WCBSURC 2007 Abstracts

Session A – ECOLOGY

S1. DO BISON FEMALES SYNCHRONIZE PARTURITION BY GESTATION ADJUSTMENT? Daniel Sullivan* (Mike Mooring), Point Loma Nazarene University, Department of Biology, 3900 Lomaland Drive, San Diego, CA 92106.

Gregarious mammals generally synchronize birthing by adjusting the time of estrus. Berger (Ecology 73: 323-329, 1992) proposed that American bison (*Bison bison*) females in good condition are capable of adjusting gestation length, as well. He hypothesized that females in good condition that breed late in the season can shorten their gestation length so as to give birth during the birthing peak. We studied a herd of bison at Fort Niobrara National Wildlife Refuge, Nebraska to test the gestation adjustment hypothesis. For a subset of females observed in 2004 and 2005, dates of conception and birth were observed in the field and confirmed by genetic parentage analysis, fecal progesterone confirmed hormonal estrus, and calves were weighed during the annual roundup in September. Average (± SD) length of gestation was 268 days (± 5). Gestation length of females that conceived after the median breeding date was an average of 3 days shorter than that of females conceiving earlier in the season. The weight of the dam was not correlated with gestation length. Calf weight was positively correlated with dam weight, but was not related to gestation length. The sex of the calf did not influence either gestation length or calf weight.

S2. MORPHOMETRICS AS A METHOD TO DETERMINE SEXUAL DIMORPHISM IN THE CONVICT CICHLID. Elizabeth Glidewell* (Ronald Coleman) California State University, Sacramento, 6000 J Street, Sacramento, CA 95819.

Sexual selection can create variation between the secondary sexual characteristics of males and females that can be clear and well defined, or imprecise and difficult to identify. Convict cichlids (*Archocentrus nigrofasciatus*), a central American freshwater fish, show only slight sexual dimorphism that can be subjective in juveniles, but becomes more pronounced as the individuals get larger. This study used geometric morphometrics (shape analysis) to quantify sexual dimorphism as a function of body size in the convict cichlid. Twenty pairs of convicts were digitally photographed, measured, and weighed. The coordinates of twenty-one landmarks (i.e., center of the eye, origin of dorsal fin) were located on the photograph of each fish. Canonical variates analysis (CVA) and multivariate analysis of variance (MANOVA) were used to test for morphological differences between the sexes. The analysis showed a significant ($p < 0.01$) difference between male and female convict cichlids, with the most variation found in forehead shape. This study suggests that the methodology could have a broad application to quantify the extent of sexual selection acting on each of the sexes in a variety of species.

S3. PROTEIN BIOCHEMISTRY OF CICHLID FISH EGGS. Kim Nelson* (Ronald Coleman), California State University, Sacramento, Dept. of Biology, 6000 J St., Sacramento, CA, 95819.

Egg size varies greatly between species of cichlid fish, ranging from 0.8mm to over 6mm in diameter. Why is this so? Females are faced with a reproductive trade-off, whether to produce a few large eggs or many small eggs. Each species of cichlid resolves this trade-off differently by producing an egg size that provides the best reproductive success for the parents. A larger egg would seemingly provide the fry with more material for development, and therefore a better chance of survival. However, it has never been demonstrated that larger eggs do in fact contain more developmental material than smaller eggs. This study examined the size and protein content of eggs from 7 species of cichlids to demonstrate that protein content does increase as egg size increases, indicating that a female puts more resources into larger eggs. My research is the first study to examine in detail the intricate biochemical trade-offs involved in parental investment decisions of cichlid fish. It lays the foundation for future work to more closely examine egg size across a range of taxa.

S4. THE EFFECTS OF A SODIUM HYPOCHLORITE SOLUTION ON THE RATE OF DECOMPOSITION AND INSECT SUCCESSION ON THE CARCASS OF *SUS SCROFA* TO MODEL HUMAN DECOMPOSITION IN THE DESERT AREA OF SOUTHERN CALIFORNIA. William Kagy*, Kristina Reed, and Tanya Zipp (James Voss), Victor Valley College, Dept. of Biology, 18422 Bear Valley Road, Victorville, CA 92392.

Sus scrofa has been established as a suitable model to replicate the taphonomic processes of human decomposition. There are several distinct stages of decomposition through which a carcass or corpse will pass which are in part dependant on environmental factors. In the case of death by homicide, suspects will sometimes use caustic chemicals to mask their crime or confound the criminal investigation. The effects of sodium hypochlorite solutions (common household bleach) on the decompositional process and insect succession on a corpse have been a subject of legal inquiry and are not completely understood. Over a four week period a comparative study was conducted of treated (bleached) and control (nonbleached) pig carcasses. Observations of the differential in rate of decomposition and insect successional data are reported.

S5. COMPARING POLLEN AIR-CONCENTRATIONS OBTAINED BY ROTOROD SAMPLER AND BURKARD SPORE TRAP DEVICES IN A PARALLEL STUDIES. Miguel Ángel Prieto Lage*, (Dale M. Benham), Nebraska Wesleyan University, Department of Biology, Lincoln, NE 68503.

The volumetric devices Rotorod Sampler and Burkard Spore Trap are the most commonly need air-sampling instruments to estimate the pollen grain concentration in the air by allergists in United States. Although both instruments were designed for the same

purpose, their principles of operation and particle recoveries differ. The objective of this project we compare the pollen counts obtained by these two instruments. The data were collected in parallel studies involving the Rotorod Sampler and Burkard Spore Trap devices in daily pollen counts for Lincoln, NE, during three months period. The collected data of each device were reviewed and analyzed. Both instruments appear to record the same relative changes on the pollen grain air concentration. In some cases the Rotorod Sampler appeared as the device able to catch smallest particles (<10μm) and in another cases, is the Burkard Spore Trap device. For the largest particles (>10μm) in most of the data sampled the Burkard Spore Trap appeared to be the best instrument to collect them.

Session B - MOLECULAR BIOLOGY

S6. SEARCHING FOR GENETIC MARKERS IN EVERY MACRONUCLEAR CHROMOSOME IN *TETRAHYMENA THERMOPHILA*. Sevwandi De Silva*, Jenna Wiley, and Chad Jalandoni (Eileen Hamilton and Eduardo Orias), Dept. of MCD Biology, University of California, Santa Barbara, CA 93106.

Completing genetic maps of *Tetrahymena thermophila* and relating them to the genome sequence is important in order to identify genes that determine useful mutant phenotypes. A better understanding of this freshwater ciliated protozoan is important because it is an excellent model organism that can be utilized for basic and biomedical research. Tetrahymena cells have two nuclei: the macronucleus (MAC) contains the expressed genome, while the micronucleus (MIC) contains the silent germline genome. During differentiation of the MAC from a mitotic sister of the MIC, the 5 MIC chromosomes are fragmented into ~225 MAC chromosomes. Additional DNA polymorphisms were searched for as follows. PCR primers flanking a tandem repeat sequence in the sequenced strain were designed and PCR amplification was used to look for a product size polymorphism by comparison to a different inbred strain. When a polymorphism was found, it was further mapped to a MIC chromosome arm by deletion mapping, then to a MIC linkage group by meiotic recombination and finally to a MAC chromosome based on linked segregation during asexual reproduction. We have now mapped two polymorphisms to MAC chromosomes that had not previously been related to the genome sequence.

S7. IDENTIFYING MICRONUCLEAR-LIMITED DNA ASSEMBLIES IN THE *TETRAHYMENA* GENOME SEQUENCE. Tai L. Lee (Eduardo Orias and Eileen Hamilton), Dept. of MCD Biology, University of California, Santa Barbara, CA 93106

Tetrahymena thermophila is a freshwater ciliated protozoan and an excellent model organism for basic and biomedical research. Tetrahymena exhibits nuclear dimorphism, resulting in both a macronucleus and a micronucleus; the macronucleus (MAC) contains the expressed genome, while the micronucleus (MIC) contains the germline genome. The MAC differentiates from a mitotic sister of the MIC. Internally eliminated sequences (IES) are MIC sequences that are not incorporated into the MAC; IES make up ~15% of

the MIC genome. Random fragments of the MAC genome were sequenced and assembled; unavoidably, ~1% of the sequence was left in many tiny assemblies and some MIC IES contamination occurred. We are currently only interested in mapping the MAC genome of Tetrahymena. By identifying the IES in Tetrahymena's MAC genome sequence, we can avoid spending time and effort in attempting to map them. After investigating the scaffold size distribution of known IES, a prediction was made of scaffolds likely to be unknown IES in the public genome sequence assemblies. Probes were prepared for predicted IES scaffolds and hybridized to a Southern Blot of purified MIC and MAC preps. 16 out of 17 tiny scaffolds tested were IES, and recent microarray data is consistent with my results.

S8. CONTIG FINISHING AND ASSEMBLY OF *D. MOJAVENSIS* FOSMID CLONES IN A DISTRIBUTED GENOMICS RESEARCH PROJECT. N. Yu*. (Dr. Gary Kuleck), Loyola Marymount University, Biology Dept., 1 LMU Drive, Los Angeles, CA 90045.

In association with Washington University, St. Louis and the Genomics Education Partnership, a comparative genomic analysis of the dot chromosome 4 in *D. melanogaster* and other *Drosophila* spp is underway. This small heterochromatic chromosome replicates in late S phase and undergoes no meiotic recombination in *D. melanogaster*. While annotation of chromosome 4 has advanced in closely, related species such as *D. virilis,* and *D. erecta*, the process of contig assembly and finishing in a more distantly related species, *D. mojavensis* is just underway. Raw sequencing reads were entered into programs which base call (phred) and then assemble (phrap). The sequences were finished to high quality using Consed, a GUI tool that allows visualization and manual editing of assembled sequences from phrap. Sequence finishing removes all gaps, ambiguities, and misassemblies. Finishing requires additional sequencing to clarify low quality regions, close gaps, and reorient and join contigs. High quality single bp discrepancies in the consensus sequence indicated that sequenced DNA contained polymorphisms. To complete finishing, a virtual restriction digest is compared to the actual digest of the cloned DNA for validation. We will discuss the finishing process and 'walk through' a finishing example. A companion poster describing annotation is also available.

S9. FORWARD GENETICS IN *TETRAHYMENA THERMOPHILA*: USE OF THE GENOME SEQUENCE TO IDENTIFY CLASSICAL DRUG RESISTANCE GENES. Andrew Findlay* (Eileen Hamilton and Eduardo Orias). Department of Molecular Cellular and Developmental Biology, University California, Santa Barbara, CA 93106.

Tetrahymena thermophila is a unicellular eukaryotic organism and a good model for studying principles in cellular and molecular biology. Tetrahymena carries homologs of many human genes and can therefore be used to understand their cell biology. For these reasons, it is important to know their sequence and function in Tetrahymena physiology.

A useful approach for investigating biological mechanisms is to start with a mutant showing a relevant phenotype of interest. Using genetic mapping of the phenotype, identification of the determinant gene and its predicted protein product is possible. To verify the ability to do forward genetics in Tetrahymena we have chosen to identify genes causing three different resistance phenotypes: 2-Deoxy D-galactose, 6-methyl-purine, and cycloheximide resistance. Candidate genes were identified based on their location in genetic linkage maps. Candidate genes from mutated strains specific for these resistance phenotypes have been cloned and are currently being sequenced and compared to wild type sequence. Several promising mutations have been identified in the mutant strains. These mutated sequences will be inserted into transgenic plasmids designed to replace the wild type allele via homologous recombination. Appearance of the mutant phenotype would confirm the identified mutation as responsible for the respective resistance phenotype.

S10. MATHEMATICAL MODELING OF THE TRANSCRIPTIONAL NETWORK CONTROLLING THE ENVIRONMENTAL STRESS RESPONSE IN *SACCHAROMYCES CEREVISIAE*. Nathan C. Wanner* (Erika Camacho and Kam D. Dahlquist), Loyola Marymount University, Department of Mathematics and Department of Biology, 1 LMU Drive, Los Angeles, CA 90045.

Gene expression is a complex biological process in which cells first transcribe genes encoded in the DNA into mRNA. Then the cell translates the mRNAs into proteins. Transcription factors are regulatory proteins which increase or decrease the rate at which a cell transcribes a gene. Recently, much work has been done on determining the relationships between transcription factors and the genes they regulate on a global scale. A number of network motifs have been identified such as autoregulation, single input motifs, and feed-forward loops. Using differential equations and network analysis, we have modeled how the concentrations of proteins in the cell changes over time for a subset of a real gene expression network of twenty-one genes controlling the environmental stress response in *Saccharomyces cerevisiae*. We varied the initial concentrations and the strengths of the regulatory relationships for each gene in the network and generated a simulated gene expression dataset giving the steady-state concentrations of each protein after a period of time has elapsed. These data show which parameters affect the behavior of the network. Then each gene in the network was deleted to determine how the steady-state concentrations of the proteins in the network changed after the deletions.

S11. ACTR1 EXPRESSION PROFILE IN THE DEVELOPING MURINE SPINE IS CONSISTENT WITH OBSERVED PHENOTYPE OF ACTR1 CONDITIONAL KNOCKOUTS. Elena Bibikova* (Robert Pogue and Karen Lyons), University of California, Los Angeles, Dept. of Molecular, Cell, and Developmental Biology, 675 Charles E. Young Dr., Rm. 2641 MRL, Los Angeles, CA 90095.

The vertebrate skeletal system develops from cartilagenous precursors. Chondrocytes (cartilage cells) within the growth plate of cartilage proliferate and produce an extracellular matrix that is eventually replaced by bone. This process is controlled through several signaling pathways, and alterations in these may lead to diseases such as dwarfism. The bone morphogenetic protein (BMP) signaling pathway is one of the main pathways in vertebrate skeletal development. Three main receptors exist for this pathway: BMPRIA (BMP receptor type 1A), BMPRIB (BMP receptor type 1B), and ActR1 (activin receptor type 1). Data on BMPRIA and BMPRIB have previously been published, but ActR1 remains uncharacterized in cartilage. Mice missing ActR1 in cartilage show defects in development of cervical cartilage and progressive intervertebral disk degeneration. This study seeks to determine the correlation between ActR1 expression during mouse development and the phenotype seen in knockout mice. The expression pattern of ActR1 was analyzed using immunohistochemistry performed on saggital sections of wild-type mice at different stages of development, raging from E12.5 to birth. The expression pattern obtained correlates with the phenotype of ActR1 conditional knockout mice. Further studies to determine the mechanism of ActR1 action, as well as its interaction with other pathways, are currently being conducted.

Session C - CELL BIOLOGY, NEUROBIOLOGY, & IMMUNOLOGY

S12. NEURONAL NOS ACTIVATED BY PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE LEADS TO SOMATODENDRITIC RELEASE OF VASOPRESSIN FROM THE SUPRAOPTIC NUCLEUS OF THE HYPOTHALAMUS. Mark Gaertner* (Curras Collazo), University of California Riverside, CA 92951.

Vasopressin is an osmoregulatory hormone that is endogenously produced in the supraoptic nucleus (SON) of the hypothalamus in response to hyperosmotic challenge. It has been shown that production of this hormone not only has systemic effects, but also a local effect where it facilitates somatodendritic VP release from the magnoclellular neuroendocrine cells (MNCs) of the SON. This facilitation ultimately leads to a regulatory effect on systemic VP release throughout the SON. Recently we have discovered a novel role for Pituitary Adenylate Cyclase Activating Peptide (PACAP) in osmoregulation. PACAP is a neuropeptide whose receptors are present throughout the SON and other osmoregulatory brain sites. Our lab has shown that during dehydration in SON MNCs, expression of PACAP receptors is upregulated along with neuronal Nitric

Oxide Synthase (nNOS). Using acutely dissected SON punches from coronal rat brain slices we have shown that dehydration causes endogenous PACAP and Nitric Oxide (NO) levels to rise (Gillard et al, 2006a;2006b). Exogenous PACAP increased somatodendritic vasopressin (VP) release. The PACAP receptor antagonist, PAC6-27 (100 nM), completely suppressed the dehydration-induced extracellular VP (Gillard et al, 2006) and NO levels in SON punches (Gillard et al, 2006, abstract). We have also shown that NO is required for dehydration-induced somatodendritic release of VP in the SON (Gillard et al., 2007). To further investigate the role of nNOS-mediated NO we used the nNOS inhibitor 1 (240-940 nM) along with exogenous PACAP application and recorded a complete suppression in local VP release and NO production (>100%). In combination, our findings suggest that PACAP is released in response to dehydration and activates its receptors to upregulate nNOS in SON MNCs, which produces NO. NO then works to increase the local somatodendritic release of VP. NO may act, in part, by stimulating glutamate (GLU) release leading to activation of GLU receptors and VP release (Gillard et al, 2007). Our long term studies are addressing whether somatodendritic VP release triggers a negative feedback loop of autoregulation modulating systemic release so that it is efficient but not exhaustive.

S13. CHARACTERIZATION OF PROTEIN MARKER INSERTIONS INTO THE VPX PROTEIN OF HUMAN IMMUNODEFICIENCY VIRUS TYPE 2. Jessica Haight*[1] (Michael Belshan[2]), [1]Nebraska Wesleyan University, [2]Creighton University, Dept. of Medical Microbiology and Immunology, 2500 California Plaza, Omaha, NE 68178.

The Human Immunodeficiency Virus (HIV) causes Acquired Immune Deficiency Syndrome (AIDS). The long term goal of this research was to find the molecular mechanism of the HIV life cycle. The main focus of the research was on the preintegration complex (PIC), especially its Vpx component. Canidate HIV-2 viruses containing different epitope tags were inserted into the Vpx region to try and allow the virus infection to be tracked and/or allow the capture of the PIC. Western blots demonstrated whether the Vpx proteins were incorporated into the virions and if the epitope tags were expressed and functional. Reverse transcription and fluorescence-activated cell sorter assays were used to determine if the viruses were viable by replication in U937 cells and if the fluorescent proteins were functional. It was found that all of the viruses replicated in the U937 cells. The only marker that was expressed and remained functional when inserted into Vpx was hemagglutin. Replication of the viruses in macrophages will tell if the Vpx remains functional with insertions.

S14. DIFFERENTIATING EARLY-STAGE VIRAL AND BACTERIAL LUNG INFECTIONS VIA INNATE IMMUNE RESPONSES. Noa Simchoni* (Paul W. Demsey and Dr. Genhong Cheng), University of California, Los Angeles, Department of Microbiology, Immunology and Molecular Genetics, 8-240 Factor Building, 10833 Le Conte Avenue, Los Angeles, CA 90095.

During an epidemic, detection of presymptomatic individuals could slow disease communication through improving quarantine capabilities and design. The ability of soluble host immune responders to enable identification of individuals exposed to a pathogen, and allow classification of either bacterial or viral infections based on responder levels, was explored. To do so, lungs were isolated from mice that were infected for 2, 8, 24, 48, 72, or 96 hours with either the bacteria *Klebsiella pneumoniae* or the virus Influenza A/PR/8/34 and the relative levels of many soluble mediators were assayed through examining transcript levels by Quantitative PCR. High levels of either Interferon-γ-Inducible Protein 10 (> 75-fold) or C-Reactive Protein (a positive result) indicated an active infection. The bacterially-infected animals additionally upregulated CC Ligand 4, CXC Ligand 5, Interleukin-1β, Interleukin-6, and the Interleukin-1 receptor agonist over 7-fold. No unique genes were upregulated in the virally-infected animals, though both infections resulted in mild or similar regulation of other mediators. The data indicates the feasibility of setting up a detection system based on innate responses, though a microarray study aiming to locate other potential mediators is still required along with a comparison of meadiator regulation in response to infections by other respiratory pathogens.

S15. DEVELOPMENT OF AN IMMUNOFLUORESCENT ASSAY FOR THE DETECTION OF HHV-8 ANTIBODIES IN HUMAN SERUM USING RECOMBINANT VIRAL PROTEINS EXPRESSED IN INSECT CELLS. Lynsey C. Crosby*[1], Veenu Minhas[2], and Kay Crabtree[2] (Charles Wood[2]), [1]Nebraska Wesleyan University, Biology Department, Lincoln, NE 68504-2794, and [2]University of Nebraska, Nebraska Center for Virology, School of Biological Sciences, 1901 Vine St., Lincoln, NE 68588.

Human herpesvirus 8 (HHV-8) has been linked to Kaposi's sarcoma (KS) and other lymphoproliferative diseases. The reliability of most currently used assays is uncertain. To establish a sensitive and specific antibody detection assay, three HHV-8 recombinant proteins, ORF 65, ORF73 and K8.1A, were over expressed in insect cells (Sf9) and used in an immunofluorescence assay (IFA). A second IFA utilizing BC3 cells, a HHV-8 infected cell line, was used (BC3-IFA). We used a panel of serum from reliably diagnosed KS patients, high and low risk patients and patients from an endemic area for evaluation of the assays. Healthy patients from a local blood bank served as a negative control. Patient plasma showing specific fluorescence in both assays was considered positive. Our results demonstrated that these two assays when combined together have a sensitivity of 90% and a specificity of 100%. The performance of these two assays when used together indicates that they may be used for reliable detection of HHV-8 antibodies in a population.

S16. SUBCELLULAR LOCALIZATION OF THE TURKEY AND HUMAN ASTROVIRAL PROTEIN ORF1-A. Jennifer Stripe*, Hei-Man Lai, Amy Garrison, Jennifer Somers (Jon Milhon) Azusa Pacific University, Department of Biology and Chemistry, 901 E. Alosta Ave., Azusa CA 91702.

Both the human and turkey astroviruses are recognized as important causes of enteric disease in infected hosts. However, while HastV has been more extensively studied, the TastV is more virulent, creating a significant financial burden for the agricultural industry. Comparisons between these two viruses show that both HastV and TastV contain three open reading frames, encoding proteins of the same names. Notably, viral protein ORF1-a encodes a protease. Early publications report contrasting results, citing HastV ORF1-a localization in either the endoplasmic reticulum or the nucleus. To justify these conflicting results, experimentation was performed to determine the cellular localization of the HastV and TastV ORF1-a proteins. A series of fluorescent studies was conducted using in-frame fusions of HastV and TasTV ORF1-a genes with either the gene for Green Fluorescent Protein (GFP) or a red fluorescent protein (DsRED). Results from both single and co-transfections into COS-7 cells indicated that human and turkey astroviral ORF1a proteins did not localize in the nucleus or endoplasmic reticulum, as previously suggested Additionally, both proteins did not localize in the golgi apparatus, nor did they co-localize in the same subcellular structure. This difference in localization could help to explain the contrasting pathology exhibited by HastV and TastV.

S17. SONIC HEDGEHOG-GLI SIGNALING IN MANTLE CELL LYMPHOMA**.** Katy Emanuel* (Ganapati V. Hegde), Nebraska Wesleyan University, Dept. of Biology, 5000 St. Paul Ave., Lincoln, NE 68504.

Mantle cell lymphoma (MCL) is associated with poor clinical outcome with a median survival of only 3-4 years. MCL cells increase Cyclin D1 (CCND1) expression. Sonic hedgehog (Shh)-GLI signaling promotes tumor cell proliferation in pancreatic cancer, & prostate cancer. However, the role of Shh-GLI signaling is unknown for B cell lymphomas. We studied the role of Shh-GLI signaling molecules in the proliferation of MCL cells *in vitro* using JVM-2, Granta-519, Jeko-1 and Z138 cell lines and human primary MCL cells. Results demonstrated that molecules involved in the Shh-GLI signaling, patched and smoothened receptors, target transcription factors, GLI were over expressed in MCL cell lines and patients' primary MCL cells compared to normal human B lymphocytes. Addition of exogenous Shh increased the proliferation of JVM-2 cells in vitro, and increased the transcript level of GLI1, BCL2 and Cyclin D1 (CCND1). Addition of Shh-signaling inhibitor, cyclopamine, abrogated Shh induced proliferation, and transcription of the above genes in JVM-2 cells. Furthermore, the GLI anti-sense oligonucleotide decreased CCND1, BCL2 transcript expression, and proliferation of JVM2 cells *in vitro*. These results suggest that Shh-GLI signaling may be one of the pathways that regulate Bcl-2 and CCND1 activation, thereby regulating proliferation and apoptosis of MCL cells.

Session D – MICROBIOLOGY

S18. DNA ISOLATION AND RESTRICTION PATTERN COMPARISON FOR NEW ISOLATES OF *ACANTHOCYSTIS TURFACEA CHLORELLA VIRUS*: DISCOVERY OF A METHYLTRANSFERASE. Angela Fenton*[1] (Ming Kang[2]), [1]Department of Biology, Nebraska Wesleyan University, Lincoln, NE 68504 and [2]Department of Plant Pathology, University of Nebraska-Lincoln, Lincoln, NE, 68583.

The *Acanthocystis turfacea Chlorella virus* (ATCV) infects specific *Chlorella* algae that are endosymbiotic with the freshwater heliozoan *Acanthocystis turfacea.* This novel virus, discovered in Germany, was isolated from several sites in North America. The virion's large dsDNA is contained in a 140-190 nm icosahedral capsid mostly made up of one major 50 kDa protein. Some of the capsid's vertices have filamentous structures that may be associated with attachment to the host cell. ATCV is affiliated with the family *Phycodnaviride*, more specifically the genus *Chlorovirus*, a group of large, icosahedral, dsDNA-containing viruses that are commonplace where *Chlorella* algae naturally live. The ATCV has previously distinguished itself from other chloroviruses, particularly the prototype *Paramecium bursaria Chlorella virus* (PBCV-1), and recently it has shown distinctions among the geographic isolates from North American based on results from analysis of restriction enzyme digests of the genome. One of those distinctions was variation in plaque size and shape. Another distinction was a possible methyltransferase gene located within the genome of one isolate, but not in others.

S19. IDENTIFYING SOIL BACTERIA AND BIOCHEMICAL PATHWAYS IN THE BALLONA WETLANDS FOR THE BIOREMEDIATION OF ORGANIC POLLUTANTS. Wesley T. Citti* (Kam D. Dahlquist and Carl R. Urbinati), Loyola Marymount University, Department of Biology, 1 LMU Drive, Los Angeles, CA 90045.

The Ballona Wetlands in Los Angeles County are contaminated with organic pollutants, such as polychlorinated biphenyls (PCBs), polyaromatic hydrocarbons (PAHs), and single-ring aromatics (e.g. toluene) from urban run-off. To determine whether biochemical pathways exist in the wetlands to degrade toluene we first attempted to culture bacteria from the soil that could metabolize toluene. We inoculated minimal media with soil samples collected from four sites in the wetlands and used toluene or citrate as the sole carbon source. Cultures grew only in the citrate-containing media. We isolated genomic DNA from a pure environmental isolate and also directly from the soil samples. Using PCR, we amplified a variable portion of the 16S rRNA gene from each sample of genomic DNA and created sub-genomic libraries. The 16S fragment from the environmental isolate was sequenced and putatively identified as *Pseudomonas sp*. Several Pseudomonas species are known to degrade toluene. Using PCR, we amplified the todC1 gene, encoding one subunit of toluene dioxygenase, the first enzyme in the toluene degradation pathway. We additionally are using Length Heterogeneity-PCR (LH-PCR) to assess the diversity of bacterial species in the soil samples. The LH-PCR results will be compared to results from direct sequencing of 16S rRNA sub-genomic libraries.

S20. CHARACTERIZATION OF HALOPHILES ISOLATED FROM A SOLAR SALTERN IN BAJA CALIFORNIA, MEXICO. Lamine Diallo*, Lauren Hays, and Shereen Sabet (Jesse Dillon), California State University Long Beach, 1250 Bellflower Blvd., Long Beach, CA 90840.

Hypersaline environments are three to ten times saltier than seawater, such as solar salterns (150 g L^{-1} – 300 g L^{-1} salt concentration), and they contain microorganisms that are adapted to tolerate extreme hypersalinity. These microorganisms are known as halophiles and include both Archaea and Bacteria. Halophiles are of interest for their biological products which are used in cosmetics, and for their potential industrial application in the oil industry and in holographic memory storage. Halophiles are also of interest as potential candidates in the search for life on other planets. Our lab is using halophiles to isolate halophilic viruses with the aim of elucidating the ecological significance of these phages in the context of host-phage dynamics in an extreme hypersaline environment. We isolated 35 halophiles of both Bacteria and Archaea from the ESSA saltworks factory in Guerrero Negro, Baja California, Mexico. Characterization of these isolates included 16S rDNA gene sequence analysis and phylogeny, metabolic analysis via the BIOLOG PM1 assay plates, and salinity tolerance over a range of 10%-30% salt concentration. Our data show that we have isolated members from a total of four halophile genera: Halorubrum, Haloarcula, Halomonas, and Salinibacter. Data is presented regarding their morphological, metabolic, and physiological profiles.

S21. THE INFLUENCE OF THE CHANGE IN SALT CONCENTRATION ON THE MICROBIAL COMMUNITY IN TWO SEASONAL SALINE LAKES IN SOUTERN UTAH. Stacy DeMill*, Cheri Tait, Coby Brown, Justin Bowles* (Charlotte Rosendahl Pedersen), Southern Utah University, Dept. of Biology, 351 West University Boulevard, Cedar City, UT 84720.

The Little Salt Lake and Quichapa Lake are two seasonal saline lakes in Iron County in Southern Utah. In seasonal lakes the amount of water varies greatly which determines the concentration of salt in both the sediment and the water in the lake. In this study we are investigating the change of the microbial community in response to the seasonal change of the salt concentration in the lake. 5 randomly selected sites are tested for salinity, temperature, water depth and microbial community structure every two weeks. Changes in the microbial community is screened using Ecolog plates and if changes from the initial community is observed microorganisms are isolated on 3 different medias and DNA is extracted to be used for 16 sDNA analysis of the community structure. Several halophilic microorganisms have been isolated from the Little Salt Lake and DNA has been extracted from Quichapa Lake.

S22. UTILIZATION OF *STREPTOMYCES* AS A MODEL ORGANISM TO STUDY QUORUM SENSING AND TRANSPOSON MUTAGENESIS IN *MYCOBACTERIA SMEGMATIS.* Megan N. Campbell*, (Angela McKinney-Williams) Nebraska Wesleyan University, Department of Biology, 5000 Saint Paul Ave., Lincoln, NE 68504.

Quorum sensing (QS) is a type density-dependent cell to cell communication, which uses chemicals as signaling molecules. Quorum sensing plays a role in a variety of cellular functions like gene expression, gene transfer, sporulation, virulence, and antibiotic production. Many QS molecules have been found in different types of bacteria. The goal of this study is to determine if QS occurs in M*ycobacteria* and to find the role of QS in mycobacterial pathogenesis. The hypothesis is that *Mycobacteria* produce QS molecules. S*treptomyces* and *Mycobacteria* are both gram-positives bacteria with a high G-C content in their genome, and QS assays are well established for *Streptomyces* and the signaling molecules identified; this makes *Streptomyces* a useful tool to study QS in *Mycobacteria*. It has been shown that *Streptomyces* responds to a signaling molecule produced by *M. smegmatis*. These results are an indication that *M. smegmatis* has a QS system and produces a QS molecule. The gene responsible for producing the QS molecule is unknown and is currently being investigated using an over expression library or *Mycobacteria*. Once the gene is identified, the information obtained from *M. smegmatis* will then be used to determine if QS plays a role in pathogenesis of *M. tuberculosis*.

S23. INHIBITORY MOLECULE AND AFFECTS OF *MYCOBACTERIUM SMEGMATIS*. Haley Capek*[1], J. Cirillo[2], and S. Kuman[2] (A. McKinney-Williams[1]), [1]Nebraska Wesleyan University, Lincoln, NE 68504 and [2]Texas A&M University, College Station, TX.

Quorum sensing (QS) is a bacterial signaling mechanism between cells that can result in aerial hyphae, pigmentation, antibiotic production and/or deterred growth. QS has been extensively studied in Streptomyces and this QS system is being used to study QS in Mycobacteria. *Mycobacterium smegmatis* is related to *Mycobacterium tuberculosis* and *Mycobacterium marinum*, however, being nonvirulent makes it appropriate to study in the laboratory setting. *Mycobacterium smegmatis* releases this unknown signaling molecule depending on the condition it is grown such as density and light exposure. Preliminary results suggest that a signaling molecule is released by *Mycobacterium smegmatis*, however the structure of this molecule remains unknown. The aim of this study is to isolate the QS molecule from *Mycobacterium smegmatis* and determine the structure of the QS molecule.

Session E - ECOLOGY

S24. EFFECTS OF SPECIES RICHNESS, SPECIES COMPOSITION, AND AVAILABLE SUBSTRATE ON LARVAL RECRUITMENT INTO FOULING COMMUNITIES OF HUMBOLDT BAY, CA. James Kealey*[1], Dean Janiak[2], and Julie Koeppel[2] (Sean Craig[2]), [1]University of California, Berkeley, [2]Humboldt State University, Dept. of Biological Sciences, 1 Harpst St., Arcata, CA, 95521.

We manipulated marine fouling communities in Humboldt Bay, CA, to examine the importance of species richness, species composition, and resource availability on the recruitment of native and non-native species. Species were selectively removed from naturally established communities on 10x15 cm plastic panels to establish low (2 spp.) and high (4 spp.) richness levels. Within these levels, panels were groomed to retain one of two unique sets of species to examine the role of species composition. In order to examine resource availability, the same panels were groomed to contain either a high or low amount of available substrate. Analysis of larval recruitment into these communities at 10, 20 and 30 days following deployment suggests a role for available free space and species composition, but not species richness per se. Specifically, communities which contained the anemone *Metridium senile* received fewer recruits of the non-native ascidian *Botrylloides* sp., and in a separate experiment, settlement of *Botrylloides* decreased with increasing *Metridium* cover. In contrast, the native *Distaplia occidentalis* was strongly affected by the availability of available substrate, but not species composition. These results suggest that recruitment depends not only on specific larval behavior, but also on resource availability and species composition within preexisting communities.

S25. COMPARISON OF FLY POPULATIONS ON STOCK AND NON-STOCK USAGE RECREATIONAL TRAILS IN THE EASTERN SIERRA, CALIFORNIA. Elizabeth Thomas* (Claremont McKenna College), Claremont McKenna College, Roberts Environmental Center, Joint Science Department of the Claremont Colleges, 925 N. Mills, Claremont, California, 91711.

Informal observations of hiking trails in the Eastern Sierra suggest that trails that allow stock usage tend to yield a higher population of flies than trails restricted to hikers. Using horse droppings, commercial fly baits, and a hiker as baits, fly population numbers were recorded on six different trails in the June Lakes area of the Eastern Sierra, California. Tests were conducted on trails and at a distance from trails to measure populations in at different distances from human and horse disturbance. The results were not consistent across all baits, suggesting different compositions of species or saturation of dung availability on stock-use trails. The information gathered from this study can help guide agencies such as the U.S. Forest Service, National Park Service, and Bureau of Land Management officials in recreational trail usage policies.

S26. ARSENIC IN SAN JOSE CALIFORNIA'S GUADALUPE RIVER. Stephen Maurano*, Kathleen Powers, and Lindsay Wenger (William Eisinger), Santa Clara University, Dept. of Biology, 500 El Camino Real, Santa Clara, CA 95053.

Arsenic is a serious human health risk and has been detected in San Jose, California's, Guadalupe River at levels that exceed EPA drinking water standards. This investigation attempted to determine if the elevated levels of arsenic were from natural or anthropogenic sources. We monitored arsenic at various sediment levels and with seasonal changes. Arsenic concentration was determined using the Gutzeit Method with a 0-500 ppb sensitivity. Although unable to fully isolate the cause, results indicate that arsenic levels in the Guadalupe River are enriched in sediments above background levels and are contingent upon flow and distance from source.

S27. DEVELOPING *SALICORNIA VIRGINICA* AS A BIOMONITOR FOR HEAVY METAL POLLUTION OF THE BALLONA WETLANDS. James R. Holmquist (Philippa M. Drennan, and James M. Landry) Departments of Biology and Natural Science, Loyola Marymount University, 1 LMU Drive, Los Angeles, CA 90045.

The coastal Ballona wetlands are a part of the highly urbanized Los Angeles watershed. Studies done on the water quality of the channel feeding the wetlands have shown high levels of heavy metals. The goal of this project is to use the widely distributed halophyte *Salicornia virginica* (commonly known as pickle weed) to establish trends in heavy metal pollution for Ballona wetlands. It is hypothesized that *S. virginica* in a contaminated wetland will take up heavy metals along with the salts. Seventy five plants were collected from 5 sites in the Ballona wetlands. The tips, lateral branches, and woody stem tissue were analyzed for water, salt, and metal content. The methods used were oven drying to establish wet and dry weights for water content, flame photometry for sodium and potassium, and atomic absorption spectroscopy for cadmium and zinc. Lateral branches had a significantly higher water content, salt content, and heavy metal content than the woody tissue. Branch tips had slightly lower, but significant, contents of water, salts, and heavy metals than lateral branches. Salts and heavy metals showed similar distribution patterns in the tissues suggesting that similar factors may affect their accumulation. The relatively high tissue concentrations for cadmium and zinc in *S. virginica* from Ballona may be associated with contaminated urban runoff in this region. Indeed, in comparing zinc levels in plants to the water content of soils a positive correlation was found between soil inundation (from the channels) and the zinc concentration in *S. virginica*. Soils from the 5 sites are currently being analyzed for the heavy metals that we have found in the plants. In the future the procedure will be refined and used to make a comprehensive map of metal pollution in the Ballona wetlands.

Session F - MOLECULAR BIOLOGY

S28. MRT4P IS INVOLVED IN 60S RIBOSOME SUBUNIT ASSEMBLY AND NUCLEAR EXPORT. Nicole S.F. Yu* (Carl R. Urbinati), Loyola Marymount University, Department of Biology, 1 LMU Drive, Los Angeles, CA 90045.

Ribosome biogenesis includes the processing of rRNA and assembly and transport of the large (60S) and small (40S) ribosome subunits from the nucleolus to the cytoplasm. The yeast *Saccharomyces cerevisiae* serves as an ideal model organism to study such a complex process. Ribosome biogenesis commences with the transcription of a 35S pre-rRNA which is extensively processed into mature 25S, 5.8S and 18S rRNAs. The mature 60S ribosome subunit includes the 25S, 5.8S and the 5S rRNAs, the latter a product of a separate transcription unit. The mature 18S rRNA is the sole RNA component of the 40S subunit. The processing of the pre-rRNA is concomitant with the assembly of pre-ribosome particles ultimately resulting in the 60S and 40S subunits. Many non-ribosomal proteins participate in pre-rRNA processing and subunit assembly. Previously Mrt4p was identified as a constituent of pre-60S particles and necessary for efficient 60S biogenesis. Genetic analysis demonstrates that *MRT4* is a non-essential gene, though *mrt4*Δ cells exhibit impaired growth. RNA analysis reveals a decrease in 25S rRNA levels in *mrt4*Δ cells and visualization of 60S subunits demonstrates perturbations in nucleocytoplasmic transport. Current experiments are focused on purification of an Mrt4p-associated ribosome assembly complex.

S29. IDENTIFICATION OF PROTEIN INTERACTING PARTNERS OF H37/RBM5 LUNG CANCER TUMOR SUPPRESSOR GENE PRODUCT. Ashley Koegel*, Idolina Delgado, and Diana Phan (Dennis Slamon/Juliana Oh), UCLA, Dept. of Medicine, 675 Charles. E. Young Dr., Los Angeles, CA 90024.

One of the first genetic alterations in lung cancer is deletion at chromosome 3p21.3 (82% of non-small cell lung carcinomas). H37/RBM5, which lies in this region, is likely a tumor suppressor gene. Using human A549 NSCLC cells transfected with H37, it has been shown that H37 is involved in G1 cell cycle arrest and increases apoptosis, significantly inhibiting human lung cancer growth both *in vitro* and *in vivo*. In order to further elucidate the cellular and molecular functions of H37, a primary yeast two-hybrid screening of 16,000 clones from the human testes cDNA library was performed. 75 positive clones were identified by the most stringent plating criteria. I am currently validating these potential targets for true interactions by purifying individual "prey" plasmids and co-transforming them with H37 "bait" plasmids into yeast cells. Based on subsequent DNA sequencing, interactions will be further validated *in-vivo* by immuno-precipitation. This research may streamline the H37 TSG mechanism in human lung cancer and the eventual development of novel therapeutics.

S30. GENETIC ANALYSIS OF THE *ARABIDOPSIS THALIANA* S15aE r-PROTEIN GENE THAT CONTAINS AN INSERTIONAL MUTATION. Stacey Abidayo*, Ammar Zanial, and Ali Zanial (Kathleen Szick-Miranda), California State University of Bakersfield, Dept. of Biology, 9001 Stockdale Hwy., Bakersfield, CA 93311-1022.

Expression of DNA relies heavily on two important process called transcription and translation whereby protein synthesis occurs with the assistance of ribosomes. The ribosome is the site where mRNA codons are translated into amino acid sequences of polypeptide chains, or proteins. Proteins are pivotal in the growth and development of *Arabidopsis thaliana* as well as all organisms because they attribute properties that are essential for life. Ribosomes, moreover, are comprised of both ribosomal proteins (r-proteins) as well as rRNA. The r-protein S15a is encoded by two evolutionary distinct groups of genes known as Type I (homologous to other eukaryotic S15a's) and Type II (distinct). The functional significance of divergent S15a is still unknown and the use of insertional mutations in Type II S15a genes may show how these divergent genes affect *Arabidopsis* phenotypically. Preliminary data suggests that there may not be a significant difference of phenotypic expression from wild type plants compared to *RPS15aE* but there was a developmental delay of *RPS15aB*. Results acquired from a future large scale study and the analysis of the data will contribute greatly to the understanding and significance of the protein function and components of the ribosome.

S31. IDENTIFICATION OF NITROGENASE *NIF*HDK PROTEIN IN NON-FRANKIA ACTINOMYCETES. Nima Milani Nejad*[1], (Peter De-Hoff [2], Ann Hirsch [1, 2]), University of California, Los Angeles, Dept. of Molecular, Cell, and Developmental Biology[1], Molecular Biology Institute[2], Los Angeles, CA, 90024.

Actinomycetes that are non-*Frankia* members have previously been isolated from the nodules of *Casuarina equisetifolia*. Based on 16s rRNA sequencing and the absence of DNA homology with other *Frankia* strains, it has been shown that these actinomycetes are not a member of the clade *Frankia*. These strains are predicted to be capable of expressing a functional nitrogenase protein, as they are capable of growth in zero nitrogen medium as well as the presence of a *nif*H gene that shares 85-98% homology with *nif*H genes from *Frankia* strains. The goal of this project is to identify the proteins involved in nitrogen fixation in *micromonospora* L5 (*mexicana*) and two new unknown streptomyces, N13 and N27. It is determined that these strains are capable of expressing putative *nif*H subunit of 31 kDa and putative *nif*DK subunits of 57 kDa in nitrogen minimal media. Further experimentations are required to identify the exact processes involved in expression of these proteins.

S32. GENETIC AND MOLECULAR MECHANISMS THAT REGULATE ORGAN BOUNDARIES DURING FLOWERING. Moni Bhattacharya* (H.M.S.Smith), Botany and Plant Sciences, University of California, Riverside, 900 University Avenue, Riverside, CA 92521.

In flowering plants, the post-embryonic growth of the shoot system is regulated by the shoot apical meristem (SAM). A key stage during development is the transition from vegetative to reproductive phase, during which SAM changes into an inflorescence meristem (IM) to produce reproductive phase-specific organs, including floral meristems (FMs). Studies from our lab show that two paralogous BELL-homeodomain transcription factors, PENNYWISE (PNY)/POUNFOOLISH (PNF) are crucial for inflorescence architecture, floral patterning, and maintaining boundaries between IMs and FMs. However, little is known about the mechanisms that regulate such boundaries. The goal of this study was to understand how PNY/PNF function with other known organ boundary genes during flowering. A recent study has elucidated the role of the GRAS transcription factor, LATERAL SUPPRESSOR (LAS) in maintaining lateral organ boundaries. Results from our genetic crosses and yeast two-hybrid studies suggest that PNY/PNF and LAS are part of a transcription factor complex to maintain boundaries between IMs and FMs. Future directions, include re-confirming the interaction between PNY/PNF and LAS by coimmunoprecipitation and possible interaction of PNY/PNF with other known boundary genes (CUPSHAPED-COTYLEDON 1, 2, 3). Such studies will allow us to place the organ boundary genes into a hierarchy.

S33. TESTING THE HYPOTHESIS OF HYBRID SPECIATION IN *PENSTEMON NEWBERRYI* VAR. *BERRYI*. Lorae' Simpson* (Shannon Datwyler), California State University, Sacramento, Dept. of Biology, 6000 J. Street, Sacramento, CA 95819.

Hybrid speciation is a central issue in plant evolutionary biology. Hybridization takes place naturally in the wild and gives rise to stabilized, genetically distinct populations. It is the goal of this project to test the hypothesis of a hybrid complex between *Penstemon newberryi var. newberryi* and *Penstemon cardwellii* with the resulting progeny of *Penstemon newberryi var. berryi*. 146 individuals representing 8 populations were examined for DNA additivity using amplified fragment length polymorphism (AFLP) protocol. ALFP is used to evaluate genetic diversity, assess genetic relationships and ultimately clarify taxonomy with the use of molecular markers. If hybridization is proven it will provide a substantial piece in the understanding of *Penstemon's* evolution. Progress towards assessment of a hybrid relationship using AFLP will be discussed.

Session G - PHYSIOLOGY AND CELL BIOLOGY

S34. A TOOL FOR CARDIOVASCULAR DISEASE: VALIDATED FOOD FREQUENY QUESTIONNAIRE FOR ASIAN INDIAN GUJARATI INDIAN IN GREATER CENTRAL VALLEY OF SACRAMENTO. Priti Patel* (Brtt-Burton Freeman), California State University, Sacramento, Department of Biological Sciences, 6000 J Street, Sacramento, CA 95819.

Among the Asian Indian population, Gujarati's have one of the highest rates of cardiovascular morbidity and mortality. Paradoxically, Gujarati's follow a predominately vegetarian diet and such a dietary pattern is typically associated with a reduced risk of cardiovascular disease. To better understand the diet-disease relationship within the Gujarati population, a thorough assessment of dietary habits relative to diseases is required. As a preliminary step in this process, this study aims to develop and validate a Food Frequency Questionnaire (FFQ) specifically designed for Gujarati's. The study examines the diet of 15 Gujarati women, between the ages of 20 and 50, to create a validated FFQ. The results of this study are intended to provide an efficient tool that can assist health professionals in appraising the dietary habits of Gujarati women relative to disease risk, and provide dietary guidelines for policy and health promotion within this population.

S35. THE INFLUENCE OF SODA AND CAFFEINE CONSUMPTION ON BONE MINERAL DENSITY. Genevieve Organist*, Diana Podlecki* (Hawley Almstedt), Loyola Marymount University, Dept. of Natural Science, 1 LMU Dr., MS 8160, Los Angeles, CA 90045.

The aim of our study was to investigate the influence of soda and caffeine consumption on bone mineral density (BMD, g/cm^2). Subjects (ages 18-25) completed 3-day diet records which were analyzed for phosphorus, calcium, and caffeine using Food Processor (version 9.8.1). Soda is a high source of phosphorus but a low source of calcium. Therefore the ratio of phosphorus to calcium was examined by dividing subjects into high (n=11) and low (n=20) ratio groups. In a second analysis, BMD was evaluated in those consuming low (<10mg, n=17) and high (>10mg, n=13) amounts of caffeine. BMD was measured using DXA. Performing an ANCOVA, revealed no significant differences in BMD at the hip, spine, or whole body according to the ratio of calcium and phosphorus intake. However, the second ANCOVA demonstrated that compared to the low caffeine group the high caffeine group had lower BMD at the femoral neck and at the trochanter. In this population, BMD was not different in the low calcium to phosphorus ratio group. However, subjects drinking higher amounts of caffeine had lower BMD at the hip than those consuming low amounts. Further research on a larger sample size would be beneficial.

S36. USE OF ULTRASOUND TO RISK-STRATIFY PREGNANCY OUTCOME IN EMERGENCY DEPARTMENT PATIENTS WITH FIRST TRIMESTER VAGINAL BLEEDING. Hee Sun Choi[*1] (John Christian Fox[2]), [1]University of California, Irvine, Department of Emergency Medicine, 200 Manchester Suite 710Q Orange, CA 92868.

Vaginal bleeding during the first trimester of pregnancy can be a result of spontaneous abortion, gestational trophoplastic disease, implantation bleeding, cervical ectropion, cervicitis and ectopic pregnancy, which must not be misdiagnosed. It is essential to include all diagnoses due to potential life threat and threatened abortion. Pelvic ultrasonography will be the best procedure to evaluate every pregnant patient with vaginal bleeding in early pregnancy due to no evidence of risk to mother or fetus, and immediate test results while providing five potential diagnoses in such situations. For example, pelvic ultraonography can reveal *NDIUP* (no definitive intrauterine pregnancy), *IUP* (intrauterine pregnancy), *Live IUP* (live intrauterine pregnancy), *Abnormal IUP* (abnormal intrauterine pregnancy), and ectopic pregnancy. Finding *NDIUP, IUP* and *Live IUP* indicates potentially viable pregnancies. Finding *Abnormal IUP* and ectopic pregnancy displays non-viable pregnancies. The goal of this research was to evaluate if and how finding *NDIUP, IUP*, and live *IUP* in first trimester vaginal bleeding predict the pregnancy outcome in patients. A total of 124 women were enrolled and of the 70 that met inclusion criteria, 23 (32%) carried to term and delivered live babies. Of the 23 live births, 18 (78%) were noted to have a documented *Live IUP* at the time of the emergency department visit. The other findings included *IUP* (13%) and *NDIUP* (8%). None of the *Abnormal IUP* resulted in a live birth. Therefore, in women with first trimester vaginal bleeding the likelihood of carrying the pregnancy to term does appear to be related to the findings on ultrasound.

S37. THE EFFECTS OF *DATISCA GLOMERATA* ON TWO BREAST CANCER CELL LINES, MDA-MB-231 AND BT-474. Pang Moua* (Mary McCarthy Hintz), California State University, Sacramento, Department of Biological Sciences, 6000 J Street, Sacramento, CA 95819.

Many Native Americans in California have used teas (aqueous extracts) of *Datisca glomerata* medicinally for treating various medical conditions. An aqueous extract of this California plant was investigated for cytotoxicity towards breast cancer cell lines MDA-MB-231 and BT-474 grown in culture. The breast cancer cells and media was inoculated with different extract concentrations and, after 48 hours, the number of live cells in inoculated wells was compared to the number of live cells in un-inoculated control wells.

S38. BACE1 ENZYME IS NECESSARY FOR NORMAL OLFACTION BEHAVIOR IN MICE. Robyn Sumpter*[1], Sharon Gracey[2], Jenny Somers[2], (Jurgen Ziesmann[2]), [1]Vanguard University and [2]Azusa Pacific University, 901 E. Alosta Ave., Azusa, CA. 91702.

One of the first signs of Alzheimer's disease is a change in the sense of smell. BACE1, a key enzyme in the disease, may have a role in olfaction. We compared olfactory behavior between BACE1 heterozygous (+/-), knockout (-/-), and wild type C57BL/6 (+/+) mice. BACE1 (-/-) adults are viable, but show some cognitive deficits. Therefore, tests of olfaction, which involve conditioning or habituation, and hence require functioning memory capabilities, could not be used. We measured spontaneous behavior of mice in response to odorants that require no learning or training. We deprived mice of food for 12h and measured the time needed to start eating unscented or scented food. In the first set of tests, the food was visible. The knockout mice needed twice as long as wildtype mice, but adding a scent had no influence. In the second set of tests, the food was buried in bedding. The scent did not influence wildtype mice. Knockout mice found the unscented food as quick as wildtype mice, but needed twice as long to find the scented food.

S39. THE ORIENTATION OF A MIDLINE MARKER IN SUPERNUMERARY EYES OF *DROSOPHILA MELANOGASTER*. Alex Altomare* (M.C. McElwain), Loyola Marymount University, Department of Biology, 1 LMU Dr. Los Angeles, California 90045.

The *extra eye* (ee) mutation in Drosophila melanogaster results in pattern duplications of the head morphology. Both the penetrance and expressivity are highly variable, responding to enhancers on chromosomes 1, 2, and 3. Extreme expression results in further duplication of the associated orbital structures. The ectopic eye often appears to be a mirror-image duplication of the ipsilateral eye. The stocks used in this experiment were constructed to carry the extra eye mutation along with a white-bearing P-element insertion on the third chromosome. This results in a stripe of dark pigmentation always running longitudinally through the middle of the eye (*Racing Stripe*, or RS). The position of the stripe of pigmentation in the supernumerary eye establishes the orientation of the extra eye and the extent of its development. Only large (>0.3mm) supernumerary eyes that are not fused to the normal eye were selected for scoring. Roughly 33% of the heads in the stock had such an eye. Although many extra eyes do not have a distinguishable stripe, among those with a stripe there is a distinct trend in orientation. This suggests that the ectopic eye is a mirror-image duplication of the ipsilateral eye.

Session H - BIOCHEMISTRY AND MICROBIOLOGY

S40. COMPARISON OF NATURAL AND ANALOG dNTP INCORPORATION INTO DNA BY T4 BACTERIOPHAGE POLYMERASE AND HUMAN DNA POLYMERASE α. Greg Timblin*[1] (Robert Kuchta[2]), [1]Nebraska Wesleyan University, Dept. of Biology, 5000 St. Paul Ave., Lincoln, NE 60504 and [2]University of Colorado, Dept. of Chemistry & Biochemistry, UCB 215, Boulder, CO 80309-0215.

B-family DNA polymerases display remarkable active site homology. The amino acids that surround an incoming dNTP and the template base during the replication process are highly conserved among enzymes within the family, suggesting that all B-family polymerases select for correct dNTPs by the same mechanism. The purpose of this study was to analyze the incorporation of various dNTPs into DNA by T4 bacteriophage polymerase and compare the results to dNTP incorporation by human pol α. Incorporation assays were ran to determine the kinetic parameters for the incorporation of both natural dNTPs and a series of analog dNTPs into radiolabeled DNA primer-templates by T4 polymerase enzyme. T4 bacteriophage polymerase showed higher discrimination against the incorporation of incorrect natural and analog dNTPs than human pol α, suggesting that it is a higher fidelity enzyme. T4 polymerase also showed a greater preference for incorporating benzimidazole analogs as purines than human pol α. Finally, upon "adding back" N-3 to a benzimadazole analog dNTP to form a 3-deazapurine analog, T4 polymerase showed both a greater preference to incorporate this analog opposite T and a greater ability to discriminate against its incorporation opposite A, G, and C than did human pol α.

S41. QUANTUM CHEMICAL QUANTIFICATION OF WEAKLY POLAR INTERACTION ENERGIES IN THE TC5B MINIPROTEIN. Marcus P. D. Hatfield*[1,2], (Sándor Lovas[2]), [1]Nebraska Wesleyan University, Lincoln, NE 68504; [2]Department of Biomedical Sciences, Creighton University, Omaha, NE 68178.

The importance of the weakly polar interactions in maintaining three-dimensional structures of polypeptides is an important topic in computational biology and chemistry. The tertiary structure of TC5B is stabilized by inter-residue weakly polar interactions of the Trp-cage ,which is composed of a tyrosyl and several prolyl residues surrounding a central tryptophanyl residue. The interactions included Ar-Ar (aromatic side-chain – aromatic side-chain), Ar-NH (Ar – backbone amide), Ar-CO (Ar – carbonyl) and CH-π (aromatic side-chain – aliphatic hydrogen) interactions. In the present work, the strength of the weakly polar interactions found in the TC5b miniprotein was quantified using state-of-the-art *ab initio* quantum chemical calculations at BhandHLYP/cc-pVTZ level of theory. The individual interaction energies of the Trp-cage ranging between 5 and 20 kcal mol^{-1} leading to a significant total stabilization energy of 52.13 kcal mol^{-1}.

S42. TOWARDS THE X-RAY CRYSTAL STRUCTURE OF P53R2, A P53 INDUCIBLE RIBONUCLEOTIDE REDUCTASE. Danny Nam Ho*, Cynthia Bui, Peter Smith (Sheryl Tsai), University of California, Irvine, Dept. of Biochemistry and Molecular Biology, West Peltason Dr., Irvine, CA 92697.

Cancer research has made great progress over the last few years. The enzyme ribonucleotide reductase (RR) is essential for providing dNTP, the building blocks in DNA replication and repair. RR is a tetramer composed of two homodimers, RRM1 and RRM2. RR is over-expressed in cancer cells and has been the topic of much cancer research. In 2000, a new protein, p53R2, was discovered and had an 80% homology to RRM2. However, unlike RRM2, p53R2 is induced in a p53-dependent manner. Further research into the structure of p53R2 will no doubt spark a plethora of new cancer research. These findings have made p53R2 an important target for cancer research. The goal of this project is to aid in the elucidation of p53R2, through crystallization and x-ray diffraction. Current progress has yielded diffraction data close to 4 angstroms. We are working towards greater resolution. The homology between p53R2 and RRM2, current progress in the project, and future paths of the research will be discussed.

S43. CRYSTALS AND KEYS: UNDERSTANDING AN IMPORTANT SUBUNIT OF ACYL CO-A CARBOXYLASE IN *MYCOBACTERIUM TUBERCULOSIS*. Shushmita M. Ahmed*, Ting-Wan Lin (Sheryl Tsai), University of California, Irvine, Dept. of Biochemistry and Molecular Biology, West Peltason Dr., Irvine, CA 92697.

Tuberculosis is a highly contagious, multi-drug resistant disease, and is the seventh leading cause of death worldwide. *Mycobacterium Tuberculosis* is characterized by a thick, waxy membrane composed of long fatty acids called mycolic acids. This contributes to the bacteria's resistance to antibiotics, disinfectants, and digestion by macrophages. As such, effective drug design should seek to block the formation of mycolic acids to make the bacteria more susceptible to treatment. A key component in mycolic acid formation is the multimeric enzyme Acyl Co-A Carboxylase. One important subunit of this complex is Acyl Co-A Carboxylase D5 (ACC D5). Through the crystallization of ACC D5 in both the apo form and with corresponding inhibitors, we hope to understand the structure of ACC D5 and effective ways in which the inhibitor interacts to prevent its activity. This will lay the foundation to future drug design in which we can specifically target ACC D5 so as to limit the production of cell wall lipids.

S44. MEASURING INTERNAL MN LEVELS AND ESTABLISHING THE UPTAKE TREND IN *CAENORHABDITIS ELEGANS* USING ICP-MS. Lihini Keenawinna* (C. Srinivasan), California State University Fullerton, Department of Chemistry and Biochemistry, 800 N. State College Blvd, Fullerton, CA 92831.

Oxidative stress is caused by toxic free radicals which are by-products of metabolism and has been associated with aging and age-related neurodegenerative diseases. Prior studies have shown that supplementing Mn in the form of $MnSO_4$ is beneficial to *Caenorhabditis*

elegans. These studies also indicated a pattern where $MnCl_2$ is detrimental to the nematodes. In the current study, the accumulation of Mn in *C. elegans* was measured in 1000 worms undergoing development (egg→ L4) with Mn supplementation in the form of $MnSO_4$ and $MnCl_2$. This study was performed to understand the discrepancy between the two forms of supplementation. A time course study was performed to establish a trend in Mn uptake. Studies were done using synchronous populations grown on plates containing $MnSO_4$ or $MnCl_2$. The nematodes were extracted, digested and the levels of Mn55, Fe57, Zn66, Cu63 and Cu65 analyzed using inductively coupled plasma- mass spectrometry (ICP-MS). Results show that $MnSO_4$ is the more preferred form of Mn in comparison to $MnCl_2$. The nematodes accumulate Mn at an increasing rate through a 10-day-period and $MnSO_4$ was accumulated at a greater rate than $MnCl_2$. Trace metal interactions need to tested more to establish the mechanism of entry and to explain the preference.

S45. ACTIVATION AND TRANSPORT FUNCTIONS IN THE *SERRATIA*-TYPE HEMOLYSIN AND TRANSPORTER OF *CHROMOBACTERIUM VIOLACEUM*. Kyle Sally-O'Keefe* (Lamont Anderson), Department of Biology, Colorado College, 14 E. Cache la Poudre, Colorado Springs, CO 80903

The *Serratia*-type hemolysin and transporter are an example of a Two-Partner Secretion system in Gram$^-$ bacteria. The *Serratia* hemolysin has shown an absolute requirement for its cognate transporter for both activation and secretion across the outer membrane. Previous work [Brumbach, Eason, and Anderson, *FEMS Microbiol Lett*, **267** (2007) 243-250] established the presence of a *Serratia*-type hemolysin (ChlA) and transporter (ChlB) in *C. violaceum*, and a lytic phenotype for *E. coli* expressing ChlA in the absence of ChlB. We have examined this ChlB-independent lytic phenotypic by enzyme assay, complementation, and osmotic protection against lysis. Our results indicate that (a) in the absence of ChlB, accumulation of ChlA in the *E. coli* periplasm leads to leakage and lysis of the bacteria; (b) ChlA released in this manner forms pores in erythrocytes that are similar in size to those formed by ChlA that is secreted by ChlB; (c) ChlA released in this manner can be activated for more effective lysis by complementation with a ChlB-secreted activation domain (ChlA'); and (d) ChlB appears to allow egress of *E. coli* periplasmic enzymes, but only if it has transported ChlA.

POSTERS

P1. CORTICAL BONE THICKNESS IN RESPONSE TO AGE IN CARNIVOROUS MAMMALS. Brian Scrivens* and Theresa Sexton* (Wendy Binder), Loyola Marymount University, Dept. of Biology, 1 LMU Drive, MS 8220, Los Angeles, CA 90045.

The diets of carnivorous mammals can lead to increased stress on the jaw. As stress increases, bone can remodel and cortical bone in the jaw can become thicker, better resisting those forces. Previous experiments have shown a correlation between cortical bone thickness and age in carnivorous mammals. We collected data which allowed us to compare age with thickness of cortical bone in the lower jaw from jaws of seven species of carnivorous mammals from families Canidae, Felidae, Ursidae, Mustelidae, and Procyonidae. Our data showed no such relationship; in fact it demonstrated a decreasing relationship for sea otters and raccoons. This data was then added to a data set previously collected by Dr. Wendy Binder. We examined whether including the data would support or weaken the findings of Dr. Binder's previous research. We observed an increase in cortical bone thickness with age for families Felidae and Ursidae which was consistent with Dr. Binder's findings. However, Canidae showed a decrease in thickness with age. We then examined how the R^2 values changed when both data sets were combined. Adding new data increased the R^2 value of the Felidae data but decreased the R^2 values of both the Canidae and Ursidae data.

P2. THE COST AND EFFECTIVENESS OF SMALL-SCALE CONTROL METHODS ON FENNEL, *FOENICULUM VULGARE,* IN NATIVIDAD CREEK PARK, SALINAS, CA. Abigail Gwinn* (Laura Lee Lienk), California State University, Monterey Bay, Return of the Natives Restoration Education Project at the Watershed Institute, Building 42, 100 Campus Center, Seaside, CA 93955.

This study examines three control methods for fennel (*Foeniculum vulgare*) in a small-scale infestation in two sites in Salinas to determine which is most effective while costing the least. The methods are: digging out individual plants, chopping the plants repeatedly during the summer with a machete, and chopping the plants and immediately spraying the stumps with an application of the herbicide Rodeo. I discovered that the most effective method was digging each plant individually, with chopping and spraying with herbicide a close second. I also found that the least expensive method was chopping and spraying with chopping repeatedly a close second. Digging the individual plants was the most time consuming and therefore the most expensive. Based upon my results, my recommendation for controlling small-scale fennel invasions for areas difficult to dig in is chopping and spraying each plant with an herbicide. For smaller infestations with softer soils digging up each individual plant is the best treatment method.

P3. ETHEPHON TRIGGERS GERMINATION IN THE SAND VERBENA *ABRONIA UMBELLATA* (NYCTAGINACEAE). Kelly Ahern, Sauda Bholat, Terry Dial, Serena Fermin, David Flick, Betty Lobanov, Natalia Michan, Theresa Sexton, Rosanna Tomiuk, Kaewalynn Wittayasiripaiboon (Philippa Drennan) Loyola Marymount University, Biology Department, 1 LMU Drive, Los Angeles, CA 90045.

Abronia umbellata has been displaced along the sandy beaches of southern California by development as well as the invasive *Carpobrotus edulis* which was often planted to stabilize dunes. Restoration efforts require the propagation of *A. umbellata* plants from seed collected from local remnant populations. In laboratory studies germination percentages for *A. umbellata* are typically low, even with pretreatments such as scarification (SEALab, Los Angeles Conservation Corps). In the present study, the effect of the plant hormone ethylene (provided by the application of ethephon) on germination was investigated. Germination exceeded 90 % at all concentrations of ethephon tested (10, 100, and 500 μmol l^{-1}). The rate of germination was highest at 500 μmol l^{-1} ethephon. Thus ethephon significantly triggered germination suggesting ethylene is the germination cue for this species. This outcome may provide a common physiological mechanism behind other successful germination pretreatments. Furthermore, identifying ethylene as a germination cue opens the potential for further investigation regarding the reintroduction of *A. umbellata* along the Pacific Coast beaches.

P4. ISOLATION OF THERMOPHILES FROM LUND HOT SPRINGS, UTAH. Kenny Robinson* (Charlotte Rosendahl), Southern Utah University, Dept. of Biology, 351 West University Boulevard, Cedar City, UT 84720.

Thermophiles are prokaryotic organisms that can grow above 45 ^{o}C. These organisms are valuable since their enzymes can be used in the biotechnology industry because they can function under conditions that would normal denature enzymes from mesophilic organisms. In this study, two different microorganisms have been successfully isolate on two different media from a pool at 65 ^{o}C at the Lund Hot Springs in Utah. Currently identification by 16s DNA sequencing is in progress and will be discussed. Data on the exact temperature ranges and the optimal growth temperature will be presented. Total DNA has also been isolated from the hot springs and future experiments investigating culturable and non-culturable microorganisms will be discussed.

P5. IN SITU MEASUREMENTS OF HYDROPHOBIC ORGANCIC CONTAMINANTS IN BALLONA WETLAND AND CREEK. Patrick M. Carter,* (Rachel G. Adams, John Dorsey) Loyola Marymount University, Dept. of Natural Science, 1 LMU Drive MS 8160, Los Angeles, CA 90045. Keith A. Maruya, and Jian Peng, Southern California Coastal Water Research Project, Costa Mesa, CA

The Ballona Creek Estuary is an impaired water body for which the development of Total Maximum Daily Loads (TMDLs) for several hydrophobic organic contaminants (HOCs) is currently underway. The Ballona Wetlands, which are part of this urban watershed,

have been designated as an ecological preserve and restoration is planned; however, the levels of HOCs in the wetlands have not yet been quantified. It is important to measure these chemicals as elevated concentrations may have adverse impacts on the wetland's ecosystem. In order to assess HOCs including selected polychlorinated biphenyls (PCBs), polycyclic aromatic hydrocarbons (PAHs), and chlorinated pesticides, passive samplers (polyethylene devices, PEDs) were used to measure the dissolved concentrations of these TMDL-regulated contaminants. PEDs were deployed at four locations within the wetland and one site in the creek. Upon sampler recovery, the HOCs were extracted from the PEDs and analyzed using a gas chromatograph-mass spectrometer (GC-MS). Using water equilibrium partitioning coefficients and corrections for non-equilibrium cases, the concentration of each analyte dissolved in water was calculated. For example, dissolved phenanthrene concentrations ranged from 20 – 50 ng/L and pyrene concentrations ranged from 2 - 20 ng/L. To our knowledge, these are the first measurements of dissolved PAHs in the wetland. This preliminary study will allow the current state of the Wetland to be assessed and facilitate future studies to examine possible sources and sinks of PCBs, PAHs, and pesticides in the Ballona Wetlands.

P6. MICROBIAL DIVERSITY OF NATIVE AND FE(III)-ENRICHED CONSORTIA FROM THE SEDIMENT-WATER INTERFACE OF AN ESTUARINE COASTAL WETLAND. Kelsey Unruh*, Amy Hebling, Stefan Spring (David Cummings), Point Loma Nazarene University, Department of Biology, 3900 Lomaland Dr, San Diego, CA, 92106.

The activity of microbes plays an important chemical role in the interface between water and soil in an estuary. This research is focused on iron reduction by iron- and sulfate-reducing bacteria (FeRB and SRB) at the Tijuana River Estuary. Estuary sediment microcosms were amended with electron donor, acceptor, or molybdate (an SRB inhibitor) to test for iron reduction. Our results indicated that additional organic carbon did not seem to affect the amount of iron reduction occurring. Additional Fe(III) (as ferrihydrite) significantly increased the amount of iron reduced overall. Fe(III) was reduced in the presence and absence of molybdate, indicating a role for both FeRB and SRB in the process. To identify specific FeRB and SRB, we created three 16S rDNA clone libraries using DNA extracted from the top 3 mm of soil from the estuary. ∗-Proteobacteria clones dominated the unamended sediment. Many clones were matched to other unidentified clones within the phylum. Microcosms with and without molybdate were dominated by (-Proteobacteria clones, 46 and 20 in each library, respectively. Members of the genera *Marinobacterium, Shewanella,* and *Pseudomonas* constituted the greatest frequency of genera present. Of all three libraries, (-Proteobacteria dominated, constituting 76 of the 187 total clones.

P7. BIOMAGNIFICATION OF WETLAND CONTAMINANTS IN GARDEN SPIDERS. Charisse Sy* (James Landry, Jeremy McCallum, Martin Ramirez), Loyola Marymount University, Dept. of Biology, 1 LMU Drive, Los Angeles, CA 90045.

As predators, spiders periodically consume insects containing heavy-metals. The purpose of this study was to assess the presence of heavy metals (Cd, Cu, Ni) in the bodies of a garden spider (*Argiope aurantia*) at a contaminated vs. a relatively uncontaminated site in the Los Angeles area. During July 2006, female spiders were collected at the Ballona Wetlands, a highly metal contaminated site, and from roadside vegetation 2 miles away. In lab, spiders were weighed (mg), and then frozen, dried, and subjected to microwave acid bomb digestion, as a prelude to atomic absorption spectroscopy to determine whole-body metal concentrations. T-tests were used to compare differences in mass specific concentrations (ppm) of the metals in spiders from the two sites [Ballona Wetlands (n=7), Westchester Parkway (n=6)]. Of the three metals, only Cu differed significantly between sites ($p < 0.01$), with Westchester Parkway having a higher mean concentration (111.48 ppm) than the Ballona sample (45.65 ppm). Thus, Ballona spiders had less than half the Cu metal load of Westchester Parkway spiders. This unexpected outcome may reflect the presence of significant heavy metal fallout due to jet engine exhaust at the Westchester Parkway site, which is adjacent to the Los Angeles International Airport.

P8. EXPLORING BACTERIAL DIVERSITY IN THE BALLONA WETLANDS BY BIOCHEMICAL IDENTIFICATION AND COMMUNITY PROFILING. P. Carter*, T. P. Nguyen and N. Yu (John Dorsey and Gary Kuleck), Loyola Marymount University, Depts. of Biology and Natural Science, 1 LMU Drive, Los Angeles, Ca 90045.

Ballona Wetlands receives water from the Ballona Creek Watershed which drains a large portion of Los Angeles. While a major health concern is the presence of pathogenic bacterial species from fecal contamination, the role of the Wetlands in reducing general microbial contamination is also of interest. To identify fecal indicator bacteria, water samples from a tidal channel were tested for the presence of *Escherichia coli* using the IDEXX Colilert Test. Samples positive for *Escherichia coli* were cultured and morphologically distinct colonies were further biochemically tested using the bioMerieux VITEK-60 system. Preliminary analysis identified three bacterial species: *Escherichia coli, Providencia stuartii,* and *Vibrio fluvialis.* To study wetlands microbial population dynamics, DNA will be isolated from community samples, the 16S rRNA and 23S rRNA gene region amplified by PCR and TOPO cloned for DNA sequencing. The 16S rRNA sequence can be used for identification; the intergenic spacer region contains species-specific length heterogeneity information. Using ARISA (Automated Ribosomal Intergenic Spacer Analysis), community profiling can provide both the identity of microbial species and semi-quantitative relative abundance without bacterial culturing. Using these techniques, we have begun to examine the factors which influence microbial populations in the Wetlands. (Sponsored by a AAAS-Merck Undergraduate Research Award, 2006-2008)

P9. THE THERMOTOLERANCE OF ALGAE IN EXTREME TEMPERATURES. Brittany Burkhead, Courtney Nau, and Stephanie Ong* (Dennis Englin and Jairaj S. Gorlla), The Master's College, Dept. of Biology, 21726 Placerita Cyn. Rd., Santa Clarita, CA 91321-1200.

Thermal tolerance may be an important mechanism by which cyanobacteria and algae adapt to novel environments. Several mechanisms of thermotolerance in plant/fungal symbionts have been documented. Algal symbionts have been shown to enable some coral to adapt to warmer water temperatures. In this study, the thermotolerance of mixed algae collected from varied ponds in Southern California was tested in a hot water bath at an average of 68°C for 5 hours. Appreciable differences in pH and iron levels were observed before and after the algae were subjected to higher temperatures. Several species survived the hot water treatment. Our data suggest that supplemented nutrients (Knop's solution) may have contributed to the survival of the algae. This study may help us to analyze and understand algal relationships which promote thermotolerance of algae in extreme environments such as the thermal hot springs of Yellowstone National Park.

P10. ABILITY OF MANGANESE SUPPLEMENTATION AT EXTENDING THE LIFESPAN OF *CAENORHABDITIS ELEGANS*. Keyan Matinpour* (T. Richard Parenteau, and Chandra Srinivasan), California State University, Fullerton Dept. of Chemistry Biochemistry 800 North State College Blvd., Fullerton, CA, 92831.

Regular cellular metabolism produces reactive oxygen species (ROS), which, if left unchecked, can cause significant biological damage. Organisms cope with oxidative stress through naturally occurring antioxidant enzymes and compounds. During aging an organism becomes less efficient at managing the balance between ROS and antioxidants, which is hypothesized to exacerbate aging and some age related diseases. Thus, discovery of antioxidant compounds could potentially increase lifespan and protect against problems associated with aging. Recent studies have revealed that manganese supplementation is capable of protecting bacteria, yeast and *C. elegans* against oxidative stress. This study investigated the efficacy of manganese supplementation at extending the lifespan of *C. elegans*. Worms were placed onto plates containing 0, 1 or 10 mM of $MnCl_2$ and $MnSO_4$ and the lifespan of the worms was measured. These results suggest manganese supplementation increases lifespan. Supplementation at 10mM increased survival by over 10% compared to control. Comparison between the two manganese salts showed at 1 mM, the sulfate extended lifespan further than chloride, while the inverse was true at 10 mM. Future studies will investigate the beneficence of higher doses of manganese salts, as well as that of various large manganese containing compounds, at extending lifespan.

P11. THE GLOBAL TRANSCRIPTIONAL RESPONSE OF *SACCHAROMYCES CEREVISIAE* TO COLD SHOCK AND RECOVERY. Elizabeth M. Liu* and Olivia S. Sakhon* (Kam D. Dahlquist), Loyola Marymount University, Department of Biology, 1 LMU Drive, Los Angeles, CA 90045.

Previous studies on the global transcriptional response of budding yeast, *Saccharomyces cerevisiae*, to cold shock have revealed that the response can be divided into a set of early response genes (after 15 minutes to 2 hours of cold temperatures) and late response genes (after 12 to 60 hours of cold temperatures). The late response genes include the ESR genes induced by many environmental stresses, but less is known about the early response genes. We have extended these earlier findings to characterize more fully the early transcriptional response at 15, 30, and 60 minutes of cold shock at 13°C and also the response to recovery after cold shock for 30 and 60 minutes at 30°C using DNA microarrays. After 60 minutes of recovery from cold shock, gene expression returned to pre-cold shock levels. Results were analyzed using the program GenMAPP (Gene Map Annotator and Pathway Profiler) to determine which biological pathways and processes were activated in response to cold shock and recovery. We found that genes involved in ribosome biogenesis, zinc ion homeostasis, and arginine biosynthesis were induced in the early response to cold shock.

P12. DETERMINATION OF THE PARAMETERS OF VIABILITY OF *BAYLISASCARIS PROCYONIS.* Jon Kibbie* and Teresa Sorvillo (Shira Shafir), Loyola Marymount University, Department of Biology, 1 LMU Drive, Los Angeles, CA 90045 and UCLA, Department of Epidemiology, 650 Charles E. Young Dr., Los Angeles, CA 90095.

Baylisascaris procyonis, the intestinal roundworm of raccoons, can result in human infection, typically in children, when embryonated eggs are ingested. While there have been fewer than 20 diagnosed cases, all human infections have either been fatal or resulted in permanent neurologic damage. This study attempted to determine the thermal death point as well as the impact of freezing and desiccation on *B. procyonis* eggs. Eggs were harvested from the uteri of adult female worms and were allowed to embryonate over three weeks. To determine the thermal death point, a mixture of infectious eggs and sterile water was heated in five degree increments over a temperature interval of 37°-67° C. To determine the length of time infectious eggs were able to withstand freezing temperatures, eggs were exposed to an environment of -15°C for six months and examined monthly. To determine the ability of infectious eggs to survive total desiccation, eggs were allowed to dehydrate over the period of seven months and examined monthly. Larval viability was determined by two methods; larval motility and affinity for Methylene blue. Loss of viability resulted when eggs were heated to 62°C, or desiccated for seven months, but not when exposed to -15°C for six months.

P13. THE SURVIVABILITY OF HUMAN SCENT AFTER ENVIRONMENTAL EXPOSURE. Krystal Crawford* and Serina Harvey* (Lisa M. Harvey), Victor Valley College, Dept. of Biology, 18422 Bear Valley Rd., Victorville, CA 92395.

Bloodhounds have been used for centuries by law enforcement to find missing persons and capture fleeing felons. Human scent collected from an article touched at the crime scene is presented to a bloodhound for trailing. Anecdotal evidence suggests that human scent does not survive in real-world scenarios longer than 24 to 48 hours. Since human scent is considered to be composed of mainly organic molecules one would assume that decomposition of these molecules would occur under various weather conditions. The aim of the study was test the prolonged survivability of human. Between five and nine bloodhounds, trained in human scent discrimination were used. These dogs were placed on trails in environments that simulated real-life scenarios. The trails were left for 48 hours, 1 week, 4 weeks and 7 years before being run by the bloodhounds. Results indicate that bloodhounds can accurately trail individuals whose scent has been laid down up to 7 years prior. These results may help to explain why some dogs have difficulty finding people in their own neighborhood, since multiple trails are laid over the years in various directions. It would appear that bloodhounds may need to be specifically trained in environments that contain aged trails.

P14. THE SURVIVABILITY OF HUMAN SCENT AFTER EXPOSURE TO NINHYDRIN. Kevin Chow* (Lisa M. Harvey), Victor Valley College, Dept. of Biology, 18422 Bear Valley Rd., Victorville, CA 92395.

Human scent is thought to be made up of a milieu of volatile chemicals both organic and inorganic in nature. These volatiles are known to be excreted from the body through sweat, saliva and urine. Since human scent can be excreted through the sweat it may be left behind in the form of a fingerprint. These same fingerprints may be the only known scent left behind by the individual. Fingerprints left on porous material cannot be lifted by the traditional powder method, but instead must be developed using ninhydrin. The present study was designed to test whether ninhydrin affects the stability of human scent. Five bloodhounds, trained in human scent discrimination were used. The dogs were presented with paper envelops that contained handprints sprayed with ninhydrin. The prints were evident by a purple discoloration of the white envelops. The dogs ran a total of 114 trails with 102 correct trails and 12 incorrect trails. Since there was no significant different in the ability of the bloodhounds to trail and find the correct person using scent found on envelops sprayed with ninhydrin verses control envelops, the ninhydrin contaminated scent may still be used as viable evidence in a criminal investigation.

P15. MEDIA OPTIMIZATION OF *HYPERICUM PERFORATUM* L. MERISTEM CULTURES. R. Donlon* (T. M. Sirvent), Vanguard University, 55 Fair Drive, Costa Mesa, CA 92626.

Hypericum perforatum L., or St. John's wort is a traditional herb that has significant and varied biological activity: antibiotic, antifungal, anti-depressive and anti-cancer effects. The hypericins are a family of at least 5 compounds that may play a role in the biological activity of the herb. Hypericins are localized within small black glands along the leaf and petal margins of *H. perforatum*. *H. perforatum* is relatively easy to culture in a sterile environment and we present our results on optimizing the media for high production of hypericins. In particular we are interested in the effect of Phytoblend.™ Phytoblend™ is a blend of multiple agars designed specifically for tissue culture produced by Caisson Labs. Phytoblend™ is comparable to "Phytagar" that was previously sold through Invitrogen. The fresh and dry weights of *H. perforatum* cultures as well as hypericin concentrations are reported.

P16. METHODS TOWARDS CLONING PKS GENES FROM *HYPERICUM PERFORATUM*. J. Badoud*, B. Lay (T. M. Sirvent), Vanguard University, 55 Fair Drive, Costa Mesa, CA 92626.

St. John's wort (*Hypericum perforatum* L.) is a perennial herb that had been traditionally used in folk medicine because it has been found to have antidepressant, antiviral and possibly anticancer properties. The antiviral properties of *H. perforatum* can be attributed to a family of hypericins localized in small black glands that dot the margins of the leaf and petal tissues. Hypericins are anthraquinones that are light activated. The hypericin family consists of at least 6 compounds: hypericin, pseudohypericin, protohypericin, protopseudohypericin, isohypericin, and cyclopseudohypericin. These compounds are thought to be synthesized via polyketide synthetases (PKS). Polyketides are secondary metabolites, which can be isolated from plants, fungi and bacteria. We present an optimized method for extracting genomic DNA suitable to be used in a degenerate PCR approach in cloning putative PKS fragments in *H. perforatum*.

P17. PLANT GENES FOR SUNSCREENS – A HYBRID CHEMISTRY/BIOLOGY APPROACH. M. Claire Edwards*[1] and James R. Furr[2] (Michelle M. Bushey[2] and James R. Shinkle[1]) Trinity University Department of Biology (1) and Department of Chemistry (2) One Trinity Place, San Antonio TX, 78212-7200.

Long before human activity altered the ozone layer plants have been responding to changes in the amount of damaging ultraviolet light (UV) in their environments. Among these responses is the synthesis of UV-absorbing pigments. A prevalent group of UV-absorbing pigments are the flavonoids, complex polyphenolic molecules that are costly to make. Plants adjust pigment synthesis in response to UV exposure. We are using analytical chemistry paired with genetic dissection of flavonoid synthesis pathways to understand how UV sensing is used to regulate the process. We are developing capillary

electrophoresis (CE) methods to identify pigments from *Arabidopsis thaliana* and cucumber seedlings, taking advantage of variations in responses to UV exposure and genetic stocks carrying mutations in genes for enzymes involved in flavonoid synthesis. Short wavelength (280-300 nm) UV-B causes accumulation of pigments that absorb specifically in this part of the spectrum. To identify these pigments, methanol extracts were analyzed by CE coupled with a photodiode array spectrophotometric detector. Candidate pigment molecules are likely present in peaks found at two retention times that exhibit absorption in the 260 nm range only in samples from UV-treated plants. Variations in responses depending on genetic backgrounds have also been characterized. Sponsored by HHMI and Merck/AAAS.

P18. EVOLUTIONARY ANALYSIS OF *CCS* AND *LCY-B* HOMOLOGS IN *CAPSICUM ANNUUM* AND RELATED SPECIES. Heather Highland*, Winston H. Bowen (Kevin Livingstone) Trinity University, Dept. of Biology, 1 Trinity Pl., San Antonio, TX 78212.

Carotenoids are the vibrant red and orange pigments seen naturally in many ripening fruits. This pigment production is thought to be under natural selection due to the role of pigments in attracting seed dispersing animals. Capsanthin and capsorubin are the main carotenoids found in *Capsicum annuum* (chile pepper) fruits. *Capsanthin-capsorubin synthase* (*Ccs*) is the result of a duplication of *Lycopene β-cyclase* (*Lcy-B*) locus, which acts earlier in the pathway. In *Capscum annuum*, this duplicated gene has developed capsanthin-capsorubin synthase activity which is not seen in other closely related species. Knowledge of the function of both *Ccs* and *Lcy-B* makes this gene duplication useful for studying the changes in gene duplicates that occur due to the pressures of natural selection. We have sequenced 15 *Ccs* homologs from *Capsicum, Solanum,* and other related *Solanaceae* species. The identity of the *Ccs* DNA sequences show identity greater than 98.5% within groups (*Capsicum, Solanaceae,* and *Tabacum*) and an average of 90% identity between groups. The protein sequences of Ccs homologs have greater than 96% identity within groups and an average of 89% identity between groups. The sequences are currently being analyzed with PAML for evidence of positive selection.

P19. RESVERATROL, A CONSTITUENT OF RED WINE, INCREASES ANTIOXIDANT LEVELS AND PREVENTS DAMAGE FROM CIGARETTE SMOKE IN HUMAN BRONCHIAL EPITHELIAL CELLS. Albert Shih*, Hongqiao Zhang, and Alessandra Rinna (Henry Jay Forman), University of California at Merced, Merced, CA95343.

Resveratrol is a compound that exists in grape skin and red wine and has been suspected to be responsible for the beneficial effects of red wine. However, the mechanism underlying these beneficial effects still need to be further identified. In this study, we investigated the effects of resveratrol on the antioxidant (glutathione) level and its potential protection of cigarette smoking in lungs. Glutathione is the master antioxidant that maintains the redox homeostasis and is critical to protect lungs from damage caused

by xenobiotics including cigarette smoke and other airborne toxins. We first found that resveratrol dose-dependently increased glutathione levels in human lung epithelial cells. To define the mechanism, we determined the mRNA levels of the catalytic and modulator subunits of glutamate cysteine ligase (GCL), the rate limiting enzyme for glutathione synthesis, and found resveratrol increased the mRNA levels of both subunits. We then checked if resveratrol could protect bronchial cells from damage caused by cigarette smoking. Resveratrol eliminated the lipid peroxidation level caused by cigarette smoking extract (CSE), and furthermore, it prevented cell death caused CSE exposure. Moreover, the protective effects of resveratrol on CSE was abrogated by L-buthionine-(S,R)-sulfoximine (BSO), a specific inhibitor of GCL. Our data suggest that resveratrol could increase the antioxidant level in the human bronchial epithelial cells and thus potentially prevent harmful effects caused by cigarette smoking and other air pollutants.

P20. METABOLIC RATE DEPRESSIONS CAUSED BY LAMOTRIGINE INDUCE ANTI-AGING ARTIFACTS IN *DROSOPHILA MELANOGASTER.* Behnood Khodayari* (Dr. Mahtab Jafari), 3103 McGaugh Hall, University of California Irvine, Irvine, CA 92697.

There are a number of potential confounds that need to be addressed in anti-aging pharmacology. Previous reports suggest that supplementing model organisms such as *C elegans* and *Drosophila melanogaster* with anticonvulsant drugs can increase life-span. None of these studies systematically evaluated the established trade-off between metabolic rate and anti-aging properties. We performed a number of dose finding assays to evaluate the impact of lamotrigine, an anticonvulsant drug, on the mortality rate of *Drosophila*. Lamotrigine at 6 and 12 mg/ml doses resulted in a significant decrease in mortality rate in male and female flies ($P < 0.05$). Dose reflects the concentration of lamotrigine in the yeast paste that flies consumed during these assays. The main objective of this study was to evaluate the impact of lamotrigine on metabolic rate using *Drosophila melanogaster* as the model system. Since we observed anti-aging properties with lamotrigine at 6 and 12 mg/ml, we proceeded to evaluate the impact of this compound at these doses on metabolic rate. Metabolic rate was measured using CO_2 as a biomarker for physiological changes in metabolic activity. CO_2 production in flies that were fed lamotrigine for ten days was compared to that of a control group handled in parallel and assayed simultaneously. Measurements of CO_2 were made using a Licor LI-6260 gas analyzer. CO2 levels were averaged and recorded every second using data acquisition software (Sable Systems). Our results indicate that lamotrigine at 6 and 12 mg/ml significantly decreased metabolic rate in compiled medicated male flies ($P<0.05$). In female flies, although not statistically significant, a trend towards metabolic rate depression was observed. These results imply that the observed lamotrigine anti-aging properties may be due to a reduction in metabolic rate. Our results suggest that metabolic rate should be systematically evaluated during the screening phase of anti-aging compounds.

P21. THE EFFECTS OF SU(VAR) $2\text{-}4^{01}$ ON THE RACING STRIPE PHENOTYPE. Aracely Dominguez, Joseph Russell, Termeh Toufanian (Catharine McElwain), Loyola Marymount University, Dept. of Biology, 1 LMU Drive, Los Angeles, CA, 90045.

The *Racing Stripe* (RS) phenotype results from a white gene located ectopically on the third chromosome in *Drosophila melanogaster* and carried on a P-transposable element. While a white gene would normally result in a completely redeye, the ectopic location of this gene results in only a red stripe across the center of the eye. It is recessively lethal, but present phenotypically in heterozygous genotypes that are homo- or hemizygous for the white mutation on the X chromosome. The gene *extra eye (ee)* is on the second chromosome, and is thought to result from a P-transposable element insertion. Selection for modifiers of *extra eye* results in alteration of the *Racing Stripe* phenotype. Su(var) has been shown to modify the expression of *extra eye*. After surveying several Su(var) stocks, it was noted that Su(var) $2\text{-}4^{01}$ had the greatest effect on the expressivity of RS phenotype. In this study, Su(var) *non-curly (Cy+)* fruit flies were compared against their non-Su(var) *Curly(Cy0)* siblings. Su(var)2-4 increases the pigmentation in RS eyes.

P22. THE EXCISION OF THE P-ELEMENT INSERTION AT 26D1, THE PUTATIVE *EXTRA EYE* MUTATION IN *DROSOPHILA MELANOGASTER*. Sauda Bholat*, Paulina Esparza*, Chris Luk*, Laura Quintero*, Kyle Webster* (M. Catharine McElwain), Loyola Marymount University, Department of Biology, 1 LMU Drive, Los Angeles, CA 90045.

The mutation *extra eye*, *ee*, in *Drosophila melanogaster* is a spontaneous mutation which often results in an ectopic eye. The mutation is usually recessive with incomplete penetrance and variable expressivity. Conditional dominance has been observed when mutant flies are mated to some P-element lines and the hetero progeny show some *ee*. *Extra eye* is thought to be due to a P-element insertion at chromosome band 26C3. It is suggested that the P-element insertion might result in the inactivation of the nearby tyrosine phosphatase gene (*Pez*). This is supported by the observation that the over expression of *Hop*, a tyrosine kinase gene, also results in ectopic eyes. However, recent evidence casts doubt on this model. We have undertaken a formal proof for this model, the excision of the P-element resulting in reversion of *ee*. Due to the variable expressivity and penetrance of *ee*, we designed our experiment to maintain the markers in the high expression line *JG*. Among the first 60 lines, we have observed 1 lethal line and 3 lines showing no *ee* expression. Preliminary PCR of 1 line with no *ee* expression indicates that the P-element has been lost.

P23. SEX DIFFERENCES IN THE EFFECTS OF ETHANOL DEPENDENCE AND WITHDRAWAL ON BODY TEMPERATURE IN RATS. Amy H. Truong*, Stephen Gardner, Christine Kim, William Lee, Chloe Sui, Delia Tio, Anna N. Taylor. UCLA, Dept. of Neurobiology, Los Angeles, CA 90095.

Studies have shown that GABAergic neuroactive steroids, such as the progesterone derivative allopregnanolone, may mediate behavioral responses in EtOH-dependence/withdrawal though their contribution to physiological adaptations such as thermoregulation remains unknown. We have been studying the effects of EtOH on thermoregulation of male and female Sprague Dawley rats. We have found that upon depletion of progesterone by combined ovariectomy and adrenalectomy procedures, differences in male and female hypothermic responses to acute EtOH challenge in EtOH-dependent and withdrawn were abolished. This suggests that neurosteroid derivatives of adrenal, ovarian, and testicular hormones play a role in mediating sex dependent effects of chronic and acute EtOH exposure on thermoregulation. The steroids that are specifically involved and responsible for these differential effects will be investigated in future studies. (Supported by Dept. of Veteran's Affairs and UCLA Academic Senate; AHTruong is a UCLA Undergraduate Research Scholar).

P24. ANALOGS OF THE ANTIHYPERTENSIVE AGENT DIAZOXIDE. Nandita Devi* (Michael P. Groziak), California State University, East Bay, Dept. of Chem. and Biochem., 25800 Carlos Bee Blvd., Hayward, CA 94542-3089.

The drug Diazoxide is a well known antihypertensive agent. As a mitochondrial ATP-sensitive K+ channel opener, it inhibits the release of insulin from the pancreas while inducing hypoglycemia. In addition, it also decreases the desensitization of the AMPA receptor—an excitatory amino acid receptor. Therefore, Diazoxide is now utilized in a therapeutic approach for treating learning and memory impairments like those in Alzheimer's disease. Studies of this receptor can reveal much about the memory and learning deficits observed in this disease. More recently, Diazoxide was discovered to have neuro-protective properties and is a potential anti-ischemic agent in the brain. Using the 3D structure of this drug as a template, we have designed, synthesized, and characterized several unique boron heterocycle analogs of Diazoxide. The characterization data supports a strong structural resemblance of these analogs to the drug itself, which is anticipated to lead to a similar, if not enhanced bioactivity.

P25. EFFECTS OF DIETARY FAT ON RETINAL DEGENERATION IN THE rd3 MOUSE MODEL. Kelly Ahern* (Michael Danciger), Loyola Marymount University, Department of Biology, 1 LMU Drive, Los Angeles, CA 90045.

In many cases, individuals inheriting the same mutation show retinal degenerative diseases (RD) with differences in severity. Much of the difference is due to background genetics, but some is due to environmental factors. One such factor may be the level of fat in the diet. To investigate this, we used two mouse strains each homozygous and

congenic for the rd3 mutation that causes a progressive RD early in life. Thus, rd3 BALB/cByJ (BALB) and rd3 C57BL/6J (B6) mice were weaned at 3 to 4 weeks of age and separated by sex and feeding regimen. One set was fed a normal diet and the other a high-fat diet. The BALB mice were sacrificed at 8 weeks of age and the B6 mice at 10 weeks – RD progresses faster in the BALB strain. After fixation, a single eye was embedded and bisected along the vertical meridian through the optic nerve head (OH). The outer nuclear layer (ONL) thickness of the retina was averaged from 18 equally-spaced sets of 3 measurements along a single section per eye from the far superior to the far inferior through the OH. Collection and analysis of results are underway and nearly completed. So far, we found that B6 males did not show any significant difference in RD between the two diets ($P = 0.838$) while B6 females showed a small, but significantly lower amount of RD on the high-fat relative to the normal diet ($P = 0.036$). Therefore, dietary fat intake may have a protective effect on females of at least one mouse strain undergoing *rd3*-induced RD. It is interesting that high-fat in the diet is protective for rd3 B6 females since some studies have shown that a high-fat diet exacerbates age-related macular degeneration, a more complex form of RD. This issue deserves further investigation.

P26. CONFORMATIONAL FLEXIBILITY IN TELOMERE-CAPPING PROTEIN-DNA COMPLEXES. Angela Hansen* (Martin P. Horvath), University of Utah, Department of Biology, 257 S 1400 E, Salt Lake City, UT 84112.

Telomeres, the protective ends of linear chromosomes, consist of tandemly repeated, species-specific DNA sequences. In *Oxytricha nova,* telomeres consist of $d(T_4G_4/C_4A_4)_n$ double-strand repeats where the GT-rich strand protrudes as a single-strand 3'-terminal extension. Previous crystal structures show telomere-binding protein (*On*TEBP-α) binds one 3'-terminal $d(T_4G_4)_{n=1}$ repeat. Because single-strand telomere extensions often exist as multiple repeats, we wondered if multiple proteins could bind at neighboring sites and if so, what such structures might look like?
We have tested repeat lengths of $d(T_4G_4)_n$, where $n = 3$, 6, or 9, allowing for multiple binding sites for *On*TEBP-α. Each single-strand telomere length was mixed with excess protein, i.e. $d(T_4G_4)_{n=3}$ received enough protein to saturate 4 binding sites. We explored these DNA-protein structures using solution-based methods: gel filtration chromatography, small angle x-ray scattering (SAX) and analytical ultracentrifugation (AUC). SAX and AUC revealed that our structure assumes multiple conformations and is surprisingly flexible. Unoccupied sites along the single-strand DNA could offer a molecular interpretation for such flexibility. Telomere-binding proteins probably evolved from proteins which bind single-strand DNA cooperatively. Non-cooperative binding detected in *On*TEBP-α has important implications for the evolution of telomere-binding proteins and their biological functions involving coordinated interactions with telomerase.

P27. LOCALIZATION OF BK CHANNELS IN MAMMALIAN VESTIBULAR SYSTEM. David Savin[1*], Rebecca Hu[2], Larry F. Hoffman[2] (Felix E. Schweizer[1]), [1]Department of Neurobiology, David Geffen School of Medicine at UCLA, [2]Division of Head and Neck Surgery, David Geffen School of Medicine at UCLA, 650 Charles E Young Dr S, Los Angeles, Los Angeles, California 90024.

Voltage and calcium activated potassium channels(BK) are important regulators of neuronal excitability. BK channels are generally thought to be colocalized with voltage gated calcium channels at presynaptic release sites and seem crucial for frequency tuning in non-mammalian vestibular and auditory hair cells. However, in mammalian auditory hair cells, BK channels have been reported to be localized towards the apical end, away from release sites (Pyott et al, 2004, 2007). We therefore decided to investigate the localization of BK channels in mammalian vestibular hair cells. Here we report on the distribution of BK channels in the rodent vestibular neuroepithelia using immunohistochemistry and laser scanning confocal microscopy. We find that a subpopulation of both Type I and Type II hair cells in the rat vestibular system do express BK channels and staining appears constrained to the medial striola in the utricle and to the central zone in the crista ampullaris. BK channel expression appears to be fairly uniform within the cell. Furthermore, we do not detect any BK-immunoreactivity in the afferent fibers. Taken together, our data indicate that BK channel expression in the mammalian vestibular system differs from the expression pattern in both the mammalian auditory and the non-mammalian vestibular system. (Supported by the NIH/NICDC DC007678 to FES.)

P28. FLAGELLAR MOTOR PROTEIN INTERACTIONS. Rithy Meas* (Donna L. Marykwas), California State University, Long Beach, Dept. of Biological Sciences, 1250 Bellflower Blvd., Long Beach, CA 90840.

Motility of *Escherichia coli* is regulated by a sequential induction of three classes of genes. Class I gene products are important for expression of 30 Class II genes culminating in the assembly of the hook basal body complex. Three of these Class II gene products (FliG, FliM, FliN) are components of the CW/CCW switching complex. This complex determines if the cell swims forward in a "run" or erratically "tumbles." Using the yeast two-hybrid system for the identification of protein interactions, we have previously characterized the interaction between FliM and FliG and further identified the global transcription factor H-NS as a FliG-interactor. To better understand FliG's role as part of the switch complex and as a potential modulator of motility gene expression, we are further characterizing an interesting subset of *fliG* mutants for their affects upon motor function, swimming motility, and motility gene expression, to be described.

P29. APOA-1 MIMETIC PEPTIDE D-4F INCREASES PARAOXONASE ACTIVITY. Dien Tran* (Greg Hough), UCLA Cardiology, Dept. of Medicine, BH-307 Center for the Health Sciences, Los Angeles, CA 90095.

There are a number of enzymes associated with High Density Lipoprotein (HDL) that have anti-oxidant properties including paraoxonase (PON), platelet-activating factor acetylhydrolase, and glutathione peroxidase. These enzymes have the ability to prevent the formation of the pro-inflammatory oxidized phospholipids and to destroy the activity of these oxidized phospholipids once formed. However, these oxidized lipids negatively regulate the activities of these HDL-associated enzymes. We have developed an apoA-I mimetic peptide (D-4F) that when added to plasma that has lower than normal PON activity, it results in increased PON activity. We have also observed that the administration of D-4F to animal models of atherosclerosis, including primates, will result in increased PON activity. We are currently studying the mechanism (s) involved in this effect, and whether other apoA-I mimetic peptides may have beneficial effects supporting HDL function under conditions that result in low PON activity.

P30. LOSS OF INTERMEDIATE FLIAMENT PROTEINS LEADS TO ABNORMAL MUELLER CELL MORPHOLOGY AND INCREASED GANGLION CELL REACTIVITY IN THE RETINA FOLLOWING EXPRIMENTAL RETINAL DETACHMENT. Gabriel Luna[*1], Geoffrey P. Lewis[1], Jiyun Byun[3], Mark Verardo[1], (Steven K. Fisher[1, 2]). University of California, Santa Barbara, [1]Neuroscience Research Institute, [2]Department of Molecular, Cellular, and Developmental Biology, and [3]Department of Electrical and Computer Engineering, Center for Bio-image Informatics, Santa Barbara, CA 93117.

Glial fibrillary acidic protein (GFAP) and vimentin are both intermediate filament proteins thought to be responsible for supplying mechanical strength and shape to glial cells of the central nervous system (CNS). In addition, they provide the cyto-architectural framework required to support cellular growth. GFAP and vimentin are expressed predominantly by Mueller cells, the radial glial cells in the vertebrate retina. Mueller cells provide nutrition, support, and maintenance to the neurons of the retina. A large increase in the expression of GFAP and Vimentin occurs in Mueller cells after retinal detachment in humans and animal models. The lack of GFAP and vimentin in $GFAP^{-/-}$ $vimentin^{-/-}$ mice led to abnormal Mueller cell responses after retinal detachment. Mueller cell end feet complexes appeared to be fragile, easily separating from the inner retina. Increased reactivity of ganglion cells in the damaged areas suggests a link between Mueller cell end foot integrity and the maintenance of normal morphology of these neurons. We also discovered that Mueller cells lacking these two proteins were not able to form “glial scars” characteristic of injury to CNS tissue. The formation of glial scars can greatly compromise the recovery of vision in humans after retinal detachment repair.

P31. HYPERMETHYLATION OF THE *KLF4* PROMOTER IN ACUTE LYMPHOBLASTIC LEUKEMIA. Vanessa M. Scarfone[1]*, Michael G. Kharas[1], Isharat Yusuf[1], Matthew R. Janes[1] (David A. Fruman [1,2]), University of California-Irvine, [1]Department of Molecular Biology and Biochemistry, [2]Center of Immunology, Irvine, CA 92697.

KLF4 is a transcription factor that has been shown to participate in cell cycle control and has been identified as a tumor suppressor gene in colon and gastric cancer. Previous results from our lab have implicated KLF4 as a potential tumor suppressor in B-cell malignancies. Using a microarray database we identified low abundance of KLF4 expression in a variety of B-cell leukemias and lymphomas and ectopic KLF4 expression induced apoptosis in a variety of transformed B-cell lines. To further identify the role of and mechanism of KLF4 silencing in B-cell leukemias and lymphomas we assessed DNA methylation. Previous reports in colon cancer have shown hypermethylation of the KLF4 promoter as a mechanism for silencing. Here we show that the KLF4 promoter is methylated in human ALL and CML patient samples by Methylation Specific PCR. Our findings suggest that the KLF4 promoter methylation is specific and may account for the low abundance of KLF4 in leukemias and lymphomas.

P32. THE CO-INFECTION OF A SINGLE HUMAN T-CELL WITH HUMAN HERPES VIRUS-6 (HHV-6), HEPATITIS C VIRUS (HCV), AND HUMAN IMMUNODEFICIENCY VIRUS (HIV) Katherine Snyder* (Dr. Dennis Revie[+], Zaki Salahuddin[++]), California Lutheran University, Dept. of Biology, 101 Memorial Pkwy, Thousand Oaks, CA 91360

The significance of simultaneous infection by HHV-6 and HCV in HIV-infected individuals emphasizes the importance of understanding the consequent biological effects. We decided to determine whether T-cells, host cell type for all three viruses, could be co-infected with HHV-6, HCV, and HIV. T-cells were infected with HHV-6, followed by HIV, and finally with HCV. At CIMM we have biologically active HCV. Co-infection within a single human T-cell by all three viruses was confirmed using RNA/DNA assays, light microscopy, and transmission electron microscopy. Assays for the presence of viral DNA or RNA were performed by PCR or RT-PCR. We performed the biological studies at the California Institute of Molecular Medicine, and the molecular part was completed at CLU. Transmission electron microscopy was performed at the City of Hope Electron Microscopy Core facility to provide photographic evidence of the co-infection of single cells. The presence of HHV-6, HCV, and HIV in a population of T-cells emphasizes the significance of this system as a tool for understanding the pathologies. The simultaneous infection will allow the elaboration of cell-virus and virus-virus interactions, induction of pathogenesis, and the resulting disease progression. Accomplishing the co-infection of a single cell was an attempt to test the outer limits of the infection process. The achievement of multiple infections in a single cell was an interesting process and one I hope to further study so that we can understand the consequences of co-infections.

P33. CREATION OF MURINE-HUMAN RECOMBINANT IGG3 ANTIBODIES AGAINST THE GLUCORONOXYLOMANNAN (GXM) POLYSACCHARIDE COMPONENT OF *CRYPTOCOCCUS NEOFORMAN'S* CAPSULE. Angelica Riestra* and Kileen Mershon (Sherie Morisson), UCLA, Dept. of Microbiology, Immunology, and Molecular Genetics, 611 Charles Young Dr., Los Angeles, CA 90095.

Cryptococcus neoformans is an opportunistic fungus that causes life-threatening meningitis. Available treatment is not effective since 10-20% of treated individuals still die from the disease and treatment in AIDS patients does not eradicate the infection. Passive antibody (Ab) therapy is an alternative treatment that has shown promise, with mouse IgG1 extending the life-span of *C.neoformans*-infected mice. Preliminary studies in our laboratory found that mouse-human chimeric IgG3 also extended the survival of BALB/c mice infected with *C. neoformans* and C57BL/6J mice infected with *Cryptococcus gatii* when the antibodies were administered as immune complexes and at lower doses than other studies. To determine this antibody's unique properties, two mutant mouse-human IgG3 chimeric antibodies against the glucoronoxylomannan polysaccharide component of *C. neoforman's* capsule were constructed. One Ab contains an N297Q mutation in the C_H2 region which should prevent its glycosylation and diminish its effector functions. The other antibody contains a shorter IgG1 hinge. Both antibodies have been expressed in NSO/1 cells. After screening for the best antibody producing subclone is complete, the antibodies will be purified, characterized and their effects tested *in vivo* and *in vitro*. These results will provide insight about the mechanisms that IgG3 uses in providing protection against Cryptococcus.

P34. THE ROLE OF PROATHEROGENIC HDL IN MONOCYTE CHEMOTACTIC ACTIVITY IN RESPONSE TO APOLIPOPROTEIN A-I MIMETIC PEPTIDES. Garrett Perrin* (Mohamad Navab, Greg Hough), University of California, Los Angeles, 11803 Folkstone Ln., Los Angeles, CA, 90077.

HDL levels are well accepted as inversely related to atherosclerotic events in the general population. However, HDL levels alone may not necessarily indicate positive cardiovascular health. Finding a measure of HDL quality would lead to improved knowledge about atherosclerosis progression and possible direct correlations between HDL protective capacity and clinical events. Since proinflammatory HDL is associated with atherosclerotic events regardless of lipid levels, a treatment to convert proinflammatory HDL to anti-inflammatory HDL is needed. In order to achieve regression in atherosclerosis, HDL must transport macrophage-LDL-derived cholesterol out of the arterial wall. The major mediator of this process is apolipoprotein A-I (apoA-I). ApoA-I is both expensive to synthesize and difficult to distribute. Treatment of proinflammatory HDL with apoA-I mimetic peptides removed oxidized lipids and restored HDL antioxidant enzymes, thereby converting proinflammatory HDL into anti-inflammatory HDL. Since apoA-I serves to mediate efflux of cholesterol from foam cells, apoA-I mimetics that have the ability to improve apoA-I function can also improve HDL quality.

P35. ACCELERATION OF LEUKEMIC TRANSFORMATION IN CALM-AF10 TRANSGENIC MICE BY RETROVIRAL INSERTIONAL MUTAGENESIS.
Rachel Pierce* (Peter D. Aplan and David Caudell), National Institutes of Health, National Cancer Institute, Center for Cancer Research, 9000 Rockville Pike, Bethesda, MD 20892.

The CALM-AF10 fusion gene is seen in patients with both acute myeloid leukemia (AML) and acute lymphois leukemia (ALL). A mouse model was generated via insertion of a CALM-AF10 transgene into the mouse germline. The mice developed acute leukemia with incomplete penetrance and a long latent period; these findings suggest that additional events are needed for leukemogenesis. Identification of candidates for these additional events is being conducted through retroviral insertional mutagenesis. Neonatal CALM-AF10 mice were infected with MOLO4070LTR retrovirus. The infected CALM-AF10 mice developed leukemia at a mean age of 5.5 months, which was considerably accelerated compared to non-infected CALM-AF10 mice. An anchored PCR approach was used to identify the retroviral insertion sites. Of the insertion sites cloned from 7 mice, 3 common insertion sites and 8 cancer-related genes were identified. Insertion sites continue to be cloned in an effort to identify additional candidate genes. A future mouse model will be created after the collaborative genes are positively identified.

P36. APOA-1 MIMETIC PEPTIDES AND TETRAPEPTIDES AS POTENTIAL THERAPEUTIC AGENTS FOR ATHEROSCLEROSIS.
Jeryl Yu* (Greg Hough), UCLA Cardiology, Dept. of Medicine, BH-307 Center for the Health Sciences, Los Angeles, CA 90095.

High density lipoprotein (HDL) is known to have anti-atherogenic properties. This relates to reverse cholesterol transport and to prevention of LDL oxidation. HDL contains many apolipoproteins including apoJ. We have made several peptides based on apoJ amino acid sequence. One peptide containing ten amino acid residues, 113-122, was found to improve cholesterol efflux from macrophages while improving HDL anti-inflammatory properties significantly as well and inhibits lesion formation in apoE null mice (mice that lacks apoE and has high levels of LDL due to the liver's inability to metabolize LDL) We developed a second peptide containing only four amino acid residues (FREL, phenylalanine-arginine-glutamic acid-leucine) and demonstrated reduction of atherosclerosis by this tetramer in apoE null mice. FREL is biologically active in both mice and primates. We have determined the potential synergistic effect of the two peptides on atherosclerotic lesions in apoE null mice. In this study, the outcome of dietary FREL combined with apo-J peptide are being studied in apoE null mice for potential enhancement of benefits compared to the two peptides on their own.

P37. HIGH THROUGHPUT SCREENING OF THE *ESCHERICHIA COLI* GENE KNOCKOUT COLLECTION FOR MUTATOR AND HYPER RECOMBINATION PHENOTYPES. Anne Liu*, Katherine Kim, Bindu Patel, Cindy Tamae, and Katherine Tran (Jeffrey H. Miller), University of California, Dept. of Microbiology, Immunology, and Molecular Genetics, and The Molecular Biology Institute, 405 Hilgard Avenue, Los Angeles, CA 90095.

We have developed a rapid screening procedure for assaying each of the 4,000 strains in the *E. coli* knockout collection for increases in either mutagenesis or recombination by employing conjugative plasmids that contain mutations that need to either revert or be converted by recombination to wild-type in order to generate blue papillae on special indicator media. Combined with the use of a cryoreplicator that allows printing of frozen microarray dishes, the entire procedure is high throughput. Further quantitation is carried out by specific tests in liquid culture.

P38. THE FUNCTIONAL SIGNIFICANCE OF EVOLUTIONARILY DISTINCT FORMS OF RIBOSOMAL PROTEIN S15a IN ARABIDOPSIS. Stacey Abidayo, Ali Zanial* and Ammar Zanial* (Kathleen Szick-Miranda), CSU, Bakersfield, Dept of Biology, 9001 Stockdale Hwy, Bakersfield, CA 93311.

The synthesis of proteins is an absolute requirement for growth and development in biological organisms, yet our understanding the core component (the ribosome) and its individual constituents (ribosomal proteins) in plants remains limited. The ribosomal protein (r-protein) S15a is encoded by six separate genes in the *Arabidopsis* genome. However, the products of those genes fall into two evolutionarily distinct categories (Type I and Type II). Recent analyses (Chang *et al*., 2005) have confirmed the presence of both Type I and Type II S15a within ribosomes of *Arabidopsis* cell cultures. Our goal is to determine the functional significance of the divergent (Type II) forms of S15a in *Arabidopsis*. Examination of the expression of individual Type II S15a genes during various developmental stages by RT-PCR demonstrates that the two genes that encode Type II S15a are differentially expressed. In addition, we are utilizing a reverse genetics approach by examining mutations that disrupt the function of individual Type II S15a genes. Preliminary results indicate that the disruption of *RPS15aB* results in a severe developmental delay, similar to the *minute* phenotype described for (r-protein gene) mutations in Drosophila. Our results will add significantly to our understanding of the protein constitution of plant ribosomes and the functional significance of ribosome heterogeneity.

P39. TOLL-LIKE RECEPTORS ON EARTHWORM COELOMOCYTES Alfredo Roesadi*, David Andrews*, Matthew Ingle*, Matthew Nalamlieng* (Dr. Joseph Francis), The Master's College, Department of Science and Mathematics, 21726 Placerita Canyon Road, Santa Clarita, CA 91321.

Coelomocytes play a central role in the earthworm immune system and are involved in immune functions characteristic of innate immunity such as phagocytosis and release of lytic factors. Earthworm coelomocytes possess several mammalian innate immune cell markers on their cell surface. Toll-like receptors (TLR) recognize conserved patterns on microbial pathogens and have been shown to play an important role in the activation of both the mammalian innate and adaptive immune systems and have been detected in invertebrates. TLRs as well as several other innate immune receptors have not yet been detected on earthworm coelomocytes. In our laboratory, we have used antibodies to detect cell associated TLRs on earthworm coelomocytes. Due to the lack of success using antibodies directed at TLR in studies analyzing the cell surface receptors, we began using a method to extract proteins and detect antibodies to TLRs using western blotting. We are using a membrane solubilization technique to free the receptors from the membrane to promote maximum binding of antibodies to epitopes on the cytoplasmic side of the receptor, as well as the extracellular part of the receptor. We are analyzing the crude protein extracts for the presence of antibodies binding to TLRs using western blotting.

P40. THE USE OF REPORTER FUSIONS TO QUANTITATE THE LEVEL OF SOS INDUCTION BY MUTAGENS AND ANTIBIOTICS IN *ESCHERICHIA COLI*. Katherine Kim*, Anne Liu, Bindu Patel, Katherine Tran, and Cindy Tamae (Jeffrey H. Miller), University of California, Department of Microbiology, Immunology, and Molecular Genetics, and the Molecular Biology Institute, 405 Hilgard Avenue, Los Angeles, CA 90095.

We have constructed a set of fusions, in collaboration with Jie Shao and Dr. Barry Wanner at Purdue University, that allow us to monitor the level of SOS induction by measuring β-galactosidase levels in strains carrying these fusions. In particular, fusion of the *lacZ* gene to the *recN* promoter provides a sensitive indicator of SOS induction. We have found that many of the common base analogs result in significant induction of the SOS system. Tests of a series of antibiotics reveal that ciprofloxacin and nalidixic acid, as previously reported, also induce the SOS system. We can quantitate these effects and compare them to those induced by mutagens. This reveals that ciprofloxacin has the highest level of induction of any agent we have tested so far.

P41. PCR-BASED COMBINATORIAL GENE SYNTHESIS FOR THE CONSTRUCTION OF A B-LACTAMASE GENE LIBRARY. Linda Khatchatourian*, Rachel Stern and Kasia Zastawnik (David Moffet), Loyola Marymount University, Department of Chemistry and Biochemistry, 1 LMU Drive, Los Angeles, CA 90045.

Natural proteins perform numerous functions vital to sustaining life. Unlike typical industrial catalysