J}*/J (B6) mice, one of which would receive the dosage of CHL or radiation, 55 samples of DNA were obtained from either snips of the tail or tumor tissue, so the samples may be labeled with Cyanine-3 and Cyanine-5 dye and prepared for a 23K CGH clone-array. The results from the 23K array will be used to confirm and enhance results obtained from a 21K CGH clone-array. After generating a fluorescence ratio graph that shows the gains and losses of copy numbers, by normalizing the data from the scanned arrays, the 23K array should provide, at least, the same results as the 21K array, or at best, deeper peaks, more clone points per peak, and less "noise" from points that do not have copy number gains or losses. Future studies will include developing arrays to provide better coverage, resolution, and sensitivity. These results will allow us to identify tumor suppressor genes and unknown genes that coordinate certain phenotypic responses.

F21-SAT

POPULATION GENETICS AND GENE FLOW OF THE ALASKAN COASTAL SHRIMP *HEPTACARPUS MOSERI* FOUND ON DEEP SEAMOUNTS

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In an expedition conducted by the National Oceanic Atmospheric Administration, several scientists conducted research on seamounts located off the Gulf of Alaska. During this expedition the submersible Alvin was used to gather specimens from deepwater seamounts. We conducted this research to study two questions regarding shrimp collected on the Gulf of Alaska Seamount Expedition. First, are unidentified shrimp collected on several different seamounts located in the Gulf of Alaska *Heptacarpus moseri*? Second, are two shrimp populations collected from different, isolated seamounts genetically different, indicating little gene flow between seamounts, or are they genetically similar, indicating significant gene flow between seamounts? To identify these shrimp we took pictures, weights, and carapace measurements of every individual. Based on the presence of epipods on the maxillipeds and on the first feet, shrimp from both seamounts were identified as *Heptacarpus moseri*. To estimate genetic differentiation of these populations we used the standard procedures from QIAGEN's DNeasy kit to extract DNA. We removed 25 mg of soft tissue from the cardiac regions of each ethanol-preserved specimen for all extractions. PCR was used to copy mitochondrial genes, which will then be sequenced to estimate any genetic differences. The two seamounts are expected to be isolated enough from each other to hinder gene flow between shrimp populations, thus the populations should display significant genetic differentiation. It is important to note that genetic analysis is not yet finished, but will be completed by fall.

F24-FRI

LANGUAGES AND GENES: THE POPULATION DYNAMICS OF SOUTHERN INDONESIA

Kevin Keys. *The University of Arizona, Tucson, Ariz.*

Analyses in macroscopic population dynamics have suggested a good correlation between languages and genes on a global scale. Recent developments have allowed researchers of population genetics to use genetic mutations in microsatellites to clock the genetic history of a group of populations. Likewise, historical linguists can chart the proximity of those populations' languages. It is therefore possible to do similar studies at smaller scales. The Indonesian archipelago, the bifurcation point into western and eastern paths of the Austronesian migration 4500 years ago from Taiwan through the rest of the Pacific, is ideal for this kind of study. This historical human migration can be reconstructed in increasing detail using the following methods. Using Swadesh word lists to compare data from four islands in southern Indonesia to proto-Austronesian, reconstructed language trees plot the historical diffusion of Austronesian languages; these trees may be subsequently compared with phylogenetic trees and cultural data, ultimately creating an accurate picture of how Austronesian peoples populated each island. This process yields new models and techniques in the study of population dynamics useful for further research into population history at the microscopic level. A complete linguistic and genetic analysis of one island, Sumba, points to an Austronesian influx and dispersion from the village of Wunga unevenly throughout the rest of the island; the Austronesian O haplogroup is represented to varying degrees in the genetic admixture. Preliminary results indicate a variance in dispersal patterns but a close correlation of languages to the degree of paternal ancestry in a given population.

F21-FRI

AN ANALYSIS OF *NEUROSPORA* SEXUAL DEVELOPMENT USING REVERSE GENETICS

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With the advent of efficient DNA sequencing and automated predition of gene structures, reverse genetics has become central to functional genomics, in which the roles of the genes and their protein products are directly investigated. The model organism, *Neurospora crassa*, was the first filamentous fungus to have its genome completely sequenced, and yet the functions of more than half of its genes are still unknown. We have initiated a pilot project to indentify and characterize the functions of these unknown *Neurospora* genes, with a particular focus on those that relate to the development of sexual structures. Knockout (KO) strains for each of the ~ 10,000 genes of *N. crassa* are being created by an NIH-supported program. Project award to Jay Dunlap (PI); limited phenotypic characterization of the KO strains is being conducted through this award. We are extending the analysis to include homozygous crosses in order to detect recessive sexual defects. In preliminary work, about 5% of the KO strains made no protoperithecia (female sexual structures) and 3% made no fruiting bodies (perithecia). A relational database was constructed to handle the complex datasets and facilitate analyses. Detailed morphological and computational analyses were conducted with selected sexual development mutants. The results of these analyses will be presented.

F20-SAT

PHANTOM, A NEW FAMILY OF *MUTATOR* TRANSPOSONS

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We previously identified a successful group of transposable elements designated *Phantom* in the genomes of two single-celled eukaryotes *Entameoba invadens* and *E. moshkovskii*. The putative encoded transposase is distantly related to the protein encoded by the canonical transposable elements of the *Mutator* superfamily. To determine the phylogenetic distribution and structural characteristics of *Phantom* elements we undertook a bioinformatic approach to identify related sequences in all taxa currently represented in public databases. Here we present the results of comprehensive database searches of the genome sequences available, which reveal the presence of *Phantom* elements in diverse taxa including stramenopiles, the trichomonad *Trichomonas vaginalis*, the fungus *Candida albicans*, insects, nematodes, the planarian *Schmidtea mediterranea*, cnidarians, urochordates, and mammals including human. We also detected coding sequences distantly related to *Phantom* within the boundaries of elements previously classified as *Foldbacks*. Based on transposase phylogenies, some elements with *Foldback*-like structure group with *Phantom* to form a well-supported monophyletic clade and we propose that they should be allied to the *Mutator-IS256* superfamily of DNA transposons.

F19-SAT

COMPOSITIONAL TRENDS MIGHT IMPROVE RNA SECONDARY STRUCTURE PREDICTION

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RNA secondary structure prediction accuracy needs to be improve, so we can be able to compare predicted structures against known compositional preferences. We want to know whether the four bases of it are differentially abundant in the different structural categories. We have three primary motivations for this analysis: First, we want to test whether a finer grained analysis of the unpaired bases would reveal differences among bulges, loops, and junctions; second, we want to test whether any compositional patterns were specific to rRNA, as previously observed, or were shared between subunits and domains of life; third, we want to test whether the compositional patterns resulted from selection on the biological sequences or would be obtain from any arbitrary sequence of the same composition. If there are consistent differences in the compositions of different structural elements that hold across many types of RNA molecule, we may be able to use these differences to refine the accuracy of secondary structure prediction programs such as BayesFold by testing whether a computed secondary structure matches the known compositional preferences. Also we test wether these differences in response to overall genome GC content hold for finer-grained structural categories, within both large and small subunit rRNAs in all three domains of life, and test whether the differences in response are due to differences in purifying selection in the different regions, or whether they are due to intrinsic differences in the amount of base-pairing expected in the sequences of different composition. The obtained natural rRNA sequences could be used for computer predictions, by stripping out all gaps and secondary structure information from our annotated data. Create randomized versions of our annotated data by shuffling the natural sequences completely, using the Fisher-Yates shuffle algorithm which is in the Python standard library.

F18-FRI

CONSTRUCTION OF BAC CLONE SHOTGUN LIBRARIES FOR COMPARATIVE SEQUENCE ANALYSIS OF THE SHORT-ARMS OF CHROMOSOME 3 OF FOUR *ORYZA* SPECIES

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To gain insight into the understanding of genome biology, that includes speciation, domestication, and gene regulation, a comparative genomics project was assembled within the *Oryza* genus. Specifically, this research compares homologous regions of the short arms of chromosome three from four of 24 *Oryza* species. These species represent diploid and polyploidy genomes: *O. glaberrima* AA, *O. punctata* BB, *O. officinalis* CC, and *O. minuta* BBCC. Physical maps of Bacterial artificial chromosome (BAC) clone libraries from each species were aligned to *O. sativa* pseudomolecules and homologous region BAC clones were selected from each target species. From each BAC clone, which contained the targeted sequence, small insert sub-clone library was constructed; called BAC clone shotgun library. BAC clone shotgun libraries are used to accommodate the limitations of the current sequencing technology which is unable to produce sufficient sequence from large 130 kb BAC inserts, but rather can process the smaller 2 to 3 kb insert sequences of shotgun libraries. To go from BACs to Shotguns, BAC DNA was isolated, sheared into random 2 to 8 kb fragments and end-repaired. Following gel electrophoresis, a range of 2 to 6 kb DNA was selected and purified. DNA was ligated into the high-copy vector, pBluescriptIIKS+, followed by electroporation into competent *E. coli* cells. Analysis of the transformants by insert size checking and sequence homology revealed the quality and utility of the BAC clone shotgun libraries. BAC subclone libraries were further sequenced to deeper coverage and assembled to determine the full sequence of a BAC clone. *(*Funded by NSF Plant Genome Program, Project Number 501877.)

F23-FRI

EVALUATING CA4 GENE MUTATIONS USING SIFT PROGRAM

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Eye diseases are a diverse area. Retinitis pigmentosa is one of the most severe genetic eye diseases. Changes of amino acid have been reported to have an effect on diseases. Why estimate the severity of observed changes instead of other things? If we can predict the severity of those changes we are going to be closer finding techniques to prevent and treat all kind of diseases. Studies of retinitis pigmentosa found sixteen genes that are involved as autosomal dominant factors. One of them is the CA4 gene also knows as RP17. It is located in chromosome 17 at locus 17q23. CA4 is part of the large family of metalloenzymes that catalyzes hydration of carbon dioxide. Mutations in CA 4 can lead to adRP (autosomal dominant retinitis pigmentosa). First we analyzed and aligned the *Homo sapiens* gene with the homologous *Rattus norvegicus* (rat), *Bos taurus* (bovine), and *Gallus gallus* (chicken) genes using a web-based Clustal server. After that we searched for the sites where the mutations occur in humans and compared the contents with the other species in terms of conserved sites. We found that, in this case all disease-associated mutations are reported as "tolerated" by SIFT. SIFT is a program that predict the severity of change in amino acids. Only one mutation is on the border line between tolerated and not tolerated and it is the amino acid at position 14. In terms of the Grantham distance, there are three mutations with high level and three mutations with low level.

F22-SAT

CONSERVED NON-CODING ELEMENTS AS TRANSCRIPTIONAL REGULATORS OF DEVELOPMENTAL GENES

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Many regions of the human genome are highly conserved between mammals. Cross species genomic similarities show that specific gene regions perform basic functions essential to many mammals. Evolution has conserved these genomic regions by allowing few mutations to occur within them. Some of the regions do not appear to code for protein (conserved non-coding elements or CNEs). Of particular interest are the ultra conserved elements (UCEs), defined as regions spanning at least 200 base pairs that are completely conserved in human, mouse, and rat genomes, and the human accelerated regions (HARs), regions highly conserved in mammals but contain a number of human-specific substitutions since our last common ancestor the chimpanzee. Both the UCEs and the HARs are often situated near key developmental transcription factors, prompting the hypothesis that CNEs may play an important role in mammalian development by regulating the expression of their neighboring genes. To test our hypothesis, we have developed an assay which measures the ability of CNEs to regulate transcription of a luciferase reporter gene in mouse embryonic stem cells. The assay confirms that several of those elements are capable of altering reporter gene expression and are likely to act as transcriptional regulators *in vivo*. This study may elucidate not only the biological functions of these CNEs, but may also shed light on important factors in mammalian development. Results will be available September 30, 2007.

F24-SAT

RETROID ANALYSIS OF THE *BOS TAURUS* GENOME

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Retroid agents are single-stranded RNA genomes that utilize the reverse transcriptase (RT) gene to transcribe the ssRNA to dsDNA, which is then integrated into a host organism's genome. These agents are the cause of AIDS (HIV) in humans, as well as bovine Jembrana (BJ) which causes anorexia and lymphadenopathy in *B. taurus*; the mortality rate is about 17%. Additionally, they have recently been shown to carry cellular genes in several plant species, as well as acting as regulatory elements for some eukaryotic genes. A preliminary analysis of the retroid content in the *B. taurus* genome is complete. This analysis provides a representative from the Artiodactyla to the catalog of Eutherian retroid agents, as well as expanding our comprehensive metagenomic study of the retroid content of the Eukaryotic domain. The method of retroid analysis is the Genome Parsing Suite (GPS) (McClure et al., 2005). The GPS program uses the RT protein, which is the most conserved of all retroid genes, to identify putative retroid agents, then extends outward to characterize additional components. By definition any genome that encodes the RT is a retroid agent, with the notable exception of the telomere elongation reverse transcriptase (TERT), which is responsible for nucleotide maintenance at the ends of chromosomes and is classified as a cellular gene. Presented is an analysis of the *B. taurus* retroid content, including the characterization of two novel putative retroid agents.

HEALTH AND MEDICINE

E26-FRI

COX-2 INHIBITS TGF-BETA SIGNALING IN BREAST CANCER

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The expression and function of cyclooxygenase 2 (COX-2) has been linked to the pathogenesis of cancer. COX-2 expression is often increased in breast cancer and is regulated by the transforming growth factor-beta (TGF-beta) cytokine, a growth suppressor deregulated in cancer progression. Normal murine mammary gland (NMuMG) cells do not express COX-2, while metastatic murine breast cancer (4T1) cells express high levels of COX-2 and are highly tumorigenic. TGF-beta induced epithelial-to-mesenchymal transition (EMT) of NMuMG cells significantly increases COX-2 mRNA and protein expression, as measured by the COX-2 promoter-driven luciferase reporter (5.21 ± 0.48 fold increase, $p < 0.05$), real-time PCR (66 ± 30 relative copy numbers, $p < 0.05$), and western blot analysis. TGF-beta-induced EMT of NMuMG cells increases protaglandin E_2 (PGE2) production ten fold through activity of COX-2. Over-expression of COX-2 inhibits TGF-beta signaling of NMuMG cells, as measured by Smad-driven luciferase reporter activity ($20 \pm 10\%$ of control, $p < 0.05$). Likewise, treatment of NMuMG cells with PGE2 activates GSK3-beta and Erk1/2 MAP kinase, and inhibits Smad-driven luciferase reporter activity. Increased beta-catenin transcriptional activity also occurs with higher COX-2 expression, assayed with the TOPflash luciferase reporter. Treatment of 4T1 cells with NS-398, an inhibitor of COX-2, decreases TOPflash reporter activity while increasing Smad-driven luciferase reporter activity. Stable over-expression of COX-2 and its effects on TGF-beta-mediated behavior are currently being evaluated in NMuMGs cells. The loss of TGF-beta tumor suppressive properties may be attributed to the over expression of COX-2 and therefore targeting COX-2 may restore certain tumor suppressive properties.

F15-SAT

MAPPING SHROOM LOCALIZATION IN HELA CELLS TO FURTHER ASSESS ITS FUNCTIONAL ROLE IN CYTOSKELETAL STABILIZATION, CYTOPROTECTION AND MAINTENANCE OF MYOCARDIAL RESPONSE AGAINST THE ONSET OF CARDIAC FAILURE

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Shroom, a PDZ domain-containing F-actin binding protein, has been shown to play an important role in neural tube morphogenesis, primarily affecting seamless closure of the neural tube. Previous work in our lab demonstrated Shroom expression in the embryo and adult heart and upregulation in cardiotrophin-1 (CT1) stimulated adult myocytes. Also, Shroom co-localizes with adherens and tight junction proteins. Since adherens junction proteins have been shown to have a role in the development of dilated cardiomyopathy, it is hypothesized that Shroom might play a role in cell-cell interaction, cytoarchitectural organization, or as a gp130 downstream signaling molecule that promotes hypertrophy and cell survival to prevent the onset of dilated cardiomyopathy. Since little is known about localization of Shroom in non-neural cells and since an antibody to Shroom is not readily available, we propose to create a Shroom-GFP fusion protein expression vector in order to study its localization in different cell types. Initially localization and validation of the expression vector fusion protein will be performed in HeLa cells using fluorescence microscopy. If this works well, similar localization experiments will be performed in cardiac myocytes.

F16-SAT

CHARACTERIZATION OF U_S9 DELETION MUTANT OF HERPES SIMPLEX VIRUS TYPE-1

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Herpes simples virus type 1 (HSV-1) is the causative agent of recurrent cold sores and affects 90% of adults worldwide. HSV-1 is a neurotropic DNA virus that replicates in epithelial cells during lytic infection, enters through nerve ending and spreads to sensory ganglia where it establishes latency. During reactivation virus travels from the neuron cell bodies in the sensory ganglia to cause lesions on epithelial or mucosal cells. Transport of virus from neuronal cell bodies to epithelial or mucosal cells represents spread in the anterograde direction. An HSV-1 envelope protein U_s9 has been shown to play a role in anterograde transport of virus. Our lab has prepared a U_s9 deletion mutant to further evaluate the role of U_s9 in anterograde transport. Here I present the characterization of an U_s9 deletion virus. A growth curve that compares the replication properties of a U_s9 deletion mutant and wild type virus indicates that the U_s9 mutant replicates to titers approximately one log higher then wild type virus. Based on this unexpected finding, I mapped the viral genome of the U_s9 mutant and wild type viruses by restriction digestion to confirm the lack of U_s9 gene in the mutant virus. I also examined the protein profile of U_s9 mutant and wild type viruses using 15% SDSPAGE. Based on the enhanced replication of the U_s9 mutant virus, we postulate that there may be an additional mutation in this strain that enhances virus replication and perhaps viral functions, such as spread in neurons.

E28-FRI

THE ROLE OF NUTRITION IN THE PREVENTION AND MANAGEMENT OF HEART FAILURE

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The effort to find a suitable replacement to methyl tert-butyl ether (MTBE) in gasoline blends has created a new demand for cereal grains in the United States, in which starch from cereal grains is fermented into ethanol. Although other cereal grains, such as sorghum, or barley, can be used to produce ethanol, the predominant cereal grain used for ethanol production in the United States is corn. Distillers grains with solubles (DDG) are co-products from the ethanol production process. As cereal grains are increasingly being used for energy production, it is likely that DDG will be used in human food production. Currently there is limited information on the ramifications of DDG consumption on human health**.** Interest in the lipid components of DDG is increasing, especially in regards to unsaturated fatty acids, which could play a preventive role in many diseases such as CVD. This study demonstrates that rats fed 30% wheat DDG 21 days prior to the mineral oil layering protocol in cardiac myocytes isolated from rat hearts demonstrated reduced ischemic cell death compared to myocytes isolated from rats fed a control diet. Therefore, it is possible that DDG used as a dietary additive may possess some health benefits. We believe research is needed to clarify the role of specific foods such as DDG in the development and progression of heart failure. Therefore this research is significant in that it will identify potential health uses for DDG, there by increasing the value for a waste product of ethanol fermentation.

F17-FRI

MUSCLE SPINDLES, TENDON VIBRATION, AND FORCE CONTROL

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Vibration of a muscle activates muscle spindles and increases afferent feedback to motor neurons. Motor neurons for different muscles may have different responses to this feedback. This exploratory project compared the effects of tendon vibration on motor neuron discharge and force control in the knee extensors (KE) and first dorsal interosseus (FDI) muscles. Vibration was applied to the KE and the FDI of seven young subjects during steady contractions. Muscle force and single motor unit (MU) discharge (intramuscular electrodes) was recorded for vibration (VIB) and no vibration (NOVIB) conditions. The mean, standard deviation, and coefficient of variation (CV) of muscle force and MU discharge rate was measured. Mean force was higher during VIB for KE (2.3% to 3.1% MVC, $P < 0.001$) and FDI (3.5% to 4.9% MVC, $P = 0.13$). The CV of force was similar between NOVIB and VIB for the KE (1.37% vs. 1.30%, $P = 0.73$) and FDI (3.20% vs. 3.50%, $P = 0.57$). MU results are for the KE only. The mean discharge rate tended to increase with VIB (11.44 Hz vs. 11.96 Hz, $P = 0.11$). The CV of discharge rate did not change (8.95 vs. 8.70%, $P = 0.56$) between the NOVIB and VIB conditions. Despite an increase in excitation to the motor neurons during VIB, the variability of KE motor neuron discharge was unaltered. The variability of KE and FDI force was also unchanged. Further study will explore differences between muscles and between young and elderly adults. (Supported by K01 AG19171 to BLT.)

E27-FRI

"SEX IS SACRED": IDENTIFYING FACTORS INFLUENCING SEXUAL HEALTH AND INDIVIDUAL RISK FOR SEXUALLY TRANSMITTED INFECTIONS IN MONTANA'S NATIVE AMERICAN POPULATION

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The state of Montana is home to seven reservations consisting of eleven Native American tribes. Sexually transmitted infection rates reported from the counties with reservations are three to five times higher than the nationally reported rates. Not much is known about the sexual health, sexual behavior and the sexually transmitted infection (STI) dynamics of these Native American reservation communities. Our objectives are to identify the physical, mental, spiritual, and emotional factors influencing individual behaviors regarding sexual health. Survey questions were developed through: (1) a review of existing literature on Native American health, sexual health, and Native American culture and tradition, (2) a review of standard government surveys for relevant questions, and (3) in-depth group discussions regarding Native American culture and lifestyles to develop culturally sensitive questions addressing the factors influencing sexual health and behaviors. A culturally oriented survey questionnaire was developed and will be administered to Native American men and women 18 years of age and older living in Montana. Several questions were taken from the literature. Standard questions developed to measure depression and post traumatic stress disorder were also included. Consultation with Native American elders helped form culturally relevant questions. Community involvement and feedback is essential for developing a culturally appropriate questionnaire.

E27-SAT

IN SEARCH FOR NOVEL ANTI-MICROBIAL DRUGS

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Community-acquired methicillin-resistant *Staphylococcus aureus* (MRSA) is now an established pathogen that is the etiologic agent of skin and soft tissue infections, as well as pneumonia, fasciitis, and osteomyelitis. Strains of MRSA that are resistant to every FDA approved antibiotic are now considered common and often lead to lethal infections. Thus, there is a genuine need to develop novel classes of antibiotics that will target MRSA. By absorbance measurements of *S. aureus* growth rates in a micro titer assay, we screened a library of idole-azo compounds as potential MRSA antibiotics. It was determined that micromolar concentrations of Compound #89 inhibit the growth of MRSA, as well as other strains of *Staphylococci.* Future experiments will compare activities of similar compounds in our library in an effort to maximize the anti-bacterial activity and to determine the optimal structure required for the antibiotic activity against MRSA and other Gram-positive and Gram-negative bacterial species. Efforts to discriminate between a bactericidal versus a bacteriostatic mode of action of this compound are underway. Furthermore, MTT assays will be conducted to assess the toxicity of these compounds to mammalian cells in culture, in order to design compounds that are maximally non-toxic to human cells. This is an essential first step toward the development of a new class of anti-MRSA agents.

E26-SAT

EFFECTIVE STRATEGIES TO RECRUIT UNDERREPRESENTED GROUPS IN CANCER PREVENTION STUDIES

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Underrepresented groups are thought to be difficult to recruit into prevention studies. Factors such as lack of trust in scientific research, competing obligations, and language barriers are often cited reasons for low participation. Using a feeding study, Carbohydrates and Related Biomarkers (CARB), which aimed to recruit 88 participants (22 Hispanics and 22 African Americans), we examined strategies for recruiting underrepresented individuals into prevention studies. Study eligibility criteria were: (1) being 18 to 45 years of age, (2) fitting into one of the study weight groups, (3) being in good health, (4) being a non-smoker, and (5) processing carbohydrates normally. Participants are given meals and beverages for two 28-day feeding periods. Participants visit the project nutrition laboratory every evening, where they are fed, weighed, and given breakfast and lunch for the following day. A compensation of $750 is given at the completion of the study. Participants were recruited through email list serves and in-person communication. Project staff attended events that targeted Hispanics and African Americans. Staff presented information at ethnic studies classes and student groups at the local university. Advertisements were placed at various locations. To date, 521 individuals (all races and ethnicities) contacted the program for study information. A total of 223 (137 female, 86 male) completed the screening questionnaire; of those, 32 were Hispanic (16 female, 16 male), and 31 were African American (22 female, 9 male). Proactive approaches involving in-person contact with participants are needed to successfully recruit underrepresented populations into prevention studies.

E25-FRI

EFFECTS OF 13-HODE ON BAX AND BCL-2 EXPRESSION IN HUMAN AORTIC ENDOTHELIAL CELLS

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Atherosclerosis is responsible for more than half of the yearly mortality in the U.S. and more than 500,000 people die annually of myocardial infarction alone. Atherosclerosis is the hardening of arteries due to plaques, which has many risk factors including smoking, high blood pressure, and elevated levels of lipoproteins in the blood. Recent research has shown that 13-Hydroxy-9Z,11E-Octadecadienoic acid (13-HODE) is one of the most abundant oxidized fatty acid metabolites released during the lipolysis of very low density lipoproteins (VLDL). Triglyceride rich lipoproteins increase apoptosis in human aortic endothelial cells (HAEC), by an unknown mechanism. In this research, the ability of 13-HODE to induce apoptosis was investigated. To determine gene expression levels of Bax and Bcl-2, a quantitative real time- polymerase chain reaction (qRT-PCR) was performed. To determine protein expression of Bax and Bcl-2, a western blot was performed. By use of qRT-PCR, it was discovered that Bax and Bcl-2 were up-regulated, but based on the gene expression of the positive control, these results were rendered inconclusive. By use of western blot, Bax protein was successfully expressed, however, there was no visible expression of Bcl-2. Based on these results, it appears that 13-HODE may have the potential to increase apoptotic cell death for the initiation of atherosclerosis.

E28-SAT

NON-LETHAL CUTANEOUS HSV-1 EFFECTS ON THE CENTRAL NERVOUS SYSTEM

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The effect of minimal HSV-1 cutaneous exposure the central nervous system was investigated in order to determine if the cutaneous disease results in central nervous system (CNS) invasion. Hairless mice were obtained from Taconic Farms or Jackson Laboratory (BALB/C) and maintained in isolation in Biosafety Level 2 housing with proper food and water. The mice were administered a non-lethal dose of HSV-1 applied through a dermabrasion wound on the lateral abdominal wall. Control mice underwent dermabrasion and application of suspension medium without virus. Mice were evaluated daily for signs of the spread of infection. Symptoms, which included lesion size, skin ulceration, and evidence of myelitis, were recorded daily. Both virus-inoculated and control mice were killed every day following inoculation. Blood, spines, and skin samples were collected for examination and preservation for later PCR analysis and immunohistochemistry. For each cross section of spinal cord, lesions of meningitis, myelitis, and ganglioneuritis were scored independently for severity. Results of these analyses will be presented.

F17-SAT

SYSTEMIC INFLAMMATION MARKERS ASSOCIATED WITH INSULIN RESISTANCE IN CHILDREN POPULATION OF TIJUANA, BAJA CALIFORNIA, MEXICO

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Type 2 diabetes mellitus (T2DM) and obesity are conditions of high prevalence in children and adult populations. Coronary vascular disease, hypertension, hyperlipidemia, and metabolic syndrome, are frequent comorbidities of T2DM. A low grade systemic inflammatory response has been postulated as an important pathological element in the emergence of those complications in T2DM and obese subjects. Previous studies show that T2DM activates certain markers of the immune system, triggering important systemic inflammatory molecules. The principal objective of this study was to analyze the pro-inflammatory response associated with pre-diabetes and insulin resistance (IR) in blood samples from a cohort of Mexican children and adolescents from Tijuana. 115 children and adolescents (56 M and 59 F) between 6 to 13 years of age with no evidence of prior disease were included in this study. A fasting blood sample was obtained to determine glucose, insulin, adiponectin and leptin levels by radioimmunoassy. Insulin resistance was determined by HOMA and anthropometric measurements by standard techniques. We obtained a significant association between IL-6 and IR ($r = 0.183$, $p < 0.05$), adiponectin ($r = 0.681$, $p < 0.043$), glucose ($r = 0.692$, $p < 0.037$) and leptin ($r = -0.322$, $p < 0.001$). A significant association was detected between CRP and BMI ($r = 0.428$, $p < 0.01$), insulin ($r = 0.342$, $p < 0.01$), IR ($r = 342$, $p < 0.01$), leptin ($r = -0.728$, $p < 0.033$) and adiponectin ($r = 0.948$, $p < 0.007$). The association between pro-inflammatory markers and insulin resistance suggests the co-existence of low-grade systemic inflammatory state and IR in children. This calls for a need of early detection of pro-inflammatory markers and aggressive strategies to prevent T2DM and complications associated with systemic inflammation in adults.

F15-FRI

EXPLORING PROTEIN MANIPULATION FOR IMPROVED DETECTION OF PROTEIN EXPRESSION FOR GENE THERAPY TREATMENT IN THE CNS

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Lysosomal storage diseases result from the deficiency of enzymes required to catabolize macromolecules. The brain is affected in most of the diseases leading to neurological symptoms. Several approaches have been used for treatment including enzyme therapy, stem cell transplant, and gene therapy. Injections of gene transfer vectors into multiple sites in the brain have shown promising results in several disease models. Only small amounts of enzyme are required to reverse storage lesions in the cell leading to increased global correction in the brain. However, better methods for understanding protein delivery in the brain are necessary in the evaluation of successful gene therapy treatment in the CNS. Protein tags can serve as a valuable alternative for detection of gene expression. When manipulating protein fusions it is possible to disrupt the structure and function of the therapeutic protein or the tag itself. In this project we analyzed the fusion of three tags (c-Myc, HA, and Venus) to β-glucuronidase (GUSB). HA and c-Myc are epitope tags that have been well characterized. Venus is a YFP mutant with improved properties to enable its use in fluorescent labeling. Using biochemical and immunohistochemical detection we evaluated the efficiency of the fusion protein's ability to express both the tags and the GUSB protein *in vivo*.

F16-FRI

REACTIVE OXYGEN SPECIES CONTRIBUTE TO SLEEP APNEA-INDUCED HYPERTENSION IN RATS

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Rats exposed to intermittent hypoxia/hypercapnia (IH/HC) during sleep to mimic sleep apnea have increased mean arterial pressure (MAP) and endothelin 1 (ET-1). We previously reported that the superoxide dismutase mimetic tempol prevents this increase in blood pressure and circulating ET-1. Because superoxide (O_2^-) can stimulate ET-1 synthesis, we hypothesized that IH/HC increases arterial O_2^- in IH/HC rats to increase ET-1 and MAP. To test this, rats were exposed to IH/HC or air cycling (Sham) for 14 days. On day 14, mesenteric arteries were dissected and used to evaluate the effect of IH/HC on superoxide generation. Absorbance at 550 mm (Ab_{550}) for ferricytochrome C (FCC, 50 μM) was recorded to determine superoxide production. Ab_{550} increased when arteries from either Sham or IH/HC rats were added but Ab_{550} was significantly greater in IH/HC than Sham (7.8±1.1 vs. 0.2±0.001, $p < 0.001$). Another group of mesenteric arteries were frozen, sectioned and stained with dihydroethidium (DHE) to detect oxidation. DHE staining also demonstrated elevated O_2^- production in IH/HC compared to Sham arteries (583±108 vs. 241±41 avg intensity IH/HC vs. Sham, $p = 0.014$). In summary, IH/HC appears to increase vascular production of O_2^-. These results support our hypothesis that vascular O_2^- *in vivo* contributes to ET-1 synthesis and hypertension in IH/HC-exposed rats.

IMMUNOLOGY

E21-FRI

DETERMINING THE EFFECT OF PHYSIOLOGICAL CONCENTRATIONS OF LEPTIN ON DENDRITIC CELL MATURATION

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Dendritic cells (DC) play a vital role in the immune response in that they are the only cells capable of activating naïve T cells. Full activation of T cells requires DC maturation, a process in which DC change to enhance interactions with T cells. Various factors can contribute to this process. Leptin, a cytokine/hormone, predominantly secreted by adipose tissue, is a pleiotropic molecule that has been linked to proinflammatory activities, including promotion of T cell responses. However, the specific effects of leptin on DC remain unknown. The aim of this study was to determine if physiological concentrations of leptin affects DC maturation since other proinflammatory molecules can both induce and/or promote this process. To address this, murine bone marrow-derived DC (BM-DC) were treated with leptin, the DC maturation molecule lipopolysaccharide (LPS), a combination of the two, or remained untreated. The cells were tested for maturation as a function of: (a) phagocytic ability, measured by ingestion of flourochrome-labeled bacteria; (b) IL-12 secretion, measured by ELISA; and (c) upregulation of activation markers, measured by flow cytometry. Results demonstrate no marked difference for any of the maturation measurements between leptin-treated and untreated BM-DC. However, co-treatment of BM-DC with LPS and Leptin, increases IL-12 production relative to treatment with LPS alone. The data suggests that physiological levels of leptin do not prokove unnecessary T cell responses and suggest that leptin assists DC to specifically prime antibacterial or antiviral T cell responses.

E25-SAT

HOXB9 IS A NOVEL TRANSCRIPTION FACTOR INVOLVED IN THE INTERFERON-BETA MEDIATED ANTIVIRAL RESPONSE

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Type I interferons (IFNs), including IFN-beta, are produced in response to viral infections and play a critical role in the establishment of a strong antiviral state. Recognition of viruses by cellular receptors triggers a signaling cascade, leading to the phosphate dependent activation of transcription factors such as IRF-3 and NF-kappaB that subsequently bind to the type I interferon promoter. Here, we establish the involvement of a novel transcription factor, HoxB9, in the regulation of IFN-beta expression. Overexpression of HoxB9 in murine fibroblast cells stimulated IFN-beta expression and generated a significant antiviral state. Viral infection susceptibility was assayed using a mouse herpes virus-68 that has been engineered to produce luciferase as it replicates. HoxB9's ability to inhibit virus replication suggests that it might be sufficient to induce type I IFNs. We then tested to see whether HoxB9 behaves as a virus inducible transcription factor, like IRF3. We showed that herpes simplex virus type 1 (HSV-1) stimulates a luciferase reporter containing the HoxB9 binding site portion of the IFN-beta promoter. Although Hox transcription factors are normally known to be involved in embryonic development, the novel role for HoxB9 as an immune modulator is here clearly established. Ongoing studies will seek to understand the importance of HoxB9 in mediating interferon response and antiviral immunity as well as its pathway of activation.

E22-SAT

THE EFFECTS OF RESISTANCE DUE TO TWO RTI'S TREATMENTS ON THE PROGRESSION OF HIV

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Didanosine and Zidovudine are the two drugs that are administered as a part of an HIV drug therapy. Both of these drugs are RTI's (Reverse Transcriptase Inhibitors) and help in inhibiting the replication of the virus in the infected CD4+ T-cells which has an effect on the rate of infection of CD4+ T-cells. We consider a mathematical model in which one drug is given at a time and is switched with the other one after a certain amount time from the date we start treatment. We perform systematic administration of drug therapy using numerical simulation and study the dynamics of T-cell count considering the mechanisms of drug resistance. We assume that a high virus count is a sign that the virus has a high resistance to the drug therapy. Running simulations we were able to see specific ranges that could be used effectively for the periods of administering drugs.

E24-FRI

NF-KB P65 AND C-REL REGULATION PATTERN DURING T CELL STIMULATION

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T cell stimulation triggers a signal cascade that causes the activation of various transcription factors. From these transcription factors NF-κB is especially important because it is necessary for expression and secretion of T cell growth factor IL-2. In this study we are interested in comparing the regulatory pattern of NF-κB proteins p65 and c-Rel. NF-κB is composed of protein subunits which form dimers that bind via the κB domain. In resting T cells, the NF-κB complex remains in the cytosol bound to the inhibitory molecule IκB. Once the T cell is activated, IκB is degraded and the NF-κB complex is translocated into the nucleus where it binds to the IL-2 promoter to initiate transcription. We compared the localization of NF-κB protein subunits p65 and c-Rel during T cells stimulation. First, we studied degradation of IκB and NF-κB proteins at different time points by Western blot. Here we found degradation of IκBα but not IκBβ during T cell activation. We also observed no degradation of either total p65 or c-Rel after 60 minutes of stimulation. We also analyzed nuclear translocation by immunofluorescence in stimulated T cells using antibodies against p65 and c-Rel. We found that p65 moves from the cytosol to the nucleus within 15 minutes and 45 minutes of stimulation. Data from immunofluorescence was also confirmed by nuclear fractionation assay. c-Rel shows a different pattern since it appears nuclear at all time points. Future studies will compare these patterns with anergic cells to determine how NF-κB is regulated in T cell anergy.

E23-SAT

PRODUCING LENTIVIRAL VECTORS EXPRESSING GENETICALLY MODIFIED HIV-1 GAG PROTEINS

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HIV-1 vaccines designed to promote cellular immunity by delivering native proteins have not been successful. We have previously shown that immunodominant HLA-A2-restricted CTL SL9 epitope of the HIV-1 Gag produces an unstable help-independent CTL response, while the subdominant TV9 provokes a response that is incapable of full maturation. We have identified an agonist peptide of SL9, SL9(p41), that elicits stable SL9-crossreactive T cells and an agonist peptide of TV9, TV9(p6), that primes CTLs that are very effective lysing virus-infected target cells. We have constructed the expression plasmids for a lentiviral vector in which the SL9- or TV9-regions of Gag have been genetically modified by introducing point mutations. Here we report on the successful production of these lentiviral vectors, including a control vector that expresses GFP. The ability of the control vector to transfect 293FT Human Embryonic Kidney cells and HT1080 tumor cells are shown. Future experiments will include verifying that these vectors will transduce dendritic cells to allow priming of CD8+ T cells *ex vivo.* In this way, we will be able to compare the T cell responses to these genetically altered Gags. Our long term goal is to see whether any of these Gags are superior immunogens to the wildtype protein. It is possible that studies on epitopes from Gag proteins may help in designing an efficient vaccine against HIV.

E23-FRI

CATIONIC STERIOID ANTIBIOTICS AS POTENTIAL CHEMOTHERAPEUTIC AGENT AGAINST *TRYPANOSOMA CRUZI*

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Trypanosoma cruzi is the causative etiological agent of Chagas' disease. Issues concerning this disease include the gaining of resistance of the *T. cruzi* parasite towards both benznidazloe and nifurtimox indicating the urgent need for an improved treatment. Ceragenins or cationic steroid antibiotics (CSAs) have a high binding affinity for membranes composed of lipid A and are able to quickly disrupt the target membranes leading to rapid cell death. The specific aims of this study are to determine the effect of CSA-13 against the trypomastigote form of the *Trypanosoma cruzi* parasite infecting LLC-MK2 cells and to determine the viability of LLC-MK_2 cells when treated with CSA-8, CSA-13, and CSA-54. *In vitro* infectivity experiments were carried out

by first treating the parasites for two hours at various drug concentrations followed by infection of the LLC-MK2 cells. The percent infectivity of the parasites treated in doses ranging from 100 μM to 1.0 μM rendered results respectively, 3.67% to 13.0%. A considerable decrease in the infection was obtained compared to the control which had 16.0 % infectivity. Along with the percent infectivity, the average number of amastigotes per cell was also calculated which rendered results ranging from, 1.12% to 1.77%. The control was calculated at 2.57 % amastigotes per cell, exemplifying a considerable half-fold decrease of the number of amastigotes infecting cells when evaluated amongst the samples containing drugs. LLC-MK_2 cells treated with all three types of CSAs at 11.11 μM demonstrated there was more 50% viability when compared to the non-treated control.

E24-SAT

EFFECT OF SIRNA-MEDIATED ATF3 KNOCKDOWN ON INTERFERON-β TRANSCRIPTION IN MACROPHAGES

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Interferons are small, secreted molecules of the immune system that help the body repel viral and possibly other types of infections. Interferon-beta (INF-β) is a member of this molecular family that is rapidly produced by macrophages and other cells following infection. While INF-β is an important component of the host defense against infection, excessive or prolonged production of this molecule can contribute to lethal septic shock and auto-immune diseases. Thus, INF-β levels must be tightly regulated in the body and multiple mechanisms are known to be involved. Recently our lab observed that macrophages from activating transcription factor 3 (ATF3)-deficient mice produce significantly elevated levels of INF-β compared to macrophages from wild type ATF3-expressing mice, leading us to hypothesize, thatATF3 is a transcriptional repressor of the INF-β gene. To directly test this hypothesis, we plan to examine whether INF-β mRNA levels are increased in macrophages that have been treated with small interfering RNA (siRNA) against ATF3 to reduce the expression of this protein. Preliminary experiments are being performed to determine the conditions that maximize siRNA-mediated ATF3 knockdown. One variable we are testing is single versus double siRNA transfection. Initial results suggest that single siRNA transfection produces a similar degree of ATF3 knockdown as double transfection. We are currently confirming this observation and examining the effect of 48 hour versus 72 hour siRNA incubation for an optimal ATF3 knockdown.

E22-FRI

SUBCELLULAR LOCALIZATION OF STAT5 FOLLOWING CD95 (FAS) LIGATION OR IL2 WITHDRAWAL OF HUMAN KIT225 CELLS

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Signal transducer and activator of transcription (Stat) molecules (Stat1-4, 5a, 5b, and 6) play diverse roles in cellular development, differentiation, proliferation, survival, and apoptosis. Stat5a and b (commonly referred to as Stat5) are highly homologous isoforms that play redundant roles in mediating IL2-induced proliferation of T cells. Stat5 is hyperactivated in a number of malignancies, including human T cell leukemia virus-1 (HTLV-1) -transformed cell lines, and tumors of breast, prostate, and lymphoid origin. We have previously established that depletion of Stat5 induced apoptotic cell death in primary blood mononuclear and lymphoid cancer cells. The role of Stat5 in mediating lymphoid cell survival is well established. However, little is known about the function of Stat5 during apoptotic cell death. The aim of this study was to investigate how Stat5 responds to apoptotic stimuli mediated by either IL2 withdrawal or ligation of the CD95/Fas death receptor pathway in a human IL2 dependent T-cell leukemia line, Kit225. Kit225 cells were treated with αCD95 antibody or cultured in medium without IL2 for various time points and cell viability/apoptosis were assessed. Subcellular localization of Stat5 will be assessed by SDS-PAGE and western blot analysis. We anticipate that the amount of nuclear-localized Stat5 decreases during apoptotic stimuli, suggesting that its presence will directly correlate with cell survival. Thus, this study will contribute to the understanding of how Stat5 is involved in cancer formation and treatment.

MARINE BIOLOGY

E20-FRI

INTERANNUAL VARIATION IN FLYINGFISH FORK LENGTHS FROM THE EASTERN TROPICAL PACIFIC

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The El Niño Southern Oscillation (ENSO) is an ocean-atmosphere coupling event that consists of warm El Niño and cool La Niña phases. The ENSO affects many systems including oceanic tropical regions like the eastern tropical Pacific (ETP). An important ETP community affected by ENSO-variation is the tuna-dolphin assemblage. Past studies concentrated on influences of ENSO-variation within apex predators, such as dolphins. This study focuses on mid-trophic level organisms, specifically

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flyingfish sampled between August and November in ten years between 1986 and 2004. The goal is to examine fork lengths of over 20 species of flyingfish to determine the possible presence of interannual variation in their growth rates. Histogram distributions of fork lengths versus abundance will compare monthly and yearly populations to establish patterns attributable to ENSO. Scatterplots and linear regression analyses will also be conducted to uncover trends and determine a correlation between fork length and El Niño/La Niña events. Preliminary results allude to the presence of interannual variation in flyingfish growth rates along with clear seasonal patterns on a monthly and annual basis. This is important to ecosystems studies, specifically for the tuna-dolphin assemblage because flyingfish are key dolphin prey. Observed variations in flyingfish can provide a possible explanation for the lack of dolphin recovery in tuna-dolphin assemblages of the ETP.

E20-SAT

THE BIOMEDICAL EFFECTS OF THE CRINOTOXIN FOUND IN THE MUCUS OF HAWAIIAN WRASSE AND PARROTFISH

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The mucous secreted by parrotfish and some species of wrasse, containing crinotoxin found on the body and composing nocturnal cocoons, serves many purposes, such as masking the fishes' scent and serving as a physical barrier against pathogens (Videler et al., 1999). Videler (1999) found that the queen parrotfish of the Caribbean Sea, *Scarus vetula*, mucous cocoon possesses antibacterial properties. The purpose of this study is to examine whether Hawaiian parrotfish and wrasse have similar biomedical effects. To test this hypothesis, mucous was collected from a variety of Hawaiian wrasses and parrotfish by fishing. The effect of mucous on heart rate of *Daphnia* and antibacterial effects of mucous on gram negative and gram positive bacteria were tested in agar plates. The mucous from the Saddleback wrasse, Christmas wrasse, Bullethead parrotfish, and Star Eye parrotfish does not possess antibacterial properties against *Staphylococcus aureus* or *Escherichia coli*. The mucous from the Christmas wrasse decreased the heart rate of the *Daphnia* while the mucous from the Bullet Head parrotfish increased the heart rate. (Supported by USDE # P217.)

E19-FRI

USING PALEONTOLOGY TO STUDY A MARINE SYMBIOSIS GENERATING A FOSSIL RECORD OF THE BIOLUMINESCENT BACTERIUM *VIBRIO FISCHERI* FROM FROZEN SEPIOLID SQUIDS COLLECTED FROM THE YEARS 1999 TO 2007

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The Australian sepiolid squid, *Euprymna tasmanica,* and the bioluminescent bacterium, *Vibrio fischeri,* are a model system to study the evolutionary ecology of environmentally transmitted symbiosis. In this partnership, the bacterium inhabits a structure called the light organ, within the mantle cavity. The experiment consists of *Euprymna tasmanica* collected annually from Botany Bay between 1999 and 2007. The bacteria were obtained by removing and homogenizing the light organ, isolating the bacteria into a 1.5-mL vial of sterile seawater. The bacterial solution was diluted with sterile seawater and plated onto sea water tryptone media. Plates were incubated for 24 hours, allowing growth of the bacteria, which were subsequently cryogenically frozen at -80˚C. This places the bacteria into a "frozen fossil record," initiating a series of *V. fischeri* taken from different years of cohorts of *E. tasmanica*. Working with these isolates has yielded data to compare differences and similarities between past and present *V. fischeri*, and to investigate what traits the symbionts are evolving as they adapt to their hosts. The further back in time we isolate bacteria from *E. tasmanica*, the larger the scale of symbiont evolution we can observe. This will eventually help us understand factors driving bacterial speciation. (Supported by NIH BRIDGES Program grant R25 GM48998.)

E18-FRI

DIFFERENCE BETWEEN POPULATIONS OF MELOCACTUS INTORTUS IN TWO DIFFERENT AREAS OF GUANICA DRY FOREST

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Melocactus intortus is a cactus that inhabits dry places such as the dry forest of Guanica in Puerto Rico. This is considered one of the best preserved and less altered by humans subtropical dry forest. This area is known to be the driest and the one that receives the greatest amount of radiation in the island. The strong salty winds and low amount of water available in the dry forest cause vegetation to have a limited growth. Species like *M. Intortus* are adapted to this kind of environment. *Melocactus* are globular cactus with a crown on its apex called cephalium. This densely spine area is where the flowers and fruits are produced and it can grow for many years. This research was conducted in the Guanica dry forest in the area of dwarf forest and in the area of coastal shrub forest. In the dwarf forest we measured a population close to the slope of the coast and in the coastal shrub forest area we measured a population close to a lagoon. We compared the distribution between the two populations and

the differences in the wind, air and soil temperature and humidity of each place. For each population we marked a central point, and from it we measured the azimuth and distances of each cactus in a radius of 30 meters. Each individual was classified according to its life cycle stage and the cephalium was measured. Spatial distribution was analyzed using the nearest neighbour method. In our study we found clumped distribution in both populations.

E21-SAT
GENETIC VARIATION IN EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) FROM THREE TEXAS BAYS
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We studied DNA variation to find whether genetic diversity is high in the eastern oyster (*Crassostrea virginica*) within and among three Texas bays, specifically Copano, Matagorda, and Carancahua. We extracted DNA using a QIAGEN DNeasy kit from 25 oysters from each of the three different bays. We amplified known microsatellite loci using PCR to estimate genetic diversity within and between each bay. Microsatellites loci are locations in the DNA of all organisms in which the nucleotides are repeated in tandem. The number of times the duplicated nucleotides are repeated varies among individuals and between chromosomes within individuals. We have completed the DNA extractions, but need the rest of the summer to complete the PCR and analysis of the microsatellite loci. We expect to find relatively high genetic diversity among the oysters from these three bays. If we find genetic variation among the bays, we will be able to test the hypotheses that high genetic variation in artificial reefs makes these reefs more resilient to change within the environment and increases larval recruitment to the reefs, as has been found for other marine species.

E19-SAT
CHARACTERIZATION OF VIBRIO ISOLATES FROM THAILAND *LOLIGINIDAE* AND *SEPIOLIDAE* (MOLLUSCA:CEPHALOPODA)
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Luminescent bacteria in the family *Vibrionaceae* (gamma-proteobacterium) are known to colonize light organs of squids in the families *Loliginidae* and *Sepiolidae*. These bacteria are harbored in morphologically similar structures which presumably enable the squids to perform a behavior known as counterillumination. Specimens of the sepiolid, *Euprymna hyllebergii*, as well as the loliginids, *Uroteuthis chinensis* and *Uroteuthis duvauceli,* were obtained from the coasts of Phuket and Rayong, and dissected to extract bacterial isolates from their light organs. Forty-one (41) symbionts were cultured and their DNA extracted and used to amplify the 16S ribosomal RNA gene. Isolates were identified by 16S rRNA sequence similarity to the NCBI database using the program BLAST. All isolates were found to be members of the family *Vibrionaceae*; this included two strains belonging to the genus *Photobacterium*, seven to the genus *Pseudoalteromonas*, and twenty to the genus *Vibrio*. Based on molecular data, eight *Vibrio* isolates were selected to execute carbon utilization experiments using Biolog MicroPlates™ for 95 different carbon sources. These results confirmed our BLAST searches and therefore verified the identity of all the strains. (Supported by NIH R25 GM48998.)

MICROBIOLOGY

E17-FRI
ANTIBACTERIAL PROPERTIES OF METHANOLIC, ETHANOLIC, AND AQUEOUS EXTRACTS OF *AURICULARIA AURICULA-JUDAE* ON SELECTED BACTERIAL CULTURES
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The emergence of antibiotic resistant bacteria has made the search for new antibiotics imperative. Basidiomycetes have not been screened for antibiotics, largely because most basidiomycetes are difficult to grow. The jelly fungus, *Auricularia auricula-judae*, is an edible basidiomycete often used in Asian cooking and methods for its commercial cultivation are approved in the U.S. An antibiotic isolated from an edible mushroom would be of particular value because it is not toxic to humans. Aqueous, ethanolic, and methanolic extracts of the mushroom *A. auricula-judae* were examined for antibacterial activity using the well-diffusion and serial dilution methods. *Staphylococcus aureus*, *Proteus vulgaris*, and *Bacillus cereus* were inhibited by all three extracts. *Pseudomonas aeruginosa* and *Escherichia coli* were resistant to all of the mushroom extracts. Commercially produced antibiotic disks were used as positive controls. *A. auricula-judae* extracts are 19% to 40% less effective than commercial antibiotic preparations. The MIC against *S. aureus* is 21.45 g/mL for all three extracts. The MIC against *P. vulgaris* is 5.36 g/mL methanolic extract, and 10.73 g/mL ethanolic and aqueous extracts.

E7-SAT

GROWTH AND DEVELOPMENT OF SHEWANELLA ONEIDENSIS MR-1 ON DIFFERENT MEDIA FOR IRON REDUCTION

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Geotechnical engineering tries to understand geological processes and the influence they have in the surrounding structures. Recent investigations have discovered that microorganisms as *Shewanella oneidensis* can reduce structural iron in smectite to illite, improving soil properties. The purpose of our research was to find an adequate media where *S. oneidensis* could achieve growth and iron reduction at an optimal level. Samples of *S. oneidensis* and Unknown bacteria were incubated in a TSB medium and cultured in two different media: LB agar Miller and tryptic soy agar. For each media, dextrose was added as a carbon source and used as electron donor while ferric citrate was added to half the samples as electron acceptor. Spreading methods were used for the bacterial culture after dilution of the inoculation. Anaerobic and aerobic conditions were used to compare the iron reduction and the development of *S. oneidensis* and Unknown bacteria samples. In our first try the bacteria was diluted by a factor of four and after 72 hours of incubation no trace of bacterial growth was found. Therefore, a second culture was made, reducing the dilution factor of *S. oneidensis* to three, and then incubated for a period of 48 hours. The Unknown bacteria samples presented a significant growth, while the *S. oneidensis* sample presented no improvement. Other methods as different dilutions and conditions are being employed to achieve our objective. Further investigations will be made to complete a growth curve and identify the best media for growth and iron reduction of *S. oneidensis*.

E17-SAT

ANTIBACTERIAL ACTIVITY OF AJOWAN, A TRADITIONAL ASIAN HERBAL MEDICINE

Paige Fulmer, Denise Owen. *Skyline College, San Bruno, Calif.*

Overuse of antibiotics has selected new strains of bacterial pathogens that are resistant to the very antibiotics used to combat them. Many plants have been used for centuries by traditional healers and may have antibacterial properties. Ajowan (*Trachyspermum ammi*) is one such plant, having been prescribed for digestive, respiratory, renal, dental, and many other maladies in Asian traditional medicine. Our research aim was to determine whether aqueous, ethanolic, and acetone extracts obtained from the plant's fruit could inhibit growth of gram-positive *Staphylococcus aureus* bacteria and gram-negative *Salmonella enterica* and *Pseudomonas aeruginosa* bacteria. Our methods included a well-diffusion assay as well as a determination of the minimal inhibitory concentration (MIC). Inhibitory effects were seen against all three bacteria, primarily as ethanolic or acetone extracts. The most effective antibacterial was the ethanolic extract, showing the greatest inhibition against *S. aureus* with an average inhibition zone of 3.9 mm and an average MIC of 6.93 mg/mL. These are valuable findings, as they may help lead to development of plant-based, affordable antimicrobials to which bacteria do not show resistance.

E9-FRI

FUNGAL COMMUNITIES ASSOCIATED WITH BIOLOGICAL SOIL CRUSTS ON GYPSIC SOIL FROM THE COLORADO PLATEAU, U.S.

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The biodiversity of microbial communities associated with biological soil crusts (BSCs) have been well documented in numerous studies; however, this area of research has almost exclusively focused on the bacterial and cyanobacterial components of these communities, while fungal constituents have been routinely overlooked. We studied fungal communities associated with BSCs on a gypsic soil site from arid-lands on the Colorado Plateau of the Western United States. This study employs the polymerase chain reaction (PCR) using fungal specific primers combined with denaturing gradient gel electrophoresis (DGGE) as a culture independent means to assess fungal diversity of this ecosystem in terms of richness and the Shannon index of diversity. The BSC associated fungal diversity from this gypsic site is comparable to that found at sandy soil sites on the Colorado Plateau and appears to be less diverse than a typical BSC site from the Sonoran desert. Our study discovered numerous fungal phylotypes, one of which appears to play a dominant role in these communities. The phylotypes, represented as DGGE 'bands', were recovered and can be sequenced for use in phylogenetic analysis in order to determine the composition of these fungal communities. In addition to this work, a culture dependent survey was initiated that can enhance our understanding of the fungal organisms that are associated with BSCs in this ecosystem.

E11-FRI

ANALYSIS OF *TRYPANOSOMA CRUZI* PHOSPHOPROTEOME BY MASS SPECTROMETRY

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The parasitic protozoan *Trypanosoma cruzi* is the etiologic agent of Chagas' disease, a chronic infection that affects over 11 million people throughout Latin America and has become a recent concern to the U.S. Lately, much research has been focused on drug and vaccine development against this parasite. In eukaryotic cells, protein phosphorylation regulates many vital pathways, such as cell cycle, and has been extensively studied as potential molecular target. Herein, we hypothesize that *T. cruzi* contains several phosphoproteins that can be successfully sequenced and mapped through mass spectrometry (MS) and can serve as drug targets. Total proteins from *T. cruzi* epimastigote form were extracted and digested with trypsin, fractionated in a strong cation-exchange (SCX) ziptip, and the phosphopeptides were purified by immobilized metal-affinity chromatography (IMAC). Purified phosphopeptides were analyzed by liquid chromatography-tandem mass spectrometry (LC-MS/MS). The resulting MS/MS spectra were searched against the TcruziDB v5.0 using TurboSequest algorithm. With this approach, we were able to identify 26 phosphopeptides from 23 distinct proteins. Several of these proteins were annotated as kinases, transcription regulatory protein and calpain-like cysteine protease, play critical roles in the cell. Currently, we are optimizing the condition for the LC-MS analysis to increase the coverage of phosphoproteins. The successful phosphoproteome analysis of *T. cruzi* may lead to the discovery of new methods to prevent or treat Chagas' disease. (Funded by NSF/REU Program grant# DBI-0353887, and NIH/SCORE grant# 2SO6GM0812-37 to ICA.)

E10-FRI

CHARACTERIZATION OF *STAPHYLOCOCCUS* ISOLATES FROM UN-PASTEURIZED COWS MILK

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Staphylococcus aureus is a leading cause of bovine mammary infection that results in decreased milk production. Epidemiology studies can be used to determine if *S. aureus* are spreading amongst animals clonally and prevent further spread of this pathogen. Initially, milk was collected from 133 dairy cows, and spread onto Baird-Parker agar. Presumptive identification of *S. aureus* isolates was determined with Gram-staining, mannitol salt agar, Petrifilm Staph Express plates, and a coagulase test. PCR amplification of a *nucA* amplicon was used to confirm *S. aureus* status. The antimicrobial susceptibility of all confirmed *S. aureus* isolates was analyzed via Kirby-Bauer disk diffusion and Sensititre veterinary MIC plates. Pulsed field gel electrophoresis (PFGE) patterns of *SmaI*-digested chromosomal DNA was used to determine clonal relatedness amongst the milk isolates. Thirty-eight presumptive *S. aureus* isolates were identified in 33 milk samples. Amplification of the *nuc* fragment confirmed all as *S. aureus*. Of the 7 isolates from 33 cows undergoing antibiotic treatment, 3 showed reduced susceptibility to 4 antimicrobials, and closely related PFGE patterns. We have demonstrated that at least one strain of *S. aureus* is spreading within a herd of New Mexican dairy cattle. (Supported by NIH Bridge Program grant R25 GM 48998.)

E16-FRI

EVALUATION OF THE POTENTIAL USE OF GINGER AS A FRUIT PRESERVATIVE

Karamjit Kaur. *Skyline College, San Bruno, Calif.*

Food preservation is critical for supplying a stable food supply and to preventing foodborne diseases. Plant-derived antimicrobials may provide nontoxic food preservatives. The purpose of this study was to determine whether *Zingiber officinale* could be used as a post-harvest fruit preservative. We prepared several extracts of ginger root (*Z. officinale)*. Aqueous unheated, aqueous heated, and acetone extracts were tested against several spoilage fungi and foodborne bacterial pathogens in culture media and in strawberries. Disk- and well-diffusion assays were used to test the extracts against gram-negative *Escherichia coli* and gram-positive *Staphylococcus aureus* bacteria and *Penicillium chrysogenum*, *Aspergillius niger*, *Botrytis cinerea*, and *Saccharomyces cerevisiae* fungi. Ginger showed moderate activity against gram-positive bacteria and *S. cerevisiae* in culture media. Aqueous and acetone ginger extracts significantly decreased fungal growth in inoculated and naturally-infected strawberries. These extracts reduced all fungal growth by an average of 55% over the conventional fruit-product preservative, sodium benzoate. This opens a new possibility of using ginger extracts as fruit preservatives.

E16-SAT

OPA NEGATIVE STRAIN OF *NEISSERIA GONORRHOEAE* TRANSCYTOSES EPITHELIAL BARRIERS

Adriana Le Van, Sam Bish, Wenxia Song, Daniel Stein. *University of Maryland, College Park, Md.*

Due to the phase and antigenic variation of *opa* genes, we constructed a derivative of *N. gonorrhoeae* strain MS11 that has the Opa-encoding genes deleted to allow us to study the role of Opa in gonococcal adherence to, invasion and transcytosis of human tissue culture cells/monolayers. The Opa-deficient strain was constructed using a PCR/replacement mutagenesis/deletion procedure, allowing us to construct a series of isogenic derivatives of MS11 that possessed different abilities to express a single defined Opa. We studied the ability of the Opa-negative strains to transcytose across polarized T84 monolayers. We found that these strains efficiently transcytosed the monolayer in less than 6 hrs, whereas a wild type strain capable of expressing all 11 Opa proteins was unable to transcytose in this time period. A strain that could only variably express Opa B could transcytose across the epithelial monolayer in 6 hrs, however, the phenotype of the colonies that arose from the basolateral media were almost exclusively Opa negative. The ability of Opa negative strains to adhere to T84 or ME180 cells was examined, and the data indicate that the presence or absence of Opa did not seem to alter the ability of the strain to adhere to these cells. Taken in toto, the data support a model of infection where Opa-expressing gonococci are better at invading into cells, while Opa negative gonococci are better at transmigrating across an epithelial barrier. This suggests that Opa expressing gonococci would be less likely to disseminate from the site of infection.

E15-SAT

MAPPING *TRANS-ACTING* REGIONS IN PRP5 PROTEIN USING TEV PROTEASE *IN VIVO* IN *SACCHAROMYCES CEREVISIAE*

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Splicing of eukaryotic nuclear precursor mRNAs (pre-mRNAs) is catalyzed by the spliceosome which consists of many proteins and five small ribonucleoproteins (snRNPs). Prp5, a DEAD-Box spliceosomal protein, is necessary for pre-spliceosome formation which requires a conformational change that involves the pre-mRNA and U2 snRNP. We hypothesize that there are regions and molecular associations in the Prp5 protein that are important for this change. To map these regions and associations we reiterated a transposon-based strategy previously utilized to investigate another spliceosomal protein. We constructed a transposon to randomly insert the TEV protease recognition site into a plasmid with the *PRP5* open reading frame (ORF) via *in vitro* transposition mutagenesis. Restriction endonuclease digestion of some of the mutant plasmids confirmed that each plasmid had one insert at a random position anywhere on the plasmid. To isolate the *PRP5* ORF with random insertions, we subcloned the mutagenized ORF into a new vector. Current work includes creating a library of *PRP5* ORF isolates with the TEV protease recognition sites but with the transposon deleted. The library will then be introduced into yeast cells in the absence and presence of the TEV protease and screened for viability. Viability and cleavage of Prp5p in the presence of TEV protease will reveal the regions of Prp5p that can function *in trans* and therefore may be involved in intramolecular or intermolecular associations. (Supported by NIH-IMSD.)

E14-FRI

INDENTIFICATION OF THE SOURCE OF FECAL CONTAMINATION IN TULALIP BAY WITH BACTEROIDES 16S RRNA GENE AND F+ COLIPHAGE MARKERS

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Previous work conducted in the Tulalip Bay has shown high total coliform counts resulting in beach closures and shellfish harvesting limitations. TB supports subsistence fishing for many Tulalip Tribal members; therefore, water quality is a significant issue for this area. This project used two genotypic microbial source tracking (MST) methods to determine the source(s) of fecal contamination in Tulalip Bay (TB). Genotyping of F+ RNA coliphage and the 16S ribosomal RNA genes of *Bacteroides* was utilized to differentiate fecal sources into human and non-human feces and human, ruminate, and dog feces, respectively. EPA protocols were used for the isolation of F+ RNA coliphage. After isolation, RT-PCR was used to amplify F+ RNA coliphage sequences using levivirus- and allolevivirus- specific primer sets. Genogroup specific oligonucleotide probes were used to genotype F+ RNA coliphage in to one of four groups in a hybridization assay. *Bacteroides* spp. were collected on membrane filters. DNA was extracted directly from filters and characterized using five host-specific PCR reactions. The F+ coliphage data suggest the presence of fecal waste in 15/16 sampling sites in TB. Out of all these sites, four areas appear to be positive during at least 50% of the sampling events. Primers specific for leviviruses and alloleviviruses confirmed the presence of fecal contamination for 10 sites. Preliminary results show that fecal contamination is present in TB; however, additional work will be conducted in order differentiate between sources.

E13-FRI

MOONMILK BIOGENICITY: ISOLATE POTENTIAL FOR BIOMINERALIZATION

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Moonmilk is a pasty carbonate deposit that occurs within various cave systems. Many secondarily formed deposits within caves (speleothems) are known to be the result of primarily physiochemical processes. However, moonmilk does not appear to be explainable via the same abiotic mechanisms, nor have the same morphologies and textures as traditional speleothems such as stalagmites and stalactites. Moonmilk is currently loosely defined as a microcrystalline aggregate cave deposit composed of various mineralogies with a distinguishable texture. Moonmilk differs from other speleothems due to its biological content, highly variable mineralogy, and texture. Moonmilk deposits were sampled from two geologically different cave systems in New Mexico: Pahoehoe Cave (lava tube) and Spider Cave (limestone cave). To investigate a possible biogenic role, various microbiological techniques were employed, including molecular phylogeny, microbial cultivation, and scanning electron spectroscopy coupled with EDS. Moonmilk displayed a low biomass yet a diverse community. Thirteen isolates were derived from moonmilk samples. In effort to identify each organism, we used the polymerase chain reaction to amplify the small subunit rRNA genes, which were then sequenced. Several isolates were closely related to other microbes from other cave systems. In addition, one isolate expressed the potential of crystal formation. Mineral composition from the isolate will be analyzed by SEM-EDS. Further media variations are being performed in order to facilitate the production of the crystals. Preliminary studies suggest a passive microbial role in the crystal formation. Our research sheds light on the moonmilk microbial inhabitants and their potential role in cave crystal formation.

E18-SAT

CALCIUM REGULATES THE ASSOCIATION OF TRANSCRIPTION FACTOR URE3-BP TO PHOSPHOLIPID-BINDING PROTEIN EHC2A AND ITS SUBCELLULAR LOCALIZATION IN *ENTAMOEBA HISTOLYTICA*

Heriberto Moreno, Carol A. Gilchrist, William A. Petri. *University of Virginia, Charlottesville, Va.*

Calcium is essential for many cellular signal transduction events. In the protozoan parasite *Entamoeba histolytica*, the transcription of the genes encoding two essential virulence factors, the lectin heavy subunit adhesin and ferredoxin is regulated by URE3-BP, an EF-hand calcium-binding transcription factor. URE3-BP binding to specific DNA promoter elements of theses genes is calcium-sensitive. Previously we demonstrated that URE3-BP is localized in the nucleus and cytoplasm of the amoebic trophozoite, yet enriched at the plasma membrane. To study this occurrence, we searched for proteins that differentially associated with URE3-BP in a calcium-dependent manner. We identified a protein that co-immunoprecipitated with URE3-BP in calcium enriched conditions by mass spectrometry. The binding partner, EhC2A, is a member of a novel *E. histolytica* protein family, and contains an N-terminal C2 domain and two C-terminal proline-rich repeats. The interaction between URE3-BP and EhC2A was confirmed to be calcium-dependent using co-immunoprecipitation and far-western blot analysis. Since some C2 domains confer proteins the ability to bind phospholipids in a calcium-dependent manner, we performed liposome binding assays using recombinant EhC2A. EhC2A exhibits apparent high affinity calcium-dependent phospholipid-binding (K_D = 3.4±2.7 μM Ca^{2+}). Immunofluorescence microscopy confirmed the presence of EhC2A in the cytoplasm and the amoebic plasma membrane. We performed liposome binding assays using amoebic cytoplasmic extracts and subcellular fractionations, and demonstrate that URE3-BP and native EhC2A association to phospholipids is calcium-dependent. These results are consistent with our hypothesis that EhC2A mediates the translocation of URE3-BP to the plasma membrane in a calcium-dependent manner regulating its transcriptional activity.

E9-SAT

CHARACTERIZATION OF RDR GENE EXPRESSION

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Arabidopsis is a model organism used for studying plant biology. The *Arabidopsis* genome has been sequenced allowing for genetic manipulation and analysis of gene expression. RDR (RNA dependent RNA Polymerase) genes were the focus of this research for gene regulation, gene expression, virus protection, and gene sequencing. Total RNA isolation from the plant tissue is a technique used to obtain the RNA for gene expression experiments. RTPCR was used after acquiring the RNA from individual parts of the plant to see precisely what genes are being expressed at different stages of the plant's life. The genes of interest are rdr-3, rdr-4, and rdr-5. These genes comprise a three gene family and have not been characterized in the literature. Research has been done on these three RDRs to see when and where these genes are expressed. Parts of the plant studied were: seed, seedling, root, adult leaf, closed bud, and inflorescence (open flower). Other genes studied are rdr-1, rdr-2, and rdr-6. Arabidopsis has a total of seven RDR genes and six of them were studied. Being able to map where the genes are being expressed will be vital in determining what genes are used for protection against viruses and the role each gene has in the plant's life.

E8-FRI

DETERMINING THE ROLE OF THE CYCLIC AMP RESPONSE ELEMENT BINDING (CREB) PROTEIN IN ANTHRAX EDEMA TOXIN-INDUCED ANTXR EXPRESSION

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Bacillus anthracis, the causative agent of anthrax, has recently been publicized as a potential agent of bioterrorism. *B. anthracis* secretes edema toxin (ET), one of two toxins that contribute to the overall disease. The receptor-binding subunit of ET, protective antigen (PA), allows ET to bind one of two anthrax toxin receptors (ANTXR1 and ANTXR2) and mediates entry of the catalytic subunit, edema factor (EF), into the host-cell cytosol. EF is an adenylate cyclase that impairs host defenses by raising cellular cAMP levels. Recently, we demonstrated that ET induces an increase in ANTXR expression that depends on the ability of EF to increase cAMP levels and requires protein kinase A (PKA)-directed signaling. Activation of PKA triggers several transcription factors including the cAMP response element binding (CREB) protein. Potential CREB binding sites are present upstream of the ANTXR1 and ANTXR2 genes suggesting that upregulation of ANTXR expression might be CREB-dependent. We have subcloned CREB variants (wtCREB, KCREB, CREB133, and ACREB) into a retroviral expression vector for efficient gene delivery. We will use ET to intoxicate RAW264.7 macrophage cells overexpressing each of the CREB variants to determine if the ET-induced increase in ANTXR expression is CREB-dependent. We will indirectly assess transcription by measuring relative ANTXR mRNA expression levels using reverse transcription quantitative PCR (RT-qPCR) and translation by measuring the ability of cells to bind a fluorescently labeled-PA using flow cytometry. This study will expand our current understanding of anthrax intoxication and could lead to development of toxin binding inhibitors.

E15-FRI

THE ROLE OF THE INSULINASE-LIKE PROTEIN TOXOLYSIN-2 IN HOST CELL INFECTION BY *TOXOPLASMA GONDII*

Michelle Palacios, Bettina Hajagos, Peter Bradley. *University of California, Los Angeles, Los Angeles, Calif.*

Toxoplasma gondii is an obligate intracellular parasite in the phylum Apicomplexa that causes severe disease in immunocompromised individuals and neonates. As the most experimentally tractable of the Apicomplexans, it also serves as a model system for studying other Apicomplexans such as *Plasmodium falciparum*, the causative agent of malaria. *Toxoplasma's* intracellular lifestyle is dependent on the ability to salvage host constituents, a process that is likely to involve parasite-derived proteases. We are focusing on the role of secreted insulinase-like metalloproteases in the establishment and maintenance of intracellular survival. To do this, we are first engineering 6His-tagged portions of the metalloproteases for recombinant expression in *E. coli*. We will then purify the recombinant protein using nickel-agarose chromatography for immunization of mice and antibody production. We are also directly assessing the role of the proteases using a gene knockout approach. This approach employs PCR amplification and subcloning of regions flanking the gene into a knockout construct that contains the selectable marker HXGPRT and a downstream GFP marker to distinguish between homologous and heterologous recombinants. The knockout construct will be transfected into *Toxoplasma* by electroporation and transfected parasites selected using mycophenolic acid and xanthine. GFP positive heterologous recombinants will be excluded and GFP null parasites will be screened for disruption of the locus by PCR. Our long-term goal is to determine if the proteins are active metalloproteases using *in vitro* assays. Studying proteases is useful for the development of therapeutic treatments such as protease inhibitors, which may block cleavage events necessary for parasitic survival.

E14-SAT

IN VITRO STUDIES OF THE EFFECT OF NOVEL ORGANOTINS ON *TRYPANOSOMA CRUZI* EPIMASTIGOTES

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Chagas is a lethal disease prominent in Latin America, caused by the parasite *Trypanosoma cruzi*. Modes of transmission include: vector transmission, blood transfusion, and organ transplants. Current treatments against Chagas are few and unsatisfactory, helping only those with acute infection. Increase in immigration, and lack of blood and organ testing has made Chagas a growing threat to the United States. Organotins have previously proven to be effective tryponicidal drugs. We hypothesize that organotins $C_{18}H_{22}SnCl_2$ (OT1) and $C_{14}H_{14}SnCl_2$ (OT2) will prove to effectively kill *T. cruzi* epimastigotes, parasite form that exists before mammalian infection. The success of these drugs on epimastigotes leads into testing trypomastigotes, the parasite form that exists after mammalian infection. An Alamar blue viability assay was used to test the effectiveness of the two organotin drugs. *Trypanosoma cruzi* epimastigotes, in OT1 and OT2, ranging from concentrations 1 μM to 100 μM, were incubated for either three or five days, at which the alamar blue was added. A statistic evaluation of results is pending, but based on current observations we conclude that biocidal qualities of the organotin drugs were not optimal. An average of 50.41% survival of epimastigotes when exposed to OT1 for three days and 64.03% survival when exposed for five days at 100 μM. After three days there was 50.41% survival when exposed to OT2 at and 65.57% when exposed for five days. Our findings might signify that organotins $C_{18}H_{22}SnCl_2$ and $C_{14}H_{14}SnCl_2$ are not strong candidates for drug development. This information is important for the development of effective trypanocydal drugs.

E12-SAT

IDENTIFYING HIV-1 TARGET CELL ENTRY VERSUS INFECTION WITH A DUAL REPORTER VIRUS

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The human immunodeficiency virus (HIV-1) is a retrovirus that infects vital cells of the human immune system. However, knowledge on how HIV-1 crosses mucosal barriers to reach the primary target cells after viral inoculation is limited. In preparation for experiments to address this question, we have produced an HIV-1 reporter virus that will allow detection of cell entry separate from replication in target cells. A two-part recombinant virus was produced by co-transfection of 293T cells using two plasmids. One plasmid contained the entire HIV-1 genome with a reporter gene (HSA) replacing the non-essential *vpr* gene, which produce whole viruses lacking Vpr. The second plasmid contained just a gene for a fusion EGFP-Vpr protein, which is expressed and packaged *in trans* into the viruses produced by the first plasmid because the Vpr protein is incorporated into HIV-1. The final virus particles contain the gene for HSA (but no HSA protein) and the protein EGFP-Vpr (but not the gene). Therefore, cells entered by the virus immediately contain EGFP-Vpr (carried directly), and cells that express virus genes will later contain detectable HSA. We plan to use this dual reporter virus as a tool to study the cells that are entered versus productively infected in a colon mucosal culture model for mucosal HIV-1 infection. Investigation of HIV-1 primary target cell types in the mucosal layer can direct further studies of HIV-1 pathogenesis and suggest vaccine targets or drug therapies focused on preventing viral propagation.

E7-FRI

MORPHOLOGICAL CHARACTERIZATION OF ENENDOLITHIC *FISCHERELLA* USING EDTA–ENABLED CALCIUM CARBONATE DISSOLUTION

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Fischerella is a marine cyanobacteria, particularly photosynthetic microbe, that bore into carbonates. They belong to a group of microbes classified as endoliths. Boring into the substrate and making a tunnel where the cells spend their life. They improve their chances of survival, and play both friend and foe in the environment taking an important role in the karstic rock cycle, and sometimes accelerating the deterioration of monuments made of carbonates. *Mastigocoleus* is another marine cyanobacteria that penetrate carbonate substrates and we hypothesized that they are the same cyanobacteria because of the change in the morphology of the *Fischerella* while inside the mineral matrix. They are isolated from the coast of Cabo Rojo, a coastal town in the archipelago of Puerto Rico. We quantified what we observed using simple measurements of the filaments inside and outside the calcite chips. Filaments where extracted from different layers of calcite chips using a 200mM EDTA solution, a chemical compound ethylenediamine tetraacetic acid. The filaments were isolated from the mineral matrix using an etching procedure which is an extraction of the endolithic *Fischerella* cells from solid crystalline calcite chips. This slowly dissolve the carbonate matrix and to reveal the different layers of the borings. Using a peristaltic pump and etching chamber, we collected three polycarbonate membrane filters with filaments. After having the extractions we prepared three slides of each fraction for microscopy. To analyze the results and to see if there is a significant difference we used one-way analysis of variance (ANOVA) and student T-test.

E12-FRI

BACTERIAL AND FUNGAL COMMUNITIES IN AERATE SOILS

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The composition of microbial and fungal soil communities greatly contributes to the success or failure of a crop. Root zone aeration has been shown to enhance crop production. Does the aeration change the composition of a bacterial community to a more beneficial or more innocuous community? The benefits of this study include finding methods to enhance good microbial communities that can lead to healthier agricultural products that whose production requires less pesticides use. Soil from a table grape vineyard was used to analyze the bacterial and fungal communities. The experimental soil was aerated with an irrigation system that delivers small bubbles of air injected with the irrigation water and the control soil was irrigated with a conventional irrigation system. The DNA of the control and experimental soils was extracted, amplified with labeled primer for bacterial and fungal organism. The terminally labeled amplification products were TRFLP analyzed by restriction digest and run on sequencing column. The results show that aeration of agricultural soil supports an increase in biomass. The concentration of DNA in experimental soils was higher than the control samples. The increased biomass contains more diverse bacterial and fungal communities and shows an increase of aerobic microorganisms. Aeration of agricultural soils enhances microbial numbers and bacterial diversity and this increased microbial biomass is compatible with enhance crop productivity. Future studies will quantify the presence of genes involved in nitrogen metabolism; including genes coding for nitrate reductase, ammonium oxidase and beneficial nitrogen fixation genes.

E13-SAT

APPLICATION OF DENATURING GRADIENT GEL ELECTROPHORESIS (DGGE) FOR IDENTIFYING FUNGAL DIVERSITY IN COASTAL PRAIRIE SOILS

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The research goal Is to identify the fungal diversity (mainly of the phyla *Ascomycota* and *Basidiomycota*) in coastal prairie grasslands, compare the change in fungal generations over three treatments: native prairie, restored prairie, and farmed prairie; as well as study the functional characteristics of fungi. My individual goal was to optimize the running conditions for the Denaturing Gradient Gel Electrophoresis in order to run soil samples from prairie grassland and isolate fungal DNA for sequencing. This also provides a mass soil fingerprint, which allows for a comparison to be done over all three treatments. DGGE is a molecular technique where rDNA is separated up to single base pair differences, causing distinct bands to be formed where each band is equivalent to a species. For the duration of this research period I used previously identified and sequenced *Basidio* DNA as controls for the DGGE. In order to optimize the conditions I had to determine ideal time, gradient, and dilution of DNA. By the end of the research session I had not yet established the ideal conditions; however, resolution of DNA strands improved on a gel of gradient 40% to 70% with a dilution of 1:20. I will continue this project in order to determine prime running conditions by using soil samples and *Ascomycota* DNA instead of only control DNA.

E11-SAT

SCREENING FOR NOVEL ANTIBIOTICS IN NEW MEXICO CAVE MICROBIAL COMMUNITIES

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Caves conjure up images of darkness and an overall absence of life. In truth, caves are one of nature's remaining terrestrial frontiers. The characteristically musty smell associated with caves is the byproduct of one group of bacteria, the actinomycetes, which are the source of the majority of the world's antibiotics. My research focuses on developing media to culture these organisms, screening for novel antibiotics produced by these microbes, and determining the abiotic factors involved in producing antibiotics. Cave formations and soil were aseptically sampled, streak-plated onto solid media (R2A or ½ R2A), and incubated in the cave for 24 hours. These were then grown in a 15˚C incubator for 5 days and subcultured onto R2A plates. To screen for antibiotic production, subcultures were spotted onto either *Escherichia coli* (Gram-negative) or *Staphylococcus saprophyticus* (Gram-positive) lawns, and monitored for the development of zones of inhibition. Preliminary data from Fort Stanton Cave, NM suggests that cave bacteria do produce antibiotics. Surprisingly, "hits" came from areas of high human visitation. Three Fort Stanton organisms produced large zones of inhibition on both lawn types. Two other organisms were effective against the Gram-positive analog, while another was effective against the Gram-negative. These preliminary results contradict the hypothesis that novel antibiotics are more frequent in low-human impacted, remote cave locations and tell us that cave microbes produce antibiotic secondary metabolites. Similar testing is currently underway for samples obtained in Carlsbad Cavern. Continuing to look to nature for next generation medications or skeletons for revolutionary synthetics remains important.

E10-SAT

ENHANCED PROPARGYL BROMIDE DEGRADATION BY SOIL BACTERIA

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Due to the recent phase-out of methyl bromide, alternative soil fumigants are currently being tested for their efficiency and fate in the environment. Propargyl bromide is an alternative that has shown promise as a fumigant but little is known about its metabolism by bacterial communities. The purpose of this study is to determine the rates of degradation within isolated strains of degraders. We have used enrichment culture techniques to isolate ten strains of bacteria from soil that are capable of using propargyl bromide as a sole source of carbon and energy. The ten different strains of microorganisms were grown in minimal media (MMO) broth and mixed with propargyl bromide and sterilized soil. After a period of growth, samples were removed from the culture and extracted. Gas chromatography was used to determine the concentration of propargyl bromide from the extracted samples. The abiotic control showed an approximate reduction of 2% over 4 hours and 10% over 7 days in MMO broth. The rate of degradation by the ten bacterial strains averaged approximately 41% over 4 hours and approximately 53% over 7 days. In soil, 64% of propargyl bromide degraded after the first 8 hours of incubation compared to 16% of the control. Work has begun to examine propargyl bromide degraders for genes known to be involved in methyl iodine and methyl bromide degradation using PCR and Southern hybridization. Results should aid in the development of bio-remediation strategies and provide insights into appropriate use of propargyl bromide in the field.

E8-SAT
BACTERIAL ABUNDANCE IN THE SOUTH PACIFIC
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Bacteria are a vital resource to the livelihood of our world. They play major roles in the cycling of important elements like carbon, nitrogen, and phosphorus. The bacteria can only take up the dissolved form of organic matter (DOM) into their cells. Bacteria participate in the microbial food web by assimilating dissolved organic carbon (DOC) into their cells that no other organisms can. Bacteria are very tiny in size, most ranging from about 0.1 μm to 1 μm in length; however, they have a very large abundance or concentration in even just a milliliter of water. Samples of water from different areas, depth, temperature, and other different parameters can give different amounts of bacterial abundance. In this project we will measure the abundance of bacteria in the South Pacific against certain parameters and have an understanding of what could be making bacteria more abundant in different regions of the South Pacific. We assume that bacterial abundance will be higher near the surface of the water because photosynthesis can occur where light penetrates. Through photosynthesis, organic molecules are made, and the bacteria respire the DOM into inorganic carbon. We predict that more moderate temperatures will give a higher abundance as opposed to really hot or cold waters. We will be counting bacteria through flow cytometry, a machine that counts individual cells. Counts will also be taken using a microscope to ensure correct numbers.

MOLECULAR AND CELLULAR BIOLOGY

E2-SAT
DIFFERENTIAL EXPRESSION OF ADHESION MOLECULES ASSOCIATED WITH HEMATOPOIETIC COMMITMENT
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Adhesion molecules mediate cell-cell interactions in a number of cell systems, but their role in murine embryonic stem cell (mESC) differentiation is incompletely understood. To better understand the molecular basis for cell-cell interactions between mESC as they differentiate, the expression of adhesion molecules in embryoid bodies (EB) was analyzed. Expression of forty adhesion molecules was analyzed with quantitative RT-PCR during EB formation. Thirteen target molecules were differentially expressed. Six out of thirteen (46%) differentially expressed proteins were junction proteins; gap junction, tight junction or adherens junction proteins. These results suggest that the six junction proteins may have a role in cell fate decisions in the differentiation of mESC into the hematopoietic lineage. Zona occludens-2 (ZO-2) was among the differentially expressed junction proteins. ZO-2 can bind to components of the gap, tight and adherens junction pathways, ultimately affecting the proliferation and differentiation of mESC. Short hairpin RNA (shRNA) sequences were generated which knockdown ZO-2 expression to evaluate the role of ZO-2 in hematopoietic commitment. Understanding the adhesion molecule interactions between mESC allows for the possibility of guiding them towards specific lineages in the future.

D44-SAT
DEVELOPMENT OF A RAPID Y ALU REPEAT SCREENING TEST FOR MALE DNA FOR FORENSIC CASEWORK
Arturo Aguilar, Steven Lee, Kimberly Clabaugh. *San Jose State University, San Jose, Calif.*

Forensic DNA has become an important tool for solving crime. Approximately 169,000 rape case samples await testing the current utilized screening tests are tedious and may lead to false positive or false negative results. The goal of this study is to develop an accurate, rapid, Y chromosome specific screening test for male DNA. The chosen target for the male DNA primers are Y Alu derived sequences, STYa and Y 90. Two different strategies for detection of amplicons have been tested: (1) molecular beacons and (2) scorpion primers. Scanning parameter optimizations have been determined for the fluorescent dye FAM used in detection of the primers and PCR products. Preliminary results indicate FAM detection is optimal with an excitation by a 488 nm laser. The use of a 577/8 nm band pass filter with a 555 nm long pass blocking filter at a focal depth 1.5 mm, and a photomultiplier tube sensitivity setting of 45% on a fluorescent scanner (FMBIO III plus, MiraiBio Inc. South San Francisco, Calif.). Optimal parameters for amplification and detection using replicate positive male DNA samples and female DNA were used to test primer specificity. Optimization of annealing temperature, primer concentration, sensitivity of input template DNA and results using different ratios of male and female mixtures will also be presented. The results will be used for further testing on previously screened samples. This new assay has the potential to greatly improve time of sexual assault screening and may alleviate the backlog evidence samples.

D55-SAT

ROLES OF YEAST RAD51, RAD55, AND RAD57 ATPASES IN DNA DOUBLE-STRAND BREAK REPAIR BY HOMOLOGOUS RECOMBINATION

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Improper repair of DNA double-strand breaks (DSBs) caused by environmental and normal metabolic processes can destabilize the genome lead to tumor formation. Homologous recombination (HR) is one mechanism that repairs DSBs. The present study focuses on gene conversion, a specific type of HR mechanism. The Rad51, Rad55, and Rad57 proteins play key roles in HR and mutant cells lacking one or more of these proteins show reduced HR efficiency and altered HR product spectra. HR results in short, continuous gene conversion tracts, but null mutants display longer tracts with frequent discontinuities. A discontinuous gene conversion tract is when a central genetic marker is not converted but flanking markers are converted. Rad51, Rad55, and Rad57 are ATPases but the roles of ATP hydrolysis by these proteins are unknown. We constructed cell lines that express ATPase-defective versions of Rad51, Rad55, and Rad57 singly and in double/triple mutant combinations. In each case, a conserved lysine residue in the ATPase domain was changed to arginine ("K→R" or "KR" mutations, which permit ATP binding but not hydrolysis). DSBs can be introduced into a target gene harboring an HO endonuclease recognition site upon ectopic expression of HO nuclease (regulated by the galactose-inducible *GAL1* promoter). Repair of these DSBs by HR using a homologous chromosome as a template is then monitored by genetic and molecular assays in wild-type and KR mutant cells. This will allow us to test the hypothesis that ATP hydrolysis by Rad51, Rad55, and/or Rad57 regulates HR efficiency and outcome.

D42-FRI

TRACKING CHROMOSOME MOVEMENTS DURING MITOSIS

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Mitosis is the process of nuclear division that results in two identical daughter cells. The mechanisms of chromosome movement during mitosis, especially during metaphase and the checkpoint, and of kinetochore attachment to microtubules are poorly understood. The current tension/strain across kinetochores model states that tension across the centromere plays a major role in coordinating chromosome movement.The goals of this research project are to monitor positions of kinetochores and spindle during mitosis and demonstrate correlation between motions of sister kinetochores. We will use spinning disc confocal microscope that will allow us to monitor kinetochore movements in mitosis. This microscope will allow us to obtain 3D images and monitor rapid movements with high temporal and spatial resolution. While a single-point scanning confocal microscope could also perform these tasks, a spinning disc confocal reduces photobleaching and phototoxicity in the cells, which is a huge advantage.We will track the distance between the sister kinetochores relative to the spindle poles during mitosis. We hope to prove that a relationship exists between the movements of the two sister kinetochores. Stable cell lines will be created with fluorescently tagged proteins to make imaging feasible. The spindle poles will be tagged with RFP (red fluorescent protein) and the kinetochores will be tagged with GFP (green fluorescent protein). The spinning disc confocal microscope will be used to image live cells undergoing mitosis. Data will be collected from the images and analyze it with particle tracking software. Statistical analysis will help determine what correlation, if any, exists between sister kinetochore movements during mitosis.

D54-SAT

EVOLUTION OF SNAIL GENE

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Snail genes are conserved in both vertebrates and invertebrate species. Members of the Snail family (sna1, sna2 and sna3) are expressed in mesodermal derivatives of species such as *Xenopus*, *Danio rerio*, *Mus musculus*, and *Tribolium*. The Snail genes encode for a zinc-finger protein that regulates various cell functions such as cell movement, cell division, cell adhesion, and cell death. The main purpose of my research project was to determine the evolutionary history of Snail genes using phylogenetic analyses. Three questions guided my investigation: (1) Was the function of Snail homologs conserved?, (2) is Snail as widely distributed as Twist (a transcriptional regulator of Snail)?, and (3) are Snail homologs expressed in species of similar lineage? My research shows that in some species the function of snail was conserved. I aligned all available (28) DNA sequences of Snail homologs using ClustalW Multiple alignment (a BioEdit application). The alignment will be used to do phylogenic analysis such as constructing a phylogenic tree, AMOVA, haplotype and nucleotide diversity measures, the number of polymorphic sites, and Tajima's D test of neutral evolution. The ZnF-domain is 60% to 70% conserved. I will use degenerate PCR primers designed from the conserved zinc-finger region to obtain sequences from organisms where Snail genes have not yet been identified (such as sea urchins, flatworms, rotifers, comb jellies, and blood worms). I expect that if Snail is present in those species, then they will be close evolutionary relatives to the Sea squirt sna1 homolog. (Supported by NSF-REU grant # DBI-0647160.)

D50-SAT

ROLE OF THE BETA ADRENERGIC RECEPTORS IN THE CARDIAC RESPONSE TO BETA BLOCKER THERAPY

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Arrhythmias are electric abnormalities leading to disruption of regular heart rhythms, causing about 5% of all cases of sudden cardiac death (SCD) in the U.S. The central nervous system releases endogenous catecholamines, which bind to adrenergic receptors such as β1 and β2 (β1/2ADR) on the heart and may increase the risk of arrhythmias. Patients with arrhythmias treated with β-blocker therapy result in a significant reduction in the incidence of cardiac events. However, not all patients respond to β-blocker therapy and the molecular basis of this lack of response is poorly understood in children. Previous studies in adults with heart failure identified S49G and G389R single nucleotide polymorphisms (SNP) in β1ADR associated with the refractoriness using β-blocker therapy. We sought to investigate whether those SNP affect this treatment in children with arrhythmias. We setup a pilot study to test non-responsive subjects, responsive individuals, patients with heart diseases without arrhythmias and general control subjects. Polymerase chain reaction (PCR) was followed by direct DNA sequencing amplicons covering the coding sequence of both *ADRB1* and *ADRB2* genes. The preliminary screening process identified the S49G and G389R SNP in β1ADR (4/6 non-responsive patients respectively), while a novel ADBR2 variant was also identified in a non-responsive patient. The S49G and G389R was also found in 5 non-arrhythmic patients. We will need to expand the patient cohorts to reach statistical significance. However, finding β1ADR or β2ADR variants in subjects with arrhythmias will greatly help understanding the role these receptors play in unsuccessful responsiveness to β-blocker therapy.

D56-SAT

SKELETAL MUSCLE FATIGUE AND RYR1

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Ca^{2+} release by the sarcoplasmic reticulum ryanodine receptor (RyR1) is essential for excitation-contraction (EC) coupling in skeletal muscle and its function is regulated by numerous bounded proteins including FKBP12 and PKA. When FKBP12 binds to the RyR1 macromolecular complex, it inhibits the channel by stabilizing the closed state. We hypothesized that PKA hyperphosphorylation of RyR1 is correlated with exercise-induced skeletal muscle fatigue and could explain the defect in Ca^{2+} release observed in skeletal muscle. A mouse model of exercise-induced skeletal muscle fatigue was developed, and the regulation of RyR1 by PKA phosphorylation during chronic and intermittent exercise was studied. Histological comparison of isolated extensor digitorium longus (EDL) muscle from exercised and unexercised mice skeletal muscles shows myofibrillar disorganization, interstitial expansion, and mild inflammatory damage consistent with previously reported intensive exercise regimens. Immunoprecipitation of RyR1 from soleus muscle of exercised and unexercised mice, followed by blotting for total RyR1 and with a S2843P phospho-specific antibody demonstrated RyR1 hyperphosphorylation at S2843 in the exercised mice. In addition, RyR1 hyperphosphorylation in the exercised mice was associated with a decrease in the bound FKBP12 that coimmunoprecipitated with the RyR1, suggestive of Ca^{2+} leak in the exercised skeletal muscles. We also found that there is a correlation between the intensity and length of exercise and RyR1 PKA phosphorylation. We conclude that exercise leads to hyperphosphorylation of RyR1 in an intensity and duration dependent manner and further speculate that it could mediate fatigue by depleting the SR of calcium.

E1-SAT

SYNTHETIC GENETIC ANALYSIS OF HISTONE H3/H4 MUTATIONS

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Eukaryotic DNA is packaged in cells as chromatin, a complex of DNA and proteins. Nucleosomes are the basic subunit of chromatin, consisting of about 146 nucleotides of DNA wrapped around a proteinaceous core composed of two copies each of the four core histones. These are arranged as two histone H2A-H2B dimers flanking a central histone H3-H4 tetramer. By binding to DNA histones block transcription initiation and elongation. To overcome this barrier, histones undergo post-translational modification in their amino-terminal tails. These modifications regulate recruitment of chromatin remodeling complexes that alter nucleosome position and conformation. These include, sites of histone-histone interactions, histone-DNA interactions, histone-remodeler interactions and residues that target post-translational modification. We have created a library of individual yeast strains carrying more than 70 distinct mutations in histones H3 and H4. Through a series of simple replica platings, the strains in this library can be crossed to a query strain containing some mutation of interest, to create a set 70-plus double mutants. These double mutants may then be assayed for phenotypes that may give insights into functions of the nucleosome and the protein encoded by the query mutation. To test this system, we crossed a strain containing a null allele of transcription elongation factor Spt4 to the histone library and screened for synthetic lethality. The majority of the interactions observed in this system were confirmed by traditional methods. Finally, based upon our data, we will present evidence for a previously unappreciated role in transcription elongation for a specific surface on the nucleosome.

D55-FRI

SILENCING OF CLAUDIN-4 IN MOUSE EMBRYONIC STEM CELLS

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Embryonic stem cells (ESC) are characterized by their ability to differentiate and self renew. Stem cell differentiation through the hematapoietic lineage can be accomplished using embryoid bodies (EB). Our lab has shown adhesion molecules are differentially expressed during hematapoietic differentiation of ESC. Adhesion molecules are expressed on the surface of the cell and are involved in cell-cell interactions. These interactions activate intracellular signaling which results in regulation of cell growth and differentiation. Claudin is an adhesion molecule that is a member of the tight junction pathway which forms impermeable barriers between cells. Claudin-4 is down regulated during early hematapoietic differentiation. My goal is to further characterize the role of Claudin-4 during hematapoietic cell fate commitment. This is accomplished by silencing the transcript levels of Claudin-4 in ESC using RNAi. DNA constructs that are specific for the inhibition of Claudin-4 transcript levels have been generated. These constructs have been introduced into ESC that have been sorted using florescent activating cell sorting. The expression of Claudin was analyzed using quantitative Reverse Transcriptase PCR (RT-qPCR) to validate silencing efficiency. Blocking the expression of adhesion molecules, such as Claudin-4, and analyzing its effect on hematapoietic differentiation will help in understanding the mechanisms involved in early hematapoietic cell fate decisions.

D49-FRI

STRATEGIES FOR CHILE PEPPER REGENERATION AND TRANSFORMATION

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Chile peppers are a high value crop in the world. Most Chile peppers are susceptible to different phytopathogenic fungi, bacteria and viruses that cause extensive losses in yield and quality of peppers. While traditional breeding techniques have been of great value for Chile pepper genetic improvement, biotechnological techniques involving plant tissue culture and recombinant DNA technologies could be powerful auxiliary tools to accelerate and achieve this goal. We are currently studying Chile regenerations in tissue culture using hypocotyls and cotyledon explants from 10 day old seedlings. We have used agro-infiltration to understand the interactions and infections capabilities of different *Agrobacterium* strains. Agro-infiltration is a powerful transient expression system which has several advantages as the gene expression can be detected in a short time after DNA delivery. Infiltration of tobacco leaves with different *A. tumefaciens* strains containing *E. coli* β-*glucuronidase* (GUS) reporter gene constructs with and without the intron showed GUS expression in 3 to 5 days post infiltration. We are currently using these *Agrobacterium* for chile transformation. Our initial assays performance on putative chile transformants show the expression of GUS reporter gene in several independent cultures. By successfully using the agro-infiltration techniques and understanding the regeneration and transformation stages we will be able to integrate the β-*glucuronidase* (GUS) reporter gene into NM-64, B-58, and 40028 chile cultivars. (Supported by NIH R25 GM48998.)

D43-FRI

A CONSTRAINT-BASED APPROACH TO MODEL AND PREDICT MIRNA SPECIFICITY

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The regulation of gene expression involves a complex network of events that occur at multiple layers of RNA processing, including control of expression both before and after transcription. Accumulating evidence suggests that a set of small RNAs, termed microRNAs (miRNAs), are important mediators of posttranscriptional regulation in higher eukaryotes that cause the degradation or translational inhibition of target mRNAs. The specificity of miRNA:mRNA target pair recognition appears to occur through conserved base pair interactions between the 3'UTR of the target mRNA and a 5' seed sequence (~8 bp) of the miRNA. Such seed sequences, however, are expected to occur every 4^8 or 65,356 bases, suggesting that miRNAs must achieve specificity through a higher order mechanism, possibly by combinatorial interactions on the mRNA. We are interested in characterizing the mechanism by which miRNA achieve specificity. We hypothesize that combinatorial interactions between multiple miRNAs and a given target mRNA confer specificity to the miRNA-mediated regulation scheme. In our model, miRNAs regulate posttranscriptional events much like transcription factors (TFs) regulate transcriptional activation/repression. TFs, like miRNAs, bind to their respective promoters through conserved binding motifs and achieve a high degree of specificity through combinatorial interactions with other TFs both *in cis* and *in trans*. We will utilize sets of known miRNA seed sequences, TF promoter binding motifs, and their respective target or promoter sequences to explore the conditions under which we can develop a coherent global and local architecture of the GRN that corresponds to experimental observations.

D52-FRI

EFFECT OF UP-REGULATING SUMOYLATION ON INFLUENZA A VIRUS REPLICATION

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SUMO (small ubiquitin-like modifier) is a post-translational modification that affects the function of proteins by altering their stability, enzymatic activity, cellular localization, and interactions with itself and other proteins. Influenza virus replication occurs in the host cell nucleus and the host cell sumoylation system is known to be more active in the nucleus. We propose that up-regulation of sumoylation in the host cell will down-regulate the virus' ability to replicate. To test our hypothesis, we increased sumoylation by transfecting HEK293 cells with a Ubc9-IRES-SUMO plasmid, and then infected the cells with H3N2 or H1N1 influenza A virus. Viral titers were used to determine if there was a difference between untransfected cells and transfected cells in term of their ability to support viral multiplication. Immunofluorescence assays were used to determine if there was a delay in infection progression with increased Ubc9 and SUMO production in each cell. The viral titers showed a substantial decrease in viral multiplication in the cells that were transfected with the Ubc9-IRES-SUMO plasmid. The immunofluorescence assays showed either a decrease or absence of expression of a late viral protein (M1) in cells that over-expressed Ubc9 and SUMO. Overall, cellular increase of sumoylation appears to exert a protective cellular effect against influenza virus infection. Our results may lead to the development of novel anti-influenza therapies that will work against the virus regardless of type, strain, and antigenic properties. Furthermore, by targeting cellular systems, such therapies will provide minimal opportunities for the development of resistant viral strains.

D54-FRI

FUNCTIONAL CHARACTERIZATION OF ENDOGLIN DOMAINS, A TGF-BETA CO-RECEPTOR ASSOCIATED WITH HEREDITARY HEMORRHAGIC TELANGIECTASIA

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Mutations in the Endoglin gene are responsible for the hereditary hemorrhagic telangiectasia, an autosomal dominant vascular dysplasia. Endoglin is an auxiliary component of transforming growth factor beta (TGF-β) receptor complex in endothelial cells, interacting with the TGF-β receptors type I (ALK-1 and ALK-5) and type II (TβRII), and modulating the cellular signaling of TGF-β. Recent studies have demonstrated that extracellular region of endoglin has two structural domains, the Orphan domain (OD) and the Zona pellucida domain (ZPD). To better understand the molecular mechanisms by which endoglin regulates vascular remodeling and angiogenesis, we have generated a novel endoglin truncated construct containing the ZPD cDNA using polymerase chain reaction (PCR) amplification. Cloning of this truncated construct into an expression vector (pDisplay, Invitrogen) has allowed the analysis of physical and functional interactions between the endoglin ZPD and the TGF-β receptors ALK1, ALK5 and TβRII. TGF-β receptors and endoglin ZPD were co-transfected in HEK 293T cells (human embryonic kidney cells), followed by cellular lysis and inmunoprecipitation with protein G using specific antibodies. Total cellular lysates and immunoprecipitates were analyzed by western blot to reveal potential associations between endoglin ZPD and the individual TGF-β receptors. To study the functional involvement of ZPD in TGF-β signaling, human endothelial cells (HMEC-1) were co-transfected with the expression vector (pDisplay/ZPD) and reporter vectors specific of the ALK5 (pCAGA-Luc) or ALK1 (pBRE-Luc) pathways. The results of these studies will help to elucidate the functional role of endoglin ZPD in the TGF-β receptor complex.

D51-FRI

TRUNCATION AND MUTATION OF CYANOBACTERIAL PHYTOCHROME-LIKE GENES TO PRODUCE RED FLUORESCENT PROTEIN

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Certain cyanobacterial genes share sequence homology with plant phytochromes. Alignments of the genes reveal common features of the domains, which describe GAF, PHY, PAS, PAC, HAMP, MCPsignal, CBS, GGDEF, EAL, HisKA, HATPase_c in both plants and cyanobacteria. We are studying five genes and their protein gene products in the Cph2 family from the cyanobacterium, *Nostoc punctiforme*. The Cph2 family was chosen to study because of its homology with Cph1N514. A mutation of CphN514 at tyrosine 176 has created a red fluorescent protein, Phytofluor1. The Cph2 genes contain several GAF domains, which are the chromophore binding domain. We have truncated our Cph2 genes to contain minimal GAF domains in order to produce small highly fluorescent red proteins that might be useful tools similar to Green Fluorescent Protein (GFP). We have completed PCR from genomic DNA, ligation into pBAD plasmid and transformation of *E. coli* for expression. We have successfully obtained 200aa and 400aa GAF containing truncations of the Cph2 genes. The expressed proteins appear green,

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which show characteristics of cyanobacterial phytochromes, but we have been unsuccessful in purification using nickel columns. We are in the process of ligating into a plasmid vector with intein tag-chitin binding domain (pBAD-CBD) to improve our purification procedure. After we have perfected our expression and purification system, we plan to mutate our Cph2 proteins at the homologous position of tyrosine 176 in Cph1N514 to produce red fluorescent proteins similar to Phytofluor1.

D53-FRI

DOES CLATHRIN HEAVY CHAIN PROTEIN HAVE A FUNCTION IN NOTCH SIGNALING?

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Mastermind (MAM) is a transcriptional co-activator important for activation of Notch target genes. MAM interacts with the intracellular domain of Notch and is required for activation of Notch specific target genes by recruiting p300, as well as yet unidentified other proteins. In an effort to identify proteins that interact with MAM, we used GST-pulldown assays and identified clathrin heavy chain (CHC17) as a potential novel protein. We hypothesize that CHC17 is also required with MAM for full, robust activation of Notch specific target genes. GST-pulldown assays were performed with full-length MAM and various truncations using a nuclear extract prepared from Hela cells. Silver stains were performed to identify proteins that interacted with Mastermind and were excised and sequenced by Maldi-TOF Mass Spectroscopy. Western blots were performed on CHC17 from pulldown experiments. CHC17 was PCR amplified and cloned using Gateway technology into pcDNA6-BIOEASE following standard cloning methods. Reporter gene assays will be performed with over-expressed CHC17 and small interfering RNA (siRNA) knockdown experiments with CHC17 to measure effect on activation of Notch specific target genes. CHC17 was found to interact with full-length MAM. Truncations of Mastermind identified that CHC17 specifically interacted with the C-terminus. Current studies are underway to clone and test CHC17 by over-expression and knockdown with siRNA to measure Notch activity in reporter gene assays. We expect CHC17, in the presence of MAM, to co-activate Notch specific target genes. (Supported by NSF-REU grant # DBI-0647160.)

E5-FRI

IDENTIFICATION OF FACTORS REGULATING H2A PHOSPHORYLATION AT A DNA DOUBLE-STRAND BREAK IN BUDDING YEAST

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DNA repair occurs in a chromatin context, and understanding how chromatin structure is regulated in response to DNA double-strand breaks (DSBs) is important for defining the role of chromatin in DSB repair pathways. Phosphorylation of histone H2A serves as an important signal in detection of DSBs and accumulation of DNA repair proteins. H2A is rapidly phosphorylated in response to DSBs in all organisms, spreading over thousands of base pairs, and as DNA repair progresses, it is dephosphorylated. My research aims to identify factors involved in the levels, spreading, and turnover of H2A phosphorylation (γH2A) at DSBs. Western blot analysis was used to determine DSB-induced global γH2A levels in nine mutant strains defective in checkpoint activation, DNA repair, chromatin remodeling, or nucleosome assembly. The results showed that deletion of *ASF1*, encoding a histone chaperone, led to increased levels of γH2A, while deletion of *MEC1*, encoding a checkpoint kinase, abolished γH2A formation when compared to wild type cells. The effects of these two mutations on γH2A formation near a defined DSB were further analyzed using chromatin immunoprecipitation. This method showed that γH2A was retained at the DSB longer in an *asf1*Δ mutant, and that local levels of γH2A were decreased in a *mec1*Δ mutant. γH2A has been found to play a key role as a tumor suppressor in humans. By understanding the factors that control the formation and turnover of γH2A, this research has the potential to reveal new insight into the role of γH2A in cancer progression.

D36-FRI

CROSSTALK BETWEEN THE G-PROTEIN AND INTEGRIN-DEPENDENT PATHWAYS: IMPLICATIONS IN ASCIDIAN SPERM ACTIVATION

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Ascidia ceratodes sperm undergo mitochondrial translocation (MTL), which is characterized by sperm mitochondria rounding and translocation off the head and tail. Binding of sperm membrane proteins (integrin, N-acetylgucosaminadase, G protein coupled receptor (GPCR)), and egg surface proteins initiate MTL. Important processes associated with MTL include: cell-cell recognition, adhesion, and activation signaling of actin and myosin. The focus of this study is on the activation of actin:myosin interactions through upsream proteins: ROCK, myosin light chain kinase (MLCK), and Rho GTPases. Samples were prepared with 5 μL of sperm cells suspended in 5 mL artificial seawater (ASW, pH 6.8). 200 μL of the mix was placed on coverslips (10 min) and incubated with an inhibitor (15 min) before induced activation (10 min) by either mAb 12G10 (integrin agonist) or Mas-7 (G-protein agonist). Sperm were fixed in 1% formaldehyde ASW, viewed under a microscope and scored for activated sperm. Inhibition of all RhoGTPases with *C. difficile* toxin A (150 pM) reduced integrin activation from 54.43% to 0.43%. Both integrin and G protein-induced activation were decreased by the Rac1 inhibitor NSC23766 (125 nM) to negative control levels.

Inhibition of ROCK with the inhibitor Y-27632 (10 uM) reduced activation levels from 33.85% to 7.35%. The MLCK inhibitor ML-9 (25 uM) decreased integrin activation from 31.5 % to 3.15%. This study supports the hypothesis that two crosstalk pathways occur in ascidian sperm activation, one being the integrin to focal adhesion kinase to RhoGTPase to ROCK to MLCK to myosin II activation pathway, and the other being the GPCR to $G_{alpha12}$ or G_o to elevated Ca^{2+} to Ca-calmodulin to MLCK to myosin II pathway.

D44-FRI

NUCLEAR PORE COMPLEX: IDENTIFICATION OF ANCHORING DOMAINS FOR FG-NUCLEOPORING

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The nuclear pore complex (NPC) is large multi-protein complex that is embedded in the nuclear envelope. Acting as a gate, the NPC regulates the import and export of large molecules (>50 kDa) but allows the diffusion of smaller molecules between the nucleus and cytoplasm of cells. The proteins that make up the NPC are known as nucleoporins or "Nups." FG-Nups, are named after their content of many phenylalanine-glycine peptide repeats, and are "natively unfolded" in structure creating a meshwork of flexible, filamentous-like proteins. These proteins, more importantly their FG domains, have been shown to participate in the translocation of cargo through the NPC and forming a size-selective gate for the NPC, but still which domain of the FG-Nups anchors them to the NPC is still unknown. In order to determine the anchoring domains of FG-Nups, we used truncated FG-Nup proteins tagged with CFP (cyan fluorescent protein). The site and length of the truncated FG-Nup protein was selected by its amino acid sequence conservation when aligned with four other Saccharomyces species. We were able to detect the localization of the CFP-tagged truncated proteins to the nucleus membrane by means of fluorescent microscopy. The deletion of non-essential FG-Nups genes intensified the localization of our CFP-tagged truncated versions by the removal of competitive endogenous FG-Nups. Here we identify specific domains in FG-Nups that are responsible for their anchoring at the NPC and through this hope to decipher the biogenesis of the NPC.

E5-SAT

NITRIC OXIDE IS REQUIRED FOR ACTIVATION OF CELLULAR ENERGY-SENSOR, AMP-ASSOCIATED PROTEIN KINASE (AMPK) IN SKELETAL MUSCLE

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We study the potential for the signaling molecule, nitric oxide (NO) to phosphorylate and activate the cellular energy-sensor AMP-associated protein kinase (AMPK). Previous studies have shown that NO is sufficient to induce metabolic adaptations in muscle cells. NO, formed enzymatically by Nitric Oxide Synthase (NOS), is involved in glucose transport and mitochondrial biogenesis in skeletal muscle. Skeletal muscle is the major site of insulin-stimulated glucose disposal, and insulin resistance. Exercise training improves insulin sensitivity and metabolic control in part by activating AMPK. AMPK induces adaptive responses such as the upregulation of the GLUT 4 glucose transporter. Thus, activation of AMPK and ensuing skeletal muscle adaptations improve metabolic efficiency and ameliorate the insulin resistant syndrome. Here we hypothesize that: (1) *treatment of L6 myotubes with the NO-donor, SNAP, will induce AMPK phosphorylation*, and (2) *treatment with the NOS inhibitor, L-NAME, will prevent the AMP-mimetic drug AICAR-induced phosphorylation of AMPK*. Rat L6 myotubes were differentiated by serum withdrawn to form confluent myotube cultures. Cells were treated with different concentrations of AICAR, L-NAME, and/or SNAP, for 1 hour. Immunoblot quantification of total and phosphor-AMPK served as assessments of AMPK activation. We concluded that $\geq$2 mM concentrations of AICAR treatment showed a significant 50% increase in AMPK phosphorylation compared to control whereas treatment with L-NAME totally prevented this effect. Also, 10 μM SNAP treatment caused a 1.6 fold increase in AMPK phosphorylation. In the future we plant to study the effect of NO on LKB1, PGC-1 alpha and GLUT4 mRNA and protein expression in skeletal muscle.

D38-SAT

DETERMINING THE PHYLOGENETIC AFFINITY OF *ENDOLIMAX NANA* THROUGH COMPARATIVE GENE SEQUENCE ANALYSES

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Taxonomy, the naming and grouping of organisms, is often at odds with true evolutionary history, or phylogeny. Comparative gene sequence analyses (molecular phylogenetics) are powerful tools and are often the only way to infer the evolutionary history of organisms that are otherwise difficult to classify. *Endolimax nana* is a specific taxon of phylogenetic importance closely related to the *Entamoeba histolytica*, the causative agent of amoebic dysentery. The primary purpose of this research is to deduce the phylogeny of *Endolimax nana* using comparative gene sequence analyses. Since molecular data for *E. nana* is almost nonexistent, heat shock protein 90 (hsp90) and alpha-tubulin genes were sequenced from the organism because they are both highly conserved, yet phylogenetically informative. Portions of the genes were PCR amplified from cDNA using degenerate primers, and were then cloned into *E. coli* and later sequenced. Once the genes were sequenced, they were conceptually

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translated to their corresponding protein sequences and added to a multiple sequence alignment that included various species of Amoebozoa and a wide array of lineages that span eukaryotic diversity. A maximum likelihood (ML) tree was created using the program "proml." The resulting tree suggests that *E. nana* is not an Entamoebae, but either is, or is sister to the pelobionts. Ultimately, the culmination of this research will lead to a better understanding of how amoebic intestinal parasites evolved and will clarify the phylogenetic relationships among the organisms.

D37-SAT

CENTRINB BINDS INTERACTING PROTEINS IN A CALCIUM DEPENDENT MANNER IN *DICTYOSTELIUM DISCOIDEUM*

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Dictyostelium discoideum is a eukaryotic cellular slime mold that inhabits forest soil. The process of cytokinesis (cell division) is remarkably similar in *Dictyostelium* and mammalian cells. Centrins are members of the calcium binding EF-hand superfamily of proteins that associate with the microtubule organizing centers during cytokinesis. Recently, centrins have also been associated with mRNA nuclear export and DNA repair. There are two known centrins in *Dictyostelium*. DdCenA is known to localize to the centrosome during cytokinesis. DdCenB (centrinB) has been demonstrated to localize to the nucleus during interphase. We hypothesize that DdCenB interacts with other *Dictyostelium* proteins in a calcium dependent manner during the cell cycle. In this study, a cDNA fragment encoding DdCenB was cloned in-frame into the pQE-30 vector behind a 6x-His tag. The DdCenB protein was expressed in M15[pREP4] *E. Coli* cells and subsequently purified on a Ni-NTA agarose matrix. Purified DdCenB will be incubated with *Dictyostelium* lysate in the presence or absence of calcium. SDS-PAGE will be performed to confirm the existence of interacting proteins, which will be identified by mass spectrometry. Since cell division is an essential physiological process and is implicated in many human diseases, it is important to understand how calcium affects the function of centrins.

D53-SAT

EXPRESSION OF THROMBOXANE A2 RECEPTOR GENE TRANSCRIPT IN RABBIT CARDIAC MYOCYTES

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Previous studies in this laboratory have shown that thromboxane A2 (TxA2), an arachidonic acid metabolite that is released by blood platelets, activates cardiovascular and pulmonary reflexes thereby altering blood pressure, breathing, and heart rate. A more recent study from this laboratory has shown that TxA2 induces arrhythmias independent of coronary blood flow changes. We hypothesize, therefore, that TxA2 many induce arrhythmias via a direct receptor mediated effect on heart tissue. We further hypothesize that TxA2 is expressed at a higher level in cardiac Purkinje cells (conducting cells) than cardiac muscle cells. This hypothesis is tested using multiplex single cell RT-PCR cardiac myocytes and Purkinje cells cultured from the rabbit heart. Individual cells were isolated, cultured, and placed into a reaction buffer containing primer sets for troponin-t (TNNT), neurofilament medium (NFM), and TxA2 receptor (TP) gene transcripts. TNNT is a cardiac muscle receptor gene transcript, NFM is a neuronal marker associated with Purkinje cells, TP is the TxA2 receptor gene transcript. Using these methods we found 18% (12 of 67) expression of TP gene transcript in NFM negative cells (non-conductile myocytes) and 28% (7 of 25) expression of TP gene transcript in NFM positive cells (conductile myocytes). The expression of TP (TxA2 receptor) gene transcripts in myocytes provides support for a possible TxA2 receptor mediated event in the heart.

E6-FRI

RESPONSE OF CD1D-RESTRICTED NATURAL KILLER T (NKT) CELLS TO ENDOGENOUS AND FOREIGN ANTIGENS

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CD1 molecules are expressed on antigen presenting cells and present several antigen structures such as lipids, glycolipids and lipopeptide antigens to T cells and are the same for everyone. By understanding the function of CD1 new treatment for inflammatory, autoimmune disorders and infectious diseases can be identified. Enzyme linked immunosorbent assays (ELISA) were used to determine the response of CD1d-restricted natural killer T (NKT) cells to particular antigens. In order to determine how NKT cells respond to various stimuli and antigen presenting cell (APC) activation states, NKT cells were incubated with APCs with and without specific stimuli. The coculture supernatants were harvested and analyzed for specific cytokines such as interferon-gamma, interlukin-13, interleukin-4 by ELISA using a standard sandwich antibody technique. The cytokine response of NKT cells to alpha-galactosyl ceramide (alpha-GC) a potent NKT agonist, were shown to be very different from their responses to endogenous antigens. NKT cells produced copious amounts of interferon-gamma in response to alpha-GC. In contrast, their response to the endogenous antigens presented by the APCs showed equal amounts of interleukin-13 and interferon-gamma. These findings suggest that the cytokines produced by NKT cells in response to endogenous antigens may be very different from those produced by foreign antigens. These findings have important implications for our understanding of NKT cell biology. Understanding how antigen presentation via CD1 molecules impacts the immune response in infection and in the maintenance of tolerance will hopefully lead to new methods of treating autoimmune disorders from asthma to diabetes.

D48-FRI

REGULATION OF SOMITOGENESIS BY RHO GTPASE DURING *X. LAEVIS* DEVELOPMENT

Mary Greene, Carmen Domingo. *San Francisco State University, San Francisco, Calif.*

The formation of somites during vertebrate development is a crucial step as these structures will give rise to the vertebrae, muscle, and dermis. In *Xenopus laevis*, somitogenesis involves the partitioning of the presomitic mesoderm into somites, which undergo a 90-degree rotation to form myotome fibers that are aligned parallel to the notochord. Prior work from our lab showed that cell contact behavior is important for this process. These cell contact behavior consists of actin-based filopodia and lamelopodia protrusions that are highly dynamic and appear to be regulated by the Rho family of GTP-binding proteins. Here we use a dominant negative of Rho A to disrupt its function during development. Confocal images of mutant embryos reveal that the cells in the paraxial mesoderm do not undergo proper segmentation and rotation. Although somites do form, they consist of myotome fibers that are mis-aligned and disorganized. These results provide evidence that the actin regulatory protein, Rho A, is associated with the changes in cell behavior that leads to the normal development of somites. This study is significant as it will make an important contribution to our understanding of the regulatory molecules underlying the cell behaviors associated with vertebrate segmentation.

E4-FRI

SEX CHANGE BY GENE CONVERSION

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The nematode *Caenorhabditis elegans* has an androdioecious mode of reproduction. Populations of *C. elegans* typically consist of hermaphrodites with a very small fraction of males. Mutations in *fog-2* (feminization of the germline) disrupt spermatogenesis in *C. elegans* hermaphrodites, but not in males, resulting in strains with an obligate outcrossing mode of reproduction and equal sex ratios. In an earlier experiment, *fog-2* populations were subjected to an RNA-i treatment of *msh-2*, a key mismatch repair gene. A knockdown of *msh-2* causes mutation rates in *C. elegans* to increase by a factor of ten. During these experiments, spontaneous reversions to hermaphroditism were observed in a *fog-2* population. The reversion from an obligately outcrossing strain to hermaphroditism could be achieved by: (1) an exact back mutation that restored the *fog-2* wild type allele, (2) an intragenic compensatory mutation, or (3) a compensatory mutation elsewhere in the sex determination pathway. We show here that the reversion to hermaphroditism resulted from a gene conversion where the donor sequence came from *ftr-1*, a gene with unknown function that is 80% identical to *fog-2*. The *ftr-1* gene in the revertant strain is intact whereas 62 to 84 nucleotides from *ftr-1* have been recombined into the mutant *fog-2* allele, restoring its function. The *fog-2*/*ftr-1* system can be exploited to examine the effect of replication and repair genes on the frequency of gene conversion in this model organism. Moreover, the results may have implications for evolution of reproductive modes in the genus *Caenorhabditis*.

D50-FRI

THE ROLE OF STROMAL DERIVED FACTOR -1α IN VERTEBRATE SOMITOGENESIS

Marisa Leal, Alyssa Bost, Carmen Domingo. *San Francisco State University, San Francisco, Calif.*

Stromal derived factor-1α (Sdf-1α), a chemoattractant chemokine, along with its exclusive receptor CXCR4, plays a major role in tumor growths, angiogenesis, metastasis and in development. Recently, the Sdf-1α signaling pathway was shown to be important for zebrafish somitogenesis (Holloway et al., 2007). Somitogenesis is an important embryological process as it establishes the segmented nature of the vertebrate body plan as well as gives rise to the adult skeletal and musculature system. During zebrafish somitogenessis, cells within the somite undergo rotation prior to myogenesis. This rotation behavior requires Sdf-1 α signaling. Interestingly, somite cell rotation also occurs in the frog, *Xenopus laevis*, however the molecular mechanism underlying this process remains unknown. Therefore, we examined whether Sdf-1α signaling is also required for somite rotation in *Xenopus laevis*. Our approach was to inject morpholino antisense oligomers to knock down the expression of Sdf-1α and its receptor CXCR4 during somitogenesis. Injected embryos were then fixed and stained with the myotome-specific antibody, 12/101. These embryos were then imaged with a confocal microscope. We found that a knock down of Sdf-1α caused a ranged of phenotypes from a complete block of somite formation to the misalignment of myotome fibers. These results suggest that Sdf-1α signaling is important in directing the cell movements during somite formation in *Xenopus*, and that this pathway is well conserved between fish and frogs.

D45-FRI

ENVIRONMENTAL SURVEY FOR ORAL-RELATED TM7 BACTERIA

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TM7 is a candidate bacterial division that was first discovered in diverse environments including soil, sludge, termite gut, and seawater, but hitherto no TM7 species has been isolated in pure culture. Most recently TM7 was found associated with adult human periodontal disease, which affects over 18% of adults in industrialized countries. If an environmental representative closely related to oral species can be found, it would circumvent limitations related to working with human specimens. The purpose of this study was to survey local environments for oral-related TM7 species to be used as model to better understand periodontitis. After bacterial genomic DNA extraction from various environmental samples via a bead beater protocol, presence of TM7 was determined by PCR amplification of the TM7 16S ribosomal DNA gene. Nearly full-length rDNA genes were cloned and sequenced to validate presence of TM7 in our environmental samples and determine phylogenetic relationship to oral strains. The relative abundance of TM7 in each sample was examined via Fluorescence *In Situ* Hybridization (FISH) and quantitative PCR (TaqMan). Though TM7 was found in various samples, it was only present as a relatively small amount (up to 5%) of the total extracted DNA. rDNA sequence analysis showed our TM7 to be >99% similar to oral TM7, suggesting oral TM7 strains exist in our local environments and may serve as a tool for new insights to this worldwide disease. (Supported by NSF-REU grant # DBI-0647160.)

D41-SAT

CREATING NEW CELL LINES EXPRESSING EGFP TO BE USED FOR CYTOTOXIC ASSAYS

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Green fluorescent protein (GFP) is a non-invasive fluorescent marker that can be easily visualized by fluorescent microscopy. As a visual marker, GFP can be used to create assays for the detection of toxic or therapeutic compounds. A HeLa cell line, HeLa-GFP, expressing a histone H2B-GFP fusion protein has already been established and used as a biosensor for a library of toxic compounds. Our goal is to establish several additional cancer cell lines expressing the H2B-GFP fusion protein to determine if there are differences in toxicities between them. In order to establish these cell lines, the H2B gene was first amplified from human cell DNA using PCR and ligated into the pGEM-T vector. After sequence verification of cloned inserts, the H2B cassette was then ligated into the pEGFP-N1 vector to create the fusion gene. The cell lines used for the transfection of the GFP cassettes were A549 Lung Cancer and Human Fibroblast cell line Hs740. Both cell lines were successfully transfected and an attempt was made to establish permanent cell lines by drug selection. Unfortunately, the transfected cells lost the plasmid (GFP-signal) after approximately two weeks of selection. We are currently attempting to reclone the same GFP into other vectors to achieve stable long term expression of the fusion protein. Once these cell lines are established, we will use them as biosensors to further investigate toxic or therapeutic compounds and determine whether or not there are differences between the cell lines.

D47-SAT

UNDERSTANDING THE ROLE OF THE YAFN GENE IN *E. COLI*

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Understand different mutation mechanisms in *E. coli* are helping to explain some aspects of bacterial evolution. One mechanism of interest is the adaptive response to environmental stress, the SOS response. Adaptive mutation in the SOS response is facilitated by the error-prone polymerase *dinB*. The *dinB* gene is the first of four genes in the *dinB* operon, which consists of the *dinB*, *yafN*, *yafO*, and *yafP* genes (McKenzie et al., 2003). The function of the *yaf* downstream genes is still unknown, but is of interest because they are induced in the SOS response and co-transcribed with *dinB*. In several adaptive mutation assays done in the laboratory, the deletion of *yafN* resulted in decreased adaptive mutations suggesting that *yafN* was required for this function. Subsequent studies revealed that a *yafN* duplication present on the chromosome, which compromised the adaptive mutation results. The presence of the second wild-type *yafN* gene suggested it might be essential. Preliminary P1 co-transduction experiments suggest *yafN* is essential for *E. coli*. Deletion of *yafO* in cells lacking *yafN* restores viability, suggesting the two genes may form a toxin-antitoxin pair similar to the known toxin-antitoxin pair *relE-relB*.

E1-FRI

PIRAGUA A NEW DORSAL CLOSURE GENE IN *DROSOPHILA MELANOGASTER*

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Embryogenesis in *Drosophila melanogaster* embraces several different morphogenetic processes such as segmentation, dorsal closure, head involution, and others. Dorsal closure occurs in late embryogenesis and requires cytomechanical mechanisms: Especially, the dynamics of non-muscle Myosin II and tubulin to effect cell shape changes during dorsal closure. This process is a highly orchestrated mechanism triggered by a series of signaling cascades. Different signaling pathways are involved. *piragua* (*prg*) (a new gene that has not been characterized before) has been observed to interact with the Jun N-terminal Kinase pathway (JNK). Homozygous *prg* mutant embryos have a characteristic dorsal hole in the cuticle, resembling a piragua (Spanish word for canoe). When *prg* is homozygous mutant in a JNK heterozygous background (*prg* and *Djun* or *prg* and *Dfos*), an enhanced mutant phenotype is obtained. Prepattern genes such as *U-shaped* (*ush*) and *pebbled* (*peb*) are required for germband retraction, a process that happens before dorsal closure. Both of these genes encode zinc-finger proteins, like *prg*. *piragua* might interact with this group of genes as well, and participate in an alternative signaling pathway in other processes besides dorsal closure. In this project we have studied the genetic interactions between *prg*, *ush*, and *peb* during development, and the physical interactions of Prg protein with other proteins.

D38-FRI

DETERMING THE FUNCTION OF ARE1 SITES ON 3' UTR OF *HRO-TWIST* IN *HELOBDELLA ROBUSTA*

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Hro-Twist mRNA is a leech homolog of the fruit fly transcription factor called *Twist*. In the leech, unlike the fruit fly, *Twist* mRNA has a maternal and a zygotic component of expression. In order to distinguish the contribution of each component, we decided to examine 3' UTR sequences that may be used to regulate mRNA stability. AU rich elements (AREs) are used in other species to target mRNA degradation of tightly-regulated transcripts. *Hro-Twist* mRNA has six AREs, two in the coding region and four in the 3' UTR. We hypothesize that mutating the 3' UTR ARE sites will increase stability of *Hro-Twist* mRNA. Mutation and transformation of the ARE sites 4, 5+6, and 4+5+6 was accomplished by the Stratagene QuikChange® Multi Site-Directed Mutagenesis Kit. Sequencing of DNA was done by Sequetech to confirm the presence of the single site mutations. Mutant strands and GFP were cut by Xba I. We than ligated the mutant 3'UTR ARE sites to our specifically designed GFP fragment. The ligated DNA-GFP will than be injected into fourth stage embryos. Using SideStep™ II QRT-PCR MM, 1 Step kit from Stratagene as well as TaqMan TAMRA probes designed from Applied Biosystems we will analyze the amount of mutated DNA present to determine stability. The designed GFP fragment will act as an indicator as it is exogenous to *Helobdella* sp. Our work thus far has concluded it is possible to mutate ARE sites 4 and 5+6. (Supported by NSF-REU grant # DBI-0647160.)

D37-FRI

MARKERS FOR DNA BARCODING AND MOLECULAR TAXONOMIC ANALYSIS OF POPULATIONS OF THE SOUTH AMERICAN FRUIT FLY *ANASTREPHA FRATERCULUS*

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Ongoing controversy over the taxonomic status of geographic populations of *Anastrepha fraterculus,* primarily from morphological and behavioral studies, emphasizes a need for information on these populations using alternative approaches such as those based on the analysis of DNA. Throughout South America these flies cause considerable economic damage through attacks on more than 80 species of plants including mango, guava, apple and coffee. The possibility also exists that these flies could invade Hawaii and cause extensive damage. In the event of such an invasion, DNA markers may prove useful for identifying the origin of the invading flies through the analysis of their genetic makeup. The objective of this study is to begin the implementation of DNA based studies of these flies using specimens from nine populations representing diverse regions including Mexico and South America. We hypothesize that DNA sequences obtained from mitochondrial genes of these species may be useful for the development of DNA barcodes, attempts to resolve taxonomic issues and for the detection of biological invasions. Using specimens from these collections, mitochondrial DNA sequences from the ribosomal 16S and cytochrome oxidase II genes have been obtained and analyzed to assess the extent of similarities and/or difference within and between these geographic populations. DNA sequence comparisons have revealed that there are approximately 0.04% and 0.06% differences, respectively, between individuals within populations and 0.7 and 0.56 times, respectively, more differences between populations. Our findings suggest genetic differences between these populations.

D40-FRI

ANALYSIS OF ADHESION MOLECULES EXPRESSION AND THEIR ROLE IN THE MIGRATION OF HSC INTO THE FETAL BONE MARROW

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Hematopoietic stem cells (HSC) produce all the cells in blood. Initially, HSC are generated in the yolk sac and the aorta-gonad-mesonephros (AGM) region. These cells migrate to the fetal liver (FL) by day 11.5 of gestation and arrive in the fetal bone marrow (FBM) by day 17.5 of gestation, where they produce blood cells for life. The factors affecting migration from the FL and colonization of FBM are not completely understood. Adhesion molecules such as, Neuronal-Cadherin (N-Cad), ICAM-1, and E-Selectin play an important role in the migration, colonization and adhesion of HSC to their bone marrow (BM) niche. We have designed primers for quantitative PCR, to evaluate the expression of these molecules in HSC and bone marrow stroma during development. Our project consisted of primer design and validation, using both bioinformatics and experimental methods. Gene sequence data and exon/intron boundaries were found in the Ensemble Project database, and primers designed using Primer3 software. To prevent nonspecific binding, primers were tested in BLAST searches against the mouse genome. Using Amplify 3 software, we assessed primer compatibility and product size. The obtained primers were used to amplify N-Cad, ICAM-1 and E-Selectin message on primary bone marrow stroma, sorted HSC, splenocytes, collagen-4 differentiated embryonic stem cells, and the BM line OP9Delta1. Our initial experiments demonstrated that we were able to successfully amplify message for both N-Cad and ICAM-1 from OP9 cells, but not E-Selectin. Understanding HSC migration and colonization of the BM niche will enable us to improve therapies for blood related diseases such as leukemia and anemia.

E6-SAT

SITE DIRECTED MUTAGENESIS OF THE YEAST CASEIN KINASE 2

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The Cdk1 kinase is responsible for inducing entry into mitosis when a critical cell size has been reached. Recent work in budding yeast has shown that Cdk1 is regulated by the opposing kinase/phosphatase activity of Swe1 and Mih1. Swe1 is a kinase that inhibits entry into mitosis by phosphorylating Cdk1 while Mih1 is a phosphatase that promotes entry into mitosis by dephosphorylating Cdk1. In order to further our understanding of how Cdk1 regulates entry into mitosis we need to understand how Swe1 and Mih1 are regulated. Yeast casein kinase (Yck) 1 and 2 are redundant homologues of a highly conserved kinase that regulates Mih1 by phosphorylation. The protein phosphatase 2A (PP2A) also regulates Mih1 by dephosphorylation. A better understanding of the relationship between Yck1/2 and PP2-A on Mih1 is needed. To address this need, the regulating effects of Yck1/2 on Mih1 will be explored by creating a yeast strain that contains an analog-sensitive kinase version of Yck2. A yck1Δ strain will be transformed with a plasmid that carries the analog sensitive yck2-as gene. Using a mating pheromone, this strain will be arrested in G1 and then released synchronously into the cell cycle. 1NM-PP1 will be added at sequential intervals to halt Yck kinase activity. Samples will be taken so that we can assay the effects on Mih1 phosphorylation by western blotting. The results will improve our knowledge about how Yck1/2 regulate Mih1. The scientific community will gain more clarity into the regulatory mechanisms that control the cell cycle.

D47-FRI

DETERMINING IF THE ARE1 SITES IN THE EXON-CODING SEQUENCE OF *HRO-TWIST* PLAY A ROLE IN MRNA STABILIZATION IN *HELOBDELLA ROBUSTA* EMBRYO

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AU-rich elements (AREs) are sequence stretches that are rich in adenosine and uridine bases. They are known to promote mRNA degradation. The leech *Twist* gene (*Hro-Twist*), which may function in the mesoderm formation in embryos, contains two ARE1 sites in its exon-coding sequence. We hypothesized that a mutation in at least one of these ARE1 sites will result in *Hro-Twist* mRNA stabilization. In order to test our hypothesis, four experimental procedures were necessary: (1) mutation of the ARE 1 sites, (2) cloning a partial 300 nucleotide GFP fragment upstream of the *Hro-Twist,* exon-coding sequence for QRT-PCR reporting, (3) producing mRNA for injections, and (4) performing QRT-PCR to quantify mRNA levels. We completed procedures 1 to 3. The two ARE1 sites were mutated using site-directed mutagenesis. A partial 300 nucleotide GFP sequence was cloned immediately upstream of the initiation codon of the ARE 1-mutated clones. Fifty picograms of exogenous, *in vitro* synthesized partial 300 bp *GFP/Hro-Twist* exon-coding, ARE1-mutated mRNA were injected into stage one *Helobdella robusta* embryos. Quantitative RT-PCR will be used to quantify the amount of *GFP/HroTwist* mRNA in injected embryos. We predict that a mutation in at least one of the ARE1 sites will inhibit mRNA degradation and result in mRNA stabilization. (Supported by NSF-REU # DBI 0647160.)

E3-FRI

SEQUENTIAL DELETIONS OF INSIG 2B PROMOTER BY CONTROLLED DIGESTIONS WITH BAL 31

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BAL 31 nuclease from *Alteromonas espejiana,* progressively degrades linear duplex DNA from both the 5' and 3' ends without the introduction of internal breaks. This controlled shortening of DNA has been used in rapid mapping of restriction fragments and placement of restriction sites next to a preselected position in cloned DNA. Our objective was to use BAL 31 endonuclease activity for generating nested deletions of Insig 2b human promoter. Insig-1 and -2 are closely related proteins of the endoplasmic reticulum (ER) that block proteolytic activation of sterol regulatory element-binding proteins (SREBPs), transcription factors that activate the synthesis of cholesterol and fatty acids in liver and other organs. When cellular cholesterol levels are high, Insig proteins bind and trap SREBP cleavage-activating protein (SCAP), retaining it in the ER and preventing it from escorting SREBPs from ER to the site of proteolytic activation in the Golgi complex. The liver-specific transcript of Insig- 2 exist on two isoforms called Insig- 2a and Insig- 2b through the use of different promoters that produce different noncoding first exons that splice into a common second exon. Although the Insig- 2a and -2b mRNAs encode identical proteins, they differ in patterns of regulation. In the present work, we generated the constructions that will be a useful tool to analyze the Insig 2b promoter and study the factors that affect their transcription.

D43-SAT

REPAIR OF DAMAGED DNA USING COMMERCIALLY AVAILABLE ENZYMES

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Biological stains like blood and semen are frequently exposed to environmental conditions in crime scenes. The DNA in these biological stains is subject to damage in the presence of environmental factors like UV, moisture, heat, chemicals and nucleases from microorganisms. It is often difficult to obtain a complete genetic profile for human identification purposes from highly damaged forensic samples. This research evaluates different DNA repair treatments and other strategies for damaged DNA using commercially available polymerases. Blood and semen samples exposed to ambient condition, UV light and sunlight over a period of 2 weeks, 1 month, 2 months, 3 months, 6 months, and 9 months were used. Quantification of the samples was performed using the qPCR Quantifiler kit (Applied-Biosystems). The extent of damage and subsequent repair was assessed by multiplex PCR amplification and analysis of the qualitative and quantitative results of 16 different genetic loci that display a range of sizes in base pairs as separated by capillary electrophoresis. DNA that displayed damage (as determined by allelic dropout of high molecular weight loci) were treated using different polymerases including, Restorase DNA Polymerase (SIGMA-ALDRICH), single and double doses of AmpliTaqGold DNA Polymerase (Applied-Biosystems) and Y-family-polymerases. Preliminary data indicate that alleles that were not detected in the 6-month-UV-exposed and 6-month-sunlight-exposed samples were recovered using a pre-incubated with Restorase DNA Polymerase before amplification with Taq Polymerase. The results for the different time points of blood and semen using different variables and enzymes will be presented. (Supported by NSF-REU grant #DBI-0647160.)

D39-FRI

DOES SPOT 14 STIMULATE LIPID DROPLET FORMATION IN MAMMARY EPITHELIAL CELLS *IN VITRO*?

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Expression of activated Akt in the mammary gland of transgenic mice stimulates precocious formation of cytoplasmic lipid droplets during pregnancy. This could result from increased biosynthesis of lipid or increased transport of lipids from the serum. Biosynthesis of lipids in the mammary gland may be regulated by the transcription factor SREBP and may be correlated with Spot 14 (S14) expression. We observed no difference in the level of SREBP RNA or protein when mammary glands from control FVB and Akt transgenic mice were compared at day 12 and 17 of pregnancy. In contrast, there was a two-fold increase in S14 RNA but no difference in S14 protein at days 12 and 17 of pregnancy. In a normal mouse mammary epithelial cell line (CIT_3), genes for SREbp1, Insig1 and FASN were induced by insulin stimulation of serum-starved cells but S14 was not induced. To test whether S14 could stimulate *de novo* lipid biosynthesis, we transfected CIT_3 cells with a S14 expression vector. Expression of lipogenic enzymes at the RNA and protein level were examined and correlated with lipid transport and/or lipid biosynthesis to determine whether exogenous S14 expression influences any of these processes. We hypothesize that elevation of S14 will stimulate lipid droplet formation *in vitro* and provide insight into the mechanism by which lipid droplet formation is regulated in the mammary glands of wildtype and Akt transgenic mice.

E3-SAT

PATHOGENICITY OF *METARHIZIUM ANISOPLIAE* EXPRESSING THE SCORPION TOXIN (AAIT) AGAINST COFFEE BERRY BORER, *HYPOTHENEMUS HAMPEI* (COLEOPTERA:CURCULIONIDAE)

Monica Pava-Ripoll[1], Francisco J. Posada[2], Momen Bahram[1], Chengshu Wang[3], Raymond StLeger[1]. *[1]University of Maryland, College Park, Md., [2]U.S. Department of Agriculture, Agricultural Research Service, Beltsville, Md., [3]Institute of Plant Physiology and Ecology, Shanghai, China.*

Coffee berry borer (CBB) is the world's most devastating coffee pest causing an estimated of U.S. $500 million annually in losses and control costs. *Beauveria bassiana* and *Metarhizium anisopliae* have been employed to control this pest but their slow kill is an important factor constraining their use. *M. anisopliae* has been modified to express the scorpion toxin (AaIT) in insect haemolymph and this dramatically increased pathogenicity against *Manduca sexta* and *Aedes aegypti*. Here, we demonstrate that the recombinant *M. anisopliae* strain expressing AaIT (MaPcTox) was also dramatically more virulent to CBB. We evaluated several spore concentrations ($1x10^1$ through $1x10^7$ spores/ml) of both wild type and recombinant strains. Results demonstrated that at concentrations of $1x10^2$ and $1x10^3$ spores/ml, the recombinant strain significantly increased mortality of CBB by 40% and 55%, respectively. The medial lethal concentration (LC_{50}) was reduced by 18 fold and the medial lethal time (LT_{50}) was reduced by 21.5% at the highest concentration evaluated. The LT_{50} was reached in 2.85 ± 0.08 days, a significant finding since it is the first occasion that an entomopathogenic fungus killed the CBB in less than 3 days. In future research we will insert the AaIT gene in *B. bassiana* and compare its efficacy against CBB.

D45-SAT

DETERMING THE SENSITIVITY OF A QPCR BASED *IN VITRO* SPLICING ASSAY

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The spliceosome, a macromolecular complex composed of protein and RNA, is critical for pre-mRNA processing during gene expression. In the splicing process, the spliceosome removes non-coding introns and ligates the coding exons from pre-mRNA to assemble an mRNA molecule with a continuous coding sequence. Spliceosomes are highly dynamic structures continuously undergoing conformational changes, thus making it difficult to elucidate structure and ultimately the structure function relationship. For detailed complex examination, we aim to identify inhibitors that will arrest spliceosome movement at multiple points during splicing. To find inhibitors of splicing, a high throughput and sufficiently sensitive assay is needed to detect the products of *in vitro* splicing reactions. QPCR is high throughput, but its range of RNA detection must be established. Using primers specific to pre-mRNA, we used reverse transcription and quantitative PCR (qPCR) to amplify and detect the products of splicing. Amplification results in the release of a fluorescent molecule which can then be monitored. Through a series of dilutions we found qPCR capable of detecting 400 to 0.128 pM of RNA, a suitable range for splicing assays. If qPCR proves to simulate splicing reactions well, it could be used in a high through-put screen for small molecule effectors of splicing using large chemical libraries. Loss of splicing activity in the presence of a particular compound may indicate it is a spliceosome inhibitor. Such inhibitors may be important tools to arrest the spliceosome at specific stages allowing detailed structural and compositional investigation.

D51-SAT

A STUDY OF THE REQUIREMENT FOR HISTONE DEACETYLASES IN GROUCHO-MEDIATED REPRESSION

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Groucho (Gro) is a ubiquitous corepressor with numerous functions in development. Studies in mammals and the fruit fly *Drosophila melanogaster* suggest that Gro recruits the class I histone deacetylase HDAC1 to silence its target genes. While there is limited information about the role of histone deacetylases in Gro-mediated repression *in vivo*, *in vitro* studies suggest that Gro recruits HDAC1 through a glycine-proline rich domain, termed the GP domain. To test the hypothesis that interaction is required for repression *in vivo*, we are using Trichostatin A (TSA), a class I histone deacetylase inhibitor. When we overexpressed Gro in wing imaginal discs the resulting flies developed severely blistered wings indicating that excess Gro leads to defects in adhesion between the dorsal and ventral epithelia comprising the wing. Exposure of these flies to TSA during metamorphosis resulted in a significant improvement in wing morphology suggesting that Gro function requires class I histone deacetylases. We have also carried out similar experiments with a Gro variant lacking the GP domain ($Gro^{\Delta GP}$). Overexpression of this mutant led to a much milder wing defect than did overexpression of wild-type Gro consistent with the idea that the Gro/HDAC1 interaction is important for Gro-mediated repression. Furthermore, the mild defect observed in response to $Gro^{\Delta GP}$ overexpression was not significantly ameliorated by TSA, suggesting that $Gro^{\Delta GP}$ functions independently of class I histone deacetylases. To extend these results, we will examine the histone deacetylase-dependence of Gro-mediated repression in other tissues and will employ additional histone deacetylase inhibitors to confirm specificity of compounds.

D48-SAT

THE FUNCTION OF THE FORK-HEAD-ASSOCIATED DOMAIN IN *ARABIDOPSIS THALIANA*

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Protein-Protein interactions are important in the regulation of signal transduction and other cellular processes. These interactions are mediated between interaction domains and target motifs. The interaction domains bind specific target motifs from proteins so that protein binding is controlled and does not happen randomly. One of the target motifs is a phosphorylated protein. Several phosphobinding domains have been identified that bind phosphorylated tyrosine, threonine, and/or serine. One of theses domains is the fork-head-associated domain (FHA). The FHA domain is a phosphothreonine binding domain and has been found in proteins that are involved in DNA repair, cell cycle control and cell proliferation. In *Arabidopsis thaliana*, FHA domains have been identified in 16 genes including *KAPP*, *ABA1*, *DDL*, and *AtNBS1*. My objective is to identify the function of other Arabidopsis genes that encode a protein with a FHA domain. The function of these genes will be deduced from the phenotype of the homozygote mutants of these genes. I focus my research on one gene, *AT5g07400*. Besides the FHA domain *AT5g07400* has a predicted tyrosyl-DNA phosphodiesterase domain, which is involved in DNA repair. I have isolated two independent homozygous mutants in *AT5g07400* and am screening for phenotypes.

D52-SAT

CHEMICAL CHARACTERIZATION OF *DATURA INNOXIA* EXTRACTS WITH NOVEL BIOACTIVITIES

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Datura innoxia (Solanaceae) a plant native to the American Southwest is under investigation for novel anti-cancer bioactivities. The tropane alkaloids in this plant have been utilized for the medical properties for centuries. Leaves were collected from plants in the wild and sequentially extracted (soxhlet) with hexane, chloroform and methanol. There were no tropane alkaloids in the methanol fraction as determined by GC/MS. The methanol soluble fraction was further fractionated by extraction with butanol and finally precipitated with diethyl ether. This last fraction was dissolved and separated by HPLC. A single fraction containing the anti-cancer bioactivity was recovered. We extracted sufficient quantities of this compound using preparative HPLC for NMR analyses on the intact compound. TLC chromatography was used to test for specific functional groups; presence of sugars presumably as glycosides and the absence of primary amines was demonstrated with spray reagents. Many of the crude fractions and partially purified extracts were also screened for anti-microbial activity. Selected extracts inhibited *Bacillus cereus,* and stimulated the growth of fungal cultures of *Candida kefy* and *Geotrichum candidum.* Preliminary interpretation of the TLC results, the NMR results along with high resolution mass spectroscopy suggest the bioactive compound to be a withanolide, however, many details about the structure remain to be determined. (Supported by NM Agricultural Experiment Station, NIH grants NIGMS GM 61222, BRIDGES NIH grant R25 GM48998, and NCI U56 CA96286.)

E2-FRI

DAMIP: DEVELOPING A NOVEL METHOD FOR DNA BINDING ELEMENTS IDENTIFICATION

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DNA-protein interactions are fundamental for critical cellular processes. The most commonly used technique for the identification of these interactions *in vivo* is Chromatin Immunoprecipitation (ChIP Assay), which involves cross-linking of DNA-Protein complexes. This method requires high quality antibodies against the protein of interest, which are often unavailable. Another method, called DamID, is based on tethering E. coli DNA adenine methyltransferase (Dam) to the protein of interest. This fusion protein methylates adenine residues in GATC sequences in DNA, a modification that is absent in eukaryotes. Adenine methylation is detected using methylation specific restriction enzymes. Our new method is based on the same principle as DamID with the differences that we tethered a Dam mutant (K9A) to the protein of interest, and that we detect the methylated sequences by immunoprecipitation with specific antibody. The K9A mutant is less specific and methylates adenines not in GATC. Methylated DNA sequences are purified using anti-methyladenosine antibodies and analyzed with real time PCR or microarray. As a starting point, we tethered K9A to the human estrogen receptor (hER) at the carboxyl and amino terminus. The estrogen receptor is good for testing this method because its binding sequences have been extensively studied. Constructs were transfected into HeLa cells, which do not express hER endogenously. Western blot results show that the fusion proteins are expressed, and Luciferase assays show that K9A-hER has some activity after the treatment with 10nM estradiol. Methylation of ER binding sites will be analyzed by qPCR.

D46-SAT

CONSTRUCTION OF A PLASMID THAT DIRECTS SYNTHESIS OF *NODAMURA VIRUS* RNA-DEPENDENT RNA POLYMERASE (RDRP) IN TRANSFORMED YEAST CELLS

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The nodavirus *Nodamura virus* (NoV) has a bipartite positive sense RNA genome. The nodaviruses are divided into two genera: alphanodaviruses, which infect insects, and betanodaviruses, which infect fish. NoV is unique in infecting both insects and mammals: NoV causes hind limb paralysis and death in suckling mice. While NoV infection is limited to a few species, purified NoV RNA can be transfected into a wide range of cells, including those from insects, mammals, and the yeast *Saccharomyces cerevisiae*. Its wide host range, its genetic simplicity, and its tremendous RNA amplification make NoV an ideal model system for studying basic mechanisms of viral RNA replication. The larger genome segment, RNA 1, encodes the viral RNA-dependent RNA polymerase (RdRp) that replicates both genome segments, while RNA2 encodes the viral capsid protein. RNA2 is dispensable for RNA1 replication and will not be considered further here. Our laboratory seeks to define the extent of RNA1 sequence that is required for its replication. Because RNA1 serves two functions during an infectious cycle (as a messenger RNA for the viral RdRp and as a template for RNA replication), mutagenesis of the RNA1 template will also affect its ability to produce RdRp. Therefore, we hypothesized that separating the mRNA and template functions of NoV RNA1 onto two different RNA molecules will facilitate the analysis of RNA1 mutants. We report here construction of a plasmid, LpG-NoV RdRp, which directs expression in transformed yeast cells of active RdRp that catalyzes replication of RNA1 mutants *in trans*.

D42-SAT

EXPRESSION AND PURIFICATION OF RECOMBINANT SREBP IN *E. COLI* FOR ANTIBODY PRODUCTION

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Regulation of cholesterol and other lipids is crucial in organisms in order to maintain metabolic balance. Sterol regulatory element binding proteins (SREBPs) are important proteins that help to ensure an adequate level of cholesterol within an organism. Good antibodies against SREBPs should be strong tools for clarifying and better understanding the regulation of different SREBP isoforms. Here, cDNAs coding amino acid 32-250 for both SREBP-1 and SREBP-2 were isolated from mouse cDNA and cloned as Glutathione S-transferase (GST) fusion proteins for expression in *E. coli*. The optimum conditions for induction for recombinant SREBP production and recovery rate of purification were measured and the recombinant SREBPs are being overexpressed in *E. coli* at high levels where they accumulate as insoluble aggregates of inclusion bodies which are solubilized and analyzed by SDS PAGE and coomassie staining. The identified SREBP bands are stained, excised from the gel and then collected by electro elution for use as antigens for antibody production and characterization. Antibody production will be carried out by a commercial vendor using rabbits, which should produce antibodies against the foreign mouse SREBPs. As the antibodies become available, they will be used in the elucidation of physiological cholesterol metabolism using such biological tools as ChIP assays and immunohistochemistry in which protein-localization and protein-DNA interactions can be observed.

D41-FRI

CHARACTERIZATION OF AN EPITHELIAL-TO-MESENCHYMAL TRANSITION IN A DROSOPHILA CELL-BASED SYSTEM

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Epithelial plasticity and epithelial-to-mesenchymal-transitions (EMT) underlie biological processes such as morphogenesis, epithelial repair, and tumor invasion. Our goal is to systematically identify and functionally characterize novel genes that control epithelial plasticity and EMT. To do so, we utilize the fruit fly, *Drosophila melanogaster*, as a model organism. *Drosophila* is a versatile genetic system, and *Drosophila* cell-based RNAi screening is advantageous over mammalian systems due to its high knockdown efficiency and low genetic redundancy. To study epithelial plasticity by cell-based RNAi, we utilize novel *Drosophila* epithelial cell lines that were established previously in our lab. One line, BrüID, shows dramatic morphological changes after stimulation with Decapentaplegic (Dpp), a member of the Transforming Growth Factor-β (TGF-β) superfamily. KaBrü1D cells undergo an EMT-like response, similar to TGF-β induced EMT in mammalian epithelial cells. To identify key players of Dpp- and other signaling pathways involved in this cellular response, we chose an RNAi approach, screening all *Drosophila* kinases and phosphatases, and known candidate genes of the Dpp pathway. As a validation of our system, we identified Dpp receptors such as thickveins (tkv) and punt (put) as suppressors of the Dpp-induced EMT- like response. Moreover, our data identify Mothers against dpp (Mad)-dependent transcriptional responses, rather than Dpp-induced transcription-independent effects, to be central for the observed cellular changes. These findings will be the basis for a more detailed dissection of the signaling pathways involved in EMT. Our findings may contribute to the understanding of normal development and pathological conditions such as tumor invasion, and may identify novel molecular targets for medical applications.

D56-FRI

CREATING CO-EXPRESSION VECTORS FOR STRUCTURAL STUDIES OF SPLICEOSOME PROTEINS

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The spliceosome complex is critical to eukaryotic cellular function. The spliceosome splices out (introns) non-coding regions from pre-messenger RNA. It is composed of five small nuclear ribonucleoprotiens (snRNPs) and many non-snRNP protein factors. Little is known about the structural dynamics of the spliceosome. The research focus of the Jurica lab is to combine different techniques such as X-ray crystallography and biochemical analysis to obtain insight into the overall shape of the spliceosome. My project involves developing a system to generate the SF3a proteins, which are an integral part of the spliceosome. The goal of the project is to create a vector that co-expresses the three SF3 proteins in bacteria together. We used PCR (polymerase chain reaction) to amplify the SF3a gene sequences. Now we are using ligase independent cloning techniques to incorporate those sequences into an expression vector. Once we have created this vector, we will test the expression of the three proteins in bacteria. Our ultimate objective is to purify these proteins for structural studies.

D40-SAT

THE IMPORTANCE OF E-CADHERIN DURING ESC DIFFERENTIATION INTO HEMATOPOIETIC CELLS

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Embryonic stem cells (ESC) can be differentiated into any cell in the body, we have hypothesized that adhesion molecules can serve a role in hematopoietic differentiation due to the cell-cell interactions. Using cells that express the green fluorescent protein (GFP) as a marker for silencing the E-Cadherin (CDH1) protein with a small hairpin RNA (shRNA), we can analyze the effect of the expression of E-Cadherin on hematopoietic differentiation. After ESC are differentiated by forming Embryo bodies (EB) in the absence of LIF, cells are sorted with the flow cytometer. During differentiation, it has been observed that 2 populations of cells (GFP+ and GFP-) appear. These populations were analyzed by sorting them to gain hematopoietic potential. During those 10 days several experiments were made: cytospin to count the different populations to see which population had more differentiated cells, RNA extraction using primers to have a separation of DNA and RNA, and reverse transcription to be able to get DNA from RNA. All these methods were used to see if our silenced protein was present. We can use ESC to get hematopoietic cells for blood therapies and blood transfusions to save lives for the near future.

D39-SAT

THE SYNTHESIS OF AN ANTIBODY AGAINST THE *ALPHA* SUBUNIT OF THE GLUCOSIDASE II ENZYME

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Glucosidase II (GII) plays a very important role in the mechanism of N-glycan quality control and glycoprotein folding in the endoplasmic reticulum (ER). Genetic evidence in previous studies has shown that the GII structure is heterodimeric, the GII-*alpha* homolog responsible for catalytic activity, and GII-*beta* responsible for retaining the enzyme in the ER. The purpose of this work is to create a specific antibody that can be used to detect the location of GII-*alpha* in the cell structure of *Schizosaccharoymeces pombe*. A PCR reaction using the *S. pombe* genomic DNA from the GII-*alpha* gene as a template generated a fragment of the enzyme of about 1000 base pairs. The pET system vector was used to transform the *E. coli* BL26 strain which was then used to clone the fragment. The transformed bacteria were induced to express the recombinant protein which was used to produce the above mentioned polyclonal antibodies against the cloned region. A protein of the desired weight of about 35 kDa was obtained with a concentration of 0.7 mg/ml. The protein has been injected into a rabbit to produce the antibodies. Results are still pending at this point since it would take another month to conduct tests on the rabbit's serum to observe signs of antibody production. It is hoped that this antibody will play a significant role in further experiments to confirm whether the *beta* subunit is necessary for retaining the *alpha* homolog of GII in the ER.

D49-SAT

EFFECTS OF PH ON DNA SYNTHESIS DURING EARLY DEVELOPMENTAL STAGES OF THE PURPLE SEA URCHIN, *STRONGYLOCENTROTUS PURPURATUS*

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Increasing levels of CO_2 in the atmosphere are expected to contribute to the continued drop in ocean pH, a process referred to as ocean acidification. Previous studies have shown fertilization and development of marine species can be significantly affected when the pH of seawater is artificially lowered. This project assesses the potential impacts that climate change will have on the development of the sea urchin, *Strongylocentrotus purpuratus.* Using artificial seawater at pH 7.0, 7.5, and 8.0 to culture

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embryos for four hours after fertilization, cleavage rates were monitored to estimate the effects of decreased seawater pH on cell cycle progression. Preliminary results have shown a significant decrease in the rates of cleavage and an increase in apoptosis as the pH is lowered. In addition, we are currently attempting to determine if the stop in cleavage is a result of a blockage in DNA synthesis by utilizing the incorporation of a chemically modified nucleotide, BrdU, and a fluorescently tagged antibody, anti-BrdU, to visualize the newly synthesized DNA in embryos. If DNA synthesis is blocked by a reduction in pH, we would expect to see a direct correlation between the reduction of sea water pH and a reduction in BrdU incorporation. These experiments are currently underway.

D46-FRI

AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE AND THE CORRELATION OF E-CADHERIN WITH RECEPTOR PROTEIN TYROSINE PHOSPHATES

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Autosomal dominant polycystic kidney disease (ADPKD) is a genetic disorder that is a common cause of renal failure later in life. Two specific genes have been found to correlate with the disease, PKD1, which codes for polycystin 1 and PKD2, which codes for polycystin 2. Together the two polycystins form the polycystin complex which is believed to have control over the major cell signaling and trafficking events linked to the disease. Other molecules are thought to interact with the polycystin complex, and thus influence the ultimate cyst formation in the kidney. One such class of molecules is receptor protein tyrosine phosphatases (RPTPs). Through confocal microscopy and co-immunoprecipitation a novel correlation between delta, sigma RPTPs, and E-cadherin, a molecule known to be in a complex with the polycystins, is shown. Future directions will investigate the mechanisms whereby the RPTPs, (specifically delta, sigma, and a third gamma isoform) and the polycystins contribute to different stages of the disease at the biochemical level.

E4-SAT

WNT4 SIGNAL IN THE DEVELOPING OVARY RESULTS IN A FEMALE-SPECIFIC PATTERN OF BETA-CATENIN LOCALIZATION TO THE CELL MEMBRANE

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The mammalian gonad has the potential to become a testis or an ovary in early fetal development. In the ovarian-determining process, a signaling molecule, Wnt4, is involved, but its mechanism of action is unknown. Previous experiments showed that cell migration from the mesonephros into the developing gonad, a critical feature of testicular development, is repressed by Wnt4. In cell culture, Wnt4 re-localizes beta-catenin, a cell adhesion molecule, to the cell membrane and cell-cell adhesion is increased. As adhesion prevents cell migration, and male-like cell migration occurs in Wnt4 knock-out (KO) ovaries, we hypothesized that Wnt4 re-localizes beta-catenin to the cell membrane in the developing ovary to inhibit male-like cell migration. To test this hypothesis, we first determined by immunohistochemistry (IHC) that expression of beta-catenin is sex-specific and localized to the membrane in some cell types during normal gonadogenesis. Next, we examined whether Wnt4 affects localization of beta-catenin using a Wnt4 KO mouse model. We found fewer somatic cells expressing beta-catenin on the membrane in Wnt4 KO ovaries compared to wild type. These findings are consistent with Wnt4 inhibition of male-like cell migration, through localization of beta-catenin on the membrane with a resulting increase in cell-cell adhesion. This research will contribute to the establishment of the molecular mechanism of mammalian sex determination.

NEUROSCIENCE

D29-SAT

EFFECTS OF ACUTE ETHANOL WITHDRAWAL ON SYNAPTIC AND EXTRASYNAPTIC GABA RECEPTORS IN HIPPOCAMPAL NEURONS

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The γ-aminobutyric acid (A) receptor ($GABA_AR$) signal transduction pathway mediates sensitivity to the effects of alcohol (EtOH). Previous research has shown decreases in α1 and increases in α4 GABAR subunit expression in response to long-term EtOH consumption and withdrawal. Changes in GABAR function due to these changes in receptor subunit composition may be responsible for the CNS hyperexcitability associated with alcohol withdrawal symptoms. Similar alterations to GABAR structure and function are thought to occur in response to single ethanol intoxications. Electrophysiological recordings reveal reversible decreases in tonic current and its potentiation by diazepam, a positive allosteric modulator of GABA, after single dose EtOH

treatments. The goal of the present study is to determine the behavioral effects of acute ethanol withdrawal using a diazepam-induced loss of righting reflex (LORR). Rats received a single intoxicating dose of EtOH (5.0 g/kg, gavauge) based on previous blood-alcohol level findings. LORR was measured 1, 2, 4, 7, or 14 days after EtOH administration. Reduced durations of diazepam-induced lLORR suggest a decrease in GABAR sensitivity to modulatory drugs. These alterations in GABAR sensitivity, which are accompanied by increases in α4 subunit cell surface protein levels and decreases in tonic current potentiation, suggest that changes in CA1 neuronal circuitry that are associated with the development of tolerance, and long-term dependence can occur temporarily after a single alcoholic bout.

D34-SAT

ASSESSING THE HEARING LOSS DUE TO OTOTOXIC DRUGS IN THE ZEBRA FINCH

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Kanamycin (KM), an ototoxic drug, causes hair cell damage/loss and threshold shift at high frequencies in birds. Behavioral studies in numerous species show both hearing loss and recovery following KM administration. Here, hearing loss and recovery were assessed in budgerigars and canaries using auditory brainstem response (ABR) and results were compared to previous behavioral data. We then used the ABR technique to measure hearing loss following KM treatment in zebra finches. Prior to treatment, ABR thresholds were measured in each bird and used as baseline data. The birds received a 10 day course of KM with thresholds assessed after the 6th dose of KM, 4 days after the completion of the KM course, and subsequently at weekly intervals. ABR thresholds in budgerigars and canaries showed high frequency threshold shifts reaching approximately 60 dB at select frequencies and recoveries that compared well with those found with behavioral methods. By contrast, while ABR audiograms in zebra finches paralleled behavioral audiograms, their threshold shifts following KM were much smaller across all frequencies (0.5 to 8 kHz), as compared to budgerigars and canaries. Examination of the basilar papilla of two zebra finches (4 days post KM course) showed stereocilia misorientation among surviving hair cells in the middle and apical regions of the basilar papilla. Some hair cell loss was observed, but not much as compared to other avian species. These data suggest that KM may have different, or perhaps less extreme, ototoxic effects on zebra finches than on other avian species. (Research supported by: DC00198S, DC001372)

D28-FRI

GENE-ENVIRONMENT INTERACTIONS: CAN POLYMORPHISMS OF THE SEROTONIN 5-HYDROXYTRYTAMINE TRANSPORTER (5-HTT) GENE BE LINKED TO DEPRESSION IN ETHNICITIES OF AFRICAN AMERICANS AND EUROPEAN AMERICANS, AGE GROUPS, AND SEXES?

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Decreased levels of the neurotransmitter, serotonin (5-HT), have been correlated with anxiety-related traits such as depression. Drugs that inhibit the serotonin transporter, 5-HTT, have been successful in the treatment of depression such as selective serotonin reuptake inhibitors (SSRIs). A mutation or polymorphism in the promoter of the 5-HTT gene has been shown to reduce the expression of the transporter protein and alter serotonin neurotransmission by decreasing transcription. We examined the prevalence of these polymorphisms between African American and European American student populations and correlate genotypes with depression symptoms, ethnicity, age, and sex. DNA from biological cheek samples has been isolated to genotype the 5-HTT polymorphism, either as homozygous short (SS), homozygous long (LL), or heterozygous (SL). A computer-based survey obtained the emotionality of an individuals' stress to determine if they possessed depression factors. P-values of $p < 0.20$ were obtained by performing an Analysis of Variance (ANOVA) to find relationships between genotype and depression as a function of ethnicity, age, and sex. The (S) allele has been associated with anxiety-related traits; therefore, we hypothesize that individuals with the (S) allele will have an increased genetic predisposition for depression symptoms.

D30-FRI

GLIAL FIBRILLARY ACIDIC PROTEIN IS DIFFERENTIALLY UP-REGULATED IN IGF2 KO AND WT MICE AFTER HYPOXIA-ISCHEMIA

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Glial fibrillary acidic protein (GFAP) is a member of the intermediate filament family that helps to provide support and strength to cells. In the central nervous system, the star-shaped cells called astrocytes react after an injury produced by trauma or disease by producing GFAP. Since the Igf2 knockout (KO) mice display less neurodegeneration than wild-type (WT) mice after a hypoxic-ischemic (HI) injury, we wanted to determine whether there were any differences in GFAP levels between these mice. Our hypothesis was that the Igf2 KO mice should have less GFAP expression than WT mice after a HI insult. Eight-week old male mice underwent unilateral carotid ligation followed by 25-minute exposure to 8% oxygen. Seven days after the insult the

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mice were perfused with 4% paraformaldehyde. Brains were post-fixed in the perfusant for 24h, cryoprotected in 30% sucrose, and sectioned using a cryostat. To examine the astrocyte reaction (gliosis), immunohistochemistry was performed using a GFAP antibody and visualized by a fluorescent secondary antibody. Our data shows that the levels of GFAP were higher in the ipsilateral hemisphere of the WT and KO brains when compared to the contralateral hemisphere after unilateral carotid ligation. Brains from Igf2 KO mice displayed less GFAP immunoreactivity compared to WT mice. These results suggest that although Igf2 KO mice have less neurodegeneration than WT mice, gliosis still takes place after a hypoxic-ischemic insult. Further studies of insulin-like growth factors and their mechanisms of action after injury may help elucidate the role of these genes in neuronal degeneration.

D30-SAT

THE INVOLVEMENT OF THE RETROSPLENIAL CORTEX IN RECENT SPATIAL MEMORIES

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The hippocampus is involved in the storage and retrieval of recent memories. As these memories mature they become increasingly dependent on neocortical sites. One of these sites, the retrosplenial cortex (RSC), was recently identified as being important for both recent and remote memories. The rostral portion of the RSC is highly connected with the prefrontal cortex, and both of these areas are crucial to the retrieval of remote spatial memories. The caudal portion of the RSC in contrast has reciprocal connections with the hippocampus, making both areas essential for recent spatial memories. However, the role of RSC in the storage and retrieval of recent spatial memories obtained via navigation through the Morris Water Maze (MWM) has not been investigated. To examine its role in recent spatial memory, we performed a behavioral study in which cannulae were first implanted into the RSC of mice. After recovering from surgery, the mice were trained in the MWM and one day after training underwent a probe test in order to evaluate their storage and retrieval of recent memories. Fifteen minutes prior to the probe test half of the mice had their RSC effectively inactivated by an infusion of CNQX, an AMPA receptor antagonist, while the other half of mice served as controls and obtained an infusion of saline. Preliminary data indicates that pharmacological inactivation of the RSC results in a behavioral memory deficit, suggesting that the RSC plays a pivotal role in the retrieval of recent spatial memories.

D36-SAT

THE EFFECTS OF CHRONIC ALCOHOL CONSUMPTION ON GAP-43 LEVELS IN THE HIPPOCAMPUS

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The brain maintains a balance of excitatory and inhibitory neurotransmitters necessary for normal brain function. This balance is particularly affected in the hippocampus by alcohol consumption. Acute ethanol exposure causes an increase of inhibitory input through the gamma-aminobutyric acid (GABA) receptors due to the suppression of excitatory input on N-methyl-D-aspartate (NMDA) receptors. Neuroadaptation occurs when NMDA receptors and GABA receptors adjust their sensitivities to compensate for the constant suppression of excitatory input on NMDA receptors. The hippocampus is a structure in the brain that is implicated in certain cognitive functions such as spatial orientation, memory, and learning. Growth-associated protein-43 (GAP-43) is a protein that is found abundantly in the hippocampus. It is a major participant in learning, memory, nerve regeneration and plasticity during neuronal development. GAP-43 levels are upregulated by NMDA receptors and downregulated by GABA receptors; therefore, chronic alcohol consumption may also affect the levels of GAP-43. This study investigates the effects of chronic alcohol consumption and withdrawal on GAP-43 gene expression in the hippocampus of alcoholic rats. Hippocampi were excised and protein isolated for Western Blot analysis (SDS-Page). We found that GAP-43 levels are significantly lower in alcoholic rats compared to alcohol naïve rats. The data suggests that impaired hippocampus function may be a result of decreased GAP-43 expression in alcoholics. This may affect the maintenance phase of long-term potentiation (LTP), which is one of the underlying mechanisms of learning.

D31-SAT

CHANGES IN VOLTAGE-GATED POTASSIUM CHANNEL EXPRESSION AFTER ACUTE SPINAL CORD INJURY IN THE ELECTROMOTOR SYSTEM OF *APTERONOTUS LEPTORHYNCHUS*

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Voltage-gated potassium (Kv) channels play an important role in setting membrane potential, regulating firing frequency, and setting action potential duration. Kv channels of the Kv1 family have been suggested to play a role in regulating the excitability of the electromotor system of *A. leptorhynchus*. The distribution of these Kv1 channels in the intact electromotor system has been well characterized in previous studies. However, the change in distribution of these channels in response to spinal cord injury has not been studied. In the present study, we used immunohistochemical methods to investigate expression of Kv channels

(Kv1.2, 1.3, 1.4, and 1.6) in the Apteronotid electromotor system following spinal cord transection. Kv1.2 immunoreactivity showed a large decrease in the pacemaker nucleus (Pn). Kv1.4 expression decreased in the electric organ (EO) over long term survival periods. Kv 1.3 immunoreactivity was low in both controls and injured electromotor neurons in the spinal cord. Kv1.6 expression remained constant in the spinal cord with exception of expression in relay axons, which disappeared as the EO degenerated. This data suggest that the downregulation of Kv1.2 channels may be an injury response of the Pn, allowing it to maintain its firing frequency after cord injury. The data also suggest the possibility of Kv1.4 immunoreactivity in the EO long after transection indicating the presence of Schwann cells that may be involved in axonal guidance during EO regeneration.

D35-SAT

EMBRYONIC BRAIN INJURY: APOPTOSIS, PROLIFERATION, AND GLIAL PRECURSORS RESPONSE

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A novel chick embryonic brain injury model was used to analyze glial precursor response to injury over time. Unilateral stab wound injuries were made in embryonic day 11 or 15 optic tecta and the response was followed by analyzing the mRNA expression of several specific markers using *in situ* hybridization and northern blot. Expression of neuronal and oligodendrocyte precursor markers was down-regulated in the injured tectum, while levels of a mature-astrocyte marker were up-regulated at the wound site and around necrotic areas and cysts. Also, the distribution extents and levels of radial glial markers (brain lipid binding protein, GLAST, and nestin) were increased at the wound site and in the ventricular zone (VZ) of the injured tectum. To explore whether the decrease of the neuronal and oligodendrocyte markers expression could be due to apoptotic cell death, levels of caspase-3/7 activity were measured in fresh tecta homogenates at different times after injury. Caspase-3/7 activity peaks one day post-injury in the injured tecta and returned to normal levels thereafter. To determine if elevated markers for astrocytes and their precursors can be attributed to increased proliferation in the VZ and injured hemisphere, BrdU incorporation, and immunocytochemistry with anti-phospho-histone H3 studies were performed. We observed no apparent increases in VZ cell division as long as four days after injury. We hypothesize that the rate of precursor differentiation increases to drive astrocytic response to injury, but that the precursor population is not replenished by increased precursor mitosis.

D33-SAT

THE EFFECT OF AGE IN A MODERATE CONTUSION SPINAL CORD INJURY

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Trauma to the spinal cord may produce a different response in young rats than in aged rats. This study was undertaken to evaluate the effect of age in recovery after a moderate mid-thoracic contusion spinal cord injury. To test the hypothesis that young rats will show greater recovery, both young (3 months) and aged (18 months) female Fisher 344/Brown Norwegian F1 hybrid rats received a moderate (200 Kdyne) contusion spinal cord injury at T9. Locomotor recovery was assessed throughout the duration of the study (28 days) using the Basso Beattie and Bresnahan (BBB) locomotor rating scale and CatWalk Gait Analysis at the end of the study (day 28). Throughout the study, young rats demonstrated to have greater locomotor recovery in comparison to aged rats (repeated measures ANOVA $p < 0.05$). At 28 days, young rats exhibited a mean BBB score of 15 (consistent stepping, coordination and toe clearance) in comparison to aged rats which showed an average score of 12.5 (frequent to consistent stepping and no coordination). CatWalk Gait Analysis showed that young rats had improved recovery in paw intensity, base of support, and swing speed ($p < 0.05$). Stereological assessment of lesion volume (day 28) showed that young rats had a statistically significantly reduced lesion volume ($4.1 \pm 0.30\ \mu m^3$) than aged rats ($7.2 \pm 0.56\ \mu m^3$) ($p < 0.001$). However, assessment of lesion volume corrected for total volume of the injured spinal cord segment showed that young rats had a reduced percent lesion volume ($4.8 \pm 0.4\%\ \mu m^3$) than aged rats ($5.6 \pm 0.4\%\ \mu m^3$), but this difference was not statistically significant ($p > 0.06$). This was done to account for the significantly greater total volume in aged rats. Additionally young rats (1338 ± 357) showed a reduced number of neutrophils (on day 2) at the injury epicenter in comparison to aged rats (2671 ± 475) ($p < 0.029$). Quantification of macrophages is underway to continue assessing the cellular inflammatory response in both age groups.

D32-FRI

NITRATION OF TAU AT TYROSINE 18; A POSSIBLE LINK BETWEEN ASTROCYTE ACTIVATION AND TAU NITRATION IN ALZHEIMER'S DISEASE

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Alzheimer's disease (AD) pathology has been characterized in part by the self-assembly of the tau molecule into neurofibrillary tangles (NFT). While different post-translational modifications have been identified that accelerate tau aggregation, nitration at tyrosine residues prevents or slows tau filament formation *in vitro.* Of the five possible tyrosine residues within the tau molecule, nitration at the first tyrosine residue from the most N-terminal end of the molecule (Tyr 18) results in the most profound inhibition of filament self assembly. In order to determine whether nitration at Tyr 18 occurs during the formation of tau filaments in AD brain, monoclonal antibodies were raised against a synthetic peptide containing the nitro-group on Tyr 18. A clone termed Tau-nY18, reacts specifically with tau proteins nitrated at Tyr 18 and fails to cross-react with other nitrated tyrosine residues spanning the length of the tau molecule (Tyr 29, 197, 310, and 394) or with other proteins known to be nitrated in neurodegenerative disease. *In situ,* Tau-nY18 robustly labels activated astrocytes intimately associated with neuritic plaques. Furthermore, Tau-nY18 also sparsely labels the pathological hallmarks of AD, including the NFT and dystrophic neurites within the amyloid plaques. Most interestingly, this antibody detects nitrated tau in soluble preparations from both severe AD brains (Braak stage V, VI) and non-demented age matched controls. Collectively, these findings suggest that nitration at Tyr 18 may be inhibitory to tau aggregation and this effect is likely mediated by astrocyte activation, an early event associated with amyloid plaque formation.

D29-FRI

PROTECTION FROM NEURONAL COPPER TOXICITY BY DOPAMINE OR THE DOPAMINE REUPTAKE BLOCKER NOMIFENSINE IN THE AQUATIC ANNELID *LUMBRICULUS VARIEGATUS*

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Previous research (O'Gara et al., *Aquatic Toxicology* 69:51-66, 2004) demonstrated copper-induced detrimental changes in locomotor escape behaviors and neuronal physiology of the freshwater oligochaete, *Lumbriculus variegatus.* In that study, copper exposure was found to reduce the action potential conduction velocity (CVs) of the medial and lateral giant nerve fibers (MGF and LGF). Paris et al. (*J. Neurochem.* 77:519-529, 2001) were able to protect cultured neurons from copper-induced toxicity by application of the dopamine reuptake inhibitor nomifensine or by an excess of the neurotransmitter dopamine. These results indicated that copper entered the neurons bound to dopamine. The goal of the current study was to determine if dopamine or nomifensine could protect the giant fibers from the copper-induced decrease in CVs. Giant fiber (GF) action potentials were elicited by tactile stimulation and were recorded from undissected worms using noninvasive methods. GF CVs were determined prior to drug exposure and following an 8-hour exposure to pond water, dopamine (0.5 or 1 mM), nomifensine (0.1 or 0.5 mM), copper (0.4 μM) or combinations of copper with dopamine or nomifensine. Copper significantly decreased GF CV after 8-hour exposure to 0.4 μM $CuSO_4$. Exposure to either concentration of dopamine alone increased GF CVs. Exposure to 0.1 mM nomifensine alone did not affect GF CVs, but 0.5 mM increased the LGF CV. Treatment with either dopamine or nomifensine protected the GF from the copper-induced CV decrease. In general, the CVs of worms treated with copper and dopamine were not significantly different than those from worms treated with dopamine alone. The results of this study suggest that copper-induced decreases in GF CV depend on dopamine-mediated transport of copper into affected cells.

D35-FRI

MECP2 IS AN EPIGENETIC REGULATOR CRITICAL TO NEURONAL MATURATION IN BRAIN DEVELOPMENT

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Mutations in MeCP2, a methylated DNA binding protein that acts as an epigenetic repressor of transcription, leads to Rett Syndrome, a severe postnatal neurological disorder. However, how deficiencies in MeCP2 could contribute to the characteristic neurological dysfunction of this disorder has remained unclear. We aimed to resolve the role of MeCP2 epigenetic regulation in brain development and found that while MeCP2 was not critical for the production of immature neurons in the dentate gyrus, these newly generated neurons exhibited pronounced deficits in synapse formation, including reduced dendritic spines. Furthermore, analysis of gene expression profiles of isolated DG granule neurons followed by immunohistological examination demonstrated altered expression of proteins previously shown to be important for cytoskeleton structure and synaptogenesis. Our studies suggest that MeCP2 plays a central role in neuronal maturation that is likely mediated through epigenetic control of expression pathways that are instrumental in dendritic development and synaptogenesis.

D33-FRI

IMAGING GENOMICS: THE COMT GENE AND FRONTOTEMPORAL DEMENTIA

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Imaging genomics is a method of studying the effects of genetic polymorphisms in which the corresponding phenotype is not a physical trait but a physiological condition of the brain. Catechol-o-methyltransferase (COMT) is a major enzyme in the brain that exhibits two functional polymorphic variants in the general population, regulates dopamine levels in cortical synapses, and is suggested to play a key role in dopamine neurotransmission at the prefrontal cortex. Furthermore, frontotemporal dementia (FTD) is the most common form of degenerative dementia after Alzheimer's disease, and is characterized by atrophy of the frontal and temporal lobes, the former being a region of the brain where the COMT enzyme is present. This study seeks to evaluate the relationship between variations in the COMT gene and the magnetic resonance imaging profiles of normal controls (N=63) and subjects with frontotemporal dementia (N=61). Genotyping is performed for determination of the COMT gene variant, neuropsychological testing for evaluation of diagnosis, and voxel-based morphometry for analysis of neuroimaging results. In this ongoing study, our preliminary data suggest that further studies are warranted in utilizing imaging genomics to further investigate the role of COMT gene expression as a putative risk factor for lobar degeneration in frontotemporal dementia.

D32-SAT

QUANTIFICATION OF MACROPHAGE RESPONSE IN CONTUSION AND LACERATION SPINAL CORD INJURIES

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Spinal cord injury (SCI) is characterized as damage to the spinal cord that leads to physiological impairment. This loss of function can be attributed to the demyelination of axons. We have previously demonstrated that contusion SCI results in widespread demyelination, whereas laceration results in localized demyelination (Keirstead et al., 2005). Additionally, transplantation of human embryonic stem cell (hESC)-derived oligodendrocyte progenitor cells (OPCs) after contusion injury resulted in enhanced remyelination and motor recovery. In contrast, adult rats with laceration injuries treated with hESC-derived OPCs did not show enhanced remyelination or locomotor improvements. An examination of the inflammatory response following SCI may elucidate different responses to contusion and laceration injuries, which may explain these observed differences. We specifically examined macrophages which have been shown to play a role in both demyelination and remyelination. 8 female Sprague-Dawley rats received contusion injuries and an additional 8 rats received laceration injuries. Animals were sacrificed 3 day and 14 day post injury. Spinal cords were removed and embedded in OCT compound. Immunohistochemistry was performed to quantify the temporal and spatial macrophage response. Our findings reveal that there are more macrophages found in contusion injuries compared to laceration injuries and there are more macrophages found in grey matter than white matter. Our data suggests that the inflammatory response and macrophage response is correlated with the extent of different pathologies in the two injury models. This knowledge will help define the differences between contusion and laceration SCI which will aid in the development of better targeted SCI therapies.

D34-FRI

TISSUE INHIBITOR OF METALLOPROTEINASE-3 KNOCKOUT MICE DISPLAY ALTERNATIVE PROTEIN EXPRESSION IN THE BRAIN DESPITE PARTIAL GENE DELETION

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Tissue inhibitor of metalloproteinase (TIMP)-3 is an endogenous metalloproteinase inhibitor that has been implicated in the regulation of apoptosis, inflammation, angiogenesis, and tumorigenesis. TIMP-3 inhibits multiple metalloproteinases (MPs), and is the major inhibitor of tumor necrosis factor-α-converting enzyme (TACE). The *TIMP-3* gene locus consists of 5 exons, with MP inhibitory activity associated with the amino acid sequence encoded by exon 1. To explore the effects of *TIMP-3* gene deletion, Leco et al. (2001) created a knock-out mouse in which exon 1 and part of exon 2 were replaced by the neomycin resistance (neo^R) gene in reverse transcriptional orientation, leaving the native promoter intact. Here, we demonstrate that partial gene deletion in $TIMP\text{-}3^{-/-}$ mice does not eliminate protein expression in the brain. Western blots using anti-TIMP-3 antibodies showed bands at the anticipated molecular weights for unglycosylated (23kDa) and glycosylated (27kDa) TIMP-3 in cultures of both knock-out and wild-type cortical neurons and neural stem cells, and immunofluorescence staining of cultured cells and histological brain sections were identical between strains. The anti-TIMP-3 antibodies were specific for TIMP-3 and did not recognize recombinant TIMP-1, -2, or -4 on western blot. rtPCR demonstrated TIMP-3 mRNA in cortical neuronal lysates from $TIMP\text{-}3^{-/-}$ mice, which contained exon 2-5, but not exon 1. These data indicate that an alternative translation start site may be present in the reverse neo^R mRNA sequence. Current work is focused on sequencing the novel mRNA transcript expressed by $TIMP\text{-}3^{-/-}$ brain and assessing MP inhibitory activity of the encoded protein.

D31-FRI

ELECTROPORATION OF GFP-ACTIN INTO THE VISUAL SYSTEM OF *XENOPUS LAEVIS*

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It is important to study the basic mechanisms of neuronal development and differentiation to understand how neuronal function may be affected in the normal brain and in disease. Studies of neuronal development and differentiation in the whole animal using a single cell approach have proven challenging; injection of DNA or RNA into one-cell stage *Xenopus laevis* frog embryos has been effective in analyzing early gene function in vertebrates. However, functional analysis of genes involved in late neuronal differentiation and axon pathfinding by available methods is often hindered by earlier function of these genes during development. Thus, it is important to establish new techniques to introduce recombinant DNA into live neurons in *Xenopus* tadpoles to alter gene expression. Electroporation of DNA presumably serves as a promising transfection technique with high efficiency and low toxicity for targeting into spatially restricted regions of the *Xenopus* CNS at a critical time-window of development (22 to 50 hour post-fertilization) when axonal tracts are first forming. We will further investigate this technique using the plasmid GFP-Actin as a fluorescent-tag in *Xenopus* tadpoles that will allow us to visualize changes in cytoskeleton in neurons in visual system as they differentiate. This technique can be used in future experiments to understand how specific genes affect neuronal development. Also, this technique has broad applications as it can be change easily for other developing systems and for other organisms by making simple adjustments.

PHARMACOLOGY

D28-SAT

DETERMINATION OF THE ROLE OF ANANDAMIDE SIGNALING IN ANXIETY INDUCED BY CORTICOTROPHIN-RELEASING FACTOR

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Although psychosocial stress is known to result in a higher prevalence of mood disorders such as anxiety and depression, the underlying neurobiological mechanisms of stress that produce this correlation are not well understood. Here we aim to mimic conditions of stress in rats using corticotrophin-releasing factor (CRF), a neuropeptide that has been demonstrated to mediate stress induced behaviors such as inhibition of feeding, enhanced grooming behavior, increased locomotor activity, and decreased exploration. Recent studies suggest that elevations of the modulatory neurotransmitter arachidonoylethanolamide (anandamide) increase feeding, decrease locomotor activity, and enhance exploratory activities in animals, leading us to hypothesize that anandamide may be released as a natural mechanism to attenuate the anxiogenic-like effects of CRF. The aim of this experiment is to determine whether administration of CRF is capable of mobilizing anandamide in the brain. To this end we have administered CRF directly into the lateral ventricle of the brain and collected several tissues at 30 minutes post injection. We will quantify anandamide in the brain regions using liquid chromatography coupled to mass spectrometry in order to compare relative levels in CRF and vehicle treated rats. Should the results support our hypothesis, pharmacological enhancers of anandamide signaling could be examined further as possible therapies for anxiety disorders.

D27-FRI

REGULATION OF HEPATIC MULTIDRUG RESISTANCE PROTEIN EXPRESSION DURING ALLYL ALCOHOL HEPATOTOXICITY

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Exposure of mice to toxic doses of the centrilobular hepatotoxicant acetaminophen (APAP) results in increased hepatic mRNA and protein levels of several members of the multidrug resistance-associated protein (Mrp) family. Mrp4 is the most significantly up-regulated transporter by APAP. Activation of Kupffer cells (KC) by APAP is critical for mediating the increase in Mrp4. The present study was performed to determine how allyl alcohol (AA), a periportal hepatotoxicant, affects the expression of hepatic efflux transporters. This study also investigated the involvement of KC-derived mediators during AA induced hepatotoxicity and transporter regulation. To investigate this, C57BL/6J mice were pretreated (0.1 ml) clodronate liposomes to deplete KC or empty liposomes 48 hrs prior to dosing with AA (60 mg/kg, i.p.). Plasma and liver samples were collected at 12 and 24 hrs following AA treatment. Hepatotoxicity was assessed by measuring plasma ALT activity and hepatic transporter mRNA and protein levels were measured using branched DNA signal amplification assay and Western blotting, respectively. Depletion of KC by clodronate liposome pretreatment resulted in increased susceptibility to AA hepatotoxicity. Exposure to AA increased Mrp3, Mrp4, and Mrp5 mRNA levels. Western blot analysis revealed increased protein levels of Mrp1, Mrp2, and Mrp4. Depletion of KC had no effect on changes in Mrp proteins induced by AA. These findings demonstrate that AA treatment causes an increase in hepatic efflux transporter levels. While KC function plays an important role in protection from AA toxicity, it is not required for induction of Mrp transporters.

PLANT BIOLOGY AND BOTANY

D22-SAT

FLORAL PHENOTYPIC INSTABILITIES IN THE ESTABLISHED ALLOPOLYPLOID ARABIDOPSIS SUECICA

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Allopolyploids are species formed by the hybridization of two different parent species. Previous work has shown that allopolyploidization may lead to the formation of new species with initially low fertility and vigor and unstable phenotypes in the immediate offspring of the new hybrid. The current dogma states that such instabilities, however, disappear over evolutionary time as the new species becomes more established. *Arabidopsis suecica*, a natural allopolyploid formed by the hybridization of *A. thaliana* and *A. arenosa* about ~ 20.000 years ago, is a vigorous, well-established species. However, we have noticed that *A. suecica* displays infrequent and unstable floral phenotypes, not previously described for an established allopolyploid. Here we present a histological analysis of the observed floral phenotypes. Abnormalities range from unusual organ fusions and supernumerary organs, to the formation of novel structures of unknown developmental origin.

D21-FRI

WATER RELATIONS AND PHYSIOLOGICAL RESPONSE OF ALFALFA UNDER DROUGHT CONDITIONS

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The effect of drought stress on midday relative water content (RWC) and physiological parameters like photosynthesis (P_{net}), stomatal conductance (g_s), vapor pressure deficit (VPD), internal CO_2 concentration (Ci), and leaf temperature (T_{leaf}) of different alfalfa genotypes (*Medicago sativa* L.) were characterized by withholding irrigation. Well watered condition (baseline) measurements were taken between 10 A.M. and 2 P.M. on April 18 and 19, 2007, 7 days after irrigation (DAI), and drought measurements were taken at the same time on June 19 and 20, 2007, 18 DAI. Comparison of well watered and drought measurements showed that the exposure of plants to progressive water stress led to noticeable decrease in midday RWC (ca. 30 %) irrespective of different alfalfa genotypes. This was accompanied by a corresponding increase in leaf temperature (ca. 30 %). Drought stress also resulted in decreased photosynthesis (ca. 55 %), stomatal conductance (ca. 70%) and internal CO_2 concentration (ca. 15 %), and an increased vapor pressure deficit (ca. 60 %) indicating a decline in physiological activity of alfalfa under water deficit conditions.

D24-SAT

USE OF RANDOMLY AMPLIFIED POLYMORPHIC DNA SEQUENCES (RAPDS) IN THE IDENTIFICATION OF SPECIES IN THE GENUS *LUPINUS*

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The genus *Lupinus* is common throughout Washington and the Yakama Valley Reservation, however, exact classification into species and variants is exceedingly difficult, time-consuming, and often imprecise with the exclusive use of morphological features. In an attempt to establish molecular techniques that will allow more exact and faster species identification, we have developed an assay based on the use of randomly amplified polymorphic DNA (RAPDs). We have screened 17 RAPD primers and six species of *Lupinus* and show unique and reproducible RAPD patterns that may provide an easier and more reliable way to plant identification than the use of morphological features alone.

D21-SAT

ANTIBACTERIAL ACTIVITY OF *ARTEMISIA* SPP. AGAINST PATHOGENS IN FOODS AND IN LABORATORY MEDIA

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Artemisia spp., sagebrush, grows in temperate climates worldwide. *Artemisia* has been used in Eastern medicine to treat stomachache and hookworm. Use of traditional medicinal plants as food preservatives is attractive because their low toxicity to humans has been demonstrated. We evaluated antibacterial properties of *A. iwayomogi* Kitamura and *A. californica*. Ethanolic extracts were investigated by the disk diffusion method against two gram-positive bacteria (*Staphylococcus aureus* and *Streptococcus pyogenes*) and two-gram negative bacteria (*Shigella sonnei* and *Pseudomonas aeruginosa*). Minimal bactericidal concentrations (MBC) were determined in 2-fold serial dilutions of extract in cell-well plates. Lysozyme activity against *Micrococcus luteus* was determined spectrophotometrically. Bactericidal activity of heated and unheated extracts were compared to look for antibacterial peptides. Growth of *S. aureus* in *Artemisia*-treated cottage cheese was measured to assess its potential as a food preservative. Both *Artemisia* extracts were more effective against gram-positive bacteria. The MBC against *St. pyogenes* and *S. aureus* for *A. iwayomogi* was 207 mg/mL and 413 mg/mL for *A. californica*. Lysozyme, comparable to egg-white lysozyme, was present in both *Artemisia* spp. No antimicrobial peptides were found. *Artemisia* extracts were as effective as sodium benzoate in preventing growth of *S. aureus* in cottage cheese. We believe *Artemisia* may provide a nontoxic food preservative.

D25-SAT

SCREENING FOR NATURALLY OCCURRING *BACILLUS CEREUS* STRAINS FOR USE IN BIOCONTROL OF CHILI WILT

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Chili peppers throughout New Mexico (NM) are affected by the soil borne pathogen, *Phytophthora capsici*, a fungus that is the greatest disease problem facing chili growers today. *P. capsici* affects the chili peppers by attacking the roots and clogging the vascular system, resulting in wilting and eventually death. The goal of our research is to build a natural approach to combat this pathogen by searching for natural bacteria that are antagonistic to the fungus, *P. capsici*. The use of natural bacteria to battle against *P. capsici* could benefit the environment by allowing control of chili wilt without the use of synthetic chemicals. One species of bacteria, *Bacillus cereus*, has been used as a biocontrol agent to control *Phytophtora* that causes diseases in several plant species. Our goal is to identify and isolate *Bacillus* species and other natural bacteria to control the fungus *P. capsici*. To do this, we isolated bacteria from chili roots. Isolations were conducted using media that were selective for *Bacillus*. Isolated bacteria were then characterized using polymerase chain reaction and DNA sequence analysis to identify the genus and species of the bacteria. The bacteria will be tested against *P. capsici* to determine potential antagonistic value in controlling the soil borne pathogen. (Supported by NIH grant R25 GM 48998.)

D25-FRI

SEXUAL REPRODUCTION AND POLLINATION AGENTS OF *CHAMAECRISTA GLANDULOSA VAR. MIRABILIS* (LEGUMINOSEAE: CESALPINOIDEA)

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The pollen transference, known as pollination, is a process on plants that involves the relationship of a physical agent. In this case, the in relationship is between hymenopterans and *Chamaecrista glandulosa var. mirabilis*, an endemic and endangered plant of Puerto Rico. Its populations are found on the Laguna Tortuguero Natural Reserve. Its habitat is open areas of silica sands with high temperatures. Individuals of *C. glandulosa* were treated to measure the pollination capability of the population. To study the autogamy possibility or buds were placed in small wire mesh bags which prevented the interaction of pollinators or visitors. Other buds were used as experimental controls. Flowers with mature anthers were collected and its pollen was

analyzed and characterized. Usually the flowers individuals were visited during early hours in the morning by hymenopterans. Some last ones of these visitors observed and analyzed in the laboratory to study the presence of the pollen on thers bodies and determine if they were pollination agents. The pollinators were identified *Xilocopa brasilianourum* (Apidae) and bees of the family Andrenidae, which apparently also visit and might pollinate other plant species. The plants with bagged buds did not produce fruits of so autogamy was discarded or reproduction in this species. The buds used as controls produced fruits, suggesting that its sexual is based on the interaction with pollinators.

D22-FRI

GENETIC TRANSFORMATION VIA *AGROBACTERIUM* IN VALERIA (*V. OFFICINALIS*)

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Valeriana officinalis leaf and petiole explants were inoculated with *Agrobacterium turmefaciens* strain PTC S5 strain to genetically transform Valeria. In this study we tested a number of different parameters were tested to optimize the transformation efficiency in *Valeria.* The parameters were co-cultivation periods (24, 48, and 72 hours), infection periods (15, 30, and 60 minutes) and optical density variations (0.2, 0.4, 0.6, 0.8). After agro-infection, explants were transferred to Murashige and Skoog's (MS) media with vitamins for 24 hours for co-cultivation and then transferred to MS media with vitamins, Benzylaminopurine solution (BAP) 3.0 mg/L, Naphthalene acetic acid (NAA) 0.5 mg/L, Cefotaxime 10mg/100 mL and Carbecillin 10 mg/100 mL to kill the excess bacteria. Samples of infected explants were then exposed to X- Gluc for the B- glucronidase detection of GUS positive spots. The optimal co-cultivation duration was 72 hour period, where a 100% of the explants were GUS possitive. The most effective infection time was 60 minutes where 100% of the explants were GUS positive. In the optical density experiment 100% of the explants were GUS positive, the highest number of GUS spots on leaves was observed at 0.6 O.D., while the highest number of GUS spots with petioles was at 0.4 O.D. In summary, using *A. turmefaciens* strain pTC S5 containing GUS gene as a visual marker *Valeria* can be successfully modified genetically to carry value added traits.

D24-FRI

THE FUNCTIONS OF SCRAMBLED AND QUIRKY PROTEINS IN *ARABIDOPSIS* FRUIT DEHISCENCE

Jacqueline Nguyen, Sangho Jeong, Marty Yanofsky. *University of California, San Diego, San Diego, Calif.*

Flowering plants develop fruits in order to form a protective structure for their seeds and to aid in seed dispersal once the seeds mature. Fruits come in different forms and one of such is a dehiscent fruit, or a fruit that shatters. Molecular mechanisms for fruit dehiscence, or pod shattering, are not fully understood. Our work focuses on two proteins, called SCRAMBLED (SCM) and QUIRKY (QKY), that are involved in regulating pod shattering in *Arabidopsis thaliana*. Both *scm* and *qky* mutants have small, twisted, and non-shattering pods, which contrast with wild type pods that are long, straight, and shattering. We found that *SCM* gene encodes a putative- receptor kinase through positional cloning. *QKY* was found to encode a transmembrane protein that binds Ca^{2+}. Through double mutant analysis, we determined that *SCM* and *QKY* are in the same genetic pathway since there were no differences observed between *scm qky* double mutants and *scm* or *qky* single mutants. We used yeast two-hybrid assay to test the interaction of SCM and QKY and found that the proteins do not interact in yeast. This suggests that there are other proteins that link SCM and QKY in a biochemical pathway. Currently, we are carrying out yeast two-hybrid screens for SCM in order to find proteins that interact with SCM. These proteins could hint on how SCM and possibly QKY function to regulate pod shattering. The results will be presented.

D23-FRI

GENETIC TRANSFORMATION OF *ARUNDO DONAX* USING MICROPROJECTILE BOMBARDMENT

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Arundo donax is a tall perennial reed, growing in fresh and moderately saline waters. This plant is well known for phytoremediation which is a way of using plants to remediate contamination by the uptake of contaminated soil. The characters of large biomass, exuberant root and good adaptability of *Arundo donax* suggested its great potential in remediation of polluted soils. With this objective in mind, we initiated *in vitro* regeneration, genetic transformation studies. Embryogenic calli were observed on Murashige and Skoog (MS) medium supplemented with 2.0 mg/L of 2,4-Dichorophenoxyacetic acid (2,4-D) using immature inflorescence tissues. Regular sub-culturing of embryogenic callus, on MS media with various concentrations of 2, 4-D (0.5 to 2.5 mg/L), 3% sucrose and 0.4% gelrite, different developmental stages of embryos including torpedo and cotyledonary stages were observed. The jellyfish green fluorescent protein (GFP) gene, a new tool to monitor gene expression was used as a reporter gene for genetic transformation stages. Embryogenic calli, induced on MS media were bombarded with 1.0 μM gold particles coated with a plasmid DNA vector containing GFP and NPTII genes fused to a 35S constitutive gene promoter. The GFP culture was observed under UV/blue light. Maximum gene expression was observed after 24 hours after culture. Prolonged exposure of high intensity blue light did not alter the number of transient events. The effect of different parameters such as

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types of tissues, distance, varying pressures on stable expression of GFP in embryogenic callus tissues will be discussed. After 12 hours of bombardment we found GFP expression in the calli. Best expression of GFP found in calli 1550 psi at 9 cm distance. In multiple bombardments the best expression of GFP found was 900 psi 6 cm of distance 3 times bombarding. Experiments demonstrated that particle bombardment could deliver biologically active DNA into plant cells.

ZOOLOGY

D26-SAT
MITOCHONDRIAL DNA SEQUENCE DIFFERENCES BETWEEN HYBRIDIZING ADMIRAL BUTTERFLIES
Yainna Hernaiz, Adam Porter. *Universidad Metropolitana, San Juan, P.R.*

We worked with two populations of butterflies (Lepidoptera) Weidemeyer's Admiral from Nevada, and Lorquin's Admiral from California, and a hybrid population located at the border between Nevada and California. The purpose of our investigation is to see how related were these populations by looking at their mitochondrial DNA (mtDNA) sequences. We tested the hybrid population to see if it showed a mixture of different mtDNA sequences. To see how related they are, we did series of steps. First, we extracted the mtDNA of the butterflies using CTAB method. After extracting the mtDNA we amplified the COI gene from the mtDNA by using Polymerase Chain Reaction (PCR). To check if our samples amplified, we used the agarose gel electrophoresis (electric field), and sent the DNA for sequencing. For data analysis we looked at each butterfly's sequence, checked it for mistakes, and put the data into a program that makes an evolutionary tree. We found there is no evidence of mtDNA mixing and that hybrids have Weidemeyer's mtDNA.

CHEMISTRY

ANALYTICAL CHEMISTRY

C15-FRI
USING INFRARED IMAGING TO DETERMINE CHANGES IN PLANT STRUCTURE OF ALFALFA PLANTS EXPOSED TO PLANT HORMONES
Libny Cabrera, Kenneth Dokken, Martha Lopez, Jose Peralta-Videa, Jorge Gardea-Torresdey. *Universtiy of Texas at El Paso, El Paso, Tex.*

Plant hormones are known to regulate many metabolic processes in plants including structure development. In this study, changes in the plant structure of alfalfa (*Medicago sativa*) grown in hydroponic solution containing plant hormones was studied using infrared microspectroscopy (IMS). IMS permits direct analysis of plant cell wall architecture combining spatially localized information and chemical information from the IR absorbances to produce a chemical map that can be linked to a particular morphology or functional group. Alfalfa plants were grown in hydroponic solutions containing 10 mM of gibberilic acid, indole-3-acetic acid, or kinetin. IMS showed changes to the concentration and spatial distribution of plant biopolymers such as cellulose, protein, and lignin in the roots and stems of alfalfa plants grown in the presence of plant hormones.

C17-FRI
THE ANALYSIS OF INTERNATIONAL AMOXICILLIN
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Amoxicillin is a widely used antibiotic around the world. People the world over seek this medication to treat bacterial infections caused by susceptible microorganisms. Because of the high expense of this medication in the United States, it has been observed that the general public tries to find other means of obtaining this medication. The research being conducted will quantitatively and qualitatively assess the purity of 500 mg amoxicillin capsules from various countries including Canada, India, Mexico, and U.K. versus the purity of the more expensive form of the drug produced in the United States. The expected conclusions from this analysis show that the amoxicillin manufactured in the United States has a significantly purer form of the drug versus its international counterparts. The methods used to assess the purity include testing samples of the pharmaceuticals using an HPLC (high performance liquid chromatography) instrument. The data is then analyzed comparing the peaks produced by each sample. The peaks produced by the amoxicillin in the various samples will be characteristic of a standard amoxicillin sample and should show a definite peak at the same retention time as the standard. Once the amoxicillin is identified the concentration of the sample will then be in question. The area underneath the peak caused by the amoxicillin is proportional to the concentration. By assessing the data acquired, it has been concluded that the hypothesis was not supported. There was no significant difference amongst the samples tested.

C16-SAT

SOL-GEL SENSOR FOR DETECTING TRACE ENVIRONMENTAL IRON

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We present here a new sensor for iron ion monitoring. The sensor was prepared by the sol-gel technique in combination with conducting grafting. Sol-gel technique has long been used in semiconductor industry. The resultant glass or ceramic material can be formed in ambient condition, in comparison to the very high temperature (2000˚C) and other harsher formation condition of conventional glass counterparts. In our new fabrication of the iron sensor, tetramethylorthosilicate (TMOS) was mixed with graphite powder and was subsequently subject to hydrolysis and further condensation/polycondensation forming sol. The sol was cast on to a glassy carbon electrode and was further poly-condensed into a thin layer of gel or xerogel. Preliminary results show the attached film is conductive and very stable in wide pH range. Different from other carbon based electrode in which the ferric/ferrous chlorides usually exhibit sluggish and quasi-reversible electrochemical response, iron (III) ion displays a highly reversible, well-defined voltammetric peak on the sol-gel electrode. Further, the current response was significantly enhanced comparing with other carbon electrodes. While both cathodic and anodic scan mode can be used to quantify iron ion concentration, an anodic voltammetry is preferred after considering potential interference from coexisting metal cations and dissolved oxygen. Various composition of the sol-gel, the doped graphite, and the operating scan rate and initial potential, have been systematically examined and the optimal sensing conditions have been obtained. By using differential pulse voltammetry technique, the sensor has been applied to monitoring real environmental samples with satisfactory results.

C16-FRI

QUANTITATION OF BLOOD NEUROTRANSMITTER METABOLITES BY MEANS OF HIGH PERFORMANCE LIQUID CHROMATOGRAPHY (HPLC) AND COULOMETRIC DETECTION

Diego Ramallo, Beth Hochreiter, Jeffrey Molloy, Gina MacDonald. *James Madison University, Harrisonburg, Va.*

Neurotransmitters play important and diverse roles in mood and behavior regulation. We are interested in improving methodologies to determine the concentrations of dopamine, serotonin, and their metabolites in blood. 3,4-dihydroxy phenyl acetic acid (DOPAC), 4-hydroxy-3- methoxyphenylacetic acid (HVA), 5-hydroxy-3-indole acetic acid (5-HIAA), and 4-hydroxy-3-methoxyphenylglycol hemipiperazinium salt (MHPG) are found in blood and are metabolites of dopamine, serotonin, and norepinephrine, respectively. Our goal is to find a highly-sensitive, reproducible method for quantitating the concentrations of these compounds in whole blood samples. Our initial studies have focused on trying to implement published procedures and use various standards in conjunction with HPLC to determine the best approach for quantitating the neurotransmitters and their metabolites. We have begun to use HPLC with coulometric detection in order to monitor their concentrations. Preliminary studies on the purification of the neurotransmitters and metabolites from blood have commenced. The methods for electrochemical and fluorescence detection will eventually be used to simultaneously quantitate the metabolite concentrations of blood samples in our laboratory.

C15-SAT

ELECTROCHEMICAL STUDIES OF DISULFIDE-MODIFIED SINGLE-STRANDED DNA SELF-ASSEMBLED MONOLAYERS ON GOLD SUBSTRATES

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The number of studies on self-assembled monolayers (SAMs) has grown over the past decades. Due to the efficiency of the self-assembly technique, immobilization of thiol- or disulfide-modified single-stranded DNA (RS-ssDNA) on solid substrates have been proposed, and are commonly used in the fabrication of DNA sensors. However, the immobilization of RS-ssDNA on solid substrates is not a simple process, since it depends on several factors, including the forces of attraction between the immobilized molecules, the interaction between terminal groups and their local environment, and the nature and structure of the metal surface, among others. We will optimize the immobilization efficiency and the packing density of the SAM by changing the immobilization time, and by using the electrochemical desorption technique. This methodology offers the possibility of controlling the concentration of the immobilized species by selectively desorbing a given amount of molecules with variations in potential and in the number of cycles used. The effect of immobilization time and number of desorption cycles on the surface coverage was probed by electrochemical techniques. The results show surface coverages greater than 0.9 for immobilization times of 15 hours or more. The coverage and charge transfer resistance increased, while capacitance decreased for higher immobilization times. The opposite trend was observed for an increasing number of desorption cycles. These results suggest that a combination of variations in immobilization time and number of desorption cycles represents an alternative to optimize the density of immobilized DNA strands, which is desirable for the development of DNA biosensors.

C14-SAT

SELECTIVE SUGAR SENSING BASED ON MIXED METAL HYDROXIDE THIN FILMS

An Vo, Caesar Tin-U, Mian Jiang, Larry Spears. *University of Houston–Downtown, Houston, Tex.*

We propose a new, electroless, facile and controllable preparation of the transitional metal hydroxide mixture and its thin film. The film, Co/Ni blended hydroxide, is formed by first dipping a carbon electrode into a mixture solution containing nickel (II) and cobalt (II) salts, then the "coated" electrode was immersed into NaOH solution for certain period. The resultant Co/Ni hydroxide film is very stable in basic media, as evidenced by its well-defined, repeated redox peaks that may associate with their II/III surface transition. This newly formed thin film demonstrated electrocatalysis towards various analytes. Most noteworthy, the film can sense monosaccharides in the presence of di- or multi-saccharids. Our results show that the oxidation of glucose, fructose, ribose, sorbose, galactose, and xylose (all monosaccharides) can be facilitated or catalyzed by the thin film, while the catalytic current relies on the respective concentration to certain extent. Equal concentration of disaccharides, including lactose, sucrose, and maltose, and polysaccharides, such as starch, have revealed insignificant oxidation responses on the prepared thin film. Mechanistic discussion revealed that electrocatalysis occurs at the site where the surface is reaching its fastest electrochemical redox transition (II/III). The thickness, the recipe of the preparation solution, were compared. Chronoamperometry has been used to qualify the monosaccharides as well. Consequently, our newly fabricated mixture film has the potential to be developed into a simple, non-enzymatic alternative. (Supported by the Undergraduate Analytical Research Program from SACP, the MARC–U*STAR program from NIH, UHD–ORC, and UHD–SA.)

BIOCHEMISTRY

C22-SAT

COMMD1 (MURR1) BINDS TO THE CUL1 COMPONENT OF SCF-TYPE UBIQUITIN-PROTEIN LIGASES

Javier Bravo, Arthur Hauenstein, Tom Huxford. *San Diego State University, San Diego, Calif.*

NF- κB is an inducible transcription factor that activates expression of genes involved in cell survival. COMMD1 (Murr1) originally discovered in dogs as a gene that if knocked out causes copper toxicity and was subsequently identified as an inhibitor of NF- κB dependent HIV expression. We are working to determine the molecular mechanism by which COMMD1 inhibits viral gene expression. We have purified COMMD1 and shown that it is a dimmer and can interact with other COMMD proteins like COMMD6, but it does not bind with NF- κB subunit p65 or transcriptional factor IKBα. To test the hypothesis that COMMD1 regulates NF- κB activation by interfering with the ubiquitination machinery of IKBα, we purified the Cul1/Rbx1 complex. Our preliminary data suggests that COMMD1 is capable of interacting with the complex. This could explain how COMMD1 interferes with NF- κB signaling and HIV expression.

C21-SAT

EFFECTS OF PXR ACTIVATION IN THE INDUCTION OF MHC-II IN HUMAN CELL LINES

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The pregnane X receptor (PXR) is known as an important nuclear receptor and a key player of the body's adaptive defense mechanism against toxic substances including foreign chemicals (xenobiotics). Adding to this classical role in detoxification, other research has shown that Pregnenolone 16α carbonitrile (PCN) a PXR activator in rodents, evokes ectopic expression of MHC class II genes in rat hepatocytes. These findings triggered further research on the role of PXR as a possible activator in the regulation of genes involved in the immune function. The Major Histocompatibility Complex class II (MCH-II) genes have recently gathered medical attention in their possible role in many disease states. There is a data suggesting that MHC-II in non-antigen presenting cells such as tumor cells can boost the immune response against itself, however, the mechanism involved in its ectopic expression is still unknown. To investigate further the possible involvement of PXR in MHCII expression we designed a series of experiments using an efficacious activator of PXR (the hypocholesterolemic drug SR12813) in two cell lines a human fibrosarcoma (HT-1080) and a hepatoma cell (HepG2). No cytotoxic effects were observed in concentrations below 10Mm as assessed by the neutral red assay. The gene expression of both PXR and MHC-II will be assessed by real-time PCR. A dose response will be conducted to determine the effective concentration of SR12813 needed to induce the transcription of MHC-II.

C17-SAT

SYNTHESIS AND CHARACTERIZATION OF CHEMO-SELECTIVE CATALYTIC METALLO-MICELLES

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Supramolecular materials that exhibit catalytic function in water will have important applications in green chemistry and decontamination sciences. This proposal synthesizes amphiphilic metal complexes that use the hydrophobic effect to self-assemble into nanoscopic micelles with encapsulated catalytic hydrolytic function and chemo-selective properties. To achieve this, the synthesis and characterization of the amphiphilic ligand and form their corresponding Cu(II) complexes that provide N(3)-coordination and can position the coordinatively unsaturated metal ions inside multi-layered micelles in water will be carried out. The coordination chemistry of the Cu center with various ligands will be studied with UV-vis spectroscopy and extended X-ray absorbance fine structure (EXAFS) spectroscopy. Metal-access of substrates having a carboxylic ester group and varying in their partition properties will be investigated. The nanoscale phase of micelles will be studied with dynamic light scattering (DLS), atomic force microscopy (AFM) and transmission electron microscopy (TEM). Metallo-amphiphiles that show catalytic activity against carboxylic esters and phosphoesters will be studied with GCMS instrumentation. These aqueous metallo-micelles will be pave the way to green catalytic systems in the future.

C18-SAT

OPEN-POND, SALTWATER CULTIVATION OF MICROALGAE FOR LIPID-BASED BIODIESEL FUEL PRODUCTION

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Increasing prices for petroleum-based transportation fuels has reenergized interest in development of renewable, biomass-based fuel technologies. The arid southwestern USA has abundant undeveloped land, sunshine and under-utilized brackish/saline ground water supplies that can be used to culture high-lipid producing, saltwater tolerant microalgae. Biodiesel fuel is produced from lipid feedstocks in a one-step transesterification of triacylglycerol with methanol. Microalgae in the genus *Nannochloropsis* grow in seawater and have been found to produce large amounts of lipids. Unknown are how long *Nannochloropsis* strain will survive competition and ecological succession in open-pond production and how environmental variables affect lipid yields. To address these questions, we are using microscopy, 18S rDNA PCR amplification and lipid analysis by gas chromatography/mass spectrometry (GC/MS) to monitor algal species and lipid profiles in open pond and laboratory grown cultures of *Nannochloropsis sp.* PCR-amplified DNA was cloned and samples analyzed by restriction enzyme digestion and agarose gel electrophoresis and DNA sequence analysis. Initial results show greater diversity of 18S rDNA sequences in open pond cultures than cultures grown under non-sterile conditions in the laboratory. Thus, green pond cultures contain a more diverse population of microorganisms. The same samples are being dried, extracted with organic solvents and analyzed for lipid content via GC/MS. (Supported by NIH grant R25 GM48998.)

C18-FRI

PEROXISOME PROLIFERATOR ACTIVATED RECEPTORS-GAMMA

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(PPAR-gamma) are nuclear-receptor transcription factors important for lipid and carbohydrate metabolism. Ligands for PPAR-gamma include Thiazolidinediones (TZD), a class of synthetic insulin-sensitizing agents used for the management of Type II diabetes. Since the skeletal muscle is the primary insulin-responsive tissue, our objective was to characterize the effect of PPAR-gamma activation on the expression of lipoprotein lipase (LPL), a key metabolic enzyme, in L6 (rat muscle) cells. Cell Treatments: L6 myoblasts were plated in DMEM containing 10% FBS. Differentiation of confluent cells into myotubes was accomplished by gradual serum-deprivation. When several areas of fused multinucleated myotubes were evident, cells were treated with 10 micromolar Troglitazone, 10 micromolar Ciglitazone, or 5 micromolar 15d-PGJ2. Two to eight days after treatment, cells were washed and harvested in TRI Reagent (Sigma). RT-PCR: Total RNA was isolated and equal mass was subjected to quantitative RT-PCR. Random hexamers were used for synthesis of total cDNA and gene-specific primer pairs were used for PCR amplification. Treatment of L6 myotubes with PPAR-gamma ligands markedly reduced LPL mRNA expression. The decrease was proportional to the dose and duration of ligand treatment. Levels of beta-actin transcript, used as a control, remained unchanged after all treatments. Our data suggest that LPL may be a primary target of PPAR-gamma, activation in the muscle. Western blot analysis and glucose uptake assays are underway to confirm this mechanism.

C20-SAT

REVEALING GENE FUNCTION USING PHENOTYPIC ANALYSIS OF *NEUROSPORA CRASSA* KNOCKOUT MUTANTS

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The *Neurospora crassa* is the most characterized among the filamentous fungus. Analysis of the genome sequence of *N. crassa* reveals many proteins of unknown function. To understand the role of these novel proteins in the biology of filamentous fungi and further annotate *N. crassa* genome, knockout mutants were made by systematically deleting each predicted gene in the *N. crassa* genome. We performed basic phenotypic analysis to assess whether the loss of each gene affects growth, morphology, linear growth rates, and asexual and sexual development in knockout mutants. We selected 20 out of 70 knockout mutants that exhibited phenotypes. The most dramatic phenotype was seen in NCU06205, a knockout mutant missing a tup-1 like protein. This protein is responsible for global transcriptional repression in the budding yeast *Saccharomyces cerevisiae*, mediating this process through chromatin remodeling. In *N. crassa,* loss of this regulatory protein slows its growth dramatically and impedes completion of its sexual cycle. Examination of information on the other missing genes revealed representation of several important classes of proteins such as transcription factors, ras proteins, chromatin remodeling factors, and DNA repair proteins. *N. crassa* is representative of the filamentous fungi that are responsible for agricultural and human diseases. Understanding the biology of this organism will aid researchers interested in preventing or controlling fungal pathogenesis and disease.

C19-FRI

LIGAND EXCHANGE BETWEEN PROTEINS: TOWARDS MAPPING THE INTERACTION REGION OF CRABP AND RAR USING MASS SPECTROMETRY

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The retinoic acid (RA) is a metabolic product of Vitamin A and exerts a variety of effects on vertebrate development, cellular differentiation and homeostasis. It is used for the treatment of skin disorders, the prevention of epidermal cancer and acute promyelocytic leukemia. Cellular retinoic acid binding proteins (CRABP) I and II, belong to the family of intracellular lipid-binding proteins. The function of the CRABP is to solubilize RA in the cytosolic environment and transport it to its nuclear receptor the retinoic acid receptor (RAR) site or modulate the amount of free RA available to the nuclear receptors by a sequestering it in the cytosol. RAR belong to the family of nuclear hormone receptors and are activated by stereoisomers of retinoic acid the interaction between CRABP and RAR is thought to be very transient as it has never been directly observed. Previously a double cys mutation was introduced in CRABP I that locks RA inside the binding cavity. We use this mutant to crosslink the CRABP I mutant with RAR because the interaction between the two proteins might be longer lived. The goal is to identify the regions on cellular retinoic acid binding protein and retinoic acid receptor that interact with one another. This will be done by cross-linking and enzymatic digestion of the cross-linked proteins. The identification of the cross-linked peptides will be done using HPLC and Mass Spectrometry.

C21-FRI

ANALYSIS OF ALPHA-SYNUCLEIN AND FUSION PROTEINS

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The aggregation of alpha-synuclein in dopaminergic neurons is a critical step in the pathogenesis of Parkinson's disease. Parkinson's disease (PD) is the second most common neurodegenerative disorder in the U.S. affecting 1% of the population over the age of 60. PD is caused by the death of cells in the substantia nigra. The cause of the loss of cells is still unknown. However, several observations have lead to the conclusion that aggregation of the presynaptic protein alpha-synuclein is a key step in the development of PD. Fluorescent proteins (e.g., yellow fluorescent protein, YFP) fused to a-synuclein are useful in *in vivo* studies. Here, we examined structural changes in alpha-synuclein and its fusion proteins to determine the interaction with lipid vesicles (POPA/POPC). We hypothesize that the interaction of alpha-synuclein with lipids may change membrane properties that might contribute to cell death. In this investigation we used alpha-synucleinCFP and alpha-synucleinYFP. We also investigated their formation of amyloid fibrils. CD data showed alpha-synuclein is unfolded; however, in the presence of lipids it adopts an alpha-helical conformation. As expected alpha-synuclein part in the fusion proteins is unfolded and adopts alpha-helical conformation in the presence of lipid vesicles.

C20-FRI
CLONING AND CHARACTERIZATION OF TELOMERASE REVERSE TRANSCRIPTASE GENES FROM *ASPERGILLUS NIDULANS* AND *NEUROSPORA CRASSA*
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Telomerase is a reverse transcriptase that adds telomeric DNA repeats to chromosomes ends. Telomerase enzyme is essential for maintaining telomere length and chromosome stability in most eukaryotic organisms. The telomerase ribonucleoprotein complex consists of two essential components, the catalytic telomerase reverse transcriptase protein (TERT) and the intrinsic telomerase RNA that provide template for telomeric DNA synthesis. In human as well as most eukaryotes, telomerase adds (TTAGGG)n sequences. Two fungi *Neurospora* and *Aspergillus* also contain human like, TTAGGG sequences in their telomeres. We hypothesize that *Neurospora* and *Aspergillus* telomerases might be more similar to human telomerase than other yeast such as *S. cerevisiae* and *S. pombe*, and serve a better model system to study telomerase biology. To test this hypothesis, we carry out RT-PCR to amplify the TERT cDNA from the total RNA sample isolated from *Neurospora crassa* and *Aspergillus nidulans.* The amplified TERT cDNA will be cloned into the pCITE plasmid vector for *in vitro* synthesis of the fungal TERT protein. The synthesize protein will be analyzed by SDS-PAGE analysis. The ultimate goal is to use the TERT protein to isolate its telomerase RNA component and establish an *in vitro* reconstitution system for the study of telomerase function.

GENERAL CHEMISTRY

C27-FRI
THE ROLE OF GAPDH IN DIABETES
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Glycolysis is the primary pathway of glucose metabolism, the pathway with the largest flux of carbon in most cells. The glycolytic breakdown of glucose is the source of metabolic energy in some mammalian tissue and cell types. We are studying the sixth step of glycolysis in which the enzyme glyceraldehyde-3-phosphate dehydrogenase (GAPDH) converts glyceraldehyde-3-phosphate into 1,3 bisphosphoglycerate, with simultaneous reduction of a molecule of NAD^+ to NADH. We hypothesize that activity of GAPDH is inhibited by high levels of glucose and also that glucose affects the NAD^+ binding site of the enzyme. GAPDH activity is measured by the amount of NADH produced which is detected at 340 nm using UV spectrometer In studies using chicken muscle GAPDH, we have shown that the activity of the enzyme is decreased with increasing modifications by glucose (0 to 25 mM, 48 hours, 37°C). Currently we are studying the Michelis-Menton kinetics of the GAPDH enzyme that has been modified by glucose to evaluate the kinetic parameters, K_M and V_{MAX}. These measures will demonstrate if the binding of the natural substrate of GAPDH is compromised by interactions with glucose.

D6-FRI
FORMATION OF A α-C-GLYCOSIDE
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Glycosidic linkages are significant bioactive natural products that are present in many antibiotics and anticancer agents. The formation of a α-C-glycoside is formed to understand the complexities of antibiotics. The improvement on the stability of the O-glycoside linkage, which is present in antibiotics, will be done by the replacing it with a C-glycoside linkage. The creation of the α-C-glycoside begins with an epoxidation process by reacting both tri-O-benzyl glucal and dimethyldioxirane (DMDO) under dichloromethane at zero degrees. The epoxidation then allows a reaction with titanocene chloride to form a radical on the anumeric center by opening up the epoxide. This makes it simple for a trapping agent, such as the sulfone used for this experiment, to be added with a stabilizing group. The trapping agent is significant allowing the compound to have a good leaving group. The Julia Olefination is then followed but first the compound is protected in order to create a double bond and bigger group linked to the compound. The results are expected to show that the reactions mentioned are possible and that a complex α-C-glycoside can be formed to have a better understanding of antibiotics and their role in treatment. The C-glycoside linkages will hopefully be able to replace the O-glycoside linkages that undergo enzyme and chemical cleavages. The enzyme and chemical cleavages make the antibiotic or anticancer agent useless since the glycosidic linkage is important for the bioactivity. The ability to improve O-glycoside linkages will help enhance the skill of creating better antibiotics and anticancer agents that are extensively useful for treatment.

C24-SAT

ELECTRODEPOSITION OF SILICON ONTO TUNGSTEN USING SILICON TETRACHLORIDE IN ACETONITRILE

Alison Carlyle, Dominic Munoz, Kyle De Herrera, Eric Miller. *San Juan College, Farmington, N.Mex.*

The electrodeposition of silicon onto tungsten is of interest for application in electronics and solar cells. This work focuses on using silicon tetrachloride as the reactant, acetonitrile as the solvent, tungsten as the cathode, graphite as the anode, and platinum as the pseudo reference electrode. The electrodes were sealed in a cell connected to a Schlenk line for vacuum and nitrogen. The reactant and solvent were introduced to the cell from separation funnels to allow entry of the chemicals without water or oxygen contamination. Chronoamperometry was done using a potentiostat with a voltage step of -2.3 V and a Pasco 750 Interface was used to record. Results of the project were confirmed by a scanning electron microscope (SEM) with X-ray microanalysis capabilities and gas chromatograph/mass spectroscopy (GC/MS). The SEM confirmed deposits of silicon on the tungsten, along with other impurities. The GC/MS verified the presence of the initial compounds from the reaction bath and no other side reactions.

C28-SAT

ENERGETICS OF ENVIROMENTAL MERCURY CYCLING THROUGH OXYGEN CONTAINING SPECIES

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Mercury contamination of marine fish and other sea food, which was detected to cause the *minamata* disease in Japan, has become a global concern. This makes the understanding of how mercury cycles in the environment very important for preventing this disease. The organic compounds of Hg are the ones that highly toxic, these consist of monomethylmercury (CH_3Hg) and dimemethylmercury (CH_3HgCH_3). For these compounds to be generated Mercury is needed in Hg (II) form. There are several reactions that yield this mercury type. Some examples of reactions that yield Hg (II) are those that involve the interaction of mercury and oxygen containing species such as OH and O_3. Computational chemistry is utilized to optimize the molecule to later find its energetics. Every molecule in the reactions must be in its most optimized state for the calculations to yield accurate and realistic results. In this project we have used the Crenbnl basis set and the Gaussian 03 software to process the molecule. The enthalpy, zero point energy and Gibb's energy is extracted from the data received from Gaussian 03. The acquired data is used to find the change in enthalpy, zero point energy and Gibb's energy of the reactions.

D4-FRI

ELECTRODEPOSITION OF SILICON ONTO TUNGSTEN USING SILICON TETRACHLORIDE IN PROPRIONITRILE

Kyle De Herrera, Dominic Munoz, Alison Carlyle, Eric Miller. *San Juan College, Farmington, N.Mex.*

This work is a study of the deposition of silicon films at room temperature for possible application in novel electronic devices. Silicon films were produced by the electroreduction of silicon tetrachloride in a proprionitrile solvent onto a tungsten working electrode using a graphite counter electrode and a platinum pseudo-reference electrode. The reaction was carried out over high purity nitrogen gas at a positive pressure. Cyclic voltammetry tests were able to establish voltage and current settings to begin the electroplating process. Using these initial settings and substances we were able to electroplate the tungsten electrode with elemental silicon over a time period of 2.5 days. Upon analysis of the electroplating solution using gas chromatography mass spectroscopy revealed only minute quantities of silicon tetrachloride indicating that most of it had been reduced and the reaction produced no significant side products. Electron microscopy of the tungsten electrode found elemental silicon had deposited successfully along with some contamination from experimental atmospheric conditions.

D1-SAT

NOVEL MULTIFERROIC CATION TEMPLATED METAL ORGANIC FRAMEWORKS

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Metal organic frameworks (MOFs) are novel crystalline hybrid materials which consist of metal ions that are connected by organic ligands to form one-, two-, or three-dimensional structures. Some of these materials show promising gas storage, optical, electrical and magnetic properties to name few. One of the classes of these materials is ion templated MOFs in which the structure grows around the central ion. In the past we have synthesized different metal formates, templated by an amine cation. These MOFs have the ABX_3 structure and same topology as those of perovskites. These novel structures are multiferroics having both magnetic and electric properties simultaneously in the structure upon cooling. In this report, we present our findings on the formation of new MOFs having same ABX_3 topology by varying the central cation and study its effect on MOF properties.

C27-SAT

QUANTUM MECHANICAL INVESTIGATIONS INTO THE MECHANISM AND FACTORS THAT CONTROL THE STEREOSELECTIVITY OF SOMO-ACTIVATED ORGANOCATALYSIS

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Organocatalysis is a rapidly growing field in synthetic organic chemistry in which organic compounds are used to effect highly stereoselective reactions. It is of particular interest to the scientific community at large as this method avoids the use of environmentally harmful metal reagents. MacMillan and his group are renowned for developing a series of amino acid derived organocatalysts for a wide range of synthetic reactions. An important recent discovery by this group is the development of efficient stereoselective alkylation reactions of carbonyl compounds via an organocatalyzed radical reaction. SOMO-activation (Singly Occupied Molecular Orbital), as the process has been named, involves the oxidation of the catalyst-substrate enamine complex, which allows for enantioselective coupling with substrates that were previously unreactive. We have established the structures of the radical cation intermediates formed in these so-called SOMO-activated processes using high accuracy quantum mechanical methods. The computed conformations of these key intermediates and the subsequent transition structures clearly show the factors that control the stereoselectivity. In addition to providing the first detailed understanding of how these reactions work, we will predict the scope of this type of reaction with various combinations of electron-rich species, and how the catalyst might be improved to give higher stereoselectivity.

D5-FRI

COMPUTATIONAL STUDIES OF ONC AND OCN REACTION PATHWAYS BY DENSITY FUNCTIONAL THEORY, CONFIGURATION INTERACTION AND COMPLETE ACTIVE SPACE SELF-CONSISTENT FIELD METHODS

Jose Gonzalez[1], Floyd A. Fayton[2], John A. W. Harkless[2]. [1]*Universidad Metropolitana, San Juan, P.R.,* [2]*Howard University, Washington D.C.*

Recent studies of the decomposition paths of ONC and OCN use the B3LYP density functional with a 6-31++G* (d,p) basis. This approach is further augmented with the configuration interaction (CI) and complete active space self-consistent field (CASSCF) methods. An orbital analysis was used to determine the dissociation of the respective carbon-oxygen, carbon-nitrogen, and oxygen-nitrogen bonds in both species. Ours results indicating the optimized geometries of the reactants and products at the B3LYP density functional with a CC-PVTZ level are: carbon-oxygen = 1.12604 å, oxygen-nitrogen = 1.14599 å, carbon-nitrogen = 1.16281 å, oxygen-nitrogen-carbon have 1.21585 å between oxygen-nitrogen and 1.20396 å between nitrogen-carbon and for oxygen-carbon-nitrogen have 1.17640 å between oxygen-carbon and 1.22146 å between nitrogen-carbon. This estimated values and reaction descriptions are consistent with experimental data and prior calculations for ONC and OCN. In this study we also try a different approach to see what happen with oxygen when we freeze the bonds between nitrogen-carbon and the coordinates of nitrogen and carbon when is bond to oxygen. With this new approach out results are: carbon-oxygen = 1.12615 å, oxygen-nitrogen = 1.14599 å, carbon-nitrogen = 1.1718 å, oxygen-nitrogen-carbon have 1.2210 å between oxygen-nitrogen and 1.1718 å between nitrogen-carbon and for oxygen-carbon-nitrogen have 1.18670 å between oxygen-carbon and 1.1718 å between nitrogen-carbon. We are going to use these results also to determine the dissociation of the respective carbon-oxygen, carbon-nitrogen, and oxygen-nitrogen bonds in both species to compare those with our estimates values and reactions descriptions from our prior calculations.

D1-FRI

HOW DOES THE COEFFICIENT OF FRICTION DEPEND ON NANOSCALE STRUCTURE?

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Friction properties of thin films, produced from various polymer templating agents, are of interest because of potential applications as coating materials for use between lightweight sliding surfaces. The coefficient of friction represents the resistance to sliding of two surfaces in contact with each other. We made mesoporous cubic titania (TiO_2) films from different polymers such as, KLE, BRIJ56, P123, and F127 to create films with different sized pores that were straight and oriented normal to the plane of the films for a desirable geometry. Atomic force microscopy (AFM) was used to achieve friction values from force-distance curves, voltage outputs from scanning, and calibration curves in the vertical and lateral direction. We calculated the coefficient of friction using: $\mu = F_{lat}/F_{ver}$ (1) where F_{lat} is the friction force and F_{ver} is the normal force applied to the sample. In past studies, mesoporous TiO_2 seems to show low coefficients of friction (values of less than 0.20), classifying mesoporous TiO_2 as a high-slip film. Investigating and comparing friction values from films with different pore sizes may increase machinability and use in fabrication of micromechanical components such as micromotors, microactuators, microsensors, and magnetic heads.

D5-SAT

LABEL-FREE DETECTION OF AMINO ACIDS

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Conventional biochemical and biomedical assay of amino acids, peptides, and proteins need coupling agents, complexing reactions, to label or to expose the active functional sites for recognition. These reaction steps extend the analysis period and cause safety precautions to the operator and environment. A label-free procedure which is based on the inherent properties of the analytes are thus attractive for a more user-friendly approach. In this work we use nickel hydroxide thin film as a sensing layer for electrochemical detection of amino acids. The resultant sensing film was made by a combination of electrodeposition of nickel and its subsequent stripping in basic media to form surface-attachable hydroxide. The film exhibits well-defined redox voltammetric peaks that correspond to Ni (II/III). A systematic examination of various amino acids (essential, and non-essential) on this film modified electrode was carried out by using cyclic voltammetry. Threonine, tryptophans have shown the most sensitive response (current vs. concentration) in basic media. Therefore the nickel hydroxide based electrode can function as a selective, voltammetric sensor for these amino acids. Various conditions for the film preparation, the detection, and comparing with other transducer techniques have been studied. Pattern recognition and data mining of the response for different amino acids were discussed. The sensory mechanism is based on the electrocatalysis occurring at Ni (II/III) and only anodic mode generates significantly enhanced voltammetric current. Owing to its facile preparation and simplicity in its sensing operation, our direct, label-free detection of amino acids adds an attractive alternative to the arsenal of existing amino assay. Further work will focus on the exploration of alloy to construct more selective sensor for individual amino acids.

D3-FRI

W.M. KECK OBSERVATORY LASER DYE PERFORMANCE

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The W.M. Keck Observatory presently has no method for determining when its laser dye should be changed in order to maintain excellent laser guide star performance. The purpose of this project is to find consistent characteristics in old dyes' spectra that will help determine when the dye should no longer be used. As the dye is actively used, its spectrum significantly changes in the ultraviolet and in the green wavelength ranges. These differences are seen when taking peak-to-valley measurements, when comparing slopes of specific regions, and when calculating the dye concentration of each sample. Data was collected from four diluted dye samples that have been used for different amounts of time: 2 different old dye samples with unknown times of usage, a relatively new sample with only 200 hours of use, and a new dye sample with no hours of use. The absolute differences are small, so new dye was used as a reference for relative difference measurements. The old dyes' spectral slopes are at least 30% different from the new dye's slope, compared to the 4% difference of the dye that has been used for only 200 hours. The goal is to create a specific procedure for analyzing laser dye samples, and to identify the spectral features that change most with dye age and overexposure. The observatory will continue to sample dye at different hours of usage to be able to determine the time the dye should be actively used.

D4-SAT

STUDIES ON THE INTERACTION BETWEEN SPINACH CUPREDOXINS AND HUMAN BREAST TUMOR CELLS

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The discovery of the effect of azurin from *Pseudomonas aeruginosa*, on the stability of tumor cells has grown a particular interest in this type of metalloprotein. It has been reported that azurin trespass the cellular membrane and forms a complex with the tumor suppressor protein p53, inducing the apoptosis of the tumor cells. Azurin is a 14kDa protein that contains a copper ion chemically bond in its structure. It is also known that the absence of the copper ion in the structure of azurin cause a significant decrease in its effect of the tumor cells observed. Thus, it can be considered that the metal bonded to the protein plays an important role in its function stabilizing p53. Based on this information, we had purified two copper proteins from the spinach leaves, plastocyanin and plantacyanin, to study their effect in the growth and possible apoptosis of human breast tumor cells. Fluorescence studies of the interaction between plastocyanin and p53 will be also present.

C24-FRI

ELECTROCHEMICAL STUDIES OF PENTYLTRICHLOROSILANE IN ACETONITRILE

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This experiment studied the electrochemical behavior of pentyltrichlorosilane in acetonitrile for possible highly ordered silicon deposition at room temperature. Cyclic voltammetry (CV) and chronoamperometry of 40% solution were performed using tungsten working, graphite counter, and platinum pseudo-reference electrodes. The deposit on the tungsten electrode was

analyzed by scanning electron microscopy–energy dispersive spectroscopy (SEM–EDS), and revealed the deposition of a possible chlorosilane compound. The liquid product from the cell was analyzed by gas chromatography–mass spectroscopy (GC–MS) revealing a possible synthesized alkane. A precipitate formed in the cell was analyzed by Fourier transform infrared spectroscopy (FTIR) indicating the formation a possible polymer.

D2-FRI

PHOTOCATALYSIS OF THE DECOMPOSITION OF CHLOROFORM BY TETRAPHENYLPORPHYRIN

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We are studying the photocatalysis of the decomposition of chloroform by tetraphenylporphyrin (TPP) on the assumption that the oxidized porphyrin would be reduced back to TPP by chloride ion, and the radicals produced during the oxidation and reduction would lead to decomposition. These decomposition products are important because during the chlorination of water chloroform is formed, and long term exposure to chloroform can lead to cancer. The study is being performed by irradiating TPP and chloroform samples using simulated sunlight. An aliquot of protonated TPP, formed after irradiation, is then added to TPP. We analyzed the formation of HCL in the resulted reaction with a UV visible spectrometer. We knew from previous studies that TPP reacted with chloroform to make HCl. It has been recently found that the protonated porphyrin continues to absorb light making extra HCl. The rates for the TPP and TPP dication reactions are the same. The rate of the reaction increases with chloride ion. The half-life of chloroform in lakes is one year, but this study will help to reduce its half-life thereby significantly decreasing the risk of cancer.

D6-SAT

SYNTHESIS AND R2PI SPECTROSCOPY OF PREBIOTIC PYRIMIDINES

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The building blocks for life can be formed from simple prebiotic precursors which may be present in interstellar bodies (e.g., comets and meteorites) and on an early Earth. Simulated prebiotic conditions involving frozen ammonium cyanide solution yield terrestrial RNA/DNA bases as well as other purine and pyrimidine derivatives. In this list of molecules lie 4,5-dihydroxypyrimidine and 5-hydroxyuracil. Details about electronic structure and exited state dynamics of nucleobases are fundamentally important to their photochemistry. For the origin of life, avoiding detrimental photochemistry may have been a selective pressure for adopting certain nucleobase structures. We can study these intrinsic molecular properties of nucleobases under isolated conditions by gas phase laser spectroscopy. 4,5-dihydroxypyrimidine was synthesized by reflux reaction, the synthesis was confirmed by an electrospray mass spectrum and a colorimetric test containing ferric chloride solution. The R2PI spectrum of 4,5-dihydroxypyrimidine could not be obtained, we studied 5-hydroxyuracil which differs only in the two position. This drastically changes the photochemical properties of the molecule. The R2PI was measured, suggesting that just by changing the two position it becomes more stable to UV radiation. To determine which structure was measured an IR hole-burning was done to determine the stretches being exited into a vibration state by the IR laser. In the future, these measurements can be used to target these molecules in a complex matrix such as a meteorite, and the structure can be used to study alternative base pairing.

C23-SAT

RED PHOSPHORS FOR SOLID STATE (LED) LIGHTING APPLICATIONS

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Solid state lighting with gallium nitride (GaN) light emitting diodes (LEDs) will be the next generation of white LEDs. The numerous advantages of LEDs over incandescent bulbs and florescent lamps include lower energy consumption and a longer life. In addition, LEDs do not contain the mercury found in compact fluorescent bulbs. The next generation white LEDs contain a GaN chip emitting light at 400 nm with red, green and blue phosphors. The purpose of my research is to create a red phosphor capable of excitation at 400 nm where the LED outputs are maximized. I will investigate the effects of adding salt fluxes and dopants, such as bismuth, to change particle morphology and tune the excitation. I use a flux method to synthesize the red phosphor, yttrium oxysulfide doped with europium (Y_2O_2S:Eu). The systems to be studied include alkali-metal phosphates. The addition of bismuth is known to shift the excitation to longer wavelengths. I plan to synthesize phosphors with different amounts of $Bi^{3+}$and see its effect. I will also try to tune the particle morphology by varying the salt fluxes as well as the other reaction parameters. The synthesized phosphors are analyzed by X-ray diffraction, scanning electron microscopy and photoluminescence spectroscopy.

C25-SAT

ANALYZING THE EFFECT OF FUNGAL GROUPS ON THE BIOGEOCHEMICAL PROCESSES OF ECOSYSTEMS AND USING THEM TO PREIDCT THE RESPONSES OF ECOSYSTEMS TO CHANGES IN THE ENVIRONMENT

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Fungal groups have a variety of impacts on ecosystems and on the natural and biogeochemical process which occur in these ecosystems. Studies have shown that fungal groups respond to change many natural occurrences and processes, which have all been affected by changes in ecosystems on a global scale. This research done examines how fungal groups can predict how ecosystems are affected by natural occurrences and environmental processes. *Glomus intraradices*, amychorrizal fungi, is a commonly used fungus for experimental purposes, and will be used for this specific research. This research is studying the many varied causes of global warming and its changes on a micro scale. It is important in finding how carbon released in the atmosphere can affect ecosystems, which affect the chemical processes of the symbiotic relationship between fungi and plants. The methods currently used are extraction and purification of the spores of *Glomus intraradices* which is done to collect glomalin. The glomalin is then put under experimental warming to collect more data on how the glomalin uses its source of carbon to help predict the effects of global warming on ecosystems. The data for the results of the research being undertaken is currently in progress and is being recorded. Looking at the predictions that fungal groups make can be used in this research to determine the effect of changes in ecosystems caused by global warming and can be used to find more means of preventing harmful changes to the environment.

C26-FRI

DO HIGH SCHOOL CHEMISTRY STUDENTS WRITE EFFECTIVE LABORATORY REPORTS?

Nahyr Rovira-Figueroa, Mary Nakhleh. *Purdue University, West Lafayette, Ind.*

In the past, there have been many claims made about the value of laboratory work in high school chemistry courses. Educators have emphasized that laboratory work helps students engage in scientific reasoning, such as critically evaluating data, debating ideas, and supporting claims with evidence. We investigated how student's perceptions/attitudes, integrated laboratory/classroom instruction, and the type of laboratory activities/experiments affected high school chemistry students' ability to write effective laboratory reports. Data sources in this analysis included questionnaire, student and teacher interviews, and classroom observations. The questionnaire assessed the qualities of the classroom learning environment and explored student's perceptions/attitudes of the laboratory instruction. We conducted semi-structured interviews to probe student and teacher ideas about how the act of writing effective laboratory reports may have impacted their understanding of chemistry and their ability to write. This study helped us to understand how writing an effective laboratory report can help students learn chemistry. Results of this study will be presented.

D3-SAT

THEORETICAL STUDY OF WINE EXTRACTS OF RED WINE AND WHITE WINE WITH RED WINE-LIKE PROPERTIES

Angel Salgado[2], Teri Robinson[1], Jerzy Lezczynski[1]. [1]*Computational Center of Molecular Structure and Interactions, Jackson, Miss.,* [2]*Metropolitan University, Cupey, Cupey, P.R.*

It has been suggested that the consumption of red wine may be associated with reduced mortality due to diseases in some populations. Some of the common diseases that red wine has been found to reduce are atherosclerosis and cancer. This is due to the antioxidant properties of the components in red wine. Its components have been examined for its potential benefits. Two of these extracts found are catechin and resveratrol. In the study made during this summer we optimized these structures to compare the ground state energies. A recently completed study in Central Israel suggests that these two extracts are found in both red wines and white wine with red wine like properties. To prove that the extract responsible for white wine health benefit is found with a low enough ground state energy to be in natural white wine. The purpose of this work was to investigate wine extracts of red wine and white wine with red wine-like properties. Theoretical calculations have been performed at the HF/6-31G(d) level of theory, the ground state Hartree fock energies are -718.70012 au for resveratrol and -1019.23724 au for catechin. To conclude, the extract responsible for white wine health benefits can be found in the ground state energy sufficient to be found in any standard white wine. This allows white wine to be as beneficial as red wine therefore the name of white wine with red wine like properties can be given to any white wine.

C25-FRI
NEW FLY ASH–POLYANILINE COMPOSITE MATERIAL: PREPARATION AND CHARACTERIZATION
Juan Tito, Antonio Tito, Rosa Villagomez, Mian Jiang, Jorge Tito, Larry Spears. *University of Houston–Downtown, Houston, Tex.*

A new application of fly ash (FA) as an active component in the composite material is presented in this work. FA is a massively generated by-product or waste from the coal-burning power plant worldwide, and its exploration and recycling have received increasingly attention because of its economic and eco-environmental impacts. In this work we proposed a surface preparation of FA-containing thin film by using *in situ* growth of a conducting polymer-imbedded FA composite structure. The conducting polymer, polyaniline (PAn), has been well studied and explored. In our approach, a FA-PAn can mix well and be coated on to substrate electrodes. Because the composite polymer was formed on site by a surface polymerization, the film thickness and surface morphology can be controlled. The resultant FA-PAn is electroactive in acidic environment, with observation of reversible voltammetric behavior. While conventional polyaniline shows three distinct redox voltammetric peaks in its conducting region, the newly formed FA-PAn demonstrates a broad voltammetric redox peak pair that revealed the surface-reaction complexity of the composite. The conductance of our newly formed FA-PAn was determined and compared with conventional PAn. While PAn alone is more redox conductive in acidic media, the FA-PAn offers wider conductive window of potential. Considering the generally insulating nature of metal oxides on the surface electrochemistry, the newly formed electroactive FA-PAn composite lies in its porosity and entrapping capacity from FA. The strong interaction between aniline and FA also take a role in surface attachment. Accordingly, our presented approach expands the FA usability and provides an alternative to use FA as a new carrier to attach active species, including electroactive monomer.

C26-SAT
AN INVESTIGATION OF QUINONES AS BIOMARKERS FOR EXPOSURE TO AIR POLLUTION
Kennedy Vu, Dianne Lim, Akihiro Ikeda, Chirstina Sabado, Tim Tyner, Alam Hasson. *California State University, Fresno, Fresno, Calif.*

Particulate matter (PM) is a component of air pollution linked to health problems such as asthma. Quinones are chemical species found within PM that are suspected of initiating chemical reactions that may lead to asthma attacks. To investigate the link between air pollutants and health effects, it is necessary to know the quantities of a pollutant that the individual has been exposed to. One approach to obtain this information is to monitor the levels of the pollutants or their metabolites in the urine or blood of the subject. This provides a convenient and relatively inexpensive method to monitor exposure if the levels of these biomarkers are correlated with the amount of pollutant inhaled.In this work the use of quinines as biomarkers for exposure to these pollutants and PM was evaluated. Urine samples were collected from Sprague-Dawley rats 24 hours after exposure to 9,10-phenanthraquinone (PQ). Samples were collected from human subjects during 2006 and 2007. Quinones were extracted from the samples and analyzed by GC/MS. Urinary levels of PQ in the rats were found to be correlated with the levels that the animals were exposed to. Levels within all exposed animals were significantly higher than in unexposed animals. The seven monitored quinones in human samples were below the detection limits during the summer, but were observable in samples collected during Spring, when ambient quinone levels are known to be higher. This study demonstrates that quinone biomarkers may be a useful method to track exposure to pollutants such as quinones and PM.

INORGANIC CHEMISTRY

D10-FRI
METALLO-LIPID COMPLEXES: SYNTHESIS, CHARACTERIZATION AND GEL-FORMATION PROPERTIES
Luis Andujo, Juan Noveron. *University of Texas at El Paso, El Paso, Tex.*

The design, synthesis and characterization of molecular materials with functional properties are an intense research area. Recently, lipid metal complexes have been proposed as a new class of molecules with mesogen properties, which can form nanoscale patterns similar to those found in liquid crystals and lyotropic media. In this poster, we will present the synthesis and characterization of N-Pyridin-4-yl-N-tetradecyl-isonicotinamideand its metal complexation with ditopic transition metal ions such as Copper (II) acetate. In addition, studies with Transmission Electron Microscopy and Atomic Force Microscopy of the mesogenic properties of the metallo-lipid complexes will be presented and discussed in the context of smart gel-materials.

D8-FRI

CARBON NANOTUBES AS CATALYSTS FOR ENVIRONMENTAL APPLICATIONS

Nayla Bezares, Louis Martin, Brady Sulivan, Tanja Pietrass. *New Mexico Institute of Mining and Technology, Socorro, N.Mex.*

The goal of this work is to synthesize and test new catalysts for ammonia decomposition that are inexpensive and operate at lower temperatures than current catalysts. These catalysts would be used as a convenient on-board source for carbon oxide-free hydrogen generation to power environmentally-friendly hydrogen fuel cell-based vehicles. Due to their thermal and mechanical stability as well as due to their unique electronic properties, carbon nanotubes are chosen as support material. Fe and Ni, both less expensive and more common metals than Ru that is used in current catalysts, are deposited on the nanotubes by wet impregnation using metallocenes as precursor. Subsequent calcination at 350 C and H2-reduction for 16 hours at 350 C yields metal nanoparticles. The carbon nanotubes were pretreated with KOH to introduce defects into the CNTs, where the metal particles can attach. The synthetic route is optimized by systematically varying conditions such as sonication, interaction time, and solvent. Catalysts are characterized by BET, TEM, and ESR to determine surface area, distribution of particles and particle size. Catalytic testing using GC for detection is currently in progress. Preliminary results based on UV/Vis spectroscopy indicate that sonication in the presence of the metal precursor and extended reaction times lead to greater metal deposition.

D8-SAT

ENERGETICS OF CHEMICAL PROCESSES WITH IMPACT ON MERCURY CYCLIING IN THE ATMOSPHERE

Federico Costa[1,2], Devashis Majumdar[2]. [1]*Universidad Metropolitana, Cupey, Cupey P.R.,* [2]*Jackson State University, Jackson, Miss.*

Since the discovery of the *Minamata* disease due to the mercury-contamination of sea food, studies regarding the environmental chemistry of mercury have become increasingly important; due to the fact that mercury contaminates water sources via atmospheric deposition. Knowledge of atmospheric mercury speciation is critical to understand its fate after biogeochemical cyclation, once released from point sources such as coal-fired power plants and small-scale gold mining. This project investigates the energetics of the chemical reactions between mercury (Hg) and bromine (Br). This process has a profound impact on mercury cycling in the atmosphere. The process by which mercury speciates to its dangerous organic forms such as monomethylmercury (CH3Hg) and dimethylmercury (CH3HgCH3), are among the most common. Using Gaussian code (software was Gaussian 94) with the CRENBL basis set, optimized structures of the molecules were generated. Computational data that was obtained from these calculations was used to determine the thermodynamic properties of these reactions. The results obtained showed that it was indeed possible to both obtain optimized molecular structures for all species involved and thermodynamic properties of said molecules and elements. However, the results are not accurate enough, so their quality must be augmented by either modifying the used basis set or experimenting with others.

D9-FRI

SILANIZATION OF TIN (IV) OXIDE NANOWIRES FOR BIOLOGICAL SENSING APPLICATIONS

Duc Duong, Andrew Morrill, Xihong Chen, Martin Moskovits. *University of California, Santa Barbara, Santa Barbara, Calif.*

Although nanowires have long been studied, their usefulness has not been fully exploited. Previously, metal oxide nanowires, such as titanium oxides and tin oxides, have been shown to exhibit sensing capabilities for oxygen, carbon dioxide, and other gases. In our research, we aim at growing and modifying SnO_2 nanowires with silane molecules that will allow our nanowires to also exhibit sensitivity to biomolecules. For our project, we first synthesize the SnO_2 nanowires through a process called chemical vapor deposition (CVD). In this process, single crystalline nanowires are produced at high temperatures on a silicon chip via gold catalysts. These nanowires are then treated with 3-Aminopropyltriethosxy silane (APS), a molecule that has an affinity for biomolecules. Finally, they are analyzed with scanning electron microscope and infrared spectroscopy. Thus far, we have seen great success in our growth of SnO_2 nanowires. CVD has given us very good control over the size of our nanowires (1 to 10 μm in length and 60 to 200 nm in diameter). Lastly, an IR spectrum for the modified SnO_2 nanowires is expected to be acquired in the near future. Through these studies, SnO_2 nanowires with tunable sizes are shown to be possible and the silanization of these nanowires are successful. Due to the fact that the APS binds onto the SnO_2 nanowires through the ethoxy groups, the amino group is now available for interactions with a variety of biomolecules. Because of this, proteins and enzymes can be attached to nanowires, giving them a plethora of new possibilities in biosensing mechanisms.

D7-SAT

SYNTHESIS OF ORGANOTIN COMPOUNDS

Tania Guardado, Keith Pannell. *University of Texas at El Paso, El Paso, Tex.*

Organotin has been use to stabilize plastics and to avoid the formation of algae in boats. The compounds used for this purpose such as tributyltin are known to affect the immune system. It is believed that the reason why these compounds are so toxic is

because the tin interacts with the oxygen, sulfur, nitrogen and carbon that make up proteins and nucleic acids. The basic idea of this research is to find alternative tin compounds which are not toxic. The hypothesis for creating compounds which are not toxic is to introduce an intramolecular oxygen, sulfur, nitrogen or carbon that will prevent tin from reacting with nucleic acids and amino acids. The particular role that I play in this research is to synthesis compound with 2-methoxybenzyl chloride, 3-methoxybenzyl chloride and 4-methoxybenzyl chloride. First 20 ml of dry toluene were added to a 3 neck round bottom flask. Next the tin was added. Next the ligand was added drop by drop. Heat was also being added. Next it was left stirring under reflux for 3 hours. After that the heat was turn of and it was left overnight. The results where 3 separate compounds with distinct NMR displacements which is evidence of the interaction of the oxygen

D7-FRI

REDOX-ACTIVE GOLD-NANOPARTICLES WITH DNA-DELIVERY PROPERTIES

Brenda Porta-Briseno, Juan Noveron. *University of Texas at El Paso, El Paso, Tex.*

Over the last three decades, DNA delivery systems, have been developed to transfer genetic material to foreign cells through transfection. These systems are powerful tools in developing gene therapy and DNA vaccination for treating and controlling diseases. Current synthetic DNA delivery systems are versatile and safe, but substantially less efficient than viruses. Therefore the synthesis and characterization of new DNA delivery systems is of great interest. The project consists of the synthesis and characterization of gold-nanoparticles with redox-active transition metals on their surface. These gold-nanoparticles systematically vary size (5 to 200 nm) and morphology (spherical, plate, and rod). Due to the cationic charge of the particles and their hydrogen bonding motifs, they have the ability to bind and condense DNA plasmids. The nanostructures revealed by atomic force microscopy and transmission electron microscopy studies will be presented. Transfection experiments with the pEGFP plasmid, which encodes for the green fluorescent protein, on eukaryotic cells mediated by the new DNA-condensates will be discussed with respect to structure-function relationships.

D9-SAT

DNA COATED GOLD NANOSHELLS FOR LASER INDUCED ANTISENSE DRUG RELEASE IN CELLS

Marcus Rosario, Gary Braun, Norbert Reich. *University of California, Santa Barbara, Santa Barbara, Calif.*

The use of gold nanoshells has been demonstrated to be a formidable tool in potential medical applications such as drug delivery. Citrate-stabilized nanoshells, coated with 5'-thiol-modified 3'-fluorescein DNA strands designed to implement antisense drug technology, are synthesized to regulate protein production within human cancer cells (HeLa). Utilizing a pulsed femtosecond laser to effectively release the DNA from the nanoshell, UV-vis spectrophotometry and fluorescence spectroscopy were used to analyze the release efficiency of the DNA through the variable salt concentrations and laser power. Yellow fluorescent protein (YFP) was incorporated into another set of DNA bound to nanoshells to help us better understand the antisense drug technology. Functionalized nanoparticle entry into cells was examined using fluorescence microscopy with dye labeling and fluorescence mapping. Glass slides treated with cationic polymer vectors such as branched-polyethylenimine (PEI) and poly-L-lysine (PLL) were also used to enhance transfection and induce cell endocytosis through a modified and adopted technique known as surfection, integrating beta-mercaptoethanol as a fake laser. PEI cytotoxicity, cell viability, DNA integrity after pulse laser firing and nanoshell characterization and stability were key throughout the study. This research will have many useful applications in speeding up the process of drug delivery.

ORGANIC CHEMISTRY

D17-FRI

NOVEL GREEN CHEMISTRY FOR ANTICANCER DRUG DISCOVERY

Lisa Anderson[1,2], Yin-Shan Wong[1], Amber Ortega[1], Madhuri Manpadi[1], Pavel Uglinskii[3], Rastogi Shiva[1], Karen Cotter[1], Severine Van slambrouck[1], Wim Steelant[1], Snezna Rogelj[1], Paul Tongwa[4], Mikhail Antipin[4,5], Igor Magedov[3,6], Alexander Kornienko[1]. *[1]New Mexico Institute for Mining and Technology, Socorro, N.Mex., [2]Albion College, Albion, Mich., [3]Timiryazev Agriculture Academy, Moscow, [4]New Mexico Highlands University, Las Vegas, N.Mex., [5]Russian Academy of Sciences, Moscow, [6]Intelbioscan Limited, Timiryazevsky Proesd 2, Moscow.*

A new multicomponent reaction of indane-1,3-dione, an aldehyde and an amine containing aromatic compound leading to the formation of indenopyridine-based heterocyclic medicinal scaffolds has been discovered and studied. The multicomponent condensations give a single desired product along with a by-product of water, therefore, they are considered an important part of green chemistry. We practiced the methods that followed the principles of green chemistry including waste prevention, atom economy, and reduction of derivatives, which are more economically and environmentally friendly. It was found that the yields

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significantly improve when oxygen gas is bubbled through the reaction mixture, facilitating the oxidation of the intermediate dihydropyridine containing compounds to their aromatic counterparts. Investigation of the reaction scope revealed that formaldehyde as well as various aliphatic, aromatic and heteroaromatic aldehydes work well as the aldehyde component. In addition, substituted anilines and diverse aminoheterocycles can be utilized in this process as the amine-containing component. Preliminary biological evaluation of the synthesized library identified a pyrimidine-based polycycle, which rivals the anticancer drug etoposide in its toxicity and apoptosis inducing properties toward a human T-cell leukemia cell line.

D18-SAT

EFFORTS TOWARD DEVELOPMENT OF ANTHRANILIC ACID-DERIVED β-KETO SULTAMS FOR LIBRARY PRODUCTION

Daniel Barrera, Thiwanka Samarakoon, Paul Hanson. *University of Kansas, Lawrence, Kans.*

Our efforts toward the development of anthranilic acid derived β-keto benzosultams are presented. This strategy employs a Dieckman-type cyclization to synthesize a number of core β-keto benzofused sultams. The core sultam was generated via the sulfonylation of anthranilic acid esters followed by a one-pot, sequential N-alkylation and Dieckman cyclization. The chemistry of the core sultam was then probed with reduction, Wittig reactions, Knoevenagel condensations, and Robinson annulations to yield a number of daughter scaffolds. Further investigation of the chemistry of the core scaffold, as well as the multi-gram synthesis of the daughter sultams are currently being carried out.

D14-FRI

COMMERCIAL VIABLE RESOLUTION OF (S)-IBUPROFEN

David Chavez, James Salvador. *University of Texas at El Paso, El Paso, Tex.*

Enzymatic esterification of racemic ibuprofen catalyzed by Candida rugosa lipase in cyclohexane at 40°C was developed with high selectivity for (*S*)-ibuprofen over the (*R*)-ibuprofen enantiomer. The length of the alcohol used changed the velocity of the esterification from 48 hours for decal-1-ol to 96 hours for butan-1-ol. Esterification with decan-1-ol was more enantioselective than that of butan-1-ol as measured by their respective enantiomeric ratios, *E*, 130 and 46. Bulb to bulb distillation of (*R*)-ibuprofen and decan-1-ol from the (*S*)-decyl ibuprofen ester, besides not requiring solvents, was run at a larger scale than chromatography. Bulb to bulb separation of ibuprofen from the butyl ibuprofen was not effective because of the close boiling points of carboxylic acid and ester. As expected total hydrolysis of (*S*)-ibuprofen esters in the native solvent of lipase, water, was possible although the reaction of the decyl ibuprofen ester was half as slow (48 hours) as the reaction of the butyl ibuprofen ester probably because of the lower solubility of the decyl ester in water. Nevertheless the combined time of esterification and hydrolysis of decyl and butyl ibuprofen esters was comparable. Chiral HPLC analysis demonstrates that pure (*S*)-ibuprofen was isolated, without racemization, by enzymatic esterification of racemic ibuprofen with decan-1-ol, effective and efficient bulb to bulb distillation and separation of products, and environmentally benign hydrolysis of the (*S*)-decyl ibuprofen ester with the same Candida rugosa lipase.

D17-SAT

SYNTHESIS OF S-TRITYL-L-CYSTEINE DERIVATIVES AS POTENTIAL EG5 INHIBITORS

Jon George[1], David Alexander[2], B.J. Bryant[2], Delany Rodriguez[2], Charles Shuster[2], Jeffrey Arterburn[2]. [1]*Diné College, Shiprock, N.Mex.,* [2]*New Mexico State University, Las Cruces, N.Mex.*

Human mitotic kinesin Eg5 plays a vital role in the establishment of the bipolar mitotic spindle, regulating centrosome separation and microtubule formation. Eg5 is a promising target for cancer therapeutics due to this critical role in the cell cycle. S-Trityl-L-cysteine (STLC) is an amino acid derivative that was recently identified as a potent inhibitor of human kinesin Eg5. The poor water solubility and membrane permeability of STLC requires high concentrations to inhibit Eg5, and limits *in vivo* applications. We hypothesized that modifying the a-amino acid functional group would provide STLC derivatives with improved properties. We initiated the synthesis of a novel series, and analyzed structure-activity relationships, resulting in more potent Eg5 inhibitors as molecular probes and potential cancer therapeutics. We have also designed and synthesized an STLC-biotin conjugate as an affinity agent for the identification of STLC binding with other biological targets. (Supported by NIH Bridge Program grant R25 GM48998 and grant no. P20 RR16480).

D13-SAT

MOLECULAR PROBES FOR PROTEOMIC PROFILING

Laurence James, Akira Kawamura. *City University of New York-Hunter College, New York, N.Y.*

The Human Genome Project identified 30,000 to 40,000 protein encoding genes. The number of proteins in our body is much higher than the number of genes in our genome because of splice variants and post-translational modifications. Functional characterization of many proteins has often been hampered by the immense heterogeneity of cellular proteins. Therefore, development of simple tools to study these proteins in cellular context is very important. Here we present a new chemical proteomics approach to selectively tag protein families in complex proteomes. In this approach, protein modelling is employed to rationally design photoactive ligands to target protein families. The resulting ligands can selectively tag targets with biotin, which enables focused functional analyses of target proteins in cellular context. Our approach can be applied to protein families that cannot be readily tagged with the existing tools, such as isotope-coded affinity tags (ICAT). As a proof-of-principle, we have generated prototype probe sets targeting kinases, and have characterized their kinase binding selectivity. Some of the prototype probes exhibited remarkable tagging selectivity toward non-receptor tyrosine kinases. It was found that a subtle structural difference in probes can make a dramatic change in protein-binding selectivity. Presently our goals are to continue the further characterization of our probe binding using cell lysate studies, and we are currently in the process of using avidin affinity column to purify tagged proteins from lysate in order to perform mass spectra analysis of the sample.

D15-FRI

ISOLATION OF BIOACTIVE COMPOUNDS FROM A MARINE-DERIVED FUNGUS *PENICILLIUM CITRINUM*

Valerie Kolm. *University of California, Santa Cruz, Santa Cruz, Calif.*

Penicillium citrinum is a filamentous fungus that is found in decaying vegetation, soil, air, and water. It has been well studied and contains very diverse chemical structures. In initial bioassay determined the fungus to have cyto-toxicity. A sample of *Penicillium citrinum* was extracted from a *Psammocinia* sponge that was collected from Papua New Guinea in 2002. Ten liters of the fungus were grown for twenty days in a malt extract Monterrey Bay seawater medium. The broth was extracted using 100% AcOEt and the mycelia was extracted using 100% MeOH. Both the mycelia and the broth fractions were then partitioned with equal parts hexane three times, and dichloromethane three times. These fractions were then analyzed using LCMS to look for interesting compounds specifically with a molecular weight between 500 and 1000 amu. An anti microbial assay was performed to determine affectivity against *Staphylococcus epidermidis*. The dichloromethane and methanol fractions showed bioactivity. A bioassay will be performed by Ford and Novartis laboratories to determine bioactivity. The bioassay-guided fractions will then be separated using HPLC to isolate the bioactive compounds. These compounds will then be analyzed using HNMR and CNMR and compared against the literature references. The bioactive compounds may, with further research, be used in the treatment of solid tumor cancers, specifically colo-rectal, breast, prostate, brain, ovarian, and lung cancer.

D11-SAT

SYNTHESIZING MONODISPERSE POLYMER MILLISPHERES IN A DROPLET-BASED MICROFLUIDIC DEVICE

Lan Huong Lai, Alexander Tucker-Schwartz, Robin Garrell. *University of California, Los Angeles, Los Angeles, Calif.*

Small polymer spheres, ranging from micrometers to millimeters in diameter, are used in many applications, including drug release, biosensors, and catalysis. A challenge in synthesizing microspheres and millispheres is controlling their size and size distribution. Suspension and emulsion polymerizations tend to yield a wide range of particle sizes, and it is difficult to make particles as large as several millimeters. These larger particles are of particular interest for solid phase extractions and inertial confinement nuclear fusion targets. We are using a droplet-based microfluidic device to synthesize individual hollow and foam-core beads with prescribed outer and inner diameters. We have found that water droplets spontaneously insert into organic liquid droplets sandwiched between hydrophobic plates. Using a two plate microfluidic device, we have used aqueous ammonium persulfate to initiate interfacial polymerization inside aniline droplets to make polyaniline beads. The beads are 2 to 4 mm in diameter, and consist of polyaniline sheets or fibers interdispersed with crystallized salts. Preliminary results indicate the possibility of using water-soluble peroxide or perester photoinitiators to polymerize styrene around the aqueous phase, in order to make hollow polystyrene shells. These studies demonstrate the feasibility of using droplet microfluidics to synthesize polymer millispheres with controlled dimensions and morphologies.

D13-FRI

SYNTHESIS OF SUBSTITUTED BENZOFURAN-2-CARBOXYLIC ACID ETHYL ESTER

Luisa Martinez Troncoso, Kenneth Yamaguchi. *New Jersey City University, Jersey City, N.J.*

In this experiment, the synthesis of a series of substituted benzofuran-2-carboxylic acid ethyl esters will be described under microwave-assisted conditions. Microwave-assisted organic synthesis allows not only for the improvement of reaction yields but also decreases reaction time. Microwave assisted organic synthesis helps shorten the synthesis and isolation of the product and, in turn, reduces environmental hazards. A variety of substituted salicylaldehyde and β-halogenated ethyl acetate esters (X) were combined using a phase-transfer agent, different microwavable solvents, and bases. The synthetic conditions for this base-catalyzed cyclocondensation reaction will be discussed. The scope of the reaction is being worked under several different modifications of the protocol in hopes of increasing reaction yields. The desired product for this synthesis is a heterocycle compound; heterocycles are an important class of organic compounds because of their biological activity and industrial importance.

D19-FRI

A DOUBLE ASYMMETRIC TITANIUM TETRAISOPROPOXIDE MEDIATED ALLENE-IMINE CROSS-COUPLING

Raul Navarro, Martin Mclaughlin, Glenn Micalizio. *Yale University, New Haven, Conn.*

Titanium-mediated reactions have long been used in organic chemistry in catalytic and stoichiometric fashions. A small subset of such stoichiometric reactions, specifically those that involve the reductive coupling of two π systems, have recently provided an efficient means by which carbon-carbon bonds are formed. In our lab, such reactions compose the basis for the convergent synthesis of biologically active natural products. We have reported titanium-mediated reactions for alkyne-alkyne, alkyne-aldehyde, and alkyne-imine cross couplings, which have efficiently generated a wide variety of natural product precursors. Recently, we have defined an imine-allene cross-coupling reaction that generates an amino diene. Although this cross-coupling has been shown to give amino dienes in good yield, a double asymmetric version of this reaction has yet to be explored. It is well known that changes in the stereochemistry of a natural product can greatly alter its biological activity; therefore, identification of the stereospecificity involved in this cross-coupling reaction is important for any possible subsequent natural product syntheses. The project involves the synthesis of enantiomerically pure imines and allenes, which will be used to test the stereospecificity of the imine-allene cross-coupling in double asymmetric reactions. We hope these studies will determine if the reaction is stereospecific and that a strategy can be found to transform the amino diene products into nitrogen-containing heterocycles, ubiquitous components of natural products.

D16-SAT

THERMODYNAMIC INTEGRATION USING REPLICA EXCHANGE

Paul Nieves[1], Hiqmet Kamberaj[2], Arjan Van Der Vaart[2]. [1]*Universidad Metropolitana, Cupey, P.R.,* [2]*Arizona State University, Tempe, Ariz.*

Computer simulations methods, such as Molecular Dynamics and Monte Carlo methods, have widely been used to characterize thermodynamic and dynamical properties of biomolecular systems. Free energy difference calculations are important for a wide range of applications, including protein/ligand binding affinities, solubility of small molecules and drug design. Free energy difference methods can be classified as either equilibrium, including free energy perturbation, thermodynamic integrations, Bennett analysis and umbrella sampling, or non-equilibrium based on Jarzynski's equality. We are particularly interested in comparison of computational efficiency and accuracy of different free energy difference approaches. In this work, we will present a new methodology for carrying out thermodynamic integration free energy difference calculations, which is implemented in a version of CHARMM program. In this method, the replica exchange simulations are performed with λ as replica coordinate. Then an algorithm will be introduced in order to identify an optimal set of λ_i replicas with modified windows width $\delta\lambda$. We will also discuss the convergence for the equilibration of the replica exchange methodology introduced and conformation sampling of high energy barriers. The test case studies presented in this work indicate the ability of the approach to reduce the computational efforts for the convergence of free energy calculations.

D12-FRI

MOLECULAR GYROSCOPES AND MOLECULAR ROTORS

Melissa Padilla, Miguel Garcia Garibay, Steven Karlen. *Univeristy of California, Los Angeles, Los Angeles, Calif.*

Macroscopic gyroscopes are used in devices to measure changes in orientation based on the principle of conservation of angular momentum. The simplest models consist of a spinning axis, a rotator whose center of mass lies on the spinning axis, and a stator which is the rigid frame of the entire system. We are interested in preparing molecular analogs of gyroscopes, fine-tuning

their rotational dynamics, and study their physical properties, with the goal of applying their knowledge to the development of molecular machines. Our group has synthesized and characterized molecular gyroscopes that have rotational barriers ranging from 2.9 kcal/mol to >20 kcal/mol. For comparison, the two methyl groups of ethane rotate past each other in the gas phase with a barrier of 3.0 kcal/mol. Currently, we are studying a family of volume conserving molecular rotors with a triphenylsilyl stator, and a diethynyl axle. The rotators in this study are 1,4-phenylene, 1,4-cubane, 1,4-bicyclo[2.2.2]octanediyl, 4,9-diamantanediyl, and 1,12- carboranediyl. We are currently working on synthesizing the diamantanediyl rotor to complete this family. To do this we are developing a new synthetic route to 4,9-diamantanedicarboxylic acid from available 4,9-diphenyldiamantane. The key step in the conversion of the phenyl groups to carboxylic acids is a ruthenium trichloride catalyzed oxidation in a mixture of acetic acid, carbon tetrachloride, and water with sodium periodate to regenerate the catalyst. This was then treated with trimethylsilyldiazomethane to yield the diester in 12%. We are currently optimizing these conditions to improve the yield.

D15-SAT

ENANTIOSELECTIVE REDUCTIONS OF KETONES USING A CHIRAL BORONIC ESTER

Kevin Park, Jinsoo Kim, Bakthan Singaram. *University of California, Santa Cruz, Santa Cruz, Calif.*

Enantioselective reductions of ketones to secondary alcohols can be accomplished by using the mild reducing agent NaBH4 with TarB-NO2. This easily prepared tartaric acid-based reagent combines a Lewis Acid with a carboxylic acid in a single bifunctional reagent. Various ketone substrates have been reduced in high enantiomeric excess using this reagent and NaBH4. Temperature studies were conducted to see whether the enantioselection could be improved at lower temperatures. As of today, studies are being done with TarB-NO2 and alpha-beta-unsaturated ketones to see if enantioselective reductions can be accomplished. Our methods include reducing the ketones with sodium triacetoxyborohydride and TarB-NO2 under inert gas under different temperatures. We expect to have more results by October 2007, which will reveal how well the TarB-NO2 affects the enantioselectivity of the alpha-beta-unsaturated ketones.

D12-SAT

CONVERGENT SYNTHESIS OF A PHOTOCHEMICALLY REACTIVE MOLECULAR DIROTOR BASED ON A DIARYLETHENE OPTICAL MOLECULAR SWITCH

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Crystalline molecular rotors have been studied in the Garcia-Garibay group and shown to have a wide range of dynamics by solid-state NMR. We are developing a molecular rotor in which an external stimulus can change the dynamics of the rotator (rotating unit) in the crystalline state. 1,2-Bis(2-methylthiophen-3-yl)cyclopentene optical molecular switches (diarylethenes) may be most useful for our research as they exhibit the photomechanical effect in the crystalline state; they convert photonic into mechanical energy. Our research aims to make diarylethenes covalently bonded to two molecular rotors, in hopes that the compression exhibited upon switching to the closed isomer will influence the dynamics of our rotators. The molecular rotors consist of a central phenylene rotator linked by two alkynes to triphenylmethane stators. We first attempted the synthesis of a photochemically reactive dirotor via a linear synthesis. Building the rotors from a disubstituted diarylethene was unsuccessful. Our current route involves a convergent synthesis with the key step being a modified Suzuki coupling between two triflate-rotors and the diboronic acid diarylethene. All intermediate structures and the final product are being characterized by NMR, FT-IR, MALDI-TOF MS, and UV-VIS. Following the completion of the synthesis of our photochemically reactive molecular dirotor, X-ray crystallography, diffuse reflectance UV-VIS, and solid state NMR will be performed on both the open and closed isomers to study differences in rotator dynamics. Ideally, this compound will behave like a crystalline nanomachine where irradiation with UV light alters the rotator dynamics, and visible light returns the rotator to its original state.

D18-FRI

EFFECTS OF 13-HODE ON BAX AND BCL-2 EXPRESSION IN HUMAN AORTIC ENDOTHELIAL CELLS

Shailise Ross, Sam-Shajing Sun, Shahin Maaref. *Norfolk State University, Norfolk, Va.*

Atherosclerosis is responsible for more than half of the yearly mortality in the U.S., and more than 500,000 people die annually of myocardial infarction alone. Atherosclerosis is the hardening of arteries due to plaques, which has many risk factors including smoking, high blood pressure, and elevated levels of lipoproteins in the blood. Recent research has shown that 13-Hydroxy-9Z,11E-Octadecadienoic acid (13-HODE) is one of the most abundant oxidized fatty acid metabolites released during the lipolysis of very low density lipoproteins (VLDL). Triglyceride rich lipoproteins increase apoptosis in human aortic endothelial cells (HAEC), by an unknown mechanism. In this research, the ability of 13-HODE to induce apoptosis was investigated. To determine gene expression levels of Bax and Bcl-2, a quantitative real time- polymerase chain reaction (qRT-PCR) was performed. To determine protein expression of Bax and Bcl-2, a western blot was performed. By use of qRT-PCR, it was

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discovered that Bax and Bcl-2 were up-regulated, but based on the gene expression of the positive control, these results were rendered inconclusive. By use of western blot, Bax protein was successfully expressed, however, there was no visible expression of Bcl-2. Based on these results, it appears that 13-HODE may have the potential to increase apoptotic cell death for the initiation of atherosclerosis.

D11-FRI

SUBSTRATE INHIBITION IN *DROSOPHILA MELANOGASTER* ACETYLCHOLINESTERASE-CATALYZED HYDROLYSIS OF ACETYLTHIOCHOLINE

Jose Tormos, Dan Quinn. *University of Iowa, Iowa City, Iowa.*

Kinetic studies of *Drosophila melanogaster* AChE (*Dm*AChE) show a deviation from the Michaelis-Menten equation that is indicative of substrate inhibition at high substrate concentrations, while at low substrate concentrations Michaelis-Menten behavior is observed. These observations were interpreted in terms of substrate binding to the acetylated enzyme. This behavior could be indicative of a change in the rate limiting step, in which substrate binding to the acetylenzyme shifts rate limitation from deacylation to acylation. In order to evaluate this suggestion, kinetic b-deuterium secondary isotope effects were measured for *Dm*AChE-catalyzed hydrolysis of acetylthiocholine (ATCh) and the corresponding acetyl-2H3 labeled substrate. Initial rate measurements show substrate inhibition that yields the following parameters: $K_m = 98 \pm 9$ μM, $V_{max} = 46 \pm 1$ mA/min, $K_A = 0.018 \pm 0.006$ M, $\beta = 0.31 \pm 0.07$ (K_A = dissociation constant at the substrate inhibition site, β = residual activity at [A] $\rightarrow \infty$). Isotope effects on the parameters V_{max}, K_m and β were determined by measuring isotope effects on initial rates ($^{D3}V_i$) as a function of [A]. These experiments gave ^{D3} V/K = 0.95 ± 0.03, ^{D3} $V_{max} = 1.12 \pm 0.01$ and $^{D3}\beta V_{max} = 0.97 \pm 0.04$. These values respectively measure the isotope effects on rate limiting acylation from the E + A reactant state, and proposed effects on rate-determining deacylation and substrate-inhibition evoked rate-limiting acylation. These results are indicative of a change in the rate limiting step. It is postulated that the thiocholine product exit is blocked, and therefore the rate-limiting step shifts from deacylation to acylation. Moreover, the marked normal isotope effect on V_{max} suggests that a tetrahedral intermediate accumulates in the deacylation stage of catalysis.

D16-FRI

MULTICOMPONENT SYNTHESIS OF A POTENTIAL ANTICANCER DRUG

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Indenopyridine-based heterocyclic compounds are known for their potent anti-cancer activity. Modern organic synthesis emphasizes green chemistry procedures by using multi-component reactions. One such process to obtain idenopyridine-containing compounds was developed in our laboratory. The reactants include a cyclic ketone, an aldehyde, and an amine containing aromatic compound. These cyclic ketones, which can be used include indane-1,3-dione, indanone, 1,3-cyclopentadione, and benzofuran-3-one. Modification of the amine and ketone components led to a new reaction. The reaction conditions include reflux for 3-4 hours at 120°C, oxygen bubbling, and a mixture of acetic acid and ethylene glycol (2:1) solvent. This multi-component reaction gave solely one desired product at the end with a single byproduct of water, which in itself is green. Atom economy is also a principle of green chemistry and is practiced in this project. The biological assays show anti-cancer activity through cell viability and apoptotic death in Jurkat, human T-cell leukemia, and HeLa, cervical cancer, cell lines. The polycyclic planar structure of indenopyridines may allow them to intercalate into the base pairs of DNA. Nuclear magnetic resonance spectra confirmed the structures of these compounds. Green chemistry is working its way into the everyday procedures of organic chemistry synthesis because of its environmental and economical advantages.

D14-SAT

DIFFERENTIATION OF NITROAROMATICS BY PORPHYRINS: TOWARDS AN ELECTRONIC NOSE

Gloria Zarate[1,2], Joshua Akhigbe[1], Yu Lei[1], Christian Brückner[1]. *[1]University of Connectic, Storrs, Conn., [2]San Diego State University, San Diego, Calif.*

Most explosives, like trinitrotoluene (TNT), are nitroaromatic compounds. It is known that the interaction of a nitroaromatic compound in solution with porphyrins causes a quenching of the porphyrin fluorescence. However, the influence of the structure of a porphyrin on the quenching by nitroaromatics is very little investigated, while it is not at all known to which degree the nitroaromatic structure affects the porphyrin quenching. This study presents the results of fluorescence quenching experiments in which 20 different nitro-aromatic compounds were titrated against 33 structurally different porphyrins and porphyrin-like macrocycles, and some of their Zn(II), Pt(II), and Pd(II) complexes. We will also detail the synthesis of selected porphyrins. We observed that each sensor element (porphyrin) responded to a given analyte (nitroaromatic) to a different

degree, generating a distinct interaction pattern. The generation of a pattern in a sensor array is the functional basis for the olfactory senses of animals. Electronic noses aim at mimicking this. Thus, the observed distinct quenching patterns for each nitroaromatic compound tested serves as proof of principle that a porphyrin-based sensor array could be assembled in an electronic nose for the specific detection of, for instance, TNT.

PHYSICAL CHEMISTRY

D20-FRI

STUDY OF HYDROXYL TERMINATED SELF-ASSEMBLED MONOLAYERS (SAMS) AFTER REACTION WITH SICL4

Diana Mars, Andrew Ichimura. *San Francisco State University, San Francisco, Calif.*

The design, synthesis, and characterization of nano-scale thin films are important in applications such as computer chip manufacture, optical coatings, and thin film displays. Thiols spontaneously assemble on gold surfaces to yield organized molecular assemblies that serve as model and practical interfaces between gold and the applied coatings. In this study, self-assembled monolayers (SAMs) were formed by reaction of 4-mercaptophenol and 4-mercaptobenzyl alcohol with gold. The structural changes of these SAMs upon reaction with $SiCl_4$ (g) were studied by reflection FTIR spectroscopy. The reaction of hydroxyl terminated SAMs with $SiCl_4$ yields a novel molecular tripod that is distinguished by Si-O stretching vibrations observed at 1106 wavenumbers. This molecular tripod forms a suitable interface for the growth of silicon dioxide based zeolites and films. It is postulated that the tripod ligand will have a much higher thermal stability compared to single S-Au linkages, which will broaden the potential applications for monolayer assemblies. This report will present structural models of the tripod SAMs deduced from reflection IR spectra and computations that employed density functional theory (DFT).

D19-SAT

THERMAL ANALYSIS OF POTENTIAL ELECTROLYTES FOR NANOCRYSTALLINE SOLAR CELLS

Nicolle Patterson, Maria Benavides. *University of Houston–Downtown, Houston, Tex.*

The thermal stability of four recently synthesized phosphonium-based ionic liquid samples was determined by TG/DSC/MS to assess their potential use as electrolyte materials for nanocrystalline solar cells. The four samples were: tetraoctyl phosphonium iodide, ethyl triooctyl phosphonium, n-butyl trioctyl phosphonium iodide, and n-butyl trihexyl phosphonium iodide. All four samples decomposed at high temperatures ranging from 250°C to 315°C. Results indicate that these materials possess significant thermal stability that makes them suitable for solar cells. Four samples were synthesized in Germany by *Ionic Liquid Technologies* for comparison purposes, namely 1-ethyl-3-methyl-imidazolium dicyamide, 1-ethyl-3-methyl-imidazolium thiocyanate, 1-hexyl-3-methyl-imidazolium iodide, and 1-methyl-3-propyl-imidazolium iodide. The four samples synthesized in Germany decomposed at lower temperatures ranging from 252°C to 275°C. The thermal analysis was carried out by simultaneous thermal gravimetry (TG), differential scanning calorimetry (DSC), and mass spectroscopy (MS) using the Netzsch 409 STA CD instrument. In addition, we have performed studies by varying parameters such as heating rates to assess their effect in various thermodynamic parameters with the aim of gaining insight into some of the kinetic processes involved in the decomposition of these materials.

COMPUTER SCIENCE

C12-FRI

ADAPTIVE OBJECT RECOGNITION USING HIGHLY SELECTIVE FEATURES

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Our purpose is to achieve recognition of similar images given a set of images and a hypothesis, where the hypothesis is the object to be identified. To perform these tasks we use a combination of highly selective features and AdaBoost. A highly selective feature, as proposed by Viola and Kinh Tieu in 2001, can be created by applying three times a sequence of filter and down-sampling. The highly selective features are then the sum of all the pixels of the final result. In our case, we use a filter bank of only six filters (variations of Laplacian, Gaussian, and Laplacian of a Gaussian). Three filters are used instead of a previously proposed 25, which would lead to 25^3 or 15625 different features, in order to reduce the time required to do such process. Each of these highly selective features are treated as weak learners and passed to the AdaBoost algorithm. The final output is a strong classifier based on a weighted combination of the highly selective features. With the final predictions and errors outputted the effectiveness of the classifier can be determined.

C12-SAT

WALLEYE: DESIGN AND INTERACTION

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Walleye is an interactive assembly of two individual 8 x 12 (at 1 foot intervals) array of lamps and photo sensors. The lamps will be dimmed so that the sensors detect this amount of light accordingly. The light sensor will detect any change and make the proper adjustment to its corresponding lamp. This summer, we will be determining how the lamps will react to the changes detected by the light sensor, how to mount the sensors and lamps, along with the chipsets that will determine their behaviour. A large part of it will also be taking into account all the factors that will cause some discrepancies in how we expect Walleye to function. One of these is the angle of detection the light sensor has, which may detect a wider range than we expect. Another is the ambient light from the other lamps and how they will affect the different sensors, especially the ones on the edge, which will have considerably less ambient light. My part of the research includes figuring out all the physical hurdles, as well as making the project completely user friendly, so we can eventually ship it to museums for display. For now, Walleye may be an array of lamps and light sensors, but in the future it may be adapted to display at higher resolutions, with more colors, and detect different changes in the environment, such as visual or temperature changes.

C8-SAT

AUTOMATION ASTRONICAL INSTRUMENT SETUP

Eric Dela Rosa. *Hawaii Community College, Hilo, Hawaii.*

ESPaDOnS is a high-resolution spectropolarimeter that was designed to collect a complete optical spectrum in a single exposure. This allows astronomers to learn about the magnetic polarization of stars. The process for setting up ESPaDOnS is tedious and frustrating for the operators because it has to be done manually. Depending on the configuration of ESPaDOnS, the process can take as long as five hours to two days. The setup process is separated into two different procedures, the physical setup and the computer-based setup. The problem is with the computer-based setup: if the setup time takes 5 hours, 1 hour is physical and the other 4 hours is computer-based. By automating the computer-based setup, it will make it easier and faster to get ESPaDOnS up and ready for observing. The goal of this project was to create a user interface using TCL/TK for this automation. The user interface allows the user to select tests needed to setup ESPaDOnS. When the setup is complete, the program will display the results, save them in a text file, and print the results. With this program, setup time is cut down to 10 to 15 minutes of user interaction. I will present the design of the user interface and how it will be implemented for the use of ESPaDOnS.

C9-SAT

MAPPING MAUI'S MAJOR ROADS WITH GLOBAL POSITIONING SYSTEM DEVICES

Augustus Elias. *Universtiy of Hawaii at Hilo, Hilo, Hawaii.*

The goal of this project at the Pacific Disaster Center is to collect the locations of all highway mile markers on the island of Maui using global positioning systems (GPS), creating a database that will be of high importance to the entire emergency management community. With the help of the County of Maui we were given rough estimates of the mile markers' positions. The project assigned was to improve the location of the mile markers using GPS units. Along with the collection of waypoints, descriptions, and pictures of each specific location were also cataloged. ArcGIS 9.1 software and mobile GarminIII GPS units were used to gather and process the data into shapefiles. Data accuracy was tested by using two GPS units and measuring the average error between the units. Other information, such as location descriptions and photographs, was written as metadata for the shapefile so it could be interpreted and used by other analysts. This shapefile will be uploaded on to a dynamic map in the Pacific Disaster Center's website. Overall results and methods used to gather this information for the database is to be presented.

C10-SAT

DESIGN OF A BIOSENSOR DATABASE AND INTEGRATION WITH IMAGE ANALYSIS TOOLS

Francisco Fernández[1,2], Estelle Glory[2], Robert Murphy[2]. *[1]Universidad Metropolitana, San Juan, P.R., [2]Carnegie Mellon University, Pittsburgh, Pa.*

Nowadays the automated analysis of microscopy images is an indispensable technique for exploring cell pathways. The design of a new way to label proteins is a critical step to improve the determination of the subcellular location of proteins. This project deals with the creation of a database, named molecular biosensor database (MBD), to assist with the creation of new protein markers. The data stored in the MBD database are annotations of newly developed biosensors which label proteins within cells. This biosensor is composed of a fluoromodule, which is a combination of an apomodule (a genetically expressed gene), a

fluorogen (a non-fluorescent dye that fluoresces in the apomodule), and a biological fusion partner (the target protein). Other important aspects of this project are to connect the MBD with the protein subcellular location imaging database (PSLID) to store and analyze biosensor images and to provide a public access to the data via an internet interface. When images of cells with biosensors are acquired, they are then analyzed with tools available in PSLID.

C13-SAT

MULTI-DOMAIN OPTICAL NETWORK PROVISIONING

Raul Garcia[1], Nasir Ghani[2], Qing Liu[2]. *[1]Universidad Metropolitana, Cupey, P.R., [2]Tennessee Technological University, Cookeville, Tenn.*

Dense wavelength division multiplexing (DWDM) has become the dominant transport layer technology for next-generation backbone networks due to its unprecedented capacity scalability. As a result, there is a pressing need to investigate lightpath provisioning in multi-domain DWDM networks. Although inter-domain provisioning has been well-studied for packet/cell-switching networks, the wavelength dimension (along with wavelength conversion) presents many added challenges. This work addresses this crucial concern. Namely, a detailed GMPLS-based hierarchical routing framework for provisioning transparent/translucent/opaque multi-domain DWDM networks is presented. The scheme adapts topology abstraction to hide internal domain state so as to resolve routing scalability and security issues. Specifically a novel full-mesh topology abstraction scheme is developed for full wavelength conversion domains, i.e., to disseminate additional wavelength converter state. Related inter-domain lightpath RWA and signaling schemes are also tabled. Performance analysis results are then presented to demonstrate the effectiveness of the proposed mechanisms along with directions for future research work.

C11-SAT

REAL-TIME SATELLITE VISUALIZATION

Vladimir Ivanov. *University of Hawaii at Hilo, Hilo, Hawaii.*

There are more than eleven thousand bodies (rockets, satellites, and debris) that are orbiting the Earth. Space surveillance is important for preventing collisions and other potential problems. Oceanit, an aerospace engineering company, is developing a product called HANDS (High Accuracy Network Determination System) which will use low-cost optical ground stations to keep track of objects orbiting the Earth. The goal of this project was to create an application that would provide visual information on the satellites and their positions in real time. The programming language C# was used in order to complete the task. An improvement providing high accuracy was developed by incorporating constant streams of satellite orbit data. Visual images of the objects' orbits are more familiar to the end user, and they transform streams of numbers into meaningful data. The finished product will integrate graphical visualization into one or more of the HANDS projects.

C13-FRI

IMAGE PROCESSING FOR DOCUMENT ANALYSIS

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My project consists in testing software that can separate the handwriting that a program generated on top of the machine printed material of the documents because we are interested to see if the program can separate the strokes (handwriting). When we first started the project we used a program to generate the handwriting on the original documents, after running the documents through the program we saw that the raw set of data we were generating we were not happy with; because most of the handwriting was not on top of the machine printed material rather on the paper itself or a background in which the document was laying. So we decided to make our own fake documents in which we searched for graphical images on the internet to paste on top of some documents so that we could make sure that handwriting that was generated with the program was on top of the machine printed material only, and not on the paper or background of the document. We ran the fake documents a couple of times, after seeing the data generated; we modified the fake documents each time so that the data that was generated was the kind of data that we were looking for. Now that we have our set of data that we are happy with; we can start running this data through the software so that we can see if the software do what is supposed to. When we get the results we are planning to take the strokes (handwriting) and do them in x3d which is a program that makes 3D figures and worlds so that the strokes can be seen at 360 degrees.

C7-SAT

DATA VISUALIZATIOIN IN AN ONLINE MAPPING NETWORK

Michael Lombardi. *Butte College, Oroville, Calif., University of California, Irvine, Irvine, Calif.*

With technological advancements in global positioning systems, mapping, and web based applications, data visualization via online mapping has demonstrated an incredible potential to improve data communications. Although online mapping has become a

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popular geographical positioning utility, the greater applications of mapping visualizations have not yet been developed to a satisfactory level in light of the current technological capability of our world. As a result, the proposed project creates a public network mechanism that uploads, visualizes, and shares location data via online Google Maps technology. We accomplish this with the use of web communication technologies that include dynamic hypertext transfer protocol (DHTML) and PHP: hypertext preprocessor (PHP) in order to transfer data to and from an Apache web server. This Apache web server hosts a MySQL database that is intended to store and retrieve the multi-user information via the Google Map user interface. As a result, we are developing an online commenting system that is intended to manage multi-user information within the online mapping network.

C10-FRI

WORD SIMILARITY AND WORD SENSE DISAMBIGUATION IN SEMANTICS

Liem Luong. *University of Houston–Downtown, Houston, Tex.*

Word is the basic unit in communication among people. From the aspect of linguistics, word is also the simplest element in a sentence. Multiple sentences make paragraphs and then paragraphs combine into articles. Semantically meaningful words include nouns, verbs, adjectives, and adverbs. These four types of words contribute to make a meaningful sentence. We focus on the word similarity/word sense disambiguation. Our project for summer 2007 is to compare the similarity between words in a large semantic network that we get from the WordNet. WordNet is a large lexical database of English words from Princeton University. This tool is very useful for computational linguistics and natural language processing. In order to conduct our project, we use Visual Studio C++. First, we search and collect data from WordNet. Second, we extract information from these huge data files. We analyze the data structure of each file and the way that four types of speech relate to other words between the other files. Third, we write a C++ program to link data structure of each file together and determine the sense of each word. Currently we are able to generate the output files for each component. These output files show exactly same results with the results as we tested with WordNet browser. In conclusion, we have done for the evaluation and the output file format. In the future, we will work on the similarity of word base on the 3D position of words in the huge semantic network.

C11-FRI

TESTING 3D FFT (FAST FOURIER TRANSFORM)-BASED REFERENCING ALGORITHMS

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In many real-life situations ranging from geoinformatics to bioinformatics, it is important to reference two images, i.e., find the shift and rotation necessary to align one image with another. There exist fast efficient algorithms for referencing 2D images; these algorithms are based on the Fast Fourier Transform (FFT). For 3D images, however, no such fast algorithms are known: shift detection is easily extended from 2D to 3D, but the 2D algorithm for finding rotation is based on the fact that rotation in 2D can be described by a single angle. We have developed a fast 3D referencing algorithm that finds 3D rotations by computing and aligning the moments of inertia of the images' Fourier transforms. This algorithm was mainly tested on no-noise cases. In practice, images are often noisy; it is therefore important to test our algorithm on noisy real-life images. Most real-life 3D images require so much space that we cannot test them on usual PCs, and access to supercomputers is often limited. To alleviate this problem, we have developed an automatic testing suite that cuts different sub-images of the larger images, uses our algorithm to reference these sub-images, and records the results. The suite relieves the need for cutting and testing by hand, and only requires human attention when verifying results. Thus, it helps us in efficiently and speedily testing our algorithm.

C8-FRI

LABVIEW CONTROL SOFTWARE FOR THE UH-HILO 0.9 M TELESCOPE

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University of Hawai'i at Hilo's (UH-Hilo) manually controlled 0.6 m telescope, built on Mauna Kea in 1968, is being replaced by their new 0.9 m telescope. This modern telescope will be in a newly-renovated educational observatory and will be electronically controlled from UH-Hilo at sea level. However, given that there is no standard telescope control software (TCS) used by all telescopes, UH-Hilo has to customize their own TCS system through LabVIEW. In order to modify and develop their TCS over time, the Physics and Astronomy Department wants to familiarize themselves with LabVIEW's graphical programming language. I helped to tailor and implement their TCS system by first observing and comparing electronically-controlled telescopes on Mauna Kea and Mauna Loa. To help the department with LabVIEW, I modified current LabVIEW telescope programs, recorded complications, created an easy-to-read manual for first-time LabVIEW users, and started a program to locate the telescope on a polar graph representing the visible sky. With this manual and base program, the faculty and students can further their research by enhancing the capabilities of their own TCS, as well as aid in operating and customizing the telescope to their convenience.

C7-FRI
APPROXIMATE SIMILARITIES WITH GAPS FOR STRINGS
Hilde Velasco, John Tsiligaridis. *Heritage University, Toppenish, Wash.*

Pattern matching is a basic problem that occurs in many domains (data processing, speech recognition, computational biology, telecommunications needs, etc.). The type of pattern matching discussed in this work is the approximate string matching. There are gaps in the matching. We do not require a perfect matching but a matching that is good enough to provide approximate similarities by satisfying certain criteria. The don't care characters may appear both in text and pattern and any character of the pattern may correspond to a different character of the text. Many string matching algorithms have been developed with various methodologies (dynamic programming, etc.) and performances depending on the size of pattern, alphabet, and the existence of repetitive subpatterns. Our major concern is to discover the similarities for patterns with various formats. For this purpose, two algorithms using the pattern matching pointers move methodology (PMM) with opposite direction moves are presented. First, the move with distance (MD) addresses the pattern case consisting of two position dependent substrings (landmarks) in distance. Secondly, the move with distances and intermediate landmarks (MDL) deals with pattern consisting of some position dependent substrings in distance. The complexity for text, and binary strings is stated and useful results are produced. We study the size interchange of the pattern's parts and its contribution to the performance of the algorithms. We also considered the construction of a suffix tree for text or biological sequences with linear running time. The experiments of this approach provided us with feasible solutions.

C9-FRI
GENOMEXPLORER: GENOMIC DATA VISUALIZATION
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Tumor genomes can be highly rearranged and, thus, may not be co-linear with host genome. Recurrent genome rearrangements involve genes that mediate a wide range of growth and signaling pathways that are increasingly targeted by anti-tumor therapeutics. Current technologies for studying tumor genome structure are not capable of elucidating the structural organization of tumor genomes at high resolution, or of relating it to the underlying host sequence. End sequence profiling (ESP) is a sequence-based method for directly determining the structural organization of tumor genomes, and for cloning all types of structural rearrangements en masse. In addition, ESP can be carried out on tumor transcriptomes for large-scale identification of fusion transcripts. We have demonstrated this by analyzing full length enriched and normalized cDNA libraries from MCF7 (breast cancer), LnCaP (prostate cancer), and a primary brain tumor. Multiple tumor-specific transcripts were identified and analyzed. The sheer amount and diversity of the data generated by ESP necessitate development of efficient and effective way to visualize and compare ESP genomic and transcriptome data. The purpose of this project, GenomExplorer, is to provide a mechanism for visualizing ESP data by means of a web based application leveraging Asynchronous Javascript and XML (AJAX) technology. We expect this tool to allow us to visualize ESP data from multiple genomes in order to facilitate the detection of common rearrangements which can later be validated in the lab.

ECOLOGY

C29-FRI
GROWTH AND POLLINATION IN *CUCUMIS SATIVA*: CUCURBITACIN EFFECTS AND RESOURCE COSTS ON CUCUMBER YIELD
Jeselyn Calderon-Ayala[1], Lynn Adler[2]. *[1]Universidad Metropolitana, San Juan, P.R., [2]University of Massachusetts, Amherst, Amherst, Mass.*

In plants, herbivores and pollinators comprise an important role in the evolution of plant chemical defense. However, chemical defenses can directly deter pollinators, while also reducing herbivory causing a cost in the plant. In order to understand if pollination and chemical defenses determine yield in cucumber (*Cucumis sativa*) we conducted a 2 x 2 factorial experiment using 88 plants, bitter versus sweet taste and natural pollination versus hand pollination. The production of bitter taste in cucumber is a mechanism of resistance and defense called cucurbitacin and is costly, and if so, we want to know if the cost is due to using up resources or deterring pollinators. The hand pollination treatment will help us understand if yield could be improved and if reproduction is limited by pollen receipt. Growth and herbivory in plants will be also measured to understand if plant is investing energy in growth and if the insecticide applied on them is working. We hypothesize that there will be lower yield in bitter plants than in sweet due to costs of defense and that hand pollination will improve yield in cucumber plants. Preliminary results of data taken in the first two weeks of growth reveal a pattern of bitter plants significantly growing larger than sweets plants. Production of flowers, pollination observations, and crop yield are yet to be measured.

C32-FRI

WIND AND INSECTS AS DISPERSAL VECTORS FOR ZOOPLANKTON SPECIES IN THE NORTHERN CHIHUAHUAN DESERT

Alma Castanon, Matthew Stensberg, Robert Wallace, Elizabeth Walsh. *University of Texas at El Paso, El Paso, Tex.*

Little research has been done on dispersal mechanisms of zooplankton in desert regions.
Patterns of dispersal and colonization of selected zooplankton species were studied in the Chihuahuan Desert at Hueco Tanks State Park (El Paso, Tex.). We hypothesized that both wind and insects are vectors for dispersal. A series of six mesocosms (67.5 L of artificial aquatic media (MBL) and food) were set out in the park. The mesocosms were covered by a 0.63 cm mesh to prevent other vectors from contributing to colonization. Two samples (10 L each) were taken weekly from each mesocosm. One sample was preserved as a quantitative sample in 70% ethanol; another sample was collected live and examined for colonists. Insects were tested as vectors by rinsing them with MBL. The rinse was incubated and examined for zooplankton. Early results suggest insects serve as poor rotifer vectors, as none (n = 229) yielded rotifers. However, algae, and ciliates were recovered from all rinses. These organisms appeared in mesocosms after one week whereas rotifers colonized the next week. Species richness was variable between samplings and among mesocosms. Eight rotifer species seven families were found representing a small proportion of the record 52 species and 18 families found at the park. No crustaceans established populations within seven weeks of the experiment. All rotifer species that colonized the mesocosms have been previously found in temporary ponds in this area including the newly described *Epiphanes chihuahuanensis*. Given our results, we believe that wind plays at least a partial role in dispersing rotifers.

C30-SAT

EFFECTS OF ENVIRONMENTAL VARIABLES ON FORMER OREGON WHITE OAK SAVANNA

Lisa Castle. *University of Oregon, Eugene, Ore., Chaminade University of Honolulu, Honolulu, Hawaii.*

Oregon white oak (*Quercus garryanna*) savanna is a highly endangered ecosystem. About 98% of this ecosystem has been lost to urban and agricultural development and the encroachment of conifer forests due to reduction in fires over the past 150 years. The purpose of this study was to examine the successional dynamics of former Oregon white oak savanna within plant communities at Mount Pisgah, Oregon, a site that includes areas of intact oak savanna and savanna that are in various stages of succession to forest. Data collected at each plot included: community type, a census of all trees present, and increment cores that were taken from two individuals of each of six size classes of each species. These cores were analyzed by dendrochronological methods, including crossdating and mensuration, to determine the relative effects of spatial and temporal variables. Two separate studies have been conducted on similar plant communities at a site in the Willamette National Forest, Oregon. In congruence with the results of these studies, I expect that Oregon white oaks will be the oldest trees and will display the lowest mean growth rate. I also expect that the composition of tree communities will be explained as a function of environmental variables, including soil nitrogen, pH, percents clay, and silt, and, to lesser degrees, slope and heat load.

B28-FRI

SONG RECOGNITION IN PLAYBACK EXPERIMENTS IN ANNA'S HUMMINGBIRD, *CALYPTE ANNA*

Carina Castro, Anne Houtman. *California State University, Fullerton, Fullerton, Calif.*

Studies have shown that some songbirds have the ability to discriminate between songs of their mate, young, or rivals. Hummingbirds, like songbirds, learn and sing complex songs. However, there are no studies to show if they can discriminate between individuals on the basis of song. Being able to distinguish neighbor from stranger can be energetically beneficial for territory maintenance. It would be wasteful to attack the neighbor bird every time it sings than a stranger bird with an unknown song. A stranger bird singing near a territory potentially indicates an invader and thus territory defense is imperative. We conducted neighbor-stranger song playbacks in February through April 2007, in Anza Borrego State Park, California, to determine if male Anna's hummingbirds distinguish between individuals' songs. We hypothesized that Anna's males will respond more strongly to playback of stranger Anna's songs than to neighbor song. We also hypothesized that they will respond more strongly to Anna's song than to Costa's hummingbird song (heterospecific competitor) and show the least response to house finch song (heterospecific non-competitor). The playbacks consisted of four trials in random order: a neighboring Anna's song, a stranger Anna's song, a Costa's song, and a house finch song. All birds reacted aggressively toward playback of conspecific songs, but did not respond to the song of Costa's or house finch. They responded more aggressively toward neighbor playback than stranger playback. Our results suggest that Anna's males can distinguish between individuals during song playback.

C31-FRI
INDUCED DEFENSES OF *MIMULUS GUTTATUS*
Ronni Chase Alone, Liza Holeski, John Kelly. *University of Kansas, Lawrence, Kans.*

Trichome density is an environmentally sensitive trait that also exhibits genetic variation in *Mimulus guttatus* (yellow monkeyflower). Trichomes often act as defense traits against insect herbivores. The first experiment, we used recombinant inbred lines (RILs) of *M. guttatus*, to investigate whether trichomes can be induced by simulated insect herbivory. We grew two plants per inbred line in a common garden environment; one plant was the control (experienced no simulated herbivore damage), and the other plant was the treatment (experienced simulated damage on the second leaf pair). Fifth leaf trichome counts were performed on control and treatment plants and the counts were compared within each genotype (inbred line). We found that simulated herbivory did induce greater trichome densities on later leaves. The second experiment had two groups in the maternal generation, damaged and undamaged. Each parental population and RIL had a replicate plant in each treatment group. Plants in the damage treatment group received simulated weevil damage on each leaf pair, starting with the second leaf pair. Plants in the undamaged treatment received no damage. These plants were selfed and grown to perform fifth leaf trichome counts on the offspring generation. One parental population and the RILs had significantly higher fifth leaf trichome densities. Both experiments are potentially examples of adaptive phenotype plasticity; plants that experience insect damage on early leaves may be able to minimize future damage through trichome induction. This adaptive phenotypic plasticity of trichome density may be induced both within and between plant generations.

C32-SAT
CRYPTIC SPECIATION IN *CHYDORUS SPHAERICUS* (CLADOCERA: CHYDORIDAE) IN CHIHUAHUAN DESERT WATERS?
Leslie Chavez[1], Thomas Schroeder[1], Marcelo Silva-Briano[3], Robert Wallace[2], Elizabeth Walsh[1]. [1]*University of Texas at El Paso, El Paso, Tex.,* [2]*Ripon College, Ripon, Wis.,* [3]*Universidad Autonoma de Aguascalientes, Aguascalientes, Mexico.*

Many freshwater zooplankton taxa with a worldwide distribution have been shown to be cryptic species complexes, and it has been assumed that cryptic speciation has occurred in the *Chydorus sphaericus* group. Morphological variation has been well documented in this cosmopolitan cladoceran. We sampled nine populations spread throughout the Chihuahuan Desert (Mexico and southwestern U.S.). These populations were found in very different aquatic habitats, including saline and freshwater springs, reservoirs, and temporary playas. Physicochemical parameters and other ecological features were recorded at each study site. *Chydorus sphaericus* DNA was isolated and the mitochondrial *cox*1 gene as well as the internal transcribed spacers of the nuclear rDNA complex were sequenced. RDA analysis of environmental data and the occurrence of *C. sphaericus* showed a weak correlation of the species' presence with algal mats. Genetic variation within the *cox*1 gene was very low among populations (< 1%). Populations found in Texas and New Mexico showed virtually no genetic differentiation, forming a distinct clade, separated from populations in Chihuahua and Coahuila (Mexico). Interestingly, when a sequence for *Chydorus brevilabris* was included, it grouped as the sister taxon to the U.S. clade. Genetic distances among *C. brevilabris* and U.S. populations ranged from 0.005 to 0.011. Frey elevated *C. brevilabris* to species status from the *sphaericus* group based on morphological differences but genetic data presented here point towards the existence of a single species. The lack of *cox*1 variation does not support cryptic speciation in this complex in the Chihuahuan Desert.

B27-SAT
RELATIONSHIPS AMONG POPULATIONS OF SIDE–BLOTCHED LIZARD (*UTA STANSBURIANA*) IN GRAND CANYON NATIONAL PARK, ARIZONA
Esther Daniells, Marlis Douglas, Michael Douglas, Mark Davis. *Colorado State University, Fort Collins, Colo.*

Biodiversity in Grand Canyon National Park is affected by numerous landscape features, such as topography, vegetation, and the Colorado River. These serve as physical barriers and may truncate gene flow from one side of the river to the other or upstream and downstream of a barrier on the same side of the river. To determine the magnitude and extent of isolation among populations, we sampled the side-blotched lizard (*Uta stansburiana*) along the river corridor throughout Grand Canyon National Park during 2000 through 2003. To determine differentiation, we extracted mitochondrial DNA (mtDNA) from pieces of tail collected non-lethally from 210 individuals representing 17 populations. We amplified two mtDNA genes (ATPase 8 and 6) via polymerase chain reaction (PCR) and sequenced 840 base pairs using an Applied Biosystems Incorporated (ABI) prism 3100 genetic analyzer. These data will not only allow us to study the potential pattern and likelihood of genetic isolation and drift in these populations, but they will also give insight into the distribution and management of biodiversity in a flagship National Park.

C29-SAT

HAS THE STATEWIDE BAN ON *CAULERPA* SPECIES BEEN EFFECTIVE? A SURVEY OF SOUTHERN CALIFORNIA AQUARIUM RETAIL STORES

Stephanie Diaz[1], Susan Zaleski[2], Jayson Smith[1], Steven Murray[1]. [1]*California State University, Fullerton, Fullerton, Calif.,* [2]*University of Southern California, Los Angeles, Calif.*

The *Caulerpa taxifolia* invasion in the Mediterranean Sea raised awareness of the potential for introduced seaweeds to impact coastal communities. Subsequent introductions of *C. taxifolia* in southern California in 2000, presumably from the release of aquarium specimens, cost ~$4.5 million for eradication efforts. Besides *C. taxifolia*, other *Caulerpa* species being sold for aquarium use also may have the potential to invade southern Californian and U.S. waters. Surveys of the availability of *Caulerpa* species in southern California aquarium retail stores in 2000 to 2001 revealed that 26 of 50 stores sold at least one species of *Caulerpa* and seven stores sold *C. taxifolia*. In late 2001, California imposed a ban on the importation, sale, or possession of nine *Caulerpa* species (DFG Code 2300); the City of San Diego expanded these regulations to include all species. To determine the effectiveness of the California ban, we surveyed *Caulerpa* availability at 44 of the southern California retail stores in 2005 to 2006 sampled in our previous study. Similar to previous methods, specimens of *Caulerpa* species were purchased, identified, and preserved. Of the 44 stores, 23 sold *Caulerpa* and three stores sold *C. taxifolia*. Three additional stores had *Caulerpa* species in stock but not for sale. These results suggest that the California ban on *Caulerpa* species has not been effective and that the retail aquarium industry continues to represent a potential vector for distributing *Caulerpa* specimens, including *C. taxifolia*. This study underscores the need for outreach and enforcement programs to increase awareness among the aquarium retail industry and aquarium hobbyists.

B28-SAT

GRAZING REDUCTION BY *TEGULA FUNEBRALIS* IN THE PRESENCE OF A KEYSTONE PREDADOR, *PISASTER OCHRACEUS*: EVIDENCE FOR TRAIT-MEDIATED INDIRECT INTERACTIONS

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Classical trophic cascade models focus on predation as the source of indirect effects (density-mediated indirect interactions, DMII) in a three-level food chain. Yet a growing body of work indicates that trait-mediated indirect interactions (TMII) complement DMII through altering the behavior and habit of the prey species. We tested the strength of TMII in rocky intertidal communities by examining interactions among a keystone predator, *Pisaster ochraceus*, an herbivore, *Tegula funebralis*, and the algal community in and around tide pools. Laboratory experiments demonstrated a strong avoidance of *Pisaster* by *Tegula*. Preliminary results from field experiments with caged *Pisaster* in tide pools reduced grazing by *Tegula* while the density remained similar. Thus, TMII appear to be an important component in structuring rocky intertidal communities and the relative importance of DMII and TMII needs to be explored.

C31-SAT

PHENOTYPIC PLASICITY AND BIOTIC INVASIONS: A COMPARATIVE STUDY BETWEEN SIX INTRODUCED GRASSES

Kyle Hernandez. *Purdue University, West Lafayette, Ind.*

The ability of introduced species to establish viable populations and ultimately become invasive has been the focus of much research over the past half century. Nonetheless, we are still unable to predict which introduced species will become invasive. An understudied potential reason for invasiveness may be attributed to phenotypic plasticity. Phenotypic plasticity is defined as the property, or trait of a given genotype to differentially express phenotypes in the presence of an environmental cue. Plasticity may allow organisms to live in a wide array of environments and may be particularly important for introduced species. To better understand the role of phenotypic plasticity in biotic invasions, I collected six introduced annual species of *Bromus* grasses across the U.S. Three of the collected species are considered to be invasive and/or noxious weeds while the other three are not. Individuals will be subject to greenhouse experiments to test the hypothesis that invasive species are more plastic in fitness-related life history traits than non-invasive species, allowing them to persist in a wider array of environments. Three environmental gradients will be used: Temperature, precipitation, and nutrient levels. The traits of interest include: flowering time, inflorescence number, number of tillers, germination success, growth rates, and biomass allocation. Germination will occur in October and the experiment will run until July. This study will allow me to better understand differences in plasticity between successful invasive species as well as the ecological and evolutionary importance of phenotypic plasticity.

C33-FRI

EXPLORATION OF ENVIRONMENTAL CORRELATES FOR THE PURPOSE OF CONSERVATION AND PROMOTION OF URBAN BEES

Ayana Heumann. *City College of San Francisco, San Francisco, Calif., San Francisco State University, San Francisco, Calif.*

According to the APIMONDIA Standing Commission for Pollination and Bee Flora, "one third of what we eat and drink is produced through service provided by pollinators." Bees are the world's most prolific pollinator and bolster ecosystem diversity and stability, but much of their native habitats are being fragmented or replaced by urban areas. Our project was developed in order to examine bees in urban habitats, about which very little is known. Our aims were two-fold: to determine what variety of sunflower would optimize local data collection, and to collect data on pollinator service in order to determine what environmental factors correlate with high levels of bee activity. Defining favourable sunflower varieties as those which were quick to germinate and flower and whose blossoms were long-persisting, we grew twelve varieties and recorded germination and flowering times. To collect field data on existing sunflowers, we surveyed six community garden sites within the city three times, recording how long it took for five bees to visit a sunflower head, and the type of each visiting bee. These data were then analyzed beside such factors as the amounts of surrounding green spaces and open spaces, ratios of urban density, and habitat mosaic. Though our data collection and analysis is not yet complete, it is our goal to determine what environmental factors correspond with high levels of bee activity in order not only to conserve, but to promote pollinator service and urban bee populations.

B27-FRI

COMPARING WATER RELATIONS OF TWO DESERT SHRUBS, *ATRIPLEX HYMENELYTRA* AND *ISOCOMA ACRADENIA*, DURING THE DRY SEASON IN THE MOJAVE DESERT

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Desert plants evolved physiological adaptations that allow them to conserve water while carrying out photosynthesis. The purpose of this study was to compare the water relations of two co-occurring, halophytic desert shrubs with differing photosynthetic pathways during the dry season in the Mojave Desert. We hypothesized that *Atriplex hymenelytra*, a C4 plant, will conserve water more than *Isocoma acradenia*, a C3 plant because, for the same net carbon gain, C4 plants transpire less than C3 plants. We examined stem and leaf water potentials, stomatal conductance, specific stem conductance, and percent loss of stem conductivity (PLC) for five individuals of each species over a 24-hour period in early June, and measured wood density. *Atriplex* had higher stomatal conductance than *Isocoma* during the night, whereas *Isocoma* had higher stomatal conductance during the day. *Isocoma* had a higher specific hydraulic conductivity and higher PLC, evidence that its xylem was more embolized than *Atriplex's,* despite the fact that *Atriplex* had lower leaf and stem water potentials. The finding that *Atriplex* had denser wood, lower specific hydraulic conductivity, lower PLC, and lower water potentials than *Isocoma*, suggests that *Atriplex* was more resistant to embolism formation than *Isocoma*. The ability of *Isocoma* to maintain a higher water potential while opening its stomata more than *Atriplex* suggests that *Isocoma* may tap into a deeper water source. Difference in rooting depths, rather than water conservation strategies, may, in part, explain the differences observed between the two species.

B26-SAT

THE EFFECTS OF ANTHROPOGENIC RUNOFF ON THE INVASION OF NATIVE ARTHROPOD COMMUNITIES BY *LINEPITHEMA* IN SOUTHERN CALIFORNIA RIPARIAN AREAS

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Runoff in semi-arid ecosystems disrupts natural water flow, impacting downstream communities. We studied the effects of anthropogenic runoff on the invasion of riparian habitats in southern California by the Argentine ant, *Linepithema humile*. We sampled ants and terrestrial arthropods at five sites at Starr Ranch Sanctuary, Orange County, California, using ten pitfalls and six bait stations per site. We hypothesized that sites with natural water flow patterns would exhibit high species richness and rare occurrences of *Linepithema*, while sites receiving increased runoff from a neighboring suburban development would have low species richness and a high abundance of *Linepithema*. The occurrence of *Linepithema* was not correlated with flow patterns of water because *Linepithema* invaded the most natural site. Sites closest to suburban developments were invaded while downstream of the suburban runoff only native ants were found. Invaded sites had a lower diversity of native ants, a maximum of 2 species versus 5 in un-invaded sites, and average lower abundance of terrestrial arthropods, with 24 ± 2.75 (SE) in invaded versus 67 ± 3.75 in un-invaded sites. The absence of *Linepithema* downstream of the suburban development could be because these sites are composed of different habitats which do not allow for invasion, or the invasion front had not yet reached these habitats. Their occurrence at the most naturally flowing site may be due to local introduction. *Linepithema* have been shown to invade disturbed habitats along a moisture gradient, but there is more to its distribution than artificial flow patterns of water.

C30-FRI
THE EFFECT OF NITROGEN ON THE POPULATION GROWTH AND SPREAD OF AN INVASIVE SPECIES, GARLIC MUSTARD (*ALLIARIA PETIOLATA*)
Renae Schmitt. *Iowa State University, Ames, Iowa.*

Invasive plant species pose a threat to many native ecosystems and increased atmospheric nitrogen deposition may increase the threat. There is growing interest in how large scale increases in nitrogen availability affect the rate of growth and spread of invasive plant populations. Garlic mustard (*Alliaria petiolata*) is a nitrophilic European species that dominates many forest understories in the nitrogen-rich Midwest. I hypothesized that nitrogen increases the persistence, growth, and rate of spread of garlic mustard populations at different spatial scales. For three years I observed garlic mustard populations in nitrogen addition plots in two Iowa forests. Preliminary results suggest that nitrogen increases survival, plant size, and seed output. Disturbance reduced population growth and spread within forests in all treatments, especially in the low nitrogen treatments. I am currently conducting a seed dispersal study to test whether increased resources or disperser movement affect the probability of dispersal between forests. I hypothesize that nitrogen increases the chance of seed dispersal by increasing the number and size of reproducing garlic mustard adults. Data from the nitrogen addition plots and dispersal study will be used to create spatial models testing the effect of nitrogen availability on the landscape-scale spread of garlic mustard. I hypothesize that the species will spread more rapidly in landscapes where forest soil nitrogen levels are high and homogenous versus in landscapes where soil nitrogen levels vary. This study will emphasize the importance of considering large-scale resource changes when predicting local and regional shifts in invasive plant species distributions.

ENGINEERING

AEROSPACE ENGINEERING

C33-SAT
ASCENT STAGE PROPULSION SYSTEMS MODELING FOR CLV FAILURE DETECTION, DIAGNOSIS, AND RESPONSE LAB
Ben Honey. *Embry-Riddle Aeronautical University, Prescott, Ariz., NASA Marshall Space Flight Center, Huntsville, Ala.*

NASA's Crew Launch Vehicle (CLV), Ares-I, will continue regular manned spaceflight operations once the Space Shuttle is retired. An important difference between the CLV and the shuttle is the CLV's Launch Abort System (LAS). In an emergency the LAS solid rockets can pull the crew away from a malfunctioning CLV. For the LAS to be effective there must be a system that can accurately and quickly assess the state of the CLV and recommend or initiate an abort. The FDDR Lab will test algorithms for possible use in this system. In order to test the accuracy of the abort failure detection algorithms, a scenario generator will output simulated sensor data as a function of flight time. For Phase 0 of the FDDR Lab, Matlab, and Simulink are being used to create low-fidelity models of key ascent stage propulsion systems. These models create data based on assumptions and approximations, in order to verify functionality and data interfaces with the rest of the FDDR Lab. In later phases the models will be physics based, in the absence of real test data, in order to accurately predict the affects of heat transfer on pressures and temperatures within the systems. Simulink allows for these models to be very adaptable on a systems level; subsystems can be modified individually to vary from nominal conditions. This allows the models to simulate how a specific failure will propagate throughout the system in ways that are detectable to the algorithms.

C34-FRI
CREATING LIGHTER AND STRONGER COMPOSITES FOR THE USE OF COMMERCIAL AIRPLANES
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Strong and light plastics, or polymers, are important for the use inside aircrafts. The purpose of this project is to develop a method to create a lighter and stronger polymer to replace the polymers that are currently being used in aircrafts today. By combining a lighter polymer with carbon nanotubes, it is possible to decrease the weight of the material while increasing the strength. To test this theory, composites of carbon nanotubes and thermoplastic polymers are molded together into a sample and measured for yield strength.

BIOMEDICAL ENGINEERING

C38-SAT

SPECKLE METROLOGY AS A TOOL TO DETERMINE SUPERHYDROPHOBIC SURFACE QUALITY

Karen Burgos[1,2], Antonio Garcia[2], John Schneider[1], Keila Arroyo[2]. [1]*Arizona State University, Tempe, Ariz.,* [2]*Universidad Metropolitana, San Juan, P.R.*

Superhydrophobic surfaces are of technological interest because they repel water by combining roughness with chemistry. Our laboratory has been synthesizing superhydrophobic polyethylene surfaces using this property to help move individual drops of biological fluids using magnetic fields in a process called digital magnetofluidics. However, the popular method for characterizing hydrophobic (aqueous contact angles) does not yield accurate data for surfaces with high macroscale roughness such as ours. In order to rapidly and accurately determine which surfaces we synthesize in the lab are better suited for digital magnetofluidics, we have been developing an optical technique based on speckle metrology. Speckle metrology is currently a useful tool to measure surface roughness for quality control purposes, but it has not previously been applied as a means to categorize superhydrophobic surfaces. In our method, a laser pointer shines on a superhydrophobic surface at a 45 degree angle and the speckle pattern is captured by a microscope with an objective directly above the surface. Through the use of image analysis software, we obtain spatially resolved intensity information for each surface. By moving the spot to different locations on the surface, the degree of variability of the macroscale roughness can also be determined. Our preliminary study of 8 different surfaces shows that the ratio of average intensity to standard deviation of intensity is a good indicator of a high quality surface for digital magnetofluidics. This poster presentation explains the speckle metrology technique also giving still images from movies of digital magnetofluidics using superhydrophobic surfaces.

C37-SAT

A MATHEMATICAL MODEL OF NOSOCOMIAL INFECTION AND ANTIBIOTIC RESISTANCE: EVALUATING THE EFFICACY OF ANTIMICROBIAL CYCLING PROGRAMS AND ISOLATION ON DUAL RESISTANCE

Karen Chow. *Arizona State University, Tempe, Ariz.*

Hospital-acquired infections caused by antibiotic-resistant bacteria pose a significant threat to public health. Antimicrobial cycling, in which antibiotic classes are alternated over time, has previously been suggested as a strategy for curbing the development of resistance in hospitals. A mathematical model of antimicrobial cycling in a hospital setting is developed to analyze the efficacy of such a program, with an emphasis on the emergence and significance of dual resistance. Simulation results compare the effects over time of antimicrobial cycling programs with mixing programs and their ability to reduce antimicrobial resistance. Our model also considers the effects of isolating patients harboring dual-resistant bacteria in the hospital.

C37-FRI

IMPEDANCE TOMOGRAPHY FOR GEOMETRIC CO-REGISTRATION OF IVUS AND FLUORESCENT SPECTROSCOPY CATHETERS

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Based on their unique tissue interrogation attributes, the serial use of an intravascular ultrasound (IVUS) catheter to survey arterial wall anatomical landmarks and a specialty side-firing optical catheter to perform time resolved laser induced fluorescence spectroscopy (TR-LIFS) can together offer a possible means for improved characterization of vulnerable plaques. Since we physically exchange the two catheter types, this serial approach necessitates a 3D geometric co-registration of the ultrasound and optical data. Precise knowledge of the intravascular location and angular orientation of both catheters is imperative. To this end we have developed a static impedance tomography (SIT) technique which allows precise intravascular catheter positioning. Each diagnostic catheter was made SIT compatible with the addition of two electrodes placed distally at diametrically opposite sites. The SIT-assisted catheter positioning was tested *in vitro* with porcine arterial segments and demonstrated satisfactory catheter tracking in both location and angular orientation within the vessel. Repeated catheter exchanges showed positional accuracy of 0.05 mm $\pm$ 0.02 mm (N = 40). This precision permits a rotational accuracy of $\pm$ 6 degrees for catheters as small as 1mm in diameter.

C40-SAT

INVESTIGATIVE STUDY OF THE IMPACT OF MICROPOSTS ON ORAL DRUG DELIVERY SYSTEM

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Oral drug delivery is known to have high patient compliance since it is a minimally invasive means of delivery. Yet, its efficiency continues to be limited by low mucosal permeability. Hence, gastrointestinal drug delivery devices fabricated using MEMS technology may address unmet medical needs related to the difficulty of drug molecules travelling through mucus layer. In this study, oral drug delivery devices are fabricated using "off wafer" fabrication techniques which entail traditional photolithography to build device, and selective etching of sacrificial layer to release devices from wafer after fabrication. During the microfabrication, we integrate microposts into these devices to enhance permeation of drug through the mucus layer and shed mucosa. Incorporation of microposts to the gastrointestinal drug delivery patch systems using microfabrication tools yields a sophisticated oral drug delivery device that has the potential to facilitate increased diffusion of compounds, provide prolonged delivery and thus reduce adverse effects. The microposts also offer mechanically driven feature as additional support, thus increasing permeability and sustaining release.

C41-FR

CHEMOTAXIS IN AN *IN VITRO* MOTILITY ASSAY

Sara Gold, William Hancock. *Pennsylvania State University, University Park, Pa.*

Kinesin is a two-headed motor protein that moves intracellular cell cargo in neurons and other cells. The motor is believed to "walk" as ATP is hydrolyzed and one of the motor heads moves 8 nm to the next binding site. Kinesin was studied *in vitro* by adsorbing the motors to glass surfaces and observing the movement of fluorescent microtubules by the immobilized motors. In this project, an *in vitro* ATP gradient was established in flow cells of motility assays. A model was tested experimentally that hypothesized that if there was a spatial gradient in the diffusion of some particle, then the particle would accumulate where the diffusion was the fastest. Because microtubules moved in random directions in the motility assay with speeds that depended on the ATP concentration, we predicted that in an ATP gradient, microtubules would accumulate over time in the region of the highest ATP concentration. Testing the model hypothesis was important because it may give insight into how gradients of an energy source may affect cellular differentiation and form asymmetry in the development of the human body. The model hypothesis was supported by evidence from bimetallic nanorods in an abiotic system. Results indicated that microtubules accumulate in the region of lower ATP. The results did not support the hypothesis that originated with the bimetallic nanorod data. A longer time period may have given the microtubules enough time to diffuse to the higher ATP region. Variations in microtubule landing or detachment rates may have also skewed the data.

C34-SAT

SMALL CELL POPULATION ISOLATION AND DETACHMENT FROM A THERMORESPONSIVE POLYMER

Kieran Gonzales, Heather Canavan, Jamie Reed. *University of New Mexico, Albuquerque, N.Mex.*

Poly(*N*-isopropyl acrylamide) (pNIPAM) has found many applications in the field of cell sheet and tissue engineering. Applied as a surface coating, pNIPAM is a proven non-destructive means of detaching cell sheets maintaining associated extracellular matrices (ECM) in the removal process. To date, the majority of work using pNIPAM has been limited to large domains, such as those in tissue engineering applications. Achieving non-destructive release of smaller populations, and even isolated cells, will allow us to translate this research to previously unavailable applications. For example, isolated cells are required to ascertain the extent of transmembrane protein receptor upregulation when assaying the efficacy of cancer therapeutics on cell populations via flow cytometry (FC). In this work, arrays of thermoresponsive domains were fabricated to isolate defined populations of cells using a variety of techniques. The surface chemistry, thermoresponse, and topography of the films generated were verified via X-ray photoelectron spectroscopy (XPS), contact angle measurements, and Secondary Ion Mass Spectrometry (SIMS), and compared to controls. The cell releasing properties of the films were characterized by several lines of incubated baby hamster kidney (BHK) and bovine aortic endothelial cells (BAECs). Cellular behavior in single cell and small populations were characterized and compared to large cell population controls.

C36-FRI

ESOPHAGEAL COOLING DURING RADIOFREQUENCY CATHETER ABLATION OF ATRIAL FIBRILLATION: EXPERIMENTAL MODELING BASED ON AN AGAR PHANTOM

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Some cases of thermal injury to the esophagus have been recently reported during radiofrequency (RF) catheter ablation of atrial fibrillation. Despite that preliminary clinical results suggested that the use of this type of device allows decrease the temperature measured in the esophageal lumen, the effect of this technique on the temperature reached at the deeper esophageal tissue (i.e., distant from the esophageal lumen) remains unknown. We built an experimental model based on an agar phantom, and conducted ablations (55°C temperature target, 120 seconds) measuring the temperature not only on the surface of an esophageal cooling probe, but also to 2 mm distant. The experimental findings suggest that: (1) it is possible to thermally protect the esophagus during an RF cardiac ablation by means of a cooling probe placed on the esophageal lumen; (2) the most important factor in this device is the coolant temperature, instead of coolant flow rate, especially to protect the esophagus lumen; (3) there is a high thermal gradient between the surface of the cooled probe and a point distant 2 mm. More distant points from esophageal lumen might be protected by combining a lower coolant temperature and a high flow rate in the cooled probe; (4) The pre-cooling periods (3 and 6 minutes) did not influence temperature reached et the end of ablation; and (5) The cooling process does not have influence on the thermal phenomenon on the interface electrode-tissue level, which suggests that the transmurality of the lesion is not influenced by the cooling process.

C39-FRI

POLYMER BASED MICROFLOW REGULATOR

Andre Paredes, Mark Bachman. *University of California, Irvine, Irvine, Calif.*

Lab-on-a-chip is a growing technology that incorporates microfluidics. Microfluidics can be controlled and regulated through microvalves and microflow regulators. Currently very little polymer based microvalves exist. This paper presents a functional polymer, polydimethylsiloxane or PDMS, based microflow regulator that can readily be applied and transformed into a microvalve. The device integrates "air cavities" protruding outward from the sides of the microchannel to establish the flow regulator and valve. Due to the polymer's hydrophobic properties, the "air cavities" are created as liquid travels down the microchannel. Upstream from the "air cavities," a thermal gradient is applied to evaporate liquid as it passes by, creating air within the microchannel. A segment of reduced width channel immediately following the "air cavities" increases flow resistance and forces air to condense into the "air cavities." The thermal gradient dictates the air concentration, and the air concentration dictates the fluidic flow. Thus, correct manipulation of the thermal gradient can result in regulation of microflow down the microchannels, functioning as a microflow regulator. In addition, with a specific thermal gradient the air can be manipulated to build up, until a bubble blockade is formed, functioning as a microvalve. Our experiment, therefore, shows a device that forms a functioning microflow regulator that can readily be transformed into a microvalve. This novel polymer based microflow regulator is simple in design and cheap. The devices' practical nature can be applied to lab-on-a-chip.

C38-FRI

A COMFORTABLE AND ACCURATE SOLUTION FOR HIGH RESOLUTION RETINAL IMAGING

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Vision science researchers at the University of California, Berkeley use an adaptive optics scanning laser ophthalmoscope (AOSLO) to capture high-resolution images of the retina. These images will allow them to monitor diseases that cause blindness. However, the AOSLO requires stable alignment between the pupil and instrument. Today, this is accomplished with a head-stabilization device called a "bite bar" (BB) which requires the patient to bite into a rigid dental impression plate fixed to the instrument. This device can be quite uncomfortable to use. Our work has found a more comfortable head-stabilization device and implemented it in the AOSLO with a pupil tracking system (PTS). The PTS consists of a tilting mirror in the AOSLO that tracks small motions of the pupil to give us a stable image of the retina. First, however, large-scale head motions must be eliminated through the use of a head-stabilization device. We measured head stability and pupil position reproducibility using three devices: a BB, a temple mount chin rest (TMCR), and an isolated chin rest (CR). As expected, the BB gave us the best results, while the isolated CR performed below average, and the TMCR performed moderately. Based on these results, we implemented the more-comfortable TMCR with a PTS in AOSLO and found it to be very successful: the pupil remained as stable as it would with a BB. This new configuration will keep patients and research subjects more comfortable, yet still provide a very accurate, high-resolution retinal image to the researcher.

C36-SAT

FABRICATION OF A PLASTIC MICROFLUIDIC DEVICE FOR DIAGNOSTIC APPLICATION

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The fabrication of plastic microfluidic devices is an intricate matter dealing with temperature, pressure, and time all of which must be optimized before a microfluidic device is produced efficiently. Using a programmable hydraulic press to maintain constant pressure and variable temperature for specified times, devices were made using poly(methyl methacrylate) (PMMA). PMMA is a clear, disposable plastic that was used as a shatterproof replacement for the more expensive glass; the device fabrication is also comparatively simple. Initially holes were drilled in the PMMA, and a channel template consisting of polycarbonate strips was placed on top of the holes. This whole ensemble was placed between aluminum blocks in the press at 15000lbs and 102°C to create the channel. The other challenge encountered was to create a cover for the channel. This was done by initiating a bond with a second piece of PMMA on top of the channel, using a bonding solution and a new recipe in the press. Essentially these recipes are found in literature but need minor modification before producing robust results. A bond was created without significantly deforming the channel as seen with fluorescent imaging. Ultimately these devices will be used for immunoassays using electrophoretic separation of proteins and protein complexes. For this application, it is important to minimize non-specific adsorption of proteins to channel walls. To this end, a fluorescently labeled protein was added to the channel and washed through with varying concentrations of detergent to determine the extent of protein adhesion to channels.

C35-FRI

MECHANOTRANSDUCTION IN VASCULAR SMOOTH MUSCLE CELLS: STRAIN-INDUCED REMODELING OF THE CELL-MATRIX INTERFACE

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Mechanotransduction refers to the process by which cells convert mechanical inputs into specific biochemical responses. A preferred subcellular location where this occurs is the interface between cells and the extracellular matrix (ECM). Consisting of either focal contacts (immature adhesion sites) or focal adhesions (mature adhesion sites), this interface plays a dual structural and signaling role, and thus is ideally situated to transduce mechanical forces. One structural proteins recruited to this interface is talin, which we believe may initiate further changes at the cell-ECM interface in response to mechanical cues. Specifically, we hypothesize that talin's expression and/or localization may be upregulated at focal contacts in response to an applied force. To test this hypothesis, we have initiated studies in which single-step changes in strain are applied to spreading vascular smooth muscle cells (SMC). The recruitment of talin to the cell-ECM interface is assessed using immunocytochemical techniques in conjunction with electrophoresis and Western blotting. Detecting changes in talin's concentration and localization in response to applied forces will demonstrate its importance in strain-induced remodeling of the cell-ECM interface. In the long-term, an improved molecular understanding of the process of mechanotransduction will facilitate our efforts to engineer functional tissues that reside in mechanically dynamic environments in the body.

C35-SAT

EVALUATION OF CELL SEGMENTATION METHODS ON CACO-2 FLUORESCENCE MICROGRAPHS

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Cell segmentation is a necessary preprocessing step in subcellular pattern recognition has been an active area of research over the last decade. Different segmentation methods have been developed, yet little has been done in the way to standardize comparison between them. In this work, we evaluate segmentation methods on fluorescence micrograph by defining criteria for comparing them. Methods we test are watershed, Voronoi, level set, and graphical models segmentation, and we use manually labeled regions as ground truth. Moreover, all of the segmentation techniques we test are highly dependent on proper seeding, so we first define a method for seeding using cell nuclei. The images we segment are fluorescence micrographs of CaCo-2 cells, grown in a monolayer. The cells are stained with DRAQ5 for the nuclei and phalloidin for the cell membrane. The multicell images are first manually segmented. One image is chosen to train parameters for the automatic segmentation. Then the automatic methods are applied to rest of the images. We calculate metrics that determine the region and pixel overlap between the automated methods and the ground truth, and use these to evaluate the different methods. Our preliminary results indicate that the Voronoi method is overall more effective than watershed. Due to the low precision-recall results we are getting between the ground truth and the segmentation methods, however, we believe that the seeding needs to be made more robust across images. We will present our results with more robust seeding and the other segmentation methods in October.

C39-SAT
THE DETECTION AND CHARACTERIZATION OF BIOLOGICAL SPECIES BY A NANOPORE/ MICROPORE
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The electrical characterization and detection of biological species using a Micropore or a Nanopore is a very promising development to detect different diseases, mechanical and electrical properties of cells, proteins, DNA and others micro-organisms. Connecting a Micropore/Nanopore setup to a measuring system, modelled as an electric circuit, we can obtain an ionic current versus time signal that is amplified, converted from analog to a digital and interpreted by a data acquisition card (DAC) in a computer. This data is analyzed to determine electrical and mechanical properties know as electrical current, viscosity, translocation time, velocity of beads and others properties. In this research we used 30 nanometer gold particles with a 40 nanometer pore to simulate the behavior of biological species. Since our research is not fully complete we do not have any final results but we expect that the behavior of the nanoparticles be similar than the biological species permitting that we can determine and characterized different kinds of biological species.

CHEMICAL ENGINEERING

C42-FRI
TRANSDERMAL DRUG DELIVERY SYSTEMS USING CHEMICAL PERMEATION ENHANCERS
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The human skin can provide a gateway for administrating therapeutics known as the transdermal drug delivery (TDD) route that can increase efficacy of drugs by circumventing hepatic first pass metabolism. TDD provides a simple and safe mode of drug delivery but the outer layer of the skin, the stratum corneum (SC), only 15 μm thick, provides the greatest barrier for transportation of molecules across the skin. Using recognized chemical permeation enhancers (CPEs) can pervade the SC, composed mainly of corneocytes and lipid bilayers, but finding the most potent and safe CPE is a challenge. The development of a hybrid CPE of mixtures from known CPEs can prove to be the answer to an effective TDD system. The development of a high throughput system to effectively test different combinations and concentrations of CPEs was developed. *In vitro* Skin impedance guided high throughput system (INSIGHT) uses the relation of skin's electrical impedance and permeability to screen through numerous combinations. Higher electrical conductivity generally exhibits higher permeability for polar solutes. Selecting over one-hundred known CPEs from the initial candidates and testing the interaction of these different mixtures are used to discover the ideal combination. Results can be confirmed using Franz diffusion cells, a time and cost consuming process. Initial data of over 80 different combinations from varied CPEs and concentrations tested through INSIGHT has proven valuable in determining very promising combinations. Although finding the ideal team is very difficult, this opens TDD as a promising breakthrough in medicinal delivery.

C44-FRI
ANAEROBIC REACTOR OPTIMIZATION
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Anaerobic digesters convert the energy stored in manure into biogas that is used for electricity production by a combustion turbine. A digester must be loaded with manure on a regular basis to ensure continuous supply of food for the anaerobic bacteria. The contents of the digester should be monitored on regular intervals to find possible digester imbalances. Indicators of imbalance include decreasing biogas production, decreasing pH, decreasing methane to carbon dioxide ratio, and an increase in volatile solids. The Inland Empire Utility Agency (IEUA) manure digester built in 2001 was modified in 2005 to improve process performance. As of July 2007, the digester is not producing the quantities of biogas projected for its known volume, influent manure characteristics, and operating temperature. IEUA would like to take steps to increase the digester biogas production, and has decided to complement the manure injection with various mixtures of food wastes. UCI will be performing laboratory studies to determine the effects of substituting portions of the digester feed with a solution of lactose. Gas production, pH, methane and carbon dioxide production, and volatile and total solid contents will carefully be monitored. The study was designed to reveal whether the feed substitution would: (1) cause an increase in foaming, (2) generate more biogas, (3) affect the biogas methane content, and (4) affect the microbial community. Although this research is in its early stages, it is expected that lactose will increase biogas production in the digesters.

C41-SAT

MODELING COMOS2 USING CERIUS2 SIMULATION SOFTWARE

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Environmental concern has led to increasingly drastic regulations on sulfur, nitrogen and aromatics content in fuels. Sulfur content in the motor and diesel fuels is continuously reduced by regulations to lower levels. The current specification in Europe and U.S. calls for maximum sulfur content of 50 ppm in gasoline and diesel by 2005, and this level will be reduced to below 10 ppm by 2010. Transition metal sulfide (TMS) catalysts play an important role in the petroleum industry. Due to their resistance to poisons, TMS are unique catalysts for the removal of heteroatoms (N, S, O) in the presence of large amounts of hydrogen. Indeed, aromatic and heteroatom-containing compounds present naturally in crude oil are the source of pollutants, such as SO_x, NO_x. Hydrodesulphurization (HDS) of mercaptanes as dibenzothiophene (DBT) is generally performed with MoS_2 or WS_2 supported on alumina and promoted by Co or Ni. The need to meet more stringent standards limiting the sulfur content of gas oils urges a deeper understanding of the mechanism by which sulfur-containing compounds are destroyed over hydrodesulphurization (HDS) catalysts. In order to understand the behavior and crystalline structure of $CoMoS_2$ synthesized by hydrothermal method during HDS reactions, it is realized molecular simulations through Cerius2, a software used to perform these simulations is Cerius2 designed to visualize structures, predict the properties and behavior of chemical systems, refine structural models, and modify the synthesis process to improve and to adapt the structure to specific necessities.

C42-SAT

IMPROVING THE WHOLE CELL BIOCATALYTIC PROPERTIES THROUGH PROTEIN ENGINEERING OF LOVD

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Simvastatin is a cholesterol-lowering compound and the main component of the top selling drug Zocor. Simvastatin has been traditionally produced through a tedious, complex chemical synthesis from the natural product lovastatin (Mevacor). Our lab has characterized an acyltransferase, LovD, able to synthesize simvastatin in one step. Through fermentation, an *Escherichia coli* strain overexpressing LovD acts as a whole cell biocatalyst to convert the precursor monacolin J and the substrate DMB-SMMP to simvastatin. Though > 98% conversion was obtained when using 10 mM monacolin J and 12 mM DMB-SMMP, higher substrate concentrations results in lower conversion of simvastatin. Low conversion is partly due to the low solubility (50% soluble) and low activity (k_{cat} = 0.6 min^{-1}) of LovD. The current goal of this research is to improve the activity and solubility of LovD through site-directed mutation of cysteine to alanine, which will prevent undesirable disulfide bonds. Through *in vivo* assay, LovD mutants overexpressed in *E. coli* will serve to measure the whole cell biocatalytic activity. Pure protein will be used in the *in vitro* assay to measure the turnover rate from monacolin J to simvastatin. If a mutant results in better activity, a double site-directed mutation will be done and checked for LovD activity. An active mutant of LovD that does not form disulfide bonds will also increase chances for successful crystallization. Crystal structures of LovD will give us the information to guide further mutations. Finally, an *E. coli* strain overexpressing the engineered LovD will be used in high-cell-density fermentation to synthesize greater yields of simvastatin.

C43-FRI

ADHESION AND DETACHMENT MECHANISM OF POLYMER SURFACES

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With the development of nanotechnology and biotechnology during the last two decades, more and more people are interested in the surface interactions (adhesion, separation) between soft materials, such as lipid bilayers, cell membranes, soft polymers, etc. The classical theories describe the adhesion and deformations of two elastic solid surfaces, and their static (equilibrium) models, which can not be directly applied to the surface interactions of the above soft materials. Understanding the adhesion and detachment mechanism of polymer surfaces is the main object of this study. The adhesion and separation of two polymer thin films was studied using a surface force apparatus (SFA). The polymer thin films are prepared by spin-coating, characterized by atomic force microscope (AFM) and contact angle measurements prior to adhesion experiments. Interesting interfacial instabilities and patterns appear during both the adhesion and separation of two viscoelastic polymer films; the patterns are highly ordered for the adhesion and coalescence process, and irregular for the detachment process. Film thickness, viscosity, and other factors can affect the lifetime and appearance of the patterns. The appearance of these patterns can be explained by both fluid mechanics theories and intermolecular and surface forces.

C43-SAT
DETECTION OF ENGINEERED TITANIUM DIOXIDE NANOPARTICLES
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The objective of this research is to differentiate and to measure the quantity of engineered and natural titanium dioxide (TiO_2) nanoparticles (NPs) in the water. With the obtained data we can identify the percentage of both natural and engineered TiO_2 NPs. Titanium dioxide has three crystal structures; they are Rutile, Anatase, and Brookite. We can identify what structure is more abundant and what type of damage is causing to the environment and health of humans. Using inductively coupled plasma (ICP) instrument we can identify the elements in the analyzed water. The ICP uses hot argon plasma to excite atoms into high energy states. As these atoms relax they emit light at characteristic wavelengths, or lines. Using X-ray diffraction (XRD) the structures of TiO_2 NPs can be characterized and can be differentiate between the structures of the engineered and natural TiO_2 NPs. The ultimate goal of this work is to identify which structure of engineered TiO_2 interacts more rapidly with biomass and how to eliminate from causing damage to the environment and humans.

ELECTRICAL ENGINEERING

C45-SAT
WALLEYE
John Aguilar, Simon Penny. *University of California, Irvine, Irvine, Calif.*

Walleye is an embodied interactive installation involving a wall-mounted grid (8 x 12 at 1 foot intervals) of discrete photo-sensors and a facing wall-mounted grid (8 x 12 at 1 foot intervals) of dimmable lamps between which users move. The amount of light hitting a particular sensor controls the brightness of the specific lamp opposite the sensor. The user's shadow on the sensors produces an image-like pattern on the light-wall. The project may be conceived as a model of a compound eye or as an exploded CCD sensor. Fundamental to the project is the absence of centralized control and the choice to work with component-level electronics and a minimum of software. Phototransistors are arranged on vertical strips, and an Atmel micro-controller performs analog to digital functions on the voltages from the phototransistors. The micro-controller (located on the Sensor Board) also handles calibration and parameterizing of the values. This data is sent serially over to a respective vertically aligned triac driven lamp strip of 8 lamps. Another Atmel micro-controller (Emitter Board) takes the sensor values and converts them into a custom AC-clocked quasi-PWM control signal. The signal is passed to the respective optoisolator triac driver circuit where a quasi-PWM signal controls the brightness of a standard AC incandescent bulb. My principle role in the project was as project manager. I was also responsible for designing the Emitter Board, writing micro-controller firmware, and developing the logical interaction between all components of Walleye. Walleye will be presented in art exhibits with the goal of locating it in a permanent indoor/outdoor installation.

C45-FRI
AN ADAPTIVE OPTICS WORKBENCH FOR EDUCATION
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An adaptive optics workbench was assembled for use in education. The workbench will be housed in a classroom / laboratory setting at Hawai'i Community College in Hilo. It will be used to demonstrate the principles of adaptive optics, and to facilitate education and training in engineering, technology, astronomical instrumentation, and fields of study that utilize adaptive optics. The major goals of this project were building and aligning the optical system, creating a graphical user interface to facilitate system control, learning and documenting the construction of the entire build process. The workbench uses a Shack-Hartmann wavefront sensor and a micro-electro-mechanical system (MEMS) 37-segment deformable mirror powered by factory-calibrated drive electronics to achieve closed loop adaptive optics operation. The deformable mirror employs a hexagonal array of 37 piston/tip/tilt segments that respond to position commands which the driver electronics convert to voltages. This mirror responds with up to 5 microns of stroke and is easily controlled via C and Matlab. The entire system is a modularly scalable and currently controls up to 128 channels. The workbench design and examples of operation and capabilities are given.

C49-SAT
WALLEYE DISPLAY LOGIC
Aaron Botello, Simon Penny. *University of California, Irvine, Irvine, Calif.*

The Walleye project was created as a way to further facilitate the integration of engineering into the arts. The approach of the Walleye project is to use electrical engineering as a way to portray a sense of complexity with the absence of centralized control. The project may be thought of as a model of a compound eye, in which sensors relay values, according to the light measured. The Walleye project is an embodied interactive installation involving a wall-mounted grid (8 x 12 sensors at 1 foot intervals) of discrete photo-sensors, facing a wall-mounted grid (8 x 12 lamps at 1 foot intervals) of dimmable lamps between which users move. The users will be able to walk between the two grids, where their shadow will project onto the photo-sensors that control the brightness of the lamp opposite to each sensor. The amount of change in brightness and its timing will depend on the amount of light hitting the particular sensor. The choice to work with non-global component-level electronics was made in order to easily replicate the Walleye for those interested in engineering art. The images created by the Walleye are produced by a horizontal system, where each component works independently from each other are put together but are not conscious of each other. It is expected that the audiences will perceive each pair of light bulb/sensor pair communicates with one another. In actuality there is no hierarchy of communication occurring in the system.

C49-FRI
UTILIZATION OF A FAST-STEERING SECONDARY MIRROR FOR LINE-OF-SIGHT STABILIZATION
Maryfe Culiat. *University of Hawaii at Manoa, Honolulu, Hawaii.*

A fast-steering mirror (FSM) is capable of rapid tips and tilts to correct jitter commonly caused by seismic movement and atmospheric turbulence. Jitter causes the images of objects viewed from a telescope to be unstable. A fast-steering secondary mirror (FSSM) allows the FSM to be close-coupled to the primary mirror, improves imaging of objects by reducing jitter, and compensates for global tilt. To achieve performance necessary to meet imaging requirement specifications, an analysis of the FSSM was done. Linear actuators are arranged in a tripod drive configuration, applying force that results in tilting the mirror. Two types of actuators were analyzed: voice coil and piezoelectric. After cost and performance analyses, it was determined that piezoelectric actuators have distinct advantages over voice coils for this application. These analyses and system recommendations will be presented.

C50-SAT
MEASURING DOME SEEING WITH A DISPLACED-BEAM SMALL APERTURE SCINTILLOMETER
Joseph Hernandez. *University of Hawaii at Manoa, Honolulu, Hawaii.*

Images obtained from land-based telescopes suffer from image degradation due to air turbulence. This phenomenon is known as "seeing" in the field of astronomy. Astronomers are concerned with many different forms of seeing that affect telescopic imaging, including optical, atmospheric and dome seeing. A displaced-beam small aperture scintillometer (DBSAS) was tested as a possible tool to measure and quantify seeing in the observatory dome environment. The ability to measure the dome turbulence may lead to the capability of mitigating dome turbulence and enhance telescope imaging. The project involved commissioning and testing the DBSAS in various folded-path configurations to ensure that it has the sensitivity to operate within the volume of the Keck telescopes. The project also tested the scintillometer's capability to measure the mean crosswind across the measurement path. The crosswind tests were performed in hopes that the DBSAS may also be used as a tool to understand the bulk airflow through the telescope structure. The project concludes that the scintillometer has the necessary sensitivity, ability to operate in folded configurations, and can measure crosswinds within the volume of the Keck telescopes. The data and process will be further analyzed and presented.

C48-FRI
DESIGNING A PORTABLE ACQUISITION UNIT: INCREASING EFFICIENCY AND MAXIMIZING PRODUCTIVITY BY USE OF STANDARDS
Dustyn Iwamoto. *Honolulu Community College, Honolulu, Hawaii, Subaru Telescopes, Hilo, Hawaii, Center for Adaptive Optics, Santa Cruz, Calif.*

Subaru Telescope uses Agilent data acquisition units to monitor vital information from their equipment such as voltage, current, temperature, and resistance. The goal of this project is to create a portable unit that is capable of conducting various measurements on test points at the summit or at the base of operations. Special considerations were the operating altitude and temperature. These factors were mitigated by using a benchmarking-type system where known good component measurements are compared to measurements from suspected faulty components. A major obstacle was encountered with the non-compatibility of connectors used at different test locations. To remedy this problem we have implemented a standard for

connecting to the data acquisition units using Mil-Spec 3111 connectors. Topics to be presented are: design process and the standard being implemented. Presentation will focus mainly on the benefits and drawbacks of the implemented standard, as these tradeoffs are relevant for many other organizations.

C47-FRI

ADHESION AND ELECTROMIGRATION PERFORMANCE OF COPPER/BARRIER INTERCONNECTIONS IN CMOS TECHNOLOGIES

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Electromigration (EM), the movement of metal atoms due to the flow of current, can cause failure in interconnects in CMOS circuits. EM performance in copper interconnect structures is largely related to diffusion of copper atoms along the barrier layer interfaces. It has been shown that the mobility of copper atoms is closely related to the adhesive strength of this copper/barrier layer interface. In the past these properties have been assessed separately. We are developing a novel technique for characterizing EM performance and adhesion of a copper/barrier layer simultaneously. Using thin film fracture mechanics techniques, adhesion in copper / barrier film stacks is analyzed in the presence of electromigration. Crack propagation rate or velocity, v, is measured versus applied strain release rate, G (which is a measure of adhesion). This is measured while different current densities are applied. Initial results at low current densities show no change in adhesion. X-ray photoelelectron spectroscopy was performed on the fracture surfaces to show that the failure does occur at the Cu/barrier interface. Further measurements of crack propagation at higher current will be done. Once this technique is developed it will provide a unique tool in optimizing EM performance in the next generation of integrated circuits and nanoelectronics.

C47-SAT

HIGH SPEED CHARACTERIZATION OF PHOTONIC INTEGRATED CIRCUITS

Maximiliano Ramirez Luna[2,3], Matthew M. Dummer[1]. *[1]University of California, Santa Barbara, Santa Barbara, Calif., [2]Internships in Nanosystems Science, Engineering and Technology Program, Santa Barbara, Calif., [3]Santa Barbara City College, Santa Barbara, Calif.*

Extensive high speed characterization of photonic integrated circuits (PIC) is essential in accelerating the time in which improvements in the functionality, performance and reliability of PICs are made. Current characterization of PICs requires the use of different measurement equipments working independently to gather data as well as requiring manual input through out the testing process reducing accuracy and increasing user error. Integrating the equipment to work as one and completely automating the testing procedures will lead to more accurate, reliable test results and faster generation of multi-dimensional tuning maps (MDTMs). Software written in Visual Basic implemented with the Keithley 4500 modular test system (MTS) will be used as a hub to integrate the use of the many source-measure channels with external optical measurement equipment. The MTS is capable of varying the operating point of multiple components simultaneously, making it possible to turn every knob in the circuit at once. Together with the integration of external optical testing equipment will allow for a greater understanding of how integrated optical components function in a single-chip system such as WCs. MDTMs for lasers as well as extinction characterization of electroabsorption and Mach-Zehnder modulators are two examples of data that are being acquired with this equipment. I hope to accomplish seamless integration of the different electrical and optical measuring equipment and the production of MDTMs at a fraction of the time required today. The high speed characterizations I develop will hopefully help improve the implementation and design of future PICs.

C46-SAT

C++ PROGRAM FOR GENERATING TETRA CAST FILLED MODELS

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The purpose of this research is to make better parts to be used as expendable patterns for investment casting. To accomplish this, C++ programming language will be used to modify pattern geometry. The C++ program will take a solid stereolithography file and generate a thin wall, while maintaining the exterior geometry of the original CAD object. A Boolean operation will be used to fill the volume within the wall with TetraCast (TC). TC is a lattice structure, made up of individual "jack" elements modeled after the bond geometry found in diamond. It will be easier to extract the TC pattern during pattern removal because it will have less density and a more fragile structure than the original object. In addition, this will reduce the amount of ash that will remain when the TC pattern is burned in comparison to a solid pattern. The new process will also have secondary benefits, which include the reduction of material and build time. It will save time because the C++ program will be able to generate a TC filled object directly from a stereolithography file, instead of manually filling an object using CAD software to design the structure for each object. The user will save money because the SLA rapid prototyping machine used to make these patterns uses expensive materials (1 gallon ~$600). This TC technology will be useful for the creation of better parts produced by investment casting.

C46-FRI
A SUN-DAY IN THE LIFE OF A SOLAR PANEL
Chad Sithar[2], Mary Liang[1]. [1]*University of Hawaii Manoa, Honolulu, Hawaii,* [2]*Maui Community College, Kahului, Hawaii.*

Though there are many sources of energy such as coal, oil and fuel, the Sun is our most abundant source of energy. Solar cells today are only about 6% to 40% efficient. Most solar cells on homes only turn 15% of the energy collected into electricity. Responding to the inefficiency of today's solar cells, I have characterized individual solar cells and their performances to try and improve upon the design and their ability to use the sun's energy more proficiently. To do this, I built a resistive load box with 30 resisters in parallel. This board controls the resistance and in return, it controls the amount of current that goes through the solar panel. The resistance is regulated by the number of switches that is turned on at any time. By varying the resistive load, the I/V curve can be easily monitored to see which resistance would be best for optimal performance. To further increase efficiency we placed the solar panel on a tracker, which is used to manually follow, or track, the Sun throughout the day. The use of the tracker has greatly improved the efficiency; however, there are still major improvements that need to be done, such as aligning the responsiveness of the panel to the Sun's entire color spectrum, not just 15%.

GENERAL ENGINEERING

C56-SAT
ACOUSTIC NOISE CANCELLING SYSTEM
Dex Alpiche. *Submillimeter Array, Hilo, Hawaii.*

Located up on Mauna Kea's slopes is SMA's maintenance facility where there is a telephone which is fairly close to an EMI (electro-magnetic interference) filter. This EMI filter produces a distinctive acoustic sound which interferes with communication within the facility. My goal in this project was to produce a replica of this acoustic sound and cancel it out with a circuit. This circuit is composed of a transformer, full bridge rectifier, buffer, active filter, power amp, power supply, and a subwoofer. I took tests using an oscilloscope and found out that the transformer was producing a clean 120 Hz sine wave in phase, as compared to 60 Hz that normally comes out from your 120 v ac outlet. I have produced a circuit that can replicate and cancel out the 120 Hz. The design of the circuit, measurements of the EMI filter with the circuit and without the circuit will be presented in the following. In conclusion the 120 Hz can be cancelled out with producing the same frequency and inverting the sine wave.

C1-FRI
EVALUATION OF PHOTOSIEVING AS A RAPID ALTERNATIVE TO PEBBLE COUNTS
Viviana Berrios. *University of Puerto Rico, Mayaguez, P.R.*

Grain size is the most fundamental physical property of sediment. This property is used to accurately measure individual particle sizes, to determine frequency distribution, and calculate statistical description of the sediments.In this project we are going to use the grain-size measurements to identify the surface composition of the Sandy River, Oregon. The measures of surface composition will be used after the Marmot Dam removal to identify changes in surface composition of the river caused by the displacement downstream of the sediment that is behind of the Marmot Dam. To carry out these grain-size measurements in the fieldwork, we will use the methods of pebble count and photo sieving to measure surface composition of the river, which measures the different grain sizes of the river bed. This research consists of making comparisons between the methods of pebble count and photo sieve. Photo sieving is new method developed to use digital photographs and Digital Gravelometer software to characterize individual particle size without measuring each individual particle. After finalizing the comparison of the data collected in the fieldwork using the methods of pebble count and Digital Gravelometer, we have reached the conclusion that the pebble count method is more precise and reliable than the method of the Digital Gravelometer.

C50-FRI
ACTIVE CONTROL OF ABERRATIONS FOR THE LARGE SYNOPTIC SURVEY TELESCOP (LSST)
Brice Cannon[1], Stacie Hvisc[2], Scot Olivier[2]. [1]*Norfoalk State University, Norfolk, Va.,* [2]*Lawrence Livermore National Laboratory, Lawrence, Calif.*

The Large Synoptic Survey Telescope is an 8.4 meter, 10 square-degree-field telescope that will provide three gigapixel digital images of the universe. The shapes of the telescope's three mirrors are affected by gravity and thermal changes, which lead to reduced image quality. To improve image quality, the mirrors are actively controlled using the information gathered from the curvature wave-front sensors (CWFS). Sky-brightness adds noise to the incoming star-light incident on the CWFS, which causes errors in the phase reconstruction and leads to lower performance for the active control of the telescope aberrations. Since sky

brightness cannot be eliminated, this research seeks to understand how it will affect phase reconstruction performance by causing errors in the curvature wavefront sensors. Using a code developed to simulate the operational performance of LSST it was possible to determine the effects that sky brightness will have on phase reconstruction. Every wavelength band of light is affected differently by atmospheric turbulence and sky-brightness, which will introduce different amounts of noise at varying wavelengths and star-brightness levels. Using the output from the code, several graphs have been constructed that show the differences in phase reconstruction performance versus star brightness for each band of light at varying sky-brightness. The graphs quantify the amount of noise that is added to the phase reconstruction as star brightness varies for many different sky-brightness levels and wavelength bands. These results will help scientists and engineers design a CWFS that will help achieve optimal phase reconstruction performance for the active control of LSST.

C55-FRI

DETERMINING THE CRITICAL DISCHARGE FOR SEDIMENT TRANSPORT IN BEDS OF DIFFERENT GRAIN SIZES

Ramsey Coronado. *University of Arizona, Tucson, Ariz.*

The Marmot Dam in Sandy, Oregon, located on the Sandy River, is a dam that is being removed, and was the setting for a case study for a quantitative and qualitative analysis of the impacts of dam removal on a river system. The area of focus was determining the critical shear stress required to cause sediment along a riverbed and the surface of a river bar with materials of different grain sizes to move. The shear stress is a force that moves parallel to a certain material, and in this case there is a certain critical shear stress that relates to some minimum water flow that works parallel to the sediment and will cause sediment transport. The methods for evaluation of the different grain sizes was with the use of the pebble count technique, which involves randomly picking up 100 pebbles from a certain facies, a homogenous area, and then measuring the intermediate axis of the pebble. Then with the use of the depth-slope product, the continuity equation, Manning's flow resistance equation a critical discharge is obtained. The results obtained were different critical flows rates at different cross-sections that will cause the sediment to move. The research conducted will be used as the baseline for the preconditions of the river prior to dam removal, and will allow for ongoing research next year after dam removal. Identifying these values will help to better determine how an increased flow after the dam removal will affect the sediment transfer rates and deposition.

C53-FRI

DEVELOPMENT OF BUILDING COMPONENT'S DAMAGE FRAGILITY CURVE

Corina De Pablo, Farzin Zareian. *University of California, Irvine, Irvine, Calif.*

There is currently a limited amount of research regarding the relationship between the damaged caused to nonstructural building components by earthquakes and repair cost. The research will implement the procedures currently available in literature for the development of damage fragility curves of building's structural and/or nonstructural components. A fragility curve is a graph which provides a relationship between an engineering demand parameter (EDP), and the probability of exceeding a specific state of damage. An EDP is the contributing factor for the damage of a structural and/or nonstructural component (i.e., displacement, maximum floor drift ratio, maximum floor acceleration). A damage fragility curve shows the probability of being in, or exceeding a damage state in a building component as function of building response (i.e., deformation or acceleration during and after a ground motion). These fragility curves will be inserted in the database of building component's fragility curves that has already been created in part of a broader performance-based assessment computer program. The database will contain photos of damaged states caused by seismic activity along with their fragility curves. They are derived from previously collected data in field reconnaissance of previous earthquakes and laboratory tests. Further analysis of this database will increase the accuracy of building monetary loss estimates during and after earthquakes.

C1-SAT

INFLUENCE OF INTERPOLATION METHODS ON THE ACCURACY OF DETECTING TOPOGRAPHIC CHANGE

Carl Ekstrand. *Illinois Institute of Technology, Chicago, Ill.*

When removing a dam that has years of sediment build up behind it, one of the major questions asked is, "Where will the sediment go?" It is clear that once the dam is removed, the flow of water will erode the delta build up and carry it downstream. What is unknown is where it will be deposited. Hopefully in the future there will be an easy, digital method for predicting the displacement of this sediment, but for the time being the best way to do this is by manually surveying thousands of points on the river and then using ArcGIS Spatial Analyst to create a 3D surface image of the river bottom. By doing this before the removal and then for several years after, the topographic change of the river can be detected. ArcGIS Spatial Analyst uses surface interpolation methods to create 3D images from large sets of data. Surface interpolation can be described as any formal technique using sampled points to predict values at unsampled points. In general, it is based on either the theory of spatial autocorrelation or spatial dependence. These both measure the degree of relationship or dependence between the many points,

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both near and distant. The method of interpolation chosen and used by ArcGIS could be a factor in determining and tracking topographic change. In order to determine the most accurate and therefore best method of interpolation, they will each be compared to one another. The differences between them can be calculated and hopefully a representation of the error in interpolation from each method can also be found. In analyzing the results, the most accurate method of interpolation can be found.

C52-FRI

DIGITALLY FABRICATING KATRINA

Alma Garcia[2], Lawrence Sass[1]. *[1]Massachusetts Institute of Technology, Cambridge, Mass.,[2]California Polytechnic State University, San Luis Obispo, Calif.*

On August 29, 2005, Hurricane Katrina caused unprecedented devastation throughout the southern part of Louisiana, wiping out entire communities. My studies aim to develop a new construction technique to overcome the challenge of rebuilding these communities with more structurally-sound approaches than conventional techniques. This approach, digital fabrication, uses Louisiana as a model but offers the possibility to mitigate housing shortages on a global scale. In recent years, the technique of prefabricated housing has been used for customizing houses which are assembled almost instantly in the field. Digital fabrication differs from prefabricated housing in several ways. It presents the opportunity to produce mass customized housing that is rapidly assembled with little material wasted and eliminates mechanical fasteners, therefore reducing the number of manual workers. Digital fabrication technique consists of a series of steps. First, a computer aided drafting (CAD) program is used to generate 3D shapes that allow for the analysis of the design. Next, the 3D shapes are translated into 2D drawings which allow for subdivision of the design into structural components with complementary attachments between them. The subdivided design is then sent to a computer numerically controlled (CNC) router which cuts the components out of a plywood sheet followed by the assembly or erection of the unit. Since the unit is sustained by friction only, the structural strength is gained by the interlocking components. The final step of the process consists of the structural analysis using the results in comparison with those of a house built with conventional techniques.

C51-SAT

ACTIVE STRUCTURAL CONTROL USING PD AND FUZZY LOGIC CONTROL SYSTEM

Zahid Hossain, Daniel Oswaku, Weining Feng. *University of Houston–Downtown, Houston, Tex.*

Civil structures vibrate or resonate due to dynamic loads. Dynamic loads cause deflection and acceleration on the structure which may create disturbance or discomfort to the people or the worst case scenario the structure may collapse creating catastrophe. Researchers have worked on structural control system using PID, fuzzy logic, or neural network algorithms to achieve vibration damping. Our research project uses a steel frame as a structural model and a perioding signal is used to generate an excitation force, which will induce the resonant vibration of the frame. The objective is to implement an active control system to minimize the deflection and vibration of the frame with a low cost lab-made electromagnet. A combined fuzzy logic and PD controller has been implemented where the proportional gain can be adapted by utilizing a fuzzy-logic-based tuning mechanism, and hence much reduce the need to for manual tuning of PD controller. The overall system has shown promising performance with significant vibration damping.

C53-SAT

USING THE FORCE FEEDBACK MOUSE TO SENSE GRAPHICAL INFORMATION ON COMPUTERIZED MAPS DEVELOPED FOR THE VISUALLY IMPAIRED

Kelly Kitagawa, Roberto Manduchi, Kee-Yip Chan. *University of California, Santa Cruz, Santa Cruz, Calif.*

A 2D haptic device, the Logitech Wingman mouse, may be utilized as a tool for blind and visually impaired users to sense graphical information on a computerized map. In this study, tests were performed to evaluate the success of the haptic mouse for identifying random polygons and their vertices by essentially feeling what was on the screen as opposed to seeing it. Participants were blindfolded while a random shape was put onto the center of the screen. With the unique tactile effects from the mouse and specialized sounds from the computer program, they were instructed to duplicate the shape they felt on the screen and to indicate the number of vertices. Preliminary results revealed a positive correlation between elapsed time using the haptic mouse and accuracy of shape recognition.

C55-SAT
CORRELATION BETWEEN RIPARIAN VEGETATION AND SEDIMENT TRANSPORT AFTER DAM REMOVAL IN THE SANDY RIVER, OR
Daniela Martinez. *Johns Hopkins University, Baltimore, Md., National Center for Earth Surface Dynamics, Minneapolis, Minn.*

Riparian vegetation, vegetation on land that is next, directly influences or is influenced by, a body of water (NWS EPA), is a fundamental part of rivers. It is does not only provide us with a good depiction of the activity and ecological diversity along streams, but it can also help us understand its functioning and several of its geomorphologic processes related to the hydrologic cycle, water budgets, soil moisture and sediment erosion, transport, and deposition (Thornes, 1990). In this research, the riparian vegetation along the Sandy River in Oregon will be used to measure and compare the conditions of the river before and after the removal of the Marmot Dam in summer 2007. In order to collect the appropriate data for this study, three weeks of pre-dam removal fieldwork in the Sandy River were required. During these weeks, surveying, and mapping techniques were used to monitor the reaches of the river that might be most sensitive to change. Similar observations will be conducted after the removal of the dam. Ultimately, this research will help to obtain a better understanding on how sediment moves, how it affects vegetation, and can provide a baseline to recognize changes in the stratigraphy and shape of the river over time.

C56-FRI
FLOATING MODULAR HYBRID PIER LONG TERM TEST ON FENDER SYSTEM
Jorge Ortiz. *University of California, San Diego, La Jolla, Calif.*

The modular hybrid pier (MHP) is a breakthrough in naval vessel berthing, with a mission to efficiently mobilize major surface combatants. The self supported floating reinforced concrete structure spans the dimension of 100 feet x 50 feet x 29 feet with two working deck levels. Horizontal loads to the structure due to berthing ships and seismic activity is transferred efficiently from the mooring shaft to the TRELLEX rubber fenders. The objective of the test is to evaluate the performance of the fender system of the modular hybrid pier to a sustained load of approximately 30 kips for a period of 45 days under a static horizontal load, wind forces, and normal fluctuating tidal conditions. The adequacy of the design will be evaluated from test results and the associated analytical studies.

C54-SAT
ACTIVE STRUCTURAL DAMPENING SYSTEMS (ASDS)
Daniel Oskaue, Zahid Hossain. *University of Houston–Downtown, Houston, Tex.*

Vibration control via active structural dampening systems (ASDS) can be improved be by incorporating a highly cost effective artificial intelligence technique called fuzzy logic (FL) to conventional control loops. Conventional control systems popularly use a PID loop or just a PD loop mathematical model. The main downfall of a PID or PD loop is that tuning can be quite tedious and difficult due to oscillation about the desired point. One basically has to use a trail and error process that can take long periods of time and resources. Fuzzy logic is a controversial artificial intelligence technique that mimics the human use of "rule of thumb" intelligence. For example, you do not need to know the exact speed of car up the nth decimal to know if it is moving to fast or slow to be safe. Your input is "fuzzy," imprecise information and yet your output is a precise, accurate, thus "logical" response, or should be. My team uses a steel frame, representing a two story structure, an electromagnet for excitation and an armature, and National Instrument's LabVIEW 8.2 as our controller. We combined our FL with our existing PD control loop by allowing FL to fully control the P term. The most important aspect of our data clear shows that incorporating FL achieved better vibration minimization of our structure. Our experience also showed FL was easier to tune. We still need to refine our fuzzy logic and expand its control to fully include the D term.

C52-SAT
DEVELOPMENT OF A POWER AND COMMUNICATION SYSTEM FOR REMOTE AUTONOMOUS GPS AND SEISMIC STATIONS IN ANTARCTICA
Ezer Patlan[1], Seth White[2], Bjorn Johns[2]. *[1]University of Texas at El Paso, El Paso, Tex., [2]UNAVCO, Boulder, Colo.*

It is a challenge to develop a permanent GPS station in the harsh environment in Antarctica. The power and communications system must operate year-round in the polar region where it is freezing, windy, and dark during the winter. We are working on three major parts of the GPS station: improving the power system, communication system, and mechanical design. My work contained five experiments to assist the design of permanent GPS stations for the Polar Regions: (1) Analysis of wind power data was performed to compare wind speed versus power generated from wind turbine in a GPS system located at Niwot Ridge west of Boulder, Colorado. (2) A test series was performed by applying varying voltages applied to power ports A and B of a GPS receiver. This was done to understand the power switching behavior of the receiver when it is powered from two independent sources. (3) A battery tester was evaluated to determine its accuracy. This tester may be used by engineers in the

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field to evaluate battery health, so ensuring its accuracy is critical. (4) Testing to determine GPS receiver and Iridium antenna interference was also done. This testing focused on understanding what distance from both antennas was necessary to reduce the interference. (5) A tent shelter was designed for permanent GPS installation so technicians can fix or install equipment comfortably. The data, experiments with the equipment, and design of the tent produced helpful results for the project, which will improve permanent GPS technology for the Polar Regions.

C54-FRI

A WIND TUNNEL STUDY OF BOUNDARY LAYER TRANSITION FROM POROUS CANOPIES TO A SMOOTH SURFACE

Angel L. Santiago Perez, Heinz Stefan, Fernando Porté-Agel. *University of Puerto Rico, Mayaguez, Mayaguez, P.R.*

The lowest layer of the atmosphere, known as the atmospheric boundary layer, is in a turbulent fluid dynamic state. This is caused by the interactions between the wind and the land surface. This study builds on a previous wind tunnel investigation in which velocity profiles and roughness properties were collected over various surface types. Here, we investigate turbulent boundary layers over surface transitions. In particular, we explore transitions in aerodynamic surface roughness and the transition of a turbulent boundary from a canopy (trees or other tall vegetation) to a smooth surface (e.g., a lake). First, we study the properties of various surfaces under homogeneous conditions by examining the effect of surface type and wind speed on the aerodynamic surface roughness and surface friction velocity. Previous experiments were conducted over different types of transitions. One transition consisted of flow from a step (foam board) to a smooth surface (the wind tunnel floor), others were a transition from a wire mesh canopy to a smooth surface and from a porous canopy (using pipe cleaners) to a smooth surface. In these cases, we measured the mean velocity profiles at different stream wise positions after the transitions to explore how the profiles adjusted to the underlying surfaces and also to find the separation region of each transition in order to understand what happened in the separation region. Also, in order to understand the atmospheric boundary layer some experiments were conducted to see what happens when the floor temperature is colder than the air temperature.

C51-FRI

EFFECTS OF TEMPERATURE VARIATION ON THE TELESCOPE POINTING AT THE SUBMILLIMETER ARRAY

Sarah Stoebner. *Smithsonian Submillimeter Array, Hilo, Hawaii.*

Temperature effects on the pointing of antennas at the Smithsonian Submillimeter Array (SMA) are important because observing can be done during the day, when there is the most temperature variation. Although temperature surveys have been done before, this project is more specific. The goal of this project was to analyze how temperature variation affects the pointing of Antenna 5 at the SMA. Although there are temperature sensors all over the antenna, we focused on the quadrapods, the reflector mount, and the base ring. The quadrapods are four legs that hold the secondary reflector in place, and the reflector mount holds the primary reflector in place. To investigate effects on the base ring—the center support of the entire antenna—I built a harness that holds temperature sensors and installed it on the base ring. I also edited a program in LabVIEW to read out the temperature output of the sensors. After installing the harness, data on temperature versus the pointing displacement was analyzed. The pointing displacement was measured using optical observations. I took snapshots of bright objects at sunset and then again after sunset, when the temperature stabilizes. The difference between the offsets of both pictures is the pointing displacement. There were significant temperature effects on the pointing of Antenna 5, up to a displacement of 0.3 inches.

C2-SAT

ACCURACY AND PRECISION OF AIRBORNE PARTICLE SIZE AND COMPOSITION MEASUREMENTS

Jose Zavala, Michael Kleeman. *University of California, Davis, Davis, Calif.*

Airborne particles have been found to be associated with adverse human health effects including illness and death. The Kleeman group at the University of California, Davis is measuring the size distribution and composition of airborne particles in California's San Joaquin Valley (SJV)—one of the most heavily polluted air basins in the U.S. Airborne particle samples were collected during the summer and winter months in Fresno, Calif., in order to cover the diverse weather conditions experienced in the SJV. Size-resolved $PM_{2.5}$ samples were collected using micro-orifice uniform deposit impactors (MOUDI) and $PM_{2.5}$ reference ambient air samplers (RAAS), using Teflon, foil, and quartz collection media to support a broad array of physical and chemical analysis. As a first step, size-resolved and $PM_{2.5}$ filters are weighed to determine particle mass concentrations using a CAHN-28 Microbalance at Crocker Nuclear Laboratory. The carbon composition of the samples is then measured using a thermal-optical carbon analyzer developed by Sunset Laboratory. These measurements help determine the source-origin, atmospheric processes, and ultimate environmental impacts of airborne particles. Quality control and quality assurance checks were performed on the airborne particle measurements to determine their accuracy and precision. Duplicate samples, co-located samples, and laboratory standards were all used to gauge the quality of the measurements. The quality control checks show that the instruments are operating properly and, therefore, all measurements obtained are reliable and valid.

MECHANICAL ENGINEERING

C5-SAT

OPTIMIZING THE ADSORPTION OF LIPID BILAYERS

Ricardo Garcia. *University of California, Santa Barbara, Santa Barbara, Calif.*

Lipid bilayers have received great attention due to their application in biosensors, semiconductors, and many other applications. They are an importance substance as they are the main composition of a cells membrane and they serve as a model for a majority of biological membranes. Numerous studies have recognized the spontaneous fusion of absorbed vesicles to form a stable planar lipid bilayer. This spontaneous fusion is not well understood and one of the goals of this research is to help clarify this phenomena by using FRAP technique. A second goal of the project is to experimentally determine the factors that optimize the adsorption of a uniform and stable lipid bilayer into a glass or silica surface from an aqueous solution of vesicles by changing the concentration of vesicles and the aqueous solution in which they will be suspended in. Although many different techniques are being used in similar projects, we currently designed a smaller scale streaming potential device that should optimize the adsorption. The purpose of this apparatus is to indicate when the substrate is completely adsorbed with lipids. The current data collected has been unsuccessful in comparison to the theoretical and a redesign is in phase of the streaming potential and better result should be expected.

C4-FRI

INVESTIGATION OF BOUNDARY SLIDING DURING DEFORMATION OF NANOCRYSTALLINE METALS

Ricardo Komai, Farghalli A. Mohamed. *University of California, Irvine, Irvine, Calif.*

Nanocrystalline metals are composed of metal grain sizes in the range of 1-200 nanometers. These metals have unique features different from their conventional grain-sized counterparts which alter the properties of the material. These types of materials are called a new type of material whose properties can be used in many areas of engineering. They are an important area in materials research. Chemical and electromagnetic properties have been explored, however many mechanical properties have not been experimentally observed. It is important to investigate and observe the properties of nanocrystalline metals because they can be used as coatings or high strength structural elements. Before these materials can be put into application, it is important to understand all of their properties and behavior to prevent future problems with their use. Computer simulations can predict occurrences of boundary sliding, the movement of grain boundaries in nanocrystalline metals, however this phenomenon has not been observed either. In order to observe how boundary sliding affects nanocrystalline mechanical properties, we intend to use and atomic force microscope to visually observe the formation of steps and voids in nanocrystalline Nickel. Boundary sliding often has a negative effect in metals. The boundary sliding that occurs in nanocrystalline metals causes voids and cavities in the structure of the metal which can cause premature failure. Research is continuing over the next few years. . It is important to understand and observe the behavior of nanocrystalline materials in order to understand and predict behavior when they are applied.

C3-FRI

COMPUTER MODELING OF THE HELIUM CLOSED-CYCLE COOLING SYSTEM IN THE GEMINI OBSERVATORY

James Linden. *University of Hawaii at Manoa, Honolulu, Hawaii., Gemini Observatory, Hilo, Hawaii., Center for Adaptive Optics, University of California, Santa Cruz, Santa Cruz, Calif.*

GMOS and NIRI, two observational instruments used at the Gemini North Observatory, share a common gas line in a helium closed-cycle cooling system. For performance, maintenance, and safety, it is important to know the thermodynamic state at any given point in the existing system. A model, which predicted the state of the gas at all points in the closed-system, was developed in the software package PIPE-FLOW Compressible. Pressure gauges and a mass flow meter were used to validate the values predicted by the computer model. The model was then used to predict the adjustments needed to operate the GMOS + GNIRS configuration, scheduled for next year, which will require a greater flow rate through the entire system. The model, measurements confirming the existing system, and predictions for the GMOS + GNIRS configuration will be presented.

C6-SAT

OPTIMIZATION OF A MINIATURE DIFFERENTIAL MOBILITY SPECTROMETER (DMS) FOR CHEMICAL ANALYSIS OF HUMAN BREATH

Mary Molina, Shankar Sankaran, Weixiang Zhao, Cristina Davis. *University of California, Davis, Davis, Calif.*

Analytical instruments can measure small amounts of chemicals in complicated samples and are useful as clinical diagnostic tools. It can often be challenging to optimize operating conditions for these sensors using clinical samples, given the heterogeneous

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background. We work with a gas chromatograph differential mobility spectrometer (GC-DMS) to analyze chemical content in human exhaled breath condensate. This system will be used for non-invasive disease diagnostics. Many parameters can be adjusted, and it is important to choose the proper combination to achieve optimum results. We implemented a factorial design of experiments (DOE), to test several combinations of parameter settings in a systematic manner and concurrently analyze effects and interactions. We examine four parameters that affect sensitivity and detection for our instrument: RF voltage, gas flow rate, SPME type, and GC cooling. Each parameter is changed between two values, requiring a 2^4 factorial design, implying 16 different configurations. We use samples of breath condensate spiked with acetone, a known clinical biomarker. We record two outputs for each experiment combination: the total number of chemicals we measure, and the amplitude of acetone. Our goal is to find the best parameter combination that yields the highest acetone peak while also preserving the larges number of other chemical peaks shown in the spectra. We have completed the experiments and are beginning analysis of the data. By optimizing the system we hope to be capable of conducting further experiments more efficiently and accurately.

C3-SAT

THE STUDY OF INDUCED-CHARGE ELECTRO-OSMOSIS

Jose Muro, Gaurav Soni. *University of California, Santa Barbara, Santa Barbara, Calif.*

Microscale devices for pumping fluids have been one of the main focuses of microfluidics. The ability to move very small amounts of fluid and mixtures has many important applications, for example: dispensing therapeutic agents into the body, cooling of microelectronic devices and chemical/biological analysis. Dealing with fluids at a very small scale (micro 10^-6 m and nano 10^-9m) allows for certain scaling laws to be used, for example electric fields can be used to attract charged ions in the fluid, causing an overall flow. As of now such microscale devices do not have a significant amount of power to move the fluid efficiently throughout the system. Recently induce-charge electro-osmosis (ICEO) has been shown to create pumping of fluid at the microscale. ICEO is the movement of fluid caused by the effect of polarizing a metal while immersed in a fluid and introduced to an electric field. My research is on the movement of fluid using ICEO at the macroscale. I first simulate ICEO numerically to see what velocities could be expected. I then build a mechanism to study ICEO, using electrodes to produces an electric field, metal cylinders for polarization, fluid with microparticles to see the movement of the fluid, and glass slides to enclose the system. Particle image velocimetry (PIV) was used to calculate the velocity of fluid due to ICEO. Comparing simulation date with experimental data will show if ICEO can be used to create microscale devices for pumping fluid.

C2-FRI

SINGLE BEAM MEMS RESONATORS FOR MASS SENSING

Kyle Owen. *University of California, Santa Barbara, Santa Barbara, Calif.*

MEMS resonators are designed to detect chemical and biological analytes. They can be used for national security to test during biological warfare and for medical research to detect strands of DNA or proteins. My research involves testing devices to determine characteristics which improve effectiveness. The best way to understand device characteristics of multi-beam mass sensors is to first understand the device characteristics of each beam on its own. By fabricating single beam devices of corresponding length and thickness to multi-beam devices it was possible to accurately characterize each individual beam. The most important characteristics of a device are its resonant frequency and dampening characteristics. The resonant frequency is where the beam will oscillate at its highest amplitude. The resonant frequency of a beam is determined by its size, shape, and material. The dampening characteristics of a device are also very important. Due to the small scale of these devices the dampening plays an interesting role. It is important to know the characteristics of the damping in order to understand how the device's response will die out. Presently, I have determined the resonant frequencies of all the beams and am in the process of observing the damping characteristics. The resonance did not come out the way I had predicted so more research will be done to determine the cause of the inconsistencies. The important aspect of this study is the method of observing single beams to understand the multi-beam devices; this will lead to new understanding and more useful MEMS resonators.

C4-SAT

AN INVESTIGATION OF THE FILTERABILITY OF SYNTHETIC BIODEGRADABLE HYDRAULIC FLUIDS

Ricardo Rivera-Lopez. *Universidad del Turabo, Gurabo, P.R., Milwaukee School of Engineering, Milwaukee, Wis.*

The purpose of this research is to determine the filterability of synthetic ester based hydraulic lubricants in the Fluid Power Institute™ through experimental procedures to obtain base data for future lubricant development. The experimental procedure followed is the one specified by the International Organization for Standardization, the ISO 13357-1. This is a very specific process; it gives restrictions of room environment, time constraints, equipment, and precision. The procedure includes a stage of sample preparation, which includes measuring and combining the different components of the mixture, followed by an aging section of four days, and finally the realization of the experiment. The filterability of lubricants in hydraulic operations is critical:

in the hydraulic industry fine filtration is necessary. To develop future hydraulic fluids and taking in account the filterability, base data is needed in order to select the proper additives and mixtures. The data obtained from filterability tests will be used in the future in the development of more efficient, cleaner, and filterable hydraulic fluids. The research done will support additional research, which will include performance, biodegradability, and field tests in order to formulate better hydraulic lubricants—an area where efficiency of machines can be improved.

C5-FRI
DEVELOPMENT OF ELECTRONIC FUEL INJECTION AND FLEX FUEL RETROFIT SYSTEM
Robert Valtierra. *University of California, San Diego, San Diego, Calif.*

Improvements in technology and recent developments towards making cars and trucks compatible with renewable fuels such as ethanol hold much promise as sources of clean, sustainable energy. However, many vehicles in use today do not utilize technology such as electronic fuel injection (EFI) that would improve their efficiency and make them compatible with renewable fuels. A retrofit system was specifically designed to convert classic carbureted (non-computerized) vehicles to EFI with Flex Fuel compatibility. Because the system is intended for use with classic automobiles and would be most likely installed by auto hobbyists, the system was designed to require minimal mechanical modifications and wiring for easy installation. Aesthetics were also an important factor in the systems design. Although they do not contribute to functionality, aesthetics can be important to consumers, especially those who own classic cars, in which aesthetics are key. The retrofit kit primarily consists of two main components: the throttle body and electronic control module (ECM). The throttle body contains most of the EFI components and is custom-designed to fit a standard Holley square bore flange, directly replacing the carburetor. Electronic control will be handled by the MegaSquirt II ECM which can be easily modified (a necessity for fine-tuning the throttle body) and has potential compatibility with Flex Fuel. By adding a GM fuel composition sensor and modifying Mega Squirts' existing program, the EFI system can be made compatible with E85 ethanol in addition to gasoline. Virtually any classic car fitted with this system can run on Flex Fuel.

ENVIRONMENTAL SCIENCE

B23-SAT
EFFECT OF PHOTOPERIOD ON GROWTH AND SURVIVAL OF RED TILAPIA *OREOCHROMIS SP.* FRY
Juan Pablo Alvarez[1], Leidy Feliz[1], Evy Osorio[1], Ruby Montoya[1], Mario Velasco[2]. *[1]Metropolitan University, San Juan, P.R., [2]Marnetec, S.L, Barcelona, Spain.*

Energy use represents one of the primary costs related to the production of fry during the hatchery phase of tilapia culture. Thus, the objective of this experiment was to evaluate the possibility of reducing electricity costs by testing different photoperiod management strategies. During a 30 day period the current study investigated the growth and survival of tilapia fry to three different photoperiods with three replicates per treatment. Light was turned on for all treatment at 6:00 A.M. and the three photoperiods were managed as follows: (A) 16 hours constant light and 8 hours dark, (B) 8 hours constant light, 8 hours dark where light was only turned on for 15 minutes for feeding and 8 hours dark, and (C) 8 hours constant light and 16 hours dark. The fish were stocked in indoor fresh water tanks (volume of 40 L) at 1.25 fry\L and an average initial weight of 0.011 g\fry. Light sources were 35W fluorescent tubes located at 21 cm from the water surface with an intensity range of 1,300-1,600 lux. Fry were weighed at day 15, 22, and 30 and were fed to satiation eight times daily every two hours, starting at 6:00 A.M., with a commercial feed. ANOVA analysis of data showed no significant differences among survival (P = 0.5974) with survivals of 87.3%, 82.0%, and 83.0% for treatments A, B, and C, respectively. Final individual weights were 0.584, 0.163, and 0.564 for treatments A, B, and C, respectively. These results suggest that it is not necessary to keep a photoperiod with constant light which warrants further research to optimize energy use and reduce production cost.

B17-SAT
INFLUENCE OF HIGH SALINITY ON SEED GERMINATION OF NATIVE GRASSES AND FORBS SPECIES
Eli Borrego, Shad Nelson. *Texas A&M University–Kingsville, Kingsville, Tex.*

Many acres of South Texas lands are afflicted with high salinity conditions stemming from both natural and man-made causes. Vegetation in these saline environments is limited to salt tolerant species, which have developed individual coping mechanisms for the excess salt. Revegetation of land improves soil quality and aids to prevent erosion, however, before any action is taken into revegetation of high salinity environments studies are required to determine the best suitable species. While some established plants may be able to thrive in these environments, they are unable to germinate in them. Therefore, it is necessary

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to monitor species for both germination and seedling salt tolerance. In this study, 21 native grasses and forbs germinated under varying salinity concentrations (0, 5, 10, 20, and 30 dS m^{-1}) measured by the solution's electro-conductivity. Separate trials were preformed comparing 20˚C 24 hour d^{-1}, 30˚C 24 hour d^{-1}, 30˚C/16˚C 12hr/12hr day/night cycle, and 30˚C/20˚C 12 hour/12 hour day/night cycle. Every two days the seeds were examined for growth and those that were deemed germinated had achieved a specified shoot and root length. The germination percentage of all the temperature and salinities were compared per species. Virtually all species had a high germination rate in the control group (0 dS m^{-1}), although some had a marked increase in the low salinity concentrations. As expected, most exhibited a decrease in germination proportional to the concentration of salt solution. Warmer temperatures promoted germination even at higher salinity.

B23-FRI

TEMPERATURE SENSITIVITY OF MICROBIAL DECOMPOSITION RATES IN ARCTIC SOILS

Monica Castañeda, Claudia Czimczik, Susan Trumbore. *University of California, Irvine, Irvine, Calif.*

Soils in the northern regions contain large amount of organic carbon and the low temperature impedes its decomposition by microorganisms. The northern areas are warming in accordance with global warming and due to the albedo feedback affect the rate of temperature change is highest in the arctic regions. Temperature affects the rates of organic matter decomposition by microorganisms which may end up releasing large amounts of carbon therefore adding to global warming. The exact effect temperature change has on rates of decomposition is unknown therefore making future CO_2 concentration predictions uncertain. Through incubation, the rate of organic matter decomposition by microorganisms from collected soils at Toolik Lake, Alaska, in July 2007 will be measured at three different temperatures for the duration of one month through an infrared gas analyzer. With a stable and accelerator isotope mass spectrometry the stable ($^{13}C/^{12}C$) and radio carbon signature (≈ mean age, $^{14}C/^{12}C$) respired will be measured. The results will be used to partition the CO_2 respiration flux. Due to variability the data is not as conclusive as expected and is still under further experimentation.

B25-FRI

USE OF COSMOGENIC ^{35}S TO TRACE THE UPTAKE PROCESS OF SO_2 IN AEROSOLS IN THE MARINE ATMOSPHERE

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Recent studies have linked environmental issues, such as acid rain and global warming, to the sulfate production in the atmosphere. Cosmogenic ^{35}S has been used to trace the process of removal and cycling of sulfate aerosols in the atmosphere. This research project will make use of a cosmogenically produced source of radioactive ^{35}S in the atmosphere to trace the uptake of SO_2 into aerosols in a marine environment using ^{35}S as a tracer of the uptake process. In addition, when coupled with measurements of the cation (Na, Ca, K, Mg, NH_4) and anion (Cl, NO_3, SO_4) concentrations in the aerosols, the ratio of $35S/SO4_{total}$ could be used to indicate the relative contribution of particulate sulfate as a function of aerosol size in the atmosphere.

B15-SAT

THE IMPACT OF FIRES IN THE AMAZON RAINFOREST ON CLIMATE WARMING

Jorge De Paz, James Randerson. *University of California, Irvine, Irvine, Calif.*

Global climate change is being caused by human activities, including emissions of greenhouse gases from fossil fuel combustion and deforestation. It is known that tropical rainforests in the equatorial area are important for a net climate cooling effect. The current common practice of land clearing with the aid of human-set fires on the perimeter of the Amazon rainforest—the biggest tropical rainforest in the world—is causing a loss of forest cover, although the exact rates of change remain uncertain. We report measurements and analysis of fire counts, fire emissions, aerosol optical depth, land cover, and precipitation in the Amazon and surrounding areas over the last decade. Results show there is an increasing trend on the seasonal fire cycle. Further results on the net climate change caused by the mentioned factors are currently being analyzed by this project. Concluding results are yet to be drawn.

B20-FRI

AN INVESTIGATION OF THE EFFECTS OF HILLSLOPE PROPERTIES ON CARBON AND NITROGEN BIOGEOCHEMISTRY IN A SEMI-ARID NEW MEXICO ECOSYSTEM

Yaika Echevarría Román, Randall D. John, Margaret S. Tammaro, Steve D. Scholle, Kimberly Bandy, Nicole E. Atencio, Enrique R. Vivoni, J. Bruce J. Harrison, Thomas L. Kieft, Michael J. Pullin. *New Mexico Institute of Mining and Technology, Socorro, N.Mex.*

The carbon and nitrogen cycles of desert soils are insufficiently studied. For example, the roles of runoff, microbial mineralization, and denitrification on the export and biogeochemical cycling of carbon and nitrogen is not understood. To properly predict what effect climate change and urban sprawl will have on these delicate ecosystems, understanding these processes is essential. Two opposing hillslopes in the Sevilleta National Wildlife Refuge (central New Mexico) were investigated to illustrate the differences in nitrogen and carbon content between north-facing and south-facing hillslopes. Additionally, the effects of hillslope elevation and soil depth on these nutrient cycles were also investigated. Soil samples were collected at four elevations on adjacent hillslopes. The soils were analyzed for organic carbon and nitrogen, nitrate, ammonium, carbon and nitrogen biomass and respiration, and denitrification activity. Runoff plots and an automatic rain gauge were used to determine the amount of carbon and nitrogen lost during heavy summer thunderstorms. An analysis of community-level sole-carbon-source utilization (BIOLOG) was conducted to assess the variability of the carbon substrates and microbial community function; factors that control the rate of microbial decomposition of organic matter. While research is currently ongoing, initial results indicate that the wetter north-facing hillslope has more organic carbon and nitrogen nutrients than the drier south-facing slope. Additionally, our results indicate that Juniper plant litter is an important source of carbon and nitrogen to the ecosystem. Finally, our results indicate that hillslope hydrology has an effect on the amount and rates of biogeochemical cycling of carbon and nitrogen.

B19-FRI

WELL WATER ON THE NAVAJO RESERVATION

Ronda Francis, Jani Ingram. *Northern Arizona University, Flagstaff, Ariz.*

There are hundreds of abandoned uranium mines on the Navajo Reservation. Mines lie in the backyard of current houses, which raises a concern of possible radiation related health problems. Two overall goals of this study is to investigate water chemistry sampled from wells located on the Navajo Reservation, specifically Leupp (east of Flagstaff, Ariz.) and Cameron, Ariz. (northeast of Flagstaff, Ariz.) and determine water usage by area citizens. After water sample collection, field pH measurements were obtained, filtered for chemical analyses, and a few acidified for metals analysis. Anionic analyses including bicarbonate, chloride, nitrate, and sulfate obtained using ion chromatography (IC). Cationic analyses including sodium, potassium, calcium, and magnesium obtained using atomic absorption spectroscopy (AAS). Elemental uranium and arsenic analyses were gathered with an inductively-coupled plasma-mass spectrometer (ICP-MS). Results revealed low sulfate level but high sodium and chloride levels Uranium investigation revealed some samples to have elevated uranium levels, especially in Cameron, Ariz. area. We are currently continuing to conduct an English-Navajo survey for these communities. The focus of the survey is to investigate well water usage in a sense of whom and how they are being utilized. (Funded by the Native American Cancer Research Partnership (NACRP) through the National Cancer Institute and by the Undergraduate Mentoring in Environmental Biology (UMEB) program.)

B13-FRI

MAIZE BRACE FORMATION AND CORRELATION WITH JUVENILE NODES AND TASSEL STRUCTURE

Dalena Hardy, Kristen Leach, Karen Cone. *University of Missouri–Columbia, Columbia, Mo.*

Global warming causing changes in weather patterns is making drought a more frequent occurrence. Drought is a major limiting factor of maize production worldwide. To maintain high production levels, it is important to identify maize lines which are tolerant to water-stress conditions. A significant trait in drought tolerance is an extensive root system. Root systems in maize are composed of not only below ground roots but also above ground roots. These above ground roots are commonly known as brace roots, and they function to keep the plant upright and provide a surface for nutrient and water uptake and gas exchange. Preliminary studies have demonstrated correlations between brace root architecture and tassel branching. There is a negative correlation between central spike length and number of nodes with brace roots. Studies also indicate brace roots emerge from juvenile nodes. The objective of this study is to examine these relationships on a set of 25 diverse maize lines. Leaf traits were measured to identify juvenile, transitional, and adult leaves. These data will be used to determine if juvenile nodes give rise to brace roots. Various measurements of tassel structure will be gathered and statistically analyzed for relationships between tassel traits and brace root architecture. Examining tassel structure and juvenile node number may help in the selection of maize lines with an increased number of brace roots which allow for adaptation to water-stressed environments.

B22-FRI
MOLECULAR ECOLOGY OF ARSENITE OXIDATION MICROBIAL
Jaime Hernandez, Chad Saltikov, Kamrun Zargar. *University of California, Santa Cruz, Santa Cruz, Calif.*

The major source of arsenic to the Los Angeles Aqueduct comes from Hot Creek, California. Geothermal springs along Hot Creek are enriched with reduced arsenic, namely arsenite As(III). Total arsenic concentration in the creek is about 2.5 μM ± 0.05 μM (Herring, 1998). When geothermal water enters the creek, arsenite is rapidly oxidized to arsenate As(V). Though it is clear that microbes are responsible for the oxidation of arsenite to arsenate, not much is known of the microbial diversity that mediates this reaction in Hot Creek. We previously isolated 18 arsenite resistant strains from the creek water. In this project I will use 16s rDNA analysis to identify the strains and also test for arsenite oxidation. Furthermore the strains will be tested for the presence of the arsenite oxidase gene using PCR. We predict that the majority of the arsenite resistant strains will be from alpha and beta protobacteria groups. Results from these experiments will benefit future research focusing on microbial diversity and arsenic transformation.

B21-SAT
ANIMATION OF 5-MINUTE RAINFALL DYNAMICS WITHIN A 4 KM X 4 KM AREA IN WESTERN PUERTO RICO
Mariana Leon Perez[1], Eric Harmsen[2]. *[1]Universidad Metropolitana, San Juan, P.R., [2]Universidad de Puerto Rico Mayaguez, Mayaguez, P.R.*

In western Puerto Rico there is limited knowledge about the spatial and temporal behavior of precipitation. Due to distance, curvature of the earth and obstructions, the radar that is used to forecast precipitation in Puerto Rico (NEXRAD) is not able to produce accurate images of rainfall events in the west of the island. The objective of this research is to improve our understanding of rainfall spatial and temporal variability within the region, and to validate quantitative precipitation estimates (QPE) based on new and existing radars and satellites. To achieve this objective we developed animations of storms within a 4 km X 4 km study area in Sector Miradero in Mayaguez, P.R. As a part of the study, twelve rain gauges were installed within a small watershed. These twelve rain gauges are located near sixteen rain gauges previously installed within the area. Five-minute rainfall data are downloaded and analyzed every two weeks. Plots from three storms were created using a contouring and 3D surface mapping program called Surfer 8 and then animated in PowerPoint. In general the measured storms exhibited a high degree of spatial and temporal variability. Small rain cells, on the order of hundreds of meters in size, appeared and disappeared randomly within the study area. We did a comparison of NEXRAD rainfall estimates and rain gauges data. The NEXRAD and rain gauge total storm rainfall amounts for August 18, 2006, January 9, 2007, and June 27, 2007, were 20.07 and 44.76, 23.88 and 7.9, and 59.11 and 38.7.

B14-SAT
OPTIMAL GRAIN-SIZE DIAMETERS FOR SALMON SPAWNING HABITAT
Michaela Long. *Univeristy of Arizona, Tucson, Ariz.*

The purpose of the Marmot Dam removal at the Sandy River is to improve habitat connectivity for salmonid population and to restore natural streamflow downstream of the dam. The nature of salmon spawning efforts depends significantly on sediment composition. The anticipated sediment transport initiated by dam removal is expected to affect salmon habitat across different reaches of the river, with the degree of severity depending on location relative to the dam and sediment composition. How will the massive amount of sediment transport affect salmon spawning? Which grain sizes are optimal for spawning? How are these particular grain-sizes distributed along the river? How will the ideal sediment transport following dam removal? Data collection consists of using Wolman's pebble-count method to determine the average grain-size diameters across several river reaches. Comparisons of grain-size diameters to salmon habitat will determine the optimal grain-size for salmon spawning efforts. Results show that the average grain-size of areas with greater salmon spawning activity is a gravel and cobble composition with diameters ranging between 16 mm and 45 mm. These results will further be used to detect change in riverbed composition over the course of the next 5 to 10 years and how dam removal affects salmonid habitat.

B21-FRI
PREDICTING MOBILE SOURCE POLLUTION LEVELS IN EL PASO COUNTY USING LAND USE REGRESSION MODELING
Teresa Madrid, Orrin Myers, Melissa Gonzales. *University of New Mexico, Albuquerque, N.Mex.*

Vehicle emissions are a major source of air pollutants such as benzene, ethyl-benzene, toluene, and xylenes (collectively known as BTEX) and nitrogen dioxide (NO_2). In El Paso County, the concentrations of these pollutants are known to vary significantly across the region. This concentration range of BTEX and NO_2 can have varied effects on human health because the air pollutants are known to be associated with increased asthma rates in adults and children. This study was conducted to measure

levels of air pollutants and utilizes a land use regression model (LUR) to predict pollution levels at unmonitored sites (prediction sites) where children with asthma are being recruited into a health study. The LUR model will use geographic information system (GIS) based predictor variables, such as road density (m/km^2), traffic volume (cars/day), population density (m/km^2) and distance to pollution point sources which have been shown to be correlated with ambient NO_2 and BTEX concentrations in air. Road densities for different functional classes (e.g., freeways, arterials, collectors) were determined for areas within 125 meters to 1000 meters of BTEX and NO_2 monitoring locations and prediction sites. This poster will show the correlation between BTEX and NO_2 and traffic across El Paso County.

B18-FRI

EFFECTS OF A NURSE CROP, ANNUAL RYEGRASS (LOLIUM MULTIFLORUM) ON ESTABLISHMENT OF FOUR SWITCHGRASS (PANICUM VIRGATUM) ECOTYPES

Katrina McClure, Bill Welton, Lorene Williams, Kinis Meyers. *Haskell Indian Nations University, Lawrence, Kans.*

Switchgrass (*Panicum virgatum)* is a warm season C_4 native perennial grass. Native to North American, it is found in 48 states though it is most prevalent east of the Rocky Mountains. Switchgrass is often utilized for erosion control but it is slow to establish. When establishing successful stands of switchgrass key factors to consider are competition prior to germination and competition during germination. Although considered a slow to moderate establishing native grass, switchgrass—due to its ability to adapt to a variety of soils and climates and its extensive root system—can prove an environmentally and economically sound long-range investment for both the military and Native American tribes wishing to return vast land holdings to native grass. Using methodical plantings in designated plot areas on Ft. Riley army installation land, research will be conducted to determine the successful establishment and growth of four ecotypes of switchgrass. The objective of this study is to note the affects of different percentages of an annual nurse crop on the establishment of the native perennial, switchgrass, planted at Ft. Riley military installation lands. What effect might a nurse crop have on successful establishment of switchgrass? What is the feasibility of Ft. Riley using switchgrass, along with the nurse crop, to reclaim training lands? Our hypothesis is as stated: Annual rye grass will establish quickly, providing soil coverage as switchgrass germinates and establishes. Annual Rye was chosen for its existing use as an annual nurse crop. The rye grass was uniformly distributed by utilizing nurse seed at three concentration rates: 0% (control), 10%, and 20% to compare effectiveness at facilitating switchgrass establishment. Delineation was made of two experimental plots in two different soil types: clay upland (Irwin series) and loamy upland (Wymore series). Measurements to determine germination rate, estimate of total plot coverage, species ratio, quality assessment scaling, % weed cover, soil moisture, pH, and texture will be taken of both plots for the months of June thru August with a final analysis to be prepared no later than September.

B24-FRI

CHEMICAL PRECIPITATION TECHNIQUES TO REMOVE VIRUSES OUT OF SEAWATER

Carolina Mendez[1], Seth John[2], Edward A. Boyle[2]. *[1]University of California, Los Angeles, Los Angeles, Calif., [2]Massachusetts Institute of Technology, Cambridge, Mass.*

Viruses play an important role in marine ecology. Viral lysis accounts for up to 50% of bacterial mortality in oceans, having a direct effect on many microbial processes. In order to study marine viruses, it is first necessary to concentrate them from seawater. However, viruses are the smallest organisms, with sizes ranging within .02 um to 0.1 um. Typical commercial filters have pores sizes within 0.1 um to 1.0 um, which makes them inefficient for removing viruses. Chemical techniques can be used to improve filtration processes. In particular, coagulation can cause viruses to become incorporated into large particles by sticking to other viruses and to the chemical precipitate. The flocculent of these larger particles can then easily be filtered. To investigate the optimal mechanism for chemical precipitation of viruses, two coagulants were tested: Magnesium hydroxide (formed by the addition of NH_4OH or NaOH to seawater) and Iron hydroxides (formed upon the addition of $FeCL_3$). In order to measure recovery efficiency, viruses were counted with SYBR-Gold staining and an epifluorescent microscope. Preliminary results suggest that 80% to 100% of the viruses are precipitated with 25 mg/L of $FeCl_3$ followed by an ethylenediamine tetraacetic acid (EDTA)-ascorbate wash. In order to minimize viral lysis during the chemical precipitation process, various washes are currently being tested: oxalate, hydroxylamine hydrochloride, and titanium-citrate. Ongoing work also includes using cloning techniques to investigate if the precipitated viruses can be sequenced for future work.

B24-SAT

TRANSPORT IN SOIL BASED ON CHEMICAL AND PHYSICAL PROPERTIES

Ranulfo Morales, Kristin Clark, Arturo Keller. *University of California, Santa Barbara, Santa Barbara, Calif.*

A demonstration project for the Los Angeles Regional Quality Board consisting of two systems; biotrenches and bioswales will be used to evaluate the efficiency for treating agricultural runoff for excess nutrient loading such as nitrates, phosphates, and

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pesticides. This field experiment is being conducted in Santa Paula between agricultural areas and the Santa Clara River. The preliminary study has looked at physical and chemical properties of soil at the sites. Methods include bulk density, specific gravity, texture analysis (particle size analysis), cat ion exchange capacity, DOM, hydraulic conductivity, soil organic matter, it is important to point out that all of these methods meet ASTM standards. These experiments will enhance our knowledge of ground water and surface runoff being transported from the fields prior to entering the river. Once wells have been drilled water quality experiments will be conducted. The predicted outcomes for both treatment systems are expected to be around 60% reduction of pesticides and 30% for nutrients which will significantly reduce total maximum daily loads (TMDLs).

B16-FRI

MICROBIAL AIR QUALITY IN A 50-YEAR-OLD MIDDLE SCHOOL

Benjamin Borgo, Mina Mostafavi. *Skyline College, San Bruno, Calif.*

Millions of children and adults across the nation spend their days in school buildings, and they need safe, healthy environments to thrive, learn, and succeed. Poor indoor air quality can affect student and teacher performance by causing eye, nose, and throat irritation, fatigue, headache, nausea, sinus problems, and other minor or serious illnesses. Almost any building surface can nourish mold growth. Elevated levels of indoor fungal spores result in significantly higher rates of illness. We enumerated the biological contaminants present in the indoor environment of a water-damaged, 50-year-old middle school in the San Francisco Bay Area. Indoor and outdoor air samples (500 to 1000 L depending on the extent of biological contamination) were taken with an impact air sampler. Swab samples and Rodac impression plates were used to culture environmental surfaces. Fungi were grown on Sabouraud dextrose agar and bacteria on nutrient agar. Indoor airborne fungal spores are 11 times higher than outdoor. Indoor and airborne bacteria are equal. Fungal and bacterial density and distribution are rank-ordered and compared with nearby buildings and outdoor air. Dominant species are identified. The significance of this contamination is discussed.

B19-SAT

NEUROTOXICITY OF NEONATAL MANGANESE EXPOSURE: GROWTH AND ANXIETY BEHAVIOR EFFECTS

Michael Niemi[1,2], Donald Smith[1], Cynthia Kern[1]. [1]*University of California, Santa Cruz, Santa Cruz, Calif.,* [2]*Monterey Peninsula College, Monterey, Calif.*

Manganese (Mn) is an essential mineral found at low levels in food, water, and the air. At excessive levels, Mn is a neurotoxicant that can produce adverse neurological, developmental, and respiratory effects in both laboratory animals and humans. A previous study in this laboratory was undertaken to determine the behavioral and cellular neurotoxic effects of oral Mn exposure at moderate levels of 0, 25, and 50 mg/kg/day using neonate rat model from postnatal day (PND) 1 to 21. This mimics some California drinking water sources and soy-based infant formula levels. Rodents exposed to varying levels of Mn were found to have a significantly reduced weight gain for which there was no clear causative agent. The rodents exposed to Mn also showed an altered response to an anxiety producing behavioral test but the instrument was not ideal for measuring disinhibition. This amended study used the same Mn dosing regimen to further explore the basis of the growth weight effects (by evaluating pup milk intake at several regular intervals) and an elevated plus-maze was used on PND 25 to better evaluate Mn effects on inhibition and anxiety response. The data generated from this study as well as future studies may help: (1) elucidate whether young children exposed to elevated Mn through drinking water and/or soy-based formulas are unable to consume as much milk or gain as much weight as normal children and (2) to explore a mechanistic approach to Mn neurotoxicity in a susceptible population.

B17-FRI

EXAMINATION OF THE MUTAGENICITY OF RDX AND ITS N-NITROSO METABOLITES USING THE *SALMONELLA* REVERSE MUTATION ASSAY

Kelly Ochoa, George Cobb, Xiaoping Pan. *Texas Tech University, Lubbock, Tex.*

The mutagenicity of Hexahydro-1,3,5-trinitro-1,3,5-triazine (RDX) and its N-nitroso derivatives hexahydro-1-nitroso-3,5-dinitro-1,3,5-triazine (MNX) and hexahydro-1-nitroso-3,5-dinitro-1,3,5-triazine (TNX) were evaluated using the *Salmonella tryphimurium* reverse mutation assay (Ames assay) with strains TA97a, TA98, TA100, and TA102. Using a preincubation procedure and high S9 (9%) activation, RDX causes weak mutagenesis to strain TA97a with Mutagenicity index (MI) of 1.5 to 2.0 at dose range of 32.7 to 1092.4 μg/plate. MNX caused mediate mutagenesis to TA97a with MI of at dose range of 21.7 to 878.1 μg/plate, and TNX caused mediate mutagenesis to TA97a with MI of 2.0 to 3.5 to TA97a at dose range of 22.7 to 1118.9 μg/plate. Additionally, TNX caused weak mutagenesis to TA100 with S9 activation at the dose of 1196.7 μg/plate. MNX and TNX also caused weak to mediate mutagenesis to TA102. TA97 is the most sensitive strain to detect RDX, MNX, and TNX induced mutagenesis among these four tested strain. No cytotoxicity of RDX, MNX, and TNX was observed in this study. Doses were verified by HPLC analysis.

B20-SAT

IMPROVING DATA QUALITY WHEN SAMPLING OXYGEN-18 ISOTOPES IN ATMOSPHERIC CARBON DIOXIDE

Lumari Pardo. *Interamerican University of Puerto Rico, San German, P.R.*

Plant respiration and photosynthesis are thought to influence the amount of oxygen-18 isotopes in atmospheric carbon dioxide, but water vapor trapped along with collected air samples affects the isotopic analysis process. If carbon dioxide exchanges Oxygen-18 isotopes with water vapor in the collection flasks, then it tends to reflect the isotopic signature of water instead of carbon dioxide. The problem is most significant in tropical and subtropical regions of the world. In this study, isotopic measurements since 1991 at two Bermuda sampling stations are compared with local meteorological data. This comparison could provide insight into the physical processes of biosphere-atmosphere interactions that may govern the measured oxygen isotopic signal. The two sampling stations on the same island offer a unique opportunity to test this hypothesis in a small region. Statistical analysis of over 360 measurements reveals that the percentage of samples rejected due to water vapor in sampling flasks is strongly correlated with specific humidity at the time of sample collection. Results from this research could significantly affect future sampling collection strategies and therefore improve the reliability of oxygen-18 measurements in carbon dioxide data in the Bermuda region. These results can enhance our understanding of interactions among meteorology, biology, environmental sciences, and could suggest that an alliance among them is needed.

B26-FRI

STUDY OF THE PROCESSES OF COLONIZATION AND ABSORPTION OF *SINORHIZOBIUM MELILOTI* OVER *MEDICAGO SATIVA* ROOTS ON DIFFERENT CONCENTRATION OF SALT

Ibis Melissa Roman Guzman. *Universidad Metropolitana, Arecibo, P.R.*

The Aral Sea in Central Asia has been drying up, because of the use of the water for irrigation of cotton crops. This Sea was a fresh water one but with the evaporation cause a rise in salt on the soil. The soil have been giving origin to the grown of leguminous plants on nears areas of the sea as *Medicago sativa* (alfalfa) how are infected by *Sinorhizobium meliloti* on conditions of extreme salinity. This infection makes a symbiotic relationship where the bacteria provide nitrogen fixation and the plant provides a place to grow and to form nodules with the purpose of obtain photo-assimilates from the plant. Those plants were recollected from this sea which grow on stress salty soil and have been analyzed. During the investigation the plants have been sterilize, induce to grow, infected and colonize by the bacteria. Also, the plants where transferred to a hydroponics' medium for a few days to study the root exudates who the plant produce in this period. On the investigation we have make a comparative study on different concentration of salt from the process of absorption and colonization of different strains of *Sinorhizobium meliloti*. The investigation pretend to characterized and assay the capacity of absorption and colonization on four (4) strains of *Sinorhizobium meliloti* (Ak 17, Ak 100, Ak 27, and Ak 21) from the Aral Sea. Those strains was selected because their competivity in front of 1021 and GR4 which are the control strains which have the capacity of colonization on different concentrations of salt as 0 mM, 50 mM, and 100 mM of sodium chloride (NaCl). The results still on investigation, the objective is to determine the resistant strain to apply on extreme saline environments.

B18-SAT

NILE RED AS A RAPID LIPID SCREENING TOOL TO IDENTIFY ALGAE FOR BIODIESEL PRODUCTION

Marisol Romero-Marquez, Russell Chianelli, Carolina Kretschmer. *University of Texas at El Paso, El Paso, Tex.*

The need for alternative and renewable fuel sources is substantiated everyday in the news media and at the pumps. Approximately, two-thirds of the petroleum imported into the U.S. comes from the Middle East, primarily from Saudi Arabia and Iran. This dependence on Middle Eastern oil shackles U.S foreign policy. Biodiesel is a renewable, carbon neutral alternative to fossil fuel that can be used with little or no modifications required on diesel engines. In the last two decades there has been much research applied to the feasibility of commercial production of microalgal lipids as a feedstock for biofuel production. The introduction of biodiesel from a domestic and renewable feedstock like microalgae will help accomplish the dual goal of energy security and improvement of the environment. Since the identification of high lipid producing microalgal strains is important for commercial biofuel production, a high throughput screening method that screens for lipid content of algae is required. We describe the use of Nile red (9-diethylamino-5H-benzo[α]phenoxazime-5-one) fluorescence as a simple and sensitive assay for determining lipid contents of microalgal strains. This assay dramatically reduces the amount of sample and preparation time by determining lipid content of microalgal strains *in situ*. The major advantages of this assay are its high sensitivity, low sample volume requirements, and reduced reaction times. We present the use of the Nile Red assay to determine neutral lipid content of various algal strains grown under nutrient replete and nutrient deplete conditions.

B15-FRI

INEGRATING OXYGEN FLUX AND GENOMICS INTO THE DEVELOPMENT OF REAL-TIME BIOMARKERS OF FISH EGG CONTAMINANT EXPOSURE

Brian Sanchez, Hugo Ochoa-Acuña, D. Marshall Porterfield, Jiri Adamec, Michael Kane, Marisol Sepúlveda. *Purdue University, West Lafayette, Ind.*

The detection of harmful chemical and biological agents in real-time is a critical need for protecting freshwater ecosystems. Currently, there are few practical and sensitive enough techniques available to identify immediate physiological effects in representative aquatic organisms. We studied the real-time effects of five environmental contaminants with differing modes of action (malathion, cadmium chloride, atrazine, pentachlorophenol or PCP, and potassium cyanide) on the oxygen flux of 2-day post fertilization fathead minnow (*Pimephales promelas*) eggs. Our objectives were twofold. First, we wanted to see whether our technique is sensitive enough to detect instantaneous changes after brief (i.e., minutes) exposures to low concentrations of contaminants. Second, we aimed at determining if there is a correlation between these responses and physiological modifications realized through changes in gene expression. Oxygen flux data indicated that the technique is indeed sensitive enough to reliably detect physiological alterations induced by four of the five contaminants. After 60 minutes of exposure, we identified significant increases in oxygen flux upon exposure to PCP (1000 and 100 μg/L) and cadmium chloride (0.002 and 0.0002 μg/L). We saw a significant decrease in oxygen flux after exposure to potassium cyanide (44 and 66 μg/L) and mixed and no effect after exposure to atrazine (1500 and 150 μg/L) and malathion (340 and 200 μg/L), respectively. Data on gene expression profiles of 2-day post-fertilization eggs exposed to the same chemicals at concentrations and times similar to those mentioned above were also collected. We have generated a "developmental" microarray consisting of three different, non-overlapping oligo-probes for over 400 genes specific to larval fathead minnows. Our work establishes this technique for the detection of real-time physiological changes as a sensitive and reliable tool ripe for development and eventual application.

B25-SAT

DYNAMICS OF DELINEATING SOURCES OF FECAL INDICATOR BACTERIA FROM AN URBAN WATERSHED: MIDDLE SANTA ANA RIVER, SOUTHERN CALIFORNIA

Helen Sanchez, Stanley Grant, Jong Ahn. *University of California, Irvine, Irvine, Calif.*

Fecal indicator bacteria (FIB) tracking studies is a way of demonstrating water quality and therefore, from this analysis we can draw out its relevance to the public health. Unfortunately, the public is running the risk of suffering from long-term safety effects if negligent maintenance of these resources is not supported by technological innovations and efforts. In this study, we prepared a set of studies that better delineate the sources of FIB in the Middle Santa Ana River, which has been found to have a high percentage of wastewater, during dry weather periods. Specifically, there are two different possibilities that can be envisioned: FIB is dispersing in the environment caused by inputs of illicit human sewage; FIB impairment is environmentally controlled giving no clear source. To account for the different exposure times, water samples will be collected every three hours for 24 hours from 4 main transect sites: upstream SAR, downstream SAR, upfront of plant, ending of Anza Channel, and then sent to the laboratory for data analysis. And accordingly to the specific data results obtained (FIB behavior and surrounding environment variant), this will lead us to choose the correct, more precise method (such as an analysis of FIB vs. time relationships) to indicate the source. The results and analysis portrayed here will stress the increasing body of evidence that management of FIB impairment in the waters of southern California will necessitate in developing long-term strategies for treatment of point/nonpoint sources of urban runoff.

B22-SAT

SIMULATION OF HURRICANE-OCEAN INTERACTION FOR HURRICANE KATRINA: DIFFERENCE BETWEEN COUPLING WRF WITH A 1-D AND 3-D OCEAN MODEL

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Given the drastic increase in shoreline habitation in hurricane zones and recent hurricane disasters such as Katrina (2005), every effort should be made to improve the accuracy of hurricane simulations. In this research project, simulations of Katrina will be run using the Advanced WRF (weather research and forecasting) atmospheric, numerical model coupled to a 1D and then to a 3D ocean model. The goal of this study is to determine if coupling with a 3D ocean model provides a more physically accurate simulation. The 1D model that will be used is the PWP (Price-Weller-Pinkel) isolated column ocean model. This ocean model is able to simulate the local mixing component of the ocean response to the hurricane. A 3D model, however, is needed to account for the upwelling component of the ocean response. Both the local mixing and the upwelling parts of the ocean response bring the deeper, colder water up to the surface which decreases the temperature of the warmer, surface mixed layer, and this decreases the amount of energy available to the storm. I am currently carrying out this project through a summer research internship, so the results are not available at this time. We anticipate that using the 3D ocean model will produce a hurricane simulation that more closely follows actual events in terms of the physics of the hurricane-ocean interaction since the 3D model can simulate both aspects of the ocean response.

B16-SAT
HIGH RESOLUTION GEOPHYSICAL SURVEY OF WESTERN LONG ISLAND SOUND OFFSHORE NEW YORK: A SEAFLOOR MORPHOLOGY SHAPED BY GLACIAL FEATURES, TIDAL CURRENTS, AND HUMAN ACTIVITY
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Western Long Island Sound (LIS) averages 16 m in water depth, with elongated depressions up to 40 m deep occurring around its axis. These depressions are currently interpreted as ancient drainage channels that were cut into its floor some 15,500 years ago, when the glacial lake that occupied LIS drained out. In June 2006, a 17 km^2 area of Western LIS was surveyed on board the R/V HUGH SHARP. High-resolution multibeam bathymetric data reveal the subtle morphology of the seafloor and chirp seismic profiling data clearly imaged the shallow sedimentary strata. Preliminary analysis details the following characteristics: (1) large sand waves on the west side of outcrops, indicating strong tidal currents, dominant to the west; (2) outcrops (possibly moraines) surrounded by moats scoured by currents; (3) pockmarks in gas-charged sediment indicating active seepage; and (4) pipelines, shipwrecks, and possible dredge spoils. Also, the lack of short mud waves suggests that currents are weak overall (< 10 cm/s), as previously documented. Preliminary analysis of the shallow gravity cores and chirp profiling data indicate that estuarine sediment deposition is relatively thin (< 1 m) (McHugh et al., Late Quaternary Depositional History and Anthropogenic Impacts of Western Long Island Sound, New York, Eos Trans., 87(52), Fall Meet. Suppl. Abstract OS31B-1638, 2006). This result is consistent with the elongated depressions corresponding to late glacial erosional channels. Grain size analysis for 9 of the gravity cores collected within the survey area will provide further test of the current energy and also help confirm (or not) this interpretation. (http://www.explore-the-sound.org)

GEOSCIENCES

ATMOSPHERIC SCIENCE

B4-SAT
NUMERICAL MODELING OF HEAT-INDUCED LARGE SCALE TROPICAL CIRCULATION
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In order to understand disturbances near the equator, transient effects due to diabatic heating in the equatorial region are explored using a nonlinear numerical model based on shallow-water equations on the equatorial β-plane. Different convective heat sources are tested in the continental areas of South America, Africa and Indonesia in the first set of studies. In the second set of studies, different convective heat sources are placed over the ITCZ and Panama bight to see wave response in an area north of Columbia where significant winds form a Caribbean low level jet. Described is the effect orography of the northwestern Andes mountain range has on the Kelvin wave response of this region, and the relationship the convective region west of Panama has with the Caribbean low level jet north of Columbia. This project increases knowledge of events and trends near the equator so meteorologists can predict the large scale evolution of the tropical atmosphere with more accuracy.

B3-FRI
UTILIZING COSMIC RADIO OCCULTATION SOUNDINGS TO ESTIMATE CONVECTIVE POTENTIALS OVER OCEANS
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Over oceans, unexpected convection can adversely affect airplane travel. To mitigate such hazards, the Federal Aviation Agency (FAA) asked the University Corporation of Atmospheric Research (UCAR) to develop techniques that warn of imminent convection. The challenge: few traditional observations are taken over the ocean, and nowcasting techniques, which rely on Doppler weather radar, are not applicable. An atmospheric sounding technique, known as GPS radio occultation (RO), offers a possible solution to this problem. The six-satellite mission Constellation Observing System for Meteorology, Ionosphere, and Climate (COSMIC) provides approximately 2,500 vertical profiles of the Earth's atmosphere daily, and is uniformly distributed around the globe including the tropical ocean. These GPS RO soundings are of high vertical resolution and accuracy. With the use of one-dimensional variational retrieval, vertical profiles of temperature and moisture can be derived from COSMIC soundings. These profiles could be used to estimate convective potentials of the atmosphere that lie ahead of an airplane travelling over the ocean. This study evaluated the accuracy of convective available potential energy (CAPE), convective inhibition (CIN), K-index (KI), total totals (TT), and 700 to 500 mb Lapse rate (L57) calculated from COSMIC GPS RO soundings against observations from balloon-based radiosonde soundings. This study also evaluated whether COSMIC-derived

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indices values are accurate enough to be useful for the FAA's over-ocean convective forecasting. With some indices proven to be useful, this technique will eventually provide real-time KI, TT, and L57 value estimates globally. Additionally, COSMIC indices values can be used in studies to map out the diurnal cycle of any index.

B5-SAT

A CLIMATOLOGY OF PINHOLE EYES IN ATLANTIC HURRICANES

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While hurricane track forecasts have continued to improve over the past decades, intensity forecasts have not significantly changed in 30 years. The intensity forecasts include large misses when rapid intensity changes are involved. Researchers have designated better guidance for rapid intensification timing and magnitude as one of the highest priorities for tropical cyclone forecasting. In recent years, several hurricanes that have undergone rapid intensification also developed a pinhole eye during that intensification. These pinhole eyes are eyes much smaller than normal, with a radius under 10 km. The appearance of these pinhole eyes appears linked to the previous period of intensification, so identifying the factors that allowed contraction to a pinhole eye could help predict future cases of pinhole eyes and the rapid intensification preceding them. This project develops a climatology of pinhole eyes occurring in Atlantic hurricanes over the period 1989 to 2006. A combination of operationally-estimated size parameters, aircraft reconnaissance fixes, and synoptic data is used to create this climatology. These datasets are examined to determine whether any environmental factors differ significantly between cases of pinhole eyes and normal eyes. It is expected that pinhole eye cases will have higher ocean heat content and lower vertical wind shear than their normal counterparts. The findings from the climatology could be used to create a statistical predictor for pinhole eye development, to assist in forecasting periods of rapid intensification.

B4-FRI

THE EFFECT OF CO_2 STABILIZATION ON UPTAKE RATES IN THE LAND AND OCEAN SINKS AS A FUNCTION OF OCEAN CIRCULATION, VEGETATION TYPE, AND CO_2 FERTILIZATION

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In order to mitigate effects of climate change, governing entities need to limit carbon dioxide (CO_2) in the atmosphere to a concentration yet to be determined. To assist policymakers, this experiment tested selected sensitivities of the land and ocean sinks to a proposed CO_2 stabilization scenario of 600 parts per million by 2100. Sensitivities evaluated were the effect of CO_2 fertilization on vegetation, the effect of long-lived forests versus short-lived steppes, and the effect of various ocean circulation rates. All simulations were done with Tethys, a four-box earth-systems model consisting of a vegetation-soil reservoir, ocean, atmosphere, and emissions source. Results are generated through a series of equations written in IDL code, parameterized to simulate key processes in the climate-carbon cycle. Results generated in response to ocean and land sink behavior included peak allowable emissions, CO_2 uptake rates in a reservoir, and the maximum amount of allowable emissions to maintain concentrations at 600 ppm. Tethys predicted that the rate of carbon uptake in the oceans will decrease with an increase in circulation time, and that the vegetation sink will cease to exist soon after atmospheric CO_2 is stabilized. Simulations suggest that grasslands will absorb more CO_2 than forests, a result that indicates a flaw in the model. The carbon cycle sensitivities tested in this experiment determine how much humans can emit and how quickly emissions need to be reduced to meet stabilization goals. Future sink behavior should be incorporated into any plan that seeks to stabilize atmospheric CO_2.

B5-FRI

AIRBORNE MEASUREMENTS OF OH, MSA, NH_3, HO_2, HO_2+RO_2 USING THE SELECTED ION CHEMICAL IONIZATION MASS SPECTROMETER

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PASE (Pacific Atmospheric Sulfur Experiment) aims to understand the sulfur cycle in a remote marine atmosphere. This study will be conducted fall 2007 at Christmas Island on board NSF/NCAR C-130 aircraft. It will focus on measurements of DMS and its contribution to formation of H_2SO_4 and MSA by oxidation of DMS by OH. PASE will also focus on subsequent production of aerosols and cloud condensation nuclei from H_2SO_4, MSA, and NH_3 concentrations in a cloud free convective boundary layer and in outflow of marine cumulus. This paper presents technique and sample measurements of OH, H_2SO_4, MSA, HO_2+RO_2, and NH_3 using the SICIMS (Selected ion chemical ionization mass spectrometer) with several adaptations to technique and instrumentation from previous studies conducted: ACE-1 (Aerosol Characterization Experiment) in, PEM-Tropics A and B (Pacific Exploratory Mission) in 1996, and INTEX-B (Intercontinental Transport Experiment) in 2006. Results are not available at present because the PASE campaign will begin August 2. Anticipated results include calculation of uncertainties in the instrument and diurnal variations of OH, H_2SO_4, MSA, HO_2+RO_2, and NH_3 in a remote marine atmosphere east of Christmas Island.

GENERAL GEOSCIENCES

B8-SAT

SEISMIC TOMOGRAPHY INTERPRETATIONS OF THE JUAN DE FUCA PLATE SUBDUCTING UNDER THE NORTH AMERICAN PLATE

Ana Luz Acevedo-Cabrera, Richard Allen, Mei Xue. *University of California Berkeley, Berkeley, Calif.*

Today, scientists are able to create pictures of the interior of the earth through the process of analyzing earthquake data called teleseismic body wave travel time tomography or more simply: seismic tomography. Recently, more seismometers have been deployed all over the western part of the United States, which aid to the creation of high-resolution pictures of the plate tectonic processes that are occurring in this tectonically active zone. Specifically, the pictures created of the interior of the earth depict the subduction of the Juan de Fuca plate, a remnant of the Farallon plate, underneath the North American Plate. Through the inversion of the analyzed data from earthquakes with a magnitude greater than or equal to 6.0 and epicentral distance greater than thirty degrees, pictures depicting the velocity gradients of the Juan de Fuca Plate subducting under the North American Plate are created. Scientists analyze these velocity pictures to find anomalies that might indicate the interaction of the subducted slab with a possible plume head or to investigate other fates of this subducted slab. Current researchers at the Berkeley Seismological Laboratory including Professor Richard Allen, and Graduate Student Mei Xue propose that the absence of the slab below 400 km today is due to the arrival of the Yellowstone plume head ~17Ma, which destroyed the Juan de Fuca slab at depths greater than the thickness of the continental lithosphere. The seismic tomography interpretations after the data is fully inverted will not only help us understand the plate tectonic interactions in the western part of the U.S., but they will also improve our understanding of plate tectonics in the Earth as a whole.

B6-SAT

PLATE KINEMATICS AND MECHANISMS: A PERSPECTIVE ON THE APRIL 2006 MAJOR RUSSIAN EARTHQUAKE

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Northeastern Asia's plate boundaries are much debated. Thus, when a magnitude 7.6 earthquake occurred in eastern Russia's Koryakia region during April 2006, seismologists were presented an opportunity to study the resulting seismic events. Data collected from both the main event and aftershocks is analyzed using moment tensors, tomography, and deformation fields. The results are given perspective against historical seismicity and regional plate tectonics. Essential to understanding the region's tectonics is plate kinematics, which is the focus of this research. Building upon existing knowledge of the local plate mechanics, moment tensor data is analyzed and patterns of consistency, gaps, and overlapping mechanisms are noted. Finally, an attempt is made to identify the process responsible for each event. Preliminary results indicate that primarily two types of shallow faulting occurred. Although the study area is geographically located near two major plates boundaries, the main event and those that followed may support evidence for existence of a microplate. To define plate boundaries, seismic events are typically tracked over an extended time period so patterns can be detected. In northeastern Asia, the sparseness of data works against scientists attempting to define plate boundaries and motions. Data analysis from the April 2006 event and following shocks will add to the body of seismic knowledge and provide a basis for future research aiming to more clearly define regional plate boundaries and kinematics.

B6-FRI

TRACKING MERCURY CONTAMINATION IN THE SEDIEMENTS OF WESTERN LONG ISLAND SOUND

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In June 22 to 29 of 2006, we surveyed western Long Island Sound from the *R/V Hugh Sharp*. We collected multibeam bathymetry, chirp sub bottom profiling, side-scan sonar imagery, and sediment samples. Chirp images provided the framework to sample five of the gravity cores for the purpose of determining Hg contamination. Cores HS06-2G and HS06-15G were recovered in a region of flat topography at 29.1 m and 15.2 m water depth, respectively, near the Connecticut shoreline. Cores HS06-21G, -22G, and -24G were recovered east and west of the main navigation channel near the Throggs Neck Bridge. Samples were run through a mercury analyzer at Wesleyan University. Cores located in closer proximity to the CT shoreline showed two distinct spikes of Hg that represent the start of the Industrial Revolution in ~1850 and a period of high precipitation in the 1970s. The cores recovered at the margins of the channel show very different Hg concentrations. Cores 24G and 21G located in an area of sediment erosion or non-deposition show one spike with low Hg concentrations of 122 ppb and 530 ppb, respectively. In contrast core 22G located in an area of sediment deposition shows Hg concentrations increasing from ~50 ppb at a depth of 50 cm to ~1500 ppb at 5 cm. This suggests that the concentration of pollutants such as Hg in LIS is to a great extent controlled by physical processes that erode, transport, and focus sediment deposition at particular locations. Bedrock and tidal currents are important factors controlling the sedimentation patterns and the channel morphology.

B7-FRI

THE DAILY CYCLE OF WINDS ALONG THE COAST OF THE GULF OF CALIFORNIA DURING THE NORTH AMERICAN MONSOON

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The North American monsoon (NAM), which occurs over the southwestern U.S. and northwestern Mexico, has been, and continues to be, an area of interest, because it has an immense affect on the populace in this region. Difficulties in understanding and predicting the convective precipitation typically seen during the NAM emerge in multiple global atmospheric general circulation models (AGCMs). Inaccurate simulations may be due to the model's inability to correctly simulate the daily cycle of winds over the NAM region. The North American Monsoon Experiment (NAME) was a study aimed at ascertaining the restricting factors and causes of the predictability associated with the summer precipitation over arid southwestern region of North America. NAME2004 was the major field campaign, however some instrumentation was redeployed in the subsequent summers. Previous researchers have studied the daily cycle of winds over northwestern Mexico during NAME2004 using winds collected by two 915-MHz Doppler wind profilers. This research builds on the two previous studies by constructing the mean daily cycle of winds for the lower troposphere during the redeployment years of 2005 and 2006. The mean daily cycles will be compared to the previous studies to document this interannual variability associated with the NAM. This study strives to provide a better understanding of the daily cycle of winds seen over northwestern Mexico. The overarching goal of this and future studies on this topic is to develop more accurate model simulations and forecasts for the region.

B7-SAT

TIME SCALE COGNITION EXPERIMENTS FOR THE TRAIL OF TIME AT GRAND CANYON NATIONAL PARK

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The *Trail of Time* is a walking timeline trail now under construction along the South Rim of Grand Canyon. It will extend 4.5 km, with each meter marked to represent one million years of geologic time. The *Time Accelerator Trail* (TAT), is a logarithmically scaled timeline designed to help visitors adjust their frames of reference from personal time scales (years to decades), to deep time (millions of years) by periodic changes in scale enroute, from one meter per year to one meter per million years. The time interval marked by the TAT begins at the present and ends at 6 million years ago (Ma), when Grand Canyon downcutting started. While linear timelines are commonly used to teach about geologic time, their effectiveness has not been fully assessed. We implemented off-Canyon studies of the proposed TAT, in which participants represented Grand Canyon visitors. The experimental setting is a scaled-down (74 m), portable rolled paper version of the TAT, on which realistic time markers were placed. Research questions include: (1) Do subjects understand the purpose of the TAT?, (2) What happens cognitively when subjects walk the variably-scaled timeline?, (3) Can subjects correctly identify the time represented at any point along the TAT?, and (4) What cognitive challenges will subjects reveal while traversing the TAT? The experiments have yielded useful recommendations for the full-scale TAT, especially clarity of scale changes and comprehensive labeling of time markers. Coding and analysis of recordings for time cognition studies are in progress.

GEOLOGICAL SCIENCE

B10-SAT

CARBON ISOTOPE (^{13}C) CHEMOSTRATIGRAPHY OF THE COTUI LIMESTONE, UPPER CRETACEOUS OF SOUTHWESTERN PUERTO RICO

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The Cretaceous limestones in Puerto Rico are exposed as non-continuous volcano-sedimentary sequences in highly deformed structural blocks. This complexity presents a serious obstacle to the understanding of the stratigraphic nomenclature of these carbonate rocks. In 1999, Santos studied the rudistid fauna in southwestern Puerto Rico and found three events of carbonate deposition. This technique proved to be a reliable tool in areas with abundant occurrence and high preservation of rudistid fossils, but is not effective in areas where both are low. To resolve problems of the correlation of areas with good fossil control and those without fossils, a carbon isotope chemostratigraphy (δ13C) is being developed for the Cotui Limestone, a Santonian age carbonate platform in southwestern Puerto Rico. To assure accuracy of the correlations between sections the carbon isotope signatures are being obtained from both the carbonates and the organic matter with a resolution of 20 cm between samples. The carbon isotope chemostratigraphic profiles suggest a correlation between carbonates with the characteristic fauna of the Cotui Limestone and a section formerly mapped as part of the younger Guaniquilla Limestone.

B13-SAT

MORPHOLOGIC AND ECOLOGICAL CHANGES IN THE HISTORY OF THE CHOWAN RIVER WATER SHED

Brian Campbell, Ann Garland. *Elizabeth City State Universtiy, Elizabeth City, N.C.*

This project, began in the fall of 2006, was designed to categorize the geomorphological, ecological, cultural setting indicative to settlements along the Chowan River in North Carolina. Historic maps ranging in date from the late 1600s to the present were gathered for review. From these maps approximations were made as to the locations of the regions major native settlements, and the significant changes to its boundaries in recent history. The distribution of recorded settlements was seen to be related to the presence of marine scarp, the relict of a Paleozoic barrier island, that has since become the path for regional highway 32. This scarp marks an abrupt 8m rise in elevation within the otherwise low lying region of the North Carolina coastal plain. We were also able to site three significant changes to the shores of the Chowan River. In 1825 and 1760 in correspondences with the closing of the Roanoke and Currituck inlets and latest in 1950 due to the hurricane Irene. The initial survey of the site began in September of 2006 with a series of shovel test preformed within the boundaries of the Chowan River off the shore of the Chowan Beach housing community. Tests at a depth of 2 feet produced artifacts including: pottery, grommets, stone and bone tools, and weapon points. It is our hypothesis that using data collected from sites along with the area's morphologic history to estimate the time of habitation and categorize some occupational habits of the regions indigenous people.

B12-SAT

HISTORICAL SEISMICITY OF THE NORTHEASTERN REGION OF RUSSIA: A PERSPECTIVE ON THE M7.6 EARTHQUAKE ON KORYAKIA, RUSSIA

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A major earthquake, which occurred near Koryakia, Russia during April 20, 2006, is analyzed and given perspective in contrast with the historical seismicity, plate tectonics, and the geology of the area. The relevance of this earthquake is that it occurred in a complex geological area, where the locations of the plate boundaries are not well known and no major earthquakes were ever recorded. This event is evaluated through comparison with past events and plate tectonic models.The methods used in the research are doing background and actual research on the geology of the area, mapping of the historical seismicity, and models of the local tomography of the region. The software used for mapping is ArcGIS; and for tomography the software is Seismic Viewer. All of these methods are going to be combined, so they can be fully analyzed and give us a new perspective of what mechanisms triggered this major 7.6 magnitude earthquake that was the cause of leaving 40 people injured and some buildings and water supply systems badly damaged with a damage estimated at 55 million U.S. dollars. The goal of this research is to make a well structured tectonic summary for reference on future events that may occur in or near the Koryakia region.

B12-FRI

PLANT-INSECT INTERACTIONS IN THE CENOZOIC

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The Cenozoic era was a time of global-scale changes not only in climate, but also in the levels of angiosperm and insect diversity. Previous work on plant-insect relationships suggests that these temporal and climatic factors may have played a role in the evolution of such interactions. To study patterns of insect-feeding damage over time, we examined six Cenozoic fossil flora assemblages from western North America: Green River Formation (45 my, 16.6˚C, 22.5 cm precipitation), Florrisant Formation (34 my, 12.2˚C, 18.5 cm), Creede Formation (27.4 my, 11.4˚C, 13.5 cm), Latah Formation (16 my, 10.2˚C, 32.5 cm), Buffalo Canyon Formation (15.6 my, 9.4˚C, 14.5 cm), and the Stewart Valley Formation (15.0 my, 10.9˚C, 12 cm). The formations span a 30 my time interval and have varying climate parameters that allowed us to determine which variables might be better predictors of the amount and types of insect damage present in assemblages. The 2390 leaves were examined for the presence or absence of insect damage. Those leaves bearing insect damage were further classified into one of five categories; hole-feeding, margin-feeding, skeletonizing, galling, or leaf-mining.

B11-SAT

ON THE NATURE OF DYNAMIC TRIGGERING OF EARTHQUAKES CAUSED BY SURFACE WAVES

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The understanding of earthquakes has grown tremendously since the turn of the century, yet many key physical processes remain a mystery. For example, recent work has shown that the passage of seismic waves from large earthquakes can trigger small earthquakes thousands of km from the epicenter. This process, called dynamic triggering, remains poorly documented and few physical explanations have been put forth. To address the fundamental physics of dynamic triggering, we study: (1) to what extent are triggered earthquakes caused by dynamic seismic waves, (2) what phases, frequencies, and amplitudes are responsible for dynamic triggering, and (3) what happens inside triggered-earthquake faults when dynamic waves pass through. We conduct a global survey of fifteen recent large to great earthquakes and optimize our analysis for automatic detection of local earthquakes. We also utilize observations from the Utah regional seismic network and closely investigate the timing, frequency, amplitude, phase, and particle motion of both Love and Rayleigh surface waves for those large events with demonstrated remote triggering. Preliminary results from both efforts indicate: (1) for many of these large earthquakes, statistically significant increases of smaller regional events coinciding with the arrival of the largest amplitude surface waves suggests a more common phenomenon than originally anticipated and (2) based on our Utah analysis, the triggering phase for remote earthquakes depends heavily on the orientation of faults and tectonic setting of the region in question. We will expand the study by applying our methods to other regions as the data become available.

B9-FRI

RISK ASSESSMENT OF EXPOSURE TO CONTAMINANTS IN WATER

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Water resources on the Reservation are more contaminated than in similar rural, non-Native communities, and are inadequately monitored. Subsistence activities and cultural practices of Reservation communities place residents at an increased risk of exposure to environmental contaminants through water sources and subsistence foods. High coliform counts in surface waters place residents at increased risk of exposure to pathogens. Extensive cattle ranching and inadequate sewage treatment are contributing factors. Surface waters used for the public drinking water supply are also at risk for chemical contamination from landfill leachates, oil spills, pesticides, and mercury deposition. Understanding exposure pathways will contribute to developing culturally appropriate mitigation strategies. Establish a sampling and analysis program to assess contaminant loadings to surface waters, groundwaters, and aquatic/wetland subsistence foods; conduct household surveys to evaluate lifestyle and cultural practices that contribute to exposure risk from water sources and subsistence foods; and, design and support implementation of culturally appropriate risk communication and management measures that minimize impacts on traditional practices, and which may be transferable to other Tribes. Conducting this research as a community based participatory research project will improve the quality of the research, help ensure our work will serve Reservation needs, and model how to provide Tribal College science majors with meaningful research experience. Initial results show significant pathogen levels in surface water resources and high mercury levels in local edible fish species. This project is ongoing through 2011.
The long term goal of our research is to improve environmental health in Reservation communities.

B10-FRI

STABLE ISOTOPIC INVESTIGATION OF MOONMILK PRECIPITATION: THRUSH AND CATARACT CAVE, ALASKA; THURSDAY MORNING CAVE, COLORADO; PAHOEHOE, LOWER AND SPIDER CAVE, NEW MEXICO

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Moonmilk is a secondary formed deposit (speleothem) within various cave systems. It is currently defined as a microcrystalline aggregate with various mineralogies and unusual texture. Unlike traditional speleothems (stalagmites and stalactites), moonmilk's origin doesn't seem to be explainable via the same physiochemical processes. Instead a microbial role is suggested to play an important component in its formation. In order to better understand moonmilk's possible biogenecity, we have employed a combination of geochemical and microbiological techniques including: scanning electron microscopy (SEM) coupled with electron dispersive spectrometry (EDS), stable isotopes, 16S ribosomal RNA sequencing, and cultural methods. We will discuss the geochemical and SEM results to date. Geological and biological processes produce isotopic fractionation, which enrichs a substance in one isotope relative to another (Hill, 1987). Stable isotopes such as carbon (^{13}C, ^{12}C), oxygen (^{18}O, ^{16}O) and hydrogen (^{2}H, ^{1}H) provide valuable information for the determination of speleothem-forming processes (Hill, 1987). Thereby, such analyses can aide to the understanding of the environmental conditions and processes under which moonmilk precipitates. Moonmilk deposits from six various cave systems (Alaska, Colorado, and New Mexico) were selected based on their environmental parameters (i.e., geology, climatic location and elevation). Moonmilk deposition and host rock were both analyzed for carbon and oxygen isotopic composition to examine the source of the carbon in the moonmilk. In addition,

dependent on hydrological activity within the various cave systems, oxygen and deuterium of pool and drip waters were analyzed to look at the source of water involved with moonmilk deposition.

B9-SAT

GEOCHEMICAL AND PETROGRAPHIC ANALYSIS OF FOSSIL BONE: UNEXPECTED RESULTS AND IMPLICATION FOR FOSSILIZATION

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Rare earth elements (REE) have a strong affinity to phosphate minerals allowing incorporation into biogenic apatite (bones and teeth) during the fossilization of vertebrates. Thus, REE incorporated into vertebrate bones (a form of carbonated apatite) are used for various taphonomic and paleoenvironmental purposes. REE have been used in taphonomic studies to detect spatial and temporal averaging, as paleoenvironmental indicators, as provenance indicators, and are proposed as a forensic tool to identify illegally removed material. Most of these studies utilize solution inductively coupled plasma mass spectrometry (ICP-MS) to analyze bone material. These methods homogenize at least 0.01 g of bone material through drilling or crushing. Solution methods usually do not detect heterogeneities of REE concentrations and proportions. Laser ablation microprobe ICP-MS (LAM-ICP-MS) analyses much smaller bone volume (~10^{-5} μm^3) allowing detection of REE heterogeneities. Two bone fragments from the dinosaur *Falcarius utahensis* were analyzed using LAM-ICP-MS. One of the bones revealed two distinct REE patterns and concentrations. Three hypotheses have been presented based on these observations: (1) REE signatures are the result of post-fossilization diagenesis; (2) fossilization occurred at a geochemical boundary; and (3) the bone, acting as a partially closed system, fossilized at different rates resulting in fractionation of the REE. Petrographic analysis using transmitted, reflected, and UV light, calculation of REE ratios, tetrad effect, and Ce anomalies, and stable isotopic analysis of bone and its surrounding carbonate matrix suggest post-fossilization diagenesis is unlikely. Fossilization between a geochemical boundary or differential rates of fossilization are more likely.

B8-FRI

DISPLACEMENT MODELING OF VOLCANIC MAGMA CHAMBERS

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Volcanoes can be hazardous if increased pressure in the magma chamber becomes great enough that magma is forced upward through a crack to the ground surface and erupts. The magma chamber which lies beneath a volcano is a large underground pool of molten rock lying under the surface of the earth's crust. The problem with the magma chamber and why it is significant is because there are unknown processes occurring inside volcanoes. Researchers have not yet understood the processes occurring inside of a volcanic magma chamber. My research is to update a mathematical displacement model which describes the magma chamber properties such as depth and volume change (e.g., inflation or deflation at surface). So far, the method used to get the displacement model to work was to move all the file structures along with the displacement program in one memory storage space in order for the program to work in Matlab. As a result, the program was able to import and export data in addition to loading geographical features of the displacement model to better understand the magma chamber for the purpose of prediction of future volcanic eruptions.

B11-FRI

KINEMATIC GPS AT KILAUEA VOLCANO

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Geologists are using global positioning systems (GPS) for deformation and to support plate tectonic theory. GPS equipment is used in multiple locations to record changes in position relative to the Earth over time. Kilauea, one of the most active volcanoes in the world often displays large movements. The GPS is able to record all of the variations in height and position quickly and easily. Kinematic GPS is most commonly used to map lava flows due to its difference in precision to static GPS. Static GPS equipment is very expensive and can be prone theft prompting the Hawaiian Volcano Observatory to use kinematic GPS systems as part of a campaign. Kinematic GPS is relying on reference GPS to pinpoint the position of the moving GPS equipment. Benchmarks have been set in many locations around Kilauea including the Kilauea Caldera, East Rift Zone and many other places. The survey would then consist of both roving and static data. A person with a kinematic GPS would move between sites while the GPS is on roving and do a sixty second static survey at each benchmark. The data is then brought back and reduced to find position using reference stations, which are established with static GPS. The results are then compared with levelling data to demonstrate kinematic GPS precision and to detect deflation and inflation. The data is also used to find differences in position that could show extension. The results are capable of centimeter to millimeter range precision in location.

MATHEMATICS

APPLIED MATHEMATICS

A6-SAT

PERMUTATIONS IN CONCATENATED ZIGZAG CODES

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Coding theory is a branch of mathematics, computer science, and electrical engineering that explores the transmission of information across noisy channels. Coding theory is used in data transmission, data storage, and telecommunications. The focus of this project is on concatenated zigzag codes, which are constructed using various permutations. We are studying the effects of permutations on the error-correcting capabilities of the coding scheme. In conjunction, we explore the behavior of average dispersion in order to further our understanding of randomness of a permutation and find correspondence with error-correction.

A11-SAT

DISCRETE GRAPH APPROACHES TO NETWORK VULNERABILITY DETECTION

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We investigate the problem of identifying vulnerabilities in electric power grid networks. An ideal power network avoids blackouts when any set of k connections in the network is removed, but testing this condition on a realistic network is computationally intractable for k larger than one. Instead, we focus on the related problem of finding critical connections in networks using a discrete graph model. A polynomial-time relaxation of the NP-hard inhibiting bisection problem is used to find vulnerable areas. The inhibiting bisection problem is to find a separation of a network into two disjoint components, with a restriction on the number of edges removed to form the separation. We compare different methods of finding optimal parameter values. Using the standard IEEE 30 and 118 bus systems as test cases, we find that a binary search is more efficient than a modified secant method when finding optimal parameter values. We analyze the frequencies of edges removed in bisections. We postulate that edges removed more frequently are more critical to the network. If this is the case, these edges can be used as candidates for the problem of finding the k most damaging edges in a network, cutting down significantly on the number of edges needed to check in an enumeration. Initial tests find a positive correlation between individual edges found frequently in bisections and those causing the most damage when removed from a network. With further analysis, we aim to find general rules for damage caused by sets of edges occurring together.

A6-FRI

A MATHEMATICAL MODEL OF POLITICAL AFFILIATIONS

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This work explores voting trends by analyzing how individuals form their political affiliations during a presidential campaign. Using a variation of the traditional epidemiological model, we construct an ODE model that represents the transition of potential voters through various levels of political interest in either the Republican or Democratic Party. We analyze variations of our model to understand the impact of various interactions between potential voters, such as those between politically-charged and apathetic individuals during a presidential campaign. Finally, we calculate and interpret threshold values to determine the stability of the steady state solution.

A14-SAT

DIMENSION REDUCTION OF GENE EXPRESSION DATA FOR SURVIVAL PREDICTION: SIMULATION AND REAL DATA ANALYSIS

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DNA microarrays are used in cancer research to collect patient's gene expression profiles. An important statistical problem is to link gene expression data to phenotypic aspects of a patient's disease. Our research pertains specifically to using a patient's gene expression data to predict survival probability. This type of statistical analysis is challenging because gene expression data is

very high dimensional ($N << p$) and death time is subject to right censoring. The general procedure for this type of modeling followed in the literature is dimension reduction of gene expression data followed by Cox proportional hazards regression on the reduced data and patient survival times for a survival analysis. This paper provides a comparison of the effectiveness of several dimension reduction techniques using simulated data. We compared principle components analysis (PCA), partial least squares (PLS), and a modified partial least squares (MPLS) proposed by Nyugen, 2005. Furthermore we looked at the results of those techniques in conjunction with a fourth: sliced inverse regression (SIR). Using real data, we determined which particular gene expressions each method considered to be most important in predicting survival time and whether the methods agreed. The results based on simulated data show that PLS outperforms PCA when the number of genes p is large. Furthermore, MPLS does not perform significantly better than PLS. SIR, in combination with the other dimension reduction techniques, improves them. The results based on real data are forthcoming.

A13-SAT

EXTENDING THE VIOLA-JONES FACE DETECTION METHOD TO THE DETECTION OF CARS

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We design a visual car detection program based on the Viola-Jones face detection algorithm, a method proven successful in rapidly identifying faces from video images. We construct the shape, size, and position of several visual detection windows, called operators, which are used to classify images as either cars or non-cars. Each of the detection windows are considered to be weak operators, as no single operator is without fairly high error rate. Using the AdaBoost algorithm, we weight all weak classifiers by testing individual effectiveness on a database of cars and non-cars. We combine the weak classifiers to form a strong classifier which can then be used to scan large images and identify cars from the rear. These findings will be used to improve the functionality of an autonomous (driverless) car—The Spirit of Berlin—in the 2007 Urban Grand Challenge.

A8-FRI

SUPERNOVA RECOGNITION THROUGH ADAPTIVE CONSTRAINT REDUCTION OF SUPPORT VECTOR MACHINES

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The support vector machine (SVM) is a common data classification technique. Data are nonlinearly classified into two categories through the use of the "kernel trick." If the data are stored as vectors in a high-dimensional space, the kernel represents a function that maps these vectors to a higher space where the classification can be done linearly. SVMs typically use data with known classification to "train" so that the method can then be used to classify new data. Supernova recognition is an area of research that requires extensive data classification. Currently, standard SVM techniques are used for this purpose. In this paper, we investigate a new adaptive constraint reduction (ACR) method for training SVMs. This method was developed to reduce SVM training times by adaptively choosing a subset of data points as support vectors. We classify type Ia supernova data using a standard SVM technique as well as the new ACR version. We perform an analysis of the parameter dependency of SVM. We also explore the use of different kernel types using both methods. We analyze the methods by training them with data sets of various sizes and testing them on two different sets of known data. We then compare the false/true positive/negative rates and training times of each method. The objective is to reduce the training times while maintaining high accuracy.

A14-FRI

POSITIVE LYAPUNOV EXPONENTS OF THE DOUBLE PENDULUM

Analee Miranda, Yuri Lvov. *Rensselaer Polytechnic Institute, Troy, N.Y.*

The chaotic behavior of a system with bounded trajectories is closely related to the systems initial conditions. This sensitive dependence to initial conditions can be quantitatively described by a lyapunov exponent. Systems with negative or zero lyapunov exponents display quasiperiodic or periodic orbits (respectively), while systems with highly positive lyapunov exponents display chaotic orbits. The aim of this work is to quantitatively and qualitatively describe the chaotic behavior of a double pendulum system. Using numerical methods, the initial conditions that yield positive lyapunov exponents are found. The lyapunov spectrum is then mapped and an estimate the entropy of the system is determined. Additionally, simulations of the pendulum's motion, using initial conditions found to yield highly positive lyapunov exponents, are observed in order to qualitatively describe the systems behavior.

A12-SAT

MIXING POPULATION EFFECT DURING A SINGLE EPIDEMIC OUTBREAK

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In recent years, communicable diseases, such as avian influenza and SARS, have shaped our public health policies. The most deadly pandemic in recent history is the 1918 to 1919 originated Spanish flu virus, which killed about 50 million people worldwide. In the event that this strain reappears, or a different mutation develops, it is important to understand the dynamics of the disease. In this report, we consider mathematical models to study the effects of the mixing parameters on the final epidemic size. We first consider a model with only one population that only interacts with itself. For the second case, we consider two different interacting populations to study its effects in the final size epidemic. In this case, our transmission coefficients are proportionate to each other. To demonstrate our analysis we consider data from the 1918 fall wave the cities of Montreal and Winnipeg in Canada.

A10-FRI

A COST ANALYSIS OF HUMANPAPILLOMAVIRUS: INDIVIDUAL EDUCATION VS. MASS MEDIA CAMPAIGN

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Human papillomavirus (HPV), a common sexually transmitted virus, contains a group of more than 100 viruses, some of which (called "high-risk" oncogenic or carcinogenic HPV) are associated with certain types of cancer. HPV 16 and 18 cause approximately 70% of all cervical cancer. An estimated 11,150 new cases of cervical cancer will develop in the U.S. in 2007. In 2006, the FDA approved the first vaccine to prevent cervical cancer, designated for females ages 9 to 26, called GARDASIL. Studies have indicated GARDASIL has a 95% to 100% success against HPV types 6, 11, 16, and 18. Many studies have shown that there exists a lack of HPV awareness, as well as knowledge of causes, effects and preventive measures. In this study we compare two strategies for controlling the spread of carcinogenic HPV in the population, while minimizing cost. The research is conducted via a cost analysis of a mandatory vaccination policy vs. a mass media awareness campaign, each individually modeled with a system of differential equations. Mandatory (but not universal) vaccination includes individual-based education at the time of vaccination only, while the mass media campaign is assumed to be ongoing. In both cases the education influences females to get vaccinated and/or reduce their sexual activity, but is of limited duration. We use qualitative analysis to derive the respective control reproductive numbers, and numerical analysis to obtain the total costs of vaccination, education, and expected cancer treatment costs for infected females in both models.

A7-FRI

COPS AND STOPS: RACIAL PROFILING AND A STATISTICAL ANALYSIS OF LOS ANGELES POLICE DEPARTMENT TRAFFIC STOPS AND SEARCHES

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With data collection efforts underway in over 45 states, racial profiling in police practice is an issue of national concern. This study focuses on Los Angeles because of its diverse racial composition and the large quantity of data collected by the Los Angeles Police Department. Under a consent decree with the U.S. Department of Justice, the Los Angeles Police Department is required to make this data available. Using records for over 600,000 traffic stops, we analyze racial disparities found in stop and search rates. Logistic regression models are used to determine which variables are significantly related to disparities in search rates and other police practices. Based on our findings, the possibility of racial profiling cannot be ruled out.

A9-FRI

SIS HOUSEHOLD MODEL WITH TARGETED TREATMENT

Samuel Potter[1], Isaac Michaud[2]. *[1]University of Minnesota, Morris, Morris, Minn., [2]University of Maine, Orono, Maine.*

SIS epidemiological household model is studied to understand the dynamics of targeted treatment. The household model splits the population into households, which may, for example, represent patches within a landscape or dorms within a school. Interactions between households occur at a much lower rate than intra-household interactions. In an agricultural setting, households are crop fields that can be infected with insect pests. Plants will recover when insecticide is applied and the insects on them are killed. Rather than using a fixed per-capita recovery or treatment rate, an individual's treatment rate will be a function of the infection level in that individual's household. This allows for targeted treatment directed towards households

with larger infections. A model is developed and a moment-closure approximation approach is used to truncate the resulting infinite system of differential equations. Numerical results from the truncated system are computed and compared to stochastic simulations. It was found that targeted treatment does not change the endemic equilibrium when the population-wide treatment rate is controlled. Surprisingly, targeted treatment decreases the amount of time it takes to reach the steady state, which could be detrimental during an epidemic.

A9-SAT

A MATHEMATICAL MODEL OF THE *DROSOPHILA* HEART

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The heart of *Drosophila melanogaster* is a tubular organ that contains two types of excitable cells which work together to pump hemolymph through the body. At the cellular level, specific ion channels involved in the heartbeat of *Drosophila* have been identified and studied using genetic mutations and pharmacological agents. In this work the *Drosophila* heart is modeled as a network of excitable cells in order to explore the biophysical mechanisms underlying the generation of the heartbeat. The model cells are arranged in a tubular shape to form a network connected by gap junctions. Pacemaker cells with an intrinsic rhythm are added at one end of the network model and generate a wave of contraction down the heart. Using the model, channel kinetics is manipulated to explore the effects of different channels on *Drosophila* heartbeat. Model results are compared to experimental data.

A13-FRI

COMPUTER EXPERIMENTS FOR FUNCTION APPROXIMATIONS

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Computer simulations are essential tools in modern science and engineering. A computer simulation can be viewed as a function evaluation at a point in a parameter space. For complex models, such function evaluations can be very time-consuming. It is then of paramount importance to intelligently choose a relatively small set of sample points in the parameter space at which to evaluate the given function, and then use this information to construct a surrogate function that is close to the original function and is inexpensive to evaluate. The objective of this study is to develop a robust and cost-effective methodology for approximating functions having characteristics that are often encountered in practice, such as linearity, continuity, monotonicity, bounded first derivative, and at most two-way interaction. This study is divided into two parts. In the first part, we compare and contrast different combinations of four experimental design methods and two function approximation methods in terms of efficiency and accuracy for the types of functions mentioned above. The sampling methods used are Monte-Carlo, quasi-random LP-tau, maximin latin hypercubes, and orthogonal-array-based latin hypercubes. The function approximation methods utilized are multivariate adaptive regression splines (MARS) and support vector machines (SVM). The second part of the study focuses on adaptive sampling methods with the ultimate goal of developing an improved methodology for generating function approximations.

A12-FRI

SENSITIVITY ANALYSIS OF MATHEMATICAL MODELS OF BLOOD FLOW AND PRESSURE REGULATION

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Cardiovascular circulation in the human body represents a complex system concerning factors such as blood flow, pressure, velocity, and resistance. While this system is involved in the development and progression of human diseases, its many dynamics are still poorly understood. A seven-compartment model of sympathetic and cerebral blood circulation exists to simulate the cardiovascular system, but the sensitivities of its many parameters are unfortunately unknown. The goal of our research is to apply the process of sensitivity analysis on two simplified Windkessel models of blood flow, interpret the results of this analysis, and then use this information to optimize all parameters and improve the solutions of both models. Through these simplified applications, we develop a procedure to analyze the sensitivity and improve the results of the entire seven-compartment model. Our first application investigates the three-parameter, single equation Windkessel model of blood circulation. After computing and ranking the sensitivity information for this system, all three parameters are then optimized using a Nelder-Mead algorithm. This same process is then applied to a five parameter, two equation Windkessel model of blood circulation. Due to the complexity of this system, certain sensitivity information must be ranked through an eigenvalue decomposition using QR factorization. Based on the procedures developed through the analysis of the Windkessel models, the sensitivity information of

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the seven-compartment model is also ranked and calculated. Researchers will now be able to use this sensitivity information to improve the seven-compartment model and achieve a better understanding of cardiovascular circulation in the human body.

A10-SAT

CATS PROTECTING BIRDS: IN SPACE

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The mesopredator release hypothesis (MRH) suggests that in the absence of large, dominant predators, a population of smaller predators increases and, in the process, generates a decline in the prey community. The MRH has been used in attempts to comprehend problems involving the management of introduced species in islands and the extinction or declination of superpredators in an ecosystem due to anthropogenic pressures. The dynamics of this system was studied using a spatial-explicit model with mean field and pair approximations. We included mathematical analysis of the mean field model as well as numerical analysis for both approximations. The analytical results were compared with spatial simulations of the superpredator-mesopredator-prey system. Spatial structure is a valuable and complex tool for studying such phenomena occurring in nature.

A7-SAT

STUDY OF ADAPTIVE QUADRATURES FOR A MODEL OF FLOW-STRUCTURE INTERACTION

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Polymers are long chain molecules that can be natural or synthetic, such as DNA or plastic. Processed in a liquid state, the interaction of the polymeric structure with the processing flow ultimately determines the properties of these soft materials. Computer simulation of these complex fluids plays a crucial role in understanding fundamental aspects of these systems as well as in aiding the design of new polymeric materials. However, the computation of coupled flow-polymer models that faithfully represent the physics of these complex fluids is an enormous challenge. In this work we employ a field theoretic model that accurately accounts for the flow-structure interaction. Specifically, we focus our work in one of the computational bottlenecks of this model: the evaluation of high dimensional integrals. Given the high volume of these integrals that need to be computed, finding an efficient method for solving them is of high priority. Using error analysis and numerical experimentation, we examine the efficiency of several adaptive quadratures and rank them according to their performance when applied to integrands that have the expected structure of the flow-polymer system.

A11-FRI

A DYNAMICAL INTERPRETATION OF THE THREE-STRIKES LAW

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California's Three-Strikes Law has been in effect since 1994. Advocates of this policy claim it acts as a deterrent for violent crime; yet critics allege it solely acts as an incapacitant—a device used to segregate a population of "undesirables" from the total population in an attempt to lower criminal susceptibility. To determine the true relationship between these two intimately connected phenomena, we construct a dynamical model of the Three-Strikes Law within the framework of inner-city communities located in Los Angeles County. We then compare this model to one of Los Angeles County before California implemented the Three-Strike policy—the classical incarceration model. Through qualitative analysis we determine the basic reproductive number, R_0, for each of the models. Using numerical simulations, we then determine the net change in the total population of reformed inmates and the total number of incarcerated individuals due to the Three-Strikes Law. We also analyze the impact of population density on crime rates in states that utilize the Three-Strikes Law. Finally, we construct and examine a hypothetical One-Strike model to determine the impact of different strike policies on the reformed and incarcerated populations.

A8-SAT

ADAPTIVE PARAMETER SELECTION FOR MINIMIZING THE KOHN-SHAM EQUATION

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Within density functional theory, the electronic ground state, which is determined by the corresponding wave function, is given by the minimum of the energy function and can be obtained by minimizing the Kohn-Sham (KS) total energy functional. Knowing these wave functions allows the determination of the electronic properties of materials. Several iterative algorithms have been designed to minimize this functional. One of the most commonly used is the Self Consistent Field (SCF) iteration. Recently, a new method for solving for the lowest energy state has been developed called the direct constrained minimization (DCM) algorithm. In addition, a version of DCM which includes a restriction on the neighborhood where the KS functional (trust region DCM) is minimized has been shown to converge for all tested molecular systems given a sufficiently small trust region. In this paper, we analyze and compare the SCF and DCM algorithms, as well as the trust region DCM, using three study cases (Silicon Bulk, SiH4, and Quantum Dot). For each system, run times, final energy results, and respective convergence criteria are compared. We develop and test rules for adaptively selecting parameter values in each of the algorithms to improve their rates of convergence.

A15-FRI

A MATHEMATICAL MODLE OF HIV AND MALARIA CO-INFECTION IN SUB-SAHARAN AFRICA

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Malaria and HIV are two of the most deadly diseases in Africa. Combined they account for 4 million deaths each year, and according to the Center for Disease Control and Prevention (CDC), there is an estimated 5 percent increase in malaria deaths due to HIV infection in Sub-Saharan Africa. Since the co-infection was discovered, malaria saw a 28 percent increase in prevalence and the death rates nearly doubled when an individual was infected with both diseases compared to either separately. We propose a system of differential equations linking the host-vector system of malaria with co-infection by HIV. We acquire data from Sub-Saharan Africa in general and Malawi in particular, where co-infection from both diseases is known to exist, and investigate the behavior of our model through stability analysis and numerical solutions.

GENERAL MATHEMATICS

A16-FRI

THE CURSED DUET: DYNAMICS OF HIV-TB CO-INFECTION IN SOUTH AFRICA

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There is an increasing public health concern for the HIV pandemic coupled with high tuberculosis (TB) prevalence in South Africa. The progression of these infectious diseases compliments each other to produce a deadly synergistic effect. We use an epidemiological model to explore the co-infection transmission dynamics of HIV-TB in South Africa, specifically in adults aged 15 to 49. We analyze our model to gauge the extent to which the HIV epidemic accentuates the TB epidemic. Will the TB I epidemic persist without the presence or prevalence of the HIV epidemic in South Africa? Some of our parameter values are estimated from demographic data. We define a basic reproductive number, *R*0, for the number of secondary cases that one infected individual will cause through the duration of the infectious period of the HIV-TB epidemic based on the local stability of the disease-free equilibrium. Uncertainty and sensitivity analyses are performed.

A15-SAT

MATHEMATICAL MODELS OF REPTILE POPULATIONS USING DELAY DIFFERENTIAL EQUATIONS

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A well-known phenomenon among reptile species is temperature-dependent sex determination (TSD) in which the temperature of egg incubation determines the sex of the hatchlings. We develop a delay differential equation (DDE) model describing the nesting habits of Alligator mississippiensis; the delay accounts for some of the dependence of birth and death rates on the age of the population members. We solve our model numerically using a modified Runge-Kutta solver in Matlab and obtain physical

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results. We compare these results to both a previous ODE model by Murray (2002) in which the age dependence of parameters is ignored. We also compare ours with a PDE model of Woodward and Murray (1993) in which a continuous age-structure is taken into account, but the complexity of the model precludes straightforward analysis of stable points. We are able to reasonably account for age structure in the population while finding equilibria and determining their stability. Additionally, we use the DDE model to investigate the effects of catastrophe on the population. Finally we modify the model to describe a sea turtle population with TSD.

PURE MATHEMATICS

A17-FRI
CYCLOIDS: THEIR GEOMETRIC AND ALGEBRAIC ASPECTS
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Cycloids, or curves defined by the path of a point on a circle rolling along a straight line, have been studied since the 14th Century, by many famous scientists such as Wren, Torricelli, and Galileo. Commonly known as spirographs, cycloids have appealing geometric realizations. The idea of tracing a fixed point on a rolling circle leads to the contraction of other curves, such as hypocycloids and epicycloids. A hypocycloid *H* (*A, B*) is generated if a rolling circle of radius *B* rolls around the inside of a larger circle of radius *A*, while an epicycloid *E*(*A, B*) is obtained when the rolling circle is rotated around the outside of the larger circle. An interesting question is to determine the relationship between the radii *A* and *B*. On this aspect, our study focuses on the condition that both *A* and *B* are integers. We show that *H* (*A, B*) and *H* (*A, A - B*) generate the same curve with opposite orientations; we also show that *H* (*A, B*) is self-crossed if and only if *B* or (*A - B*) does not divide *A*. Similar result holds for epicycloids. Furthermore, we define a correspondence between hypocycloids and the rings $\boldsymbol{Z}_n$. Preliminary results indicate that by using the curves *H* (*n, B*) as geometric representations, we can visualize the operations on $\boldsymbol{Z}_n$, some useful properties (such as orders of elements, multiplicative inverses, and so on), substructures, and homomorphisms of $\boldsymbol{Z}_n$. Further results are expected if time permits. (Supported by USDE #P217.)

A16-SAT
SYNCING UP WITH THE QUINN-RAND-STROGATZ CONSTANT: THE ROLE OF HURWITZ-ZETA ZEROS IN NONLINEAR PHYSICS
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This work extends the analytical and computational investigation of the Quinn-Rand-Strogatz (QRS) constants from non-linear physics. The QRS constants (c1, c2, ... , cN) are found in a Winfree oscillator mean-field system used to examine the transition of coupled oscillators as they lose synchronization. The constants are part of an asymptotic expansion for large N of a function related to the oscillator synchronization. There is interest in determining the exact values of these constants. Previous work used high-precision computer programs to evaluate c1 to 42 decimal-digits, which made it possible to recognize and prove that c1 was the root of a Hurwitz-zeta function. This allowed a value of c2 to be conjectured in terms of c1. In our work we compute the values of subsequent constants (c3, c4, etc.) to 42-digit precision by extending an algorithm developed by D.H. Bailey, J.M. Borwein and R.E. Crandall. The values of these constants are used to aid in the recognition of a relationship between the computed values. The conjectured relationships can then help provide an analytical proof of the value of cN for arbitrary N. Furthermore, we investigate alternative analytic and computational methods for finding the constants.

PHYSICS

A5-SAT
ELASTIC RESPONSE OF SINGLE STRANDED NUCLEIC ACIDS TO SHARP BENDS
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We investigate the elastic energy to sharp bends, in particular, the question of whether DNA and RNA behave differently. To do this we look at the stability of polynucleotide hairpins. A hairpin is composed of a single nucleic acid strand folded back on itself and is comprised of two parts, a self-complimentary sequence, the stem, and a short connective region, the loop with varying length (1 to 5 nucleoties). The stem stabilizes the hairpin through intramolecular base-pair binding, while the loop destabilizes the structure by contributing both an entropic and elastic energy term. The transition from hairpin to random-coil is driven by heating; the temperature at which 50% of the molecules are found in a hairpin conformation and 50% exist as random

coils is known as the melting temperature (Tm). The conformational changes are explored by measuring the ultraviolet (UV) melting profile with the use of UV spectroscopy at varying temperatures. We propose a different approach from previous studies by fitting a modified Ising model that includes nucleotide base pairing and base unstacking. The obtained measurements indicate that for a sequence with constant stem nucleotide number and varying loop length, Tm varies significantly with the size of the loop. The goal of these experiments is to probe the mechanical response of nucleotides to sharp bends through modeling of the elastic term.

A4-SAT

IMPROVED IMAGE QUALITY IN AO-OCT THROUGH SYSTEM CHARCTERIZATION

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Optical coherence tomography (OCT) has become a fundamental tool in diagnosing and monitoring the treatment of human retinal disease and offers a considerable advantage in terms of cross sectional imaging, as compared to other leading imaging modalities. OCT provides high axial resolution, enabling retinal layers to be imaged; however, lateral resolution is limited by wavefront error. Combing adaptive optics (AO) with OCT improves lateral resolution allowing individual retinal structures to be imaged. Imperfections in AO correction will limit the image contrast of those structures, in particular calibration errors, which are not seen by the wavefront sensor. We have introduced a Far-field imaging camera which captures real-time images of the PSF, that can be compared to the simultaneous wavefront measurements made by the AO system. The wavefront measurements, produced by the Far-field imaging camera, are used to simulate the PSF for comparison with the experimental data and to estimate the calibration error of the wavefront sensor. The results from the comparison between the experimental data and our simulated PSF are presented, as well as our estimates of the calibration errors. These results will allow us to better understand calibration error and also see how measured residual errors affect OCT image quality. Using the calibration error estimations mitigation techniques can be investigated in order to improve the performance of the AO-OCT systems.

A5-FRI

RESPONSE OF FOAM TO SHEAR

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Aqueous foam (gas bubbles with fluid walls) has a range of interesting responses to applied shear. For small stresses, the foam acts like a solid. As the stress increases, the foam will flow. The flow occurs through rearrangements of the bubbles. An interesting question is whether or not these rearrangements generate the equivalent of molecular diffusion, only for the bubbles. In order to study the effects of shear on the bubble rearrangements, we use a system of bubbles floating on the water surface that are driven by parallel bands. We hope to shed light on the impact of applied stresses on the shear induced rearrangements of bubbles not just in foam, but in a range of other complex materials, including granular matter and colloids.

A4-FRI

USING GPS RADIO OCCULTATION SOUNDINGS TO STUDY MESOSCALE CONVECTIVE SYSTEMS

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Mesoscale convective systems, or MCSs, formed particularly in the mid latitudes, are responsible for a great deal of damage especially in the summer time. These systems are hard to forecast since most observing systems do not provide reliable data inside these storms. In this study we use high vertical resolution GPS radio occultation (RO) data to investigate the vertical structure of temperature and water vapor in these destructive storms. We examine GPS RO data from the Constellation Observing System for Meteorology, Ionosphere, and Climate (COSMIC) that occur inside MCSs in North America between May and August 2006 and April and July 2007. Data from rawinsondes and numerical weather prediction analyses are used to validate the RO sounding data. From the results of several case studies, there is no evidence that MCSs elevate the tropopause, but they do excite gravity waves above it. There is also some evidence of small temperature inversions below the tropopause.

SOCIAL AND BEHAVIORAL SCIENCE

EDUCATION

A17-SAT

ASSESSMENT TO INFORM PROGRAMING TO INCREASE CANCER SCREENING IN NATIVE HAWAIIAN HOMESTEAD COMMUNITIES

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According to Fong et al., 2003, and the Intercultural Cancer Council (ICC, 2001), Native Hawaiians, who comprise 20% of the state of Hawaii's population, have the lowest life expectancy and are underserved in access to health and social services. The purpose of this project is to find out if a cancer screening day and other educational activities would be both desirable and useful in the Waimanalo Native Hawaiian Homestead Community and to assess barriers and facilitators to cancer screening. The hypothesis is that a cancer screening day and other educational activities would be desirable in the Waimanalo Native Hawaiian Homestead Community. To assess this question 50% (322) of the households (644) of the Waimanalo Native Hawaiian Homestead Community are to be surveyed. The survey includes questions on general health, knowledge of cancer, education, and whether activities aimed at helping to reduce cancer among Hawaiians would be desired. Presently, 228 of the 322 homes have been visited and 174 agreed to participate. The results of the completed surveys, analyzed by SPSS statistics, showed that the residents of the Waimanalo Native Hawaiian Homestead Community would like to see a cancer-screening day (74% favor) and other educational activities. The barriers and facilitators to cancer screening were also found. The final results of the Ke Ola Mamo Native Hawaiian Assessment will not be available until December 2007. (Supported by USDE # P217A030070 and the National Cancer Institute # 3U01CA114630-02S2.)

GENERAL SOCIAL AND BEHAVIORAL SCIENCE

A23-SAT

PROFILE OF THE LONG TERM CARE REGISTERED NURSE IN VERMONT

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Work dissatisfaction and turnover continue to contribute to a serious nursing shortage, especially in long term care facilities. Little research has been conducted which examines demographics, satisfaction, and intent to leave of the long term care registered nurse. We conducted a survey of 301 registered nurses working in long term care facilities in rural Vermont. Statistical (t-tests and chi square analyses) and descriptive statistics will be presented. Conclusions of this study will inform retention and recruitment initiatives for registered nurses in long term care facilities which are necessary to meet the growing need of our aging society.

A25-SAT

THE COLLEGIATE CANCER COUNCIL OF THE INTERCULTURAL CANCER COUNCIL

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The goals of the Collegiate Cancer Council (CCC) are to: (1) educate the public (primarily the college/university student audience) about cancer prevention and associated health disparities; (2) influence policy to reduce cancer morbidity, mortality, and health disparities; and (3) promote careers in cancer control among all college/university students and disciplines. Keeping in mind the intercultural/multicultural aspects of our communities, student leaders established the CCC as a college-based cancer control initiative while participating in the student-mentoring track of the 2004 Biennial Symposium on Minorities, the Underserved & Cancer. The Intercultural Cancer Council and C-Change: Collaborating to Conquer Cancer organizations have sponsored summer internships through which CCC participants have developed a well-formulated step-by-step toolkit (available by CD and on the web) to help establish a CCC chapter on campus. C-Change and the National Partnership for Comprehensive Cancer Control have actively promoted the CCC to a national audience of state cancer control coalitions as well as private, public, and nonprofit cancer organizations. The University of Houston Charter Chapter of the CCC (www.uh.edu/cccatuh) has led and participated in over 13 cancer and health related events including educational activities, cancer career speakers groups, and community-based activities. Graduates have pursued careers and/or graduate studies in cancer related professions (medicine, public health, and social work). Two more universities have founded CCC chapters and at least 5 additional chapters are in process of being established across the U.S. In terms of sustainability, after being established,

CCCs require minimal financial support. CCCs thus represent an efficient and effective mechanism to promote careers in cancer control while engaging college/university students in community-based educational endeavors.

A24-SAT

7-3-3-1, HEALTHY FAMILIES HAVING FUN: AN AFTER-SCHOOL NUTRITION EDUCATION PROGRAM

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The *7-3-3-1: Healthy Families Having Fun* nutrition curriculum, developed by the University of Maryland, was adapted for implementation in our after-school setting and was used to encourage children to consume more fruits and vegetables and low-fat/non-fat milk, and to increase physical activity. The nutrition classes were implemented with children (5 to 12 years old) who participated in the after care program in Title I Elementary Schools in Prince George's County. A series of four lessons were conducted over a four-week period in each school. A parental education component was also developed to provide parents with knowledge about the nutrition topics being covered in the after-school lessons. Flyers were disseminated to parents on a weekly basis. The nutrition education program has been implemented in a total of 60 schools and has reached approximately 2,900 youth. A Pre-/Post-Assessment was used to measure the children's knowledge and behavioral changes. Approximately 62% of the children showed an increase in knowledge in choosing healthful snacks/beverages and identifying the recommended servings of each group in MyPyramid. In addition, approximately 45% showed positive behavioral changes or demonstrated intent to positively change their consumption of fruits and vegetables, low-fat/non-fat milk, and/or participation in physical activity.

A24-FRI

DEVELOPMENT OF A MOUSE MODEL OF POST TRAUMATIC STRESS DISORDER

Alexandria Bachicha, Kevin Caldwell, Andrea Allen. *University of New Mexico, Albuquerque, N.Mex.*

Post-traumatic stress disorder (PTSD) is a persistent emotional and physiologic response to a traumatic event such as war, physical or sexual abuse, or natural disaster. It is characterized by several symptoms including re-experiencing of the event, altered startle responses, depression, and irritability. Not every person who experiences a traumatic event will exhibit PTSD so it is important that predisposition to this disorder be studied. Several factors contributing to predisposition to PTSD have been identified including pre-trauma factors (e.g., environment, genes, and gender), trauma-related factors (e.g., severity, duration, and reaction to the situation during the trauma), and post-trauma factors (e.g., exposure to other traumatic events). Neurological dysfunction of the prefrontal cortex is an area that is currently of interest in examining its role in patients with PTSD. The present studies aimed to develop a mouse model of PTSD using exposure to rat odor (rat bedding in a clean rat cage) as the traumatic event. Preliminary results demonstrate that the model exhibits a cluster of symptoms related to PTSD. Compared to odor control mice, who were exposed to fresh bedding, odor-exposed mice showed impaired prepulse inhibition (PPI) of the startle response, indicating altered sensory gating, and increased learned helplessness, a laboratory model of depression. Control and odor exposed mice did not show differences in anxiety (light/dark box and open field/novel object) tests. This model of PTSD will be useful for future studies designed to identify factors which may predispose an animal to the development of PTSD-like behaviors. (Supported by NIH grant #GM060201-07.)

A19-FRI

PERSPECTIVES CONCERNING PREVENTION OF HEALTH PROBLEMS

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Our project examined the perspectives of hospital clients and personnel about prevention of health problems. We also surveyed residents from a low-income community served by the hospital who attended a health fair organized in collaboration with the hospital. We asked about what prevention meant to them, what specific health conditions they suffered from, and about their ideas and opinions of current and future strategies for prevention efforts. We conducted surveys, interviews, and an internationally validated food security survey. The data analysis revealed patterns of responses in terms of individual, socio-economic and environmental factors associated with health. The main conditions that both clients and hospital personnel frequently mentioned were asthma, cardiovascular disease (mainly hypertension), and gastroenteritis. Health fair participants identified asthma, cardiovascular diseases (mainly hypertension) and diabetes as the three major conditions they were suffering from. In addition, clients stated they would like to receive health promotion information by way of televised programs and ad campaigns and events. The results of the food security survey indicated that 45% of the health fair participants experienced food insecurity. Results from the study were presented to hospital and community audiences.

A26-SAT

CORRELATES OF METHAMPHETAMINE USE AMONG AMERICAN INDIANS

Sarah Brokenleg, Megan O'Brien. *University of Kansas, Lawrence, Kans.*

Methamphetamine (MA) use is a major public health concern in the United States. Rates of MA use are particularly high among American Indians. This study seeks to describe characteristics of American Indian methamphetamine users in the United States. Our main findings indicate that American Indians are 1 to 2 times more likely to have ever used MA than Whites. Alcohol dependence is strongly associated with methamphetamine use among American Indians. Analysis of past year users revealed similar patterns to lifetime users. Future studies will further describe these associations and apply advanced statistical techniques to account for the small sample size.

A22-SAT

HURRICANE AND TROPICAL STORM IMPACTS OVER THE SOUTH FLORIDA METROPOLITAN AREA: MORTALITY AND GOVERNMENT

Ian Carlos Colon Pagan. *Universidad de Puerto Rico, San Juan, P.R.*

Since 1985, the South Florida Metropolitan area (SFMA), which covers the counties of Miami-Dade, Broward, and Palm Beach, has been directly affected by 9 tropical cyclones: four tropical storms and 5 hurricanes. This continuous hurricane and tropical storm activity has awakened the conscience of the communities, government, and private sector, about the social vulnerability, in terms of age, gender, ethnicity, and others. Several factors have also been significant enough to affect the vulnerability of the South Florida Metropolitan area, like its geographic location which is at the western part of the Atlantic hurricane track, with a surface area of 6,137 square miles, and elevation of 15 feet. And second, from the 2006 Census estimate, this metropolitan area is the 7th most populous area in the U.S. supporting almost 1,571 individuals per square mile. Mortality levels due to hurricanes and tropical storms have fluctuated over the last 21 years without any signal of a complete reduction, a phenomenon that can be related to both physical characteristics of the storms and government actions. Results reflect a lack of focus on hurricane and tropical storm related themes, while a decrease in funding can be the consequence of less interest and much more attention on less probable hazards with a long term recovery period. Even though the government has an important role in hurricanes and tropical storms mitigation, some of the main ideas to decrease mortality are focused in networking between private and public sector and the understanding of self-vulnerability of each individual.

A21-SAT

EVALUATION OF HOME BASED COLORECTAL CANCER EDUCATION METHODS AMONG HISPANICS

Avigail Galvan[1,2], Ilda Islas[1], Gloria Coronado[1], Ruby Godina[1], Genoveva Ibarra[1], Beti Thompson[1]. [1]*Fred Hutchinson Cancer Research Center, Seattle, Wash.,* [2]*Heritage University, Toppenish, Wash.*

Colorectal cancer is the second most common cancer in the U.S. Hispanics are more likely than non-Hispanics whites to be diagnosed with later stages of colorectal cancer and are less likely to receive regular screening tests. One strategy to promote colorectal cancer screening is home health parties, which are home-based, promotora-led education sessions about a given health topics. The aim of the study is to determine if Hispanics are more likely to receive cancer screening tests after participating in a home health party. The study uses a pre-test/post-test (6 months later) design. In person interviews are conducted among individual aged 50 to 79 who participate in a home health party. Follow-up telephone interviews are conducted 6 months after the baseline survey. Survey items include screening practices, knowledge and attitudes about colorectal cancer, and demographic characteristics. A total of 143 follow up surveys have been completed. The results show that 25% of participants received fecal occult blood testing (FOBT) or colonoscopy after attending the home health party and of those who had not yet received screening, over 20% had made a clinic appointment to receive an FOBT. The findings demonstrate that home parties are an effective method of increasing rates of colorectal cancer screening among Hispanics in rural communities.

A21-FRI

CALIFORNIA'S PUBLIC HEALTH SYSTEM POST-9/11

Sara Garcia. *University of California, Davis, Davis, Calif.*

This presentation aims to present research on the status of the California public health system with a focus on California Public Health Laboratories in the post-9/11 era. This research details California's ability, post-9/11, to address potential attacks of bio-terrorism, flu pandemics, and other public health crisis. Furthermore, it details California's response to developing qualified teams of scientists with expertise in microbiology and molecular science fields. Due to a shortage of Microbiologists and other laboratory scientists, California is funding a new initiative designed to prepare graduate students for work in California Public Health Laboratories as Assistant Public Health Laboratory Directors that will eventually lead to the position of Public Health

Laboratory Director. With a population of nearly 35 million people and only 39 understaffed Public Health Laboratories, the State of California is taking a necessary step in addressing one of the many faults in the California public health system. Surveys are currently being conducted to determine the capabilities of each California Public Health Laboratory and the manner in which they recruit qualified employees. Internet research is also in progress to compile information regarding the status of California Public Health Laboratories and the California public health system in general. The expected result of this investigation is to find the state of the California public health system to be disorganized and ineffective in the event of a major public health crisis. This may be attributed to understaffed and insufficient facilities, a decentralized infrastructure, and a severe shortage of qualified scientists.

A20-SAT

FROM SPACE FLIGHT TO FORESIGHT: EXPLORING THE SOCIAL MOVEMENT SPILLOVER BETWEEN SPACE AND NANOTECHNOLOGY

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This ongoing research investigates the connections between the 1970s pro-space movement and the 1980s pro-nano movement, two important pro-technology social movements, in order to discover what evoked public imagination about nanotechnology. We postulate that the advocates of the 1970s pro-space movement dominated the public impression of nanotechnology when it began in the 1980s. Once such case study of this social movement spillover is the space elevator endeavor through data analysis of numerous texts including primary source materials from relevant social movement organizations and interviews with individuals from the target population. Preliminary findings showed commonality of histories by network entrepreneurs during these periods. Hence, we speculate that shared people, ideologies, and resources paved the way for the social movement spillover between pro-space and pro-nano movements.

A18-FRI

AUDIENCE SURVEYS AND GIS: LOOKING AT PATTERNS OF CONNECTION TO THE KLAMATH RIVER THROUGH SPATIAL ANALYSIS

Adriana Guzman. *Humboldt State University, Arcata, Calif.*

This study combines geographic information systems (GIS) with survey research by analyzing place attachment to the Klamath River in northern California. Objectives were to analyze people's strength of connection to the river compared to where they reside and illustrate how GIS can enhance the survey results through visualization of analysis. My hypotheses were that people living closer to the river would feel more connected to it and that socio-demographics would also predict how connected individuals feel to the river. Methodology included spatial analysis and surveying audiences learning about river issues. When comparing residence and strength of connection to the river, linear regression analysis showed no significant difference for two out of the three survey locations. GIS mapping visually revealed that patterns of connection can be due to similar patterns (similar colors) or large variations in those patterns (many random colors). GIS mapping also visually illustrated any unequal response rates for each location. ANOVA tests revealed that most socio-demographic characteristics could not predict an individuals' strength of connection to the river. Sample size issues may explain the one positive connection found. GIS mapping illustrates the geography of survey responses, occurrences of over or under representation in the sampling frame and visualization of important differences/patterns only maps can reveal. Statistical findings indicate that a strong conclusion cannot be drawn and variability in distance-connection patterns warrants further investigation. Other variables need to be taken into account such as sample size issues, the complex human-environment relationship, and people's reasoning for attachment to the landscape.

A25-FRI

SUPPORT IN HELPING THE INDIAN HEALTH SERVICE IN DELIVERING HIGH QUALITY HEALTH CARE TO OUR COMMUNITY

Alacea Head, Suzanne Christopher, Deborah Laveaux. *Montana State University, Bozeman, Mont.*

Messengers for Health is a community-based participatory research project with a goal to increase the proportion of women who receive cancer screenings. This talk will focus on the development of an advocacy program between community members and health care providers at the Indian Health Service. Recognizing that providers find themselves in a cross-cultural situation, we hope that this advocacy program will foster greater mutual understanding and respect, ultimately removing barriers to broader community involvement for all health care providers. Our goals are for health care providers in the Indian Health service to increase their knowledge of and sensitivity to the Native American traditional practices, to extend their cultural competence and learn spiritual and religious beliefs and practices of Native Americans, and to foster mutual understanding between IHS and the community. Community and university partners are going through a 15-step process to develop the

... continues on next page

advocate program. Steps include defining the process, ensure support from community members, to name the participants and the initiative, define the health provider pool, create the community member pool, and to identify roles and responsibilities for health care provider and community members.

A23-FRI

EVALUATION OF HOME HEALTH PARTIES TO IMPROVE DIABETES KNOWLEDGE AND MANAGEMENT PRACTICES

Cierra Mendoza[1,2], Henedina Tavares[1], Ilda Isles[1], Gloria Coronado[1], Beti Thompson[1], Ruby Godina[1], Genoveva Ibarra[1]. *[1]Fred Hutchinson Cancer Research Center, Seattle, Wash., [2]Heritage University, Toppenish, Wash.*

Hispanics in the United States are 1.9 times more likely than non-Hispanic Whites to have non-insulin dependent diabetes mellitus (type 2 diabetes). Little is known about effective interventions to improve diabetes awareness and self-management practices among Hispanics. The objective is to evaluate whether home health parties, which are promotora-led education sessions conducted in participants' homes, are effective in improving knowledge about diabetes self- and medical-management. Home health party participants were recruited at community events, grocery stores, and community churches. An in-person baseline interview was administered among home health party participants aged 18 and older and a follow-up telephone survey will be administered six months after the baseline. The questionnaire consists of items about diabetes knowledge, family history, dietary practices, and demographics. A total of 109 participants completed the baseline questionnaire. Over one-third (37%) of participants had diabetes, of which 57.5% had type 2. Over two-thirds (68%) of participants reported having a family member with diabetes. Among those with diabetes, 43% have had it for five or fewer years and nearly two-thirds (65%) had not had a foot exam in the last 12 months. Results also show that 60% believed that eating foods high in sugar is a cause of diabetes. The follow-up questionnaires are currently being conducted. Follow-up data showing changes in diabetes knowledge and management practices will be presented. Home health parties may be an effective strategy at improving diabetes knowledge and prevention among Hispanics.

A22-FRI

MIGRATION OF MEXICAN INDIGENOUS WOMEN FROM OAXACA

Nadia Merino. *San Diego State University, San Diego, Calif.*

The findings of research on the growing feminization of migration have revealed that women migrate for a variety of reasons; they migrate from one country to another on their own; their migration is facilitated by social networks; the migration may be of a new type, circular or transnational, instead of permanent or temporary; after arrival in the host country the women often engage in reproductive work; and, migration may have positive or negative effects/consequences for the women's status and gender roles. My research project is an exploratory investigation of Mexican immigrant women from the "new" sending region in Mexico, the state of Oaxaca. It seeks to interrogate the reasons, tools, nature, work, and consequences of migration for Oaxacan female migrants in the San Diego County. Data was obtained from Mexican immigrant women through interviews. In so doing, my project seeks to assess the applicability of recent findings of scholarly research to female migrants from Oaxaca. Women from this state have not been the specific foci/subjects of extensive research. The potential benefits of this study include contributing to the basic knowledge about immigrant women from Mexico and the feminization of migration.

A18-SAT

HEALTH: A COMMUNITY'S PRIORITY

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During the summer of 2007, the Institute of Interdisciplinary Research at the University of Puerto Rico in collaboration with the University of South Florida, offered a four-week internship to engage students in applied community-based research on public health issues. Fieldwork was conducted in a low-income rural community in order to obtain a local understanding of the relationships between "community health" and "individual health." We obtained our data using quantitative and qualitative methods including cultural mapping, surveys, focus groups, and individual interviews. Data showed that 31% of the 39 residents surveyed agreed that addiction to both drugs and alcohol was major factors that compromised community health. Forty-nine percent of participants also believed the group most affected by factors that compromised community health were its adolescent population. Focus groups with 5 adolescents between 17 and 22 years of age also revealed family concerns, lack of transportation and public safety as other factors that affected the overall health of their community. In addition, personal interviews were conducted with four adult residents that allowed us to gain a more in depth understanding of "community health" and its interrelation to their individual health. Collectively, the interdisciplinary approach taken in this investigative process allowed us to collect data that connected "community health" with social, economic, political, physiological, and environmental factors.

A26-FRI

EXPLORATORY PREFERENCE IN RATS: MEMORY FOR OBJECTS AND PLACE

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The aim of the present study was to develop a paradigm that can be used for object exploratory behavior in rats. In the present study, rats were tested in two versions of an object recognition task. Based on previous research, it was hypothesized that rats would exhibit a preference towards novel objects and target objects in novel locations. Seven male rats were habituated to an open field apparatus on 3 consecutive days (20 min/day). Following habituation, rats were tested in object and place tasks using a counterbalanced design. For the object task, rats were placed in the apparatus for 5 min with two identical objects (familiarization phase). Following a 3 min delay, rats were placed in the apparatus with one object replaced by a novel object (testing phase). Place testing followed the same procedure except one of the identical objects was moved to a new location. This procedure was repeated using different objects. Data were collected using an automated tracking system. A repeated measure ANOVA was used to evaluate the data. We found that animals exhibited a preference for the novel object and objects moved to a new location. Preference towards target objects varied during the initial 1 to 2 min of testing. In conclusion, rats exhibit preferences for novelty in object and place tasks. The complexity of target objects, and experience with objects prior to testing may be important. This testing paradigm will be used in future experiments to evaluate the behavioral effects of hippocampal damage following ischemic insult in rats.

A20-FRI

TUBERCULOSIS IN THE ROMA POPULATION OF SLOVAKIA (POSTER)

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The Roma population has experienced a history of marginalization which may impact the epidemiology of tuberculosis (TB) in their community. The aims of this study were to compare Roma and non-Roma TB cases according to demographic characteristics, describe the epidemiology of TB and identify predictors of treatment outcome in the Roma. A retrospective cohort study was conducted using data from surveillance records of 652 Roma and 5,949 non-Roma cases reported to the National TB Registry in Vyšné Hágy, Slovakia from 1999 to 2004. T-tests and Chi^2 tests for differences in demographic factors such as age, gender, site of primary infection, and year of report between Roma and non-Roma cases were conducted. Logistic regression was used to assess the relationship between demographic and psychosocial covariates and treatment outcome among Roma. Roma cases were significantly younger than non-Roma cases, more likely to be female and to have pulmonary TB (all $p < 0.05$). Twelve percent of Roma cases experienced treatment failure. Older age, history of TB, initial sputum-smear positivity, and being designated as asocial were associated with poorer treatment outcomes among Roma cases (all $p < 0.05$). There is a disproportionate burden of TB among Roma children. Treatment outcomes in the Roma population could be improved by detecting cases earlier, reducing the number of recurrent cases and understanding why Roma patients are characterized as asocial. This is the first study to describe TB in the Roma population. Further studies examining sociodemographic disparities among the Roma are warranted.

PSYCHOLOGY

A28-SAT

ACCULTURATION, ACCULTURATIVE STRESS, AND ACADEMIC SELF-ESTEEM AMONG LATINA/O COLLEGE STUDENTS

Marlyn Garcia, Donna Castañeda. *San Diego State University–Imperial Valley Campus, Calexico, Calif.*

Very little research is available that examines Latina/o college students' academic self-esteem, despite research with non Latinas/os that shows that higher academic self-esteem is related to higher academic achievement. The purpose of this study is to investigate the relationship between acculturation, acculturative stress, immigration status, and gender and academic self-esteem among 150 Latina/o community college students. The majority of Latinas/os who enter higher education do so through the community college system, thus, research on their academic experience in this system is important. Students filled out self-administered questionnaires in their classes. Result will be analyzed in mid-August using multiple regression. It is expected that those with higher acculturation, lower acculturative stress, born in the U.S., and men will have higher academic self-esteem. Results from this study may be useful in developing programs to help Latina/o students succeed in college.

B1-FRI

PIGEONS (COLUMBA LIVIA) RESPOND TO OBSERVE A CLOCK THAT SIGNALS IMMINENT REINFORCEMENT

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Behavioural studies are one of the oldest ramifications in psychology area, specifically experimental analysis of rats and pigeons, particularly old from early 20th century. These animals are exposed to different conditions and reinforcement schedules. The objective of this experiment was to determine if the pigeons would respond to obtain a stimulus that indicated the imminence of food reinforcement. This experiment had two conditions: during testing, a white-illuminated response key turned red when the pigeons peck it 10 s before the delivery of food. In the second condition, the response key turned red for 10 s on the first peck and never within 5 s of food. The time between feedings was not changed between training and testing. In this experiment the independent variable was the temporal association between the red light and food; the dependent variables, were the rates of responding to the red and white lights. When the association between red light and food was eliminated, responses to the red light decreased and responding to the white light first increased after then decreased. In conclusion, the association between red light and food maintain responding to the red light, but it is unknown why responding to the white light increased after this association was eliminated.

A2-FRI

IN HARMONY WITH SELF: IMPROVING SEXUAL HEALTH

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Montana reports low rates of sexually transmitted infections; however, some counties have rates three to five times higher than national rates. Many of these are reservation counties. Sexual health research is lacking in Native American communities. "In Harmony with Self: Improving Sexual Health" is part of the Montana Sexual Health project. The purpose of this project was to develop a set of questions for evaluating the role of mental and psychosocial health on sexual health and STI transmission for rural Native American peoples in Montana. A literature review was conducted of previous work in the area of mental and psychosocial health. Over 50 interviews with key informants were conducted. A content analysis of the interviews was conducted by the research team discovering key themes. Themes included: drugs, alcohol, family dynamics, and self esteem. This suggests that mental and psycho-social factors may influence sexual health and STI transmission among Montanans, including Native Americans. This co-occurrence has been ignored in Native American populations. We are now developing a survey to examine the role of mental and psycho-social factors on sexual health. Relevant questions have been drafted. Decisions made concerning the questions are meant to be culturally sensitive. The Mental Health section of the survey is a recent addition, as always, one hopes to cause as little distress to the participant as possible. The questions concerning sexual behavior, decisions, and experience are indeed a delicate subject. Future work includes administering this survey to reservations.

A27-FRI

PARENT-CHILD INTERACTION: A COMPARISON OF GENDER ROLES & GENDER EGALITARIAN ATTITUDES OF COLLEGE STUDENTS FROM SAME-SEX AND HETEROSEXUAL PARENT COUPLES

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It is the purpose of this research to test claims about the nature of parenting by homosexual couples, given the 8 to 11 million children being raised in families with a gay or lesbian parent in the U.S. whom have been characterized as maladaptive for a child's gender identity and/or sexual orientation. Moreover, we currently have access to a population of young adults who have been raised by gay and lesbian couples to share their experiences. Thus, research will be possible to examine the validity of the claims made in the past about children raised by homosexual parents empirically and understand parent-child interaction in terms of gender development and egalitarian attitudes. A cohort of college students (N = 251, 72% female, 2% transgendered, mean age of 21 years) was gathered in two ways: (1) by distributing the survey in an undergraduate class at a local university (89% of the sample) and (2) by using the online survey provider SurveyMonkey.com (11% of sample). Measures used were the Bem Sex Role Inventory (BSRI) and the Sex-Role Egalitarianism Scale. Two groups were identified: 89% of students were raised by a heterosexual parent couple (control group), and 79% within the same-sex parent couple group (experimental group) were female/female parent couples. There was no significant difference between the two groups' BSRI scores. However, there was an overall effect of sex on egalitarianism; males had more stereotypical attitudes than both females and transgendered individuals. There were no significant effects of group (control vs. experimental) or an interaction between group and sex. However, the less stringent Fisher's PLSD did reveal a significant effect of group. This effect was driven by lower scores of experimental females (i.e., had higher egalitarian attitudes) relative to control females. Students raised by gays and lesbians show no "negative" effects on their gender expression and actually show a positive effect on their sex-egalitarian attitudes. With that in mind, this study has shown that same-sex parent couples are not maladaptive for the children they raise.

B2-FRI

DURATION OF MOTHER VOCALIZATION TO INFANT AND DEPRESSION IN FIRST TIME MOTHERS

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Over the years there has been much research regarding mother and infant communication. Communication and interaction help to form a bond between mother and infant. Vocalizations of mothers to infants change throughout the first year of life. The purpose of this study was to analyze the duration of maternal vocalizations to infants at 3, 6, and 9 months of age. Additionally, vocalization duration at 3 months was analyzed with maternal depression, based on the BDI (Beck Depression Index) survey. Fifteen participants took part in the study, all of whom were first time mothers. The Noldus Observer program was used to obtain duration of vocalizations from mother to infant from ten minute videotapes. Analysis is still in progress. (Supported by NIH grant R25 GM 48998.)

A27-SAT

PERCEPTIONS OF ROOMMATE RELATIONSHIPS: STEREOTYPE CHANGES OVER TIME

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Stereotypes color many parts of impressions and decisions. Various factors can affect stereotype formation and activation over time. These factors were explored in the context of the Greek system. Specifically, the study looked at roommate relationships and how stereotypes can change over time as people learn more individuating information about the roommates. Forty-seven participants, recruited from a large Midwestern university, rated their roommates on positive and negative stereotypes and described their relationships with their roommates at two points in time, six to eight weeks apart. It was hypothesized that stereotypes about sorority women in general would not change over time, but that participants who are close with their roommates would rate the roommates as less stereotypic as they got to know them. The results showed that in many cases, stereotype ratings for roommates actually increased over time. The results also showed that stereotype ratings for sorority women in general were related to whether the participant was a sorority member. These findings are interesting because they did not support the research hypotheses, which were based on previous research.

B2-SAT

THE EFFECTS OF SEXUAL AND FRIENDLY PRIMES ON CONFLICT RESOLUTION STRATEGIES IN ROMANTIC RELATIONSHIPS

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The current study compared the effects of subliminal sexual, friendly, and neutral priming on the tendency to maintain close relationships as manifested in higher preference for positive conflict resolution strategies (pcrs) and lower preference of negative conflict resolution strategies (ncrs). Previous research has shown that subliminal sexual priming (brief exposure to picture of naked opposite sex member) actives the sexual system, leading to an increased tendency to maintain one's close relationship (Gillath et al., in press). An alternative explanation for the effects of the sexual prime is that the prime evoked friendliness (another person in an inviting posture results in feeling close or friendly). The present study was set to examine this alternative by comparing the effects of sexual priming and friendly priming on the tendency to use pcrs and ncrs. Forty heterosexual students were primed with a sexual (picture of naked opposite sex), a friendly (group of people smiling), or a neutral prime for 30 milliseconds before completing each item on the Rahim's (1983) Conflict Resolution Measure. Partially supporting our hypothesis, sexual priming led to a higher preference of pcrs; however, this finding was qualified by gender, such that the effect occurred only among men. No effects of prime were found with regard to the preference of ncrs. The current results shed further light on the role of the sexual system in close relationships, especially among men. Future research should find new ways to test the effects of sexual priming when its friendliness aspect is eliminated or controlled for.

B3-SAT

CLASSICAL AND INSTRUMENTAL CONDITIONING IN PIGEONS

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The behavioral studies have been considered one of the oldest branches of psychology. In the 1900s the first experimental analysis were applied to rats and pigeons. These animals were exposed to different conditions and reinforcement schedules. The objective of the experiment was to compare the effectiveness of two different CSs in maintaining the dot tracking. Sign tracking is a movement toward and possibly contact with a stimulus that signals the availability of positive reinforcer, such as food. Four pigeons were tested in an experimental chamber with a touchscreen mounted on one side. Every session is signaled by the illumination of a house light. Following a VI 40-sec schedule, a circle (8 mm) appeared in either the top left or bottom right of the touchscreen and will travel to the opposite side and reverse direction. A peck on the dot after the VI time expires will

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result in the activation of the food hopper for 2.5 sec. The hypothesis states that the pigeons will peck more toward the hopper than away from it. Three phases of the experiment were analyzed. Two of them were instrumental and one was classical conditioning. On the instrumental condition the animal had to respond in order to receive the positive reinforcer and in the classical condition they would get it regardless of their behavior. The data showed that the classical conditioning phase showed the desired behavior in comparison with the instrumental phases. This means that in the autoshape condition the dot is a good predictor of food.

B1-SAT

THE EXPRESSION OF ANGER AMONG INDIVIDUALS WITH CONDUCT AND IED DISORDERS: A QUESTIONNAIRE AND INTERVIEW COMPARISON

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Conduct disorder and intermittent explosive disorder are categories in the DSM-IV describing people with aggressive behavior problems. Differential diagnosis of these disorders is important for designing appropriate treatment strategies. 198 participants were recruited: 24 meeting criteria for conduct disorder, 47 meeting criteria for IED, and 11 meeting criteria for both. Each participant completed the State Trait Anger Expression Inventory and anger interviews, consisting of 3 situations involving anger provocations by family members. Anger interview responses were coded by 8 raters on 18 dimensions of anger expression. Conduct disorder is operationally defined as meeting criteria for both the Entitlement and Poor Self Control schemas on the Young Schema Questionnaire, while IED is operationally defined as a BSI hostility scale score greater than or equal to 60. Questionnaire results indicate that people with conduct disorder scored higher on measures of anger in and had statistically similar scores on anger-control-in and anger-control out, while people with IED scored higher on measures of anger out but lower on measures of anger control-out, when compared to those who did not have either disorder. No interactions existed between conduct and IED for anger expression variables. The study discusses implications for formulating appropriate treatments, for both conduct and IED disorders.

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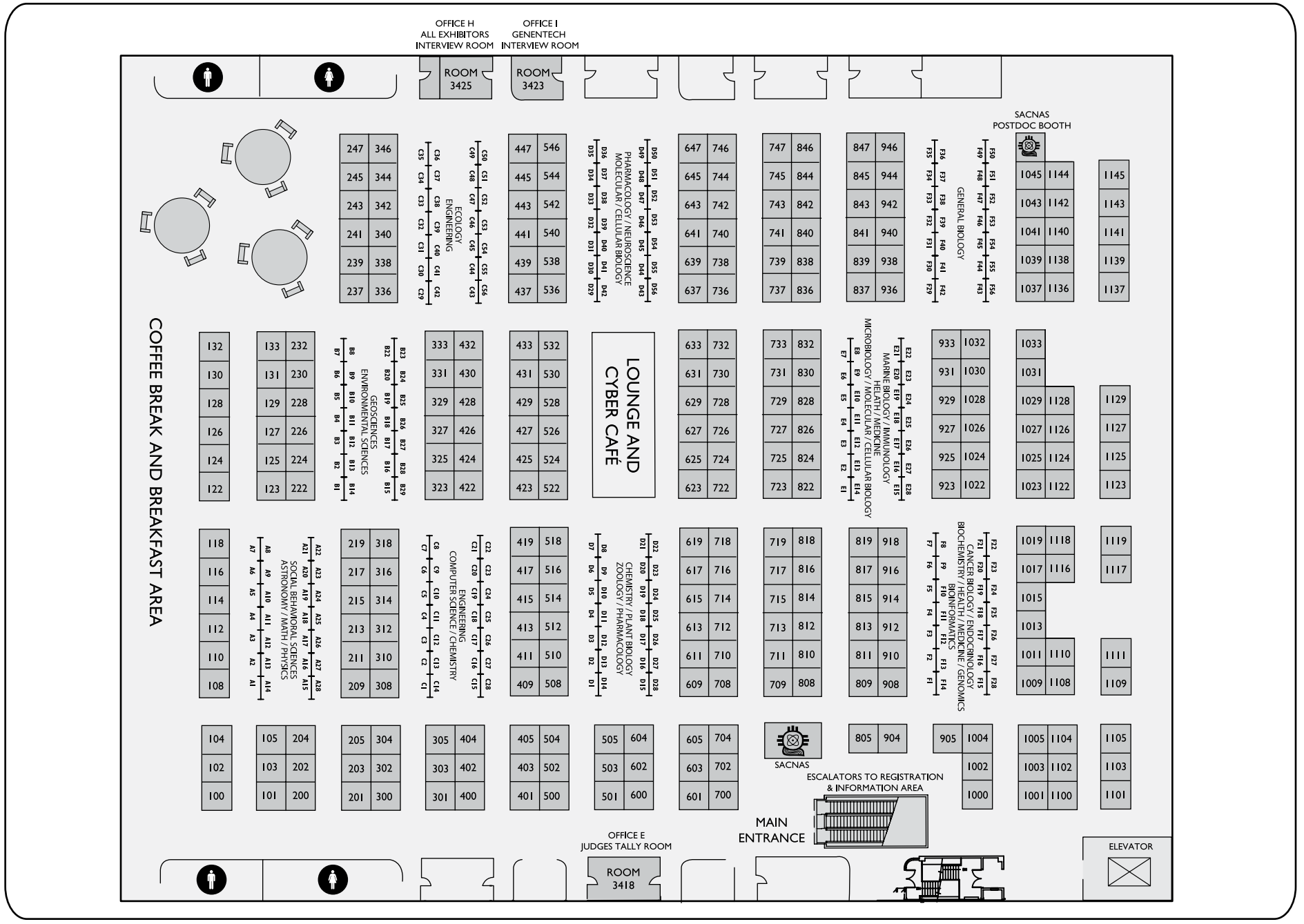




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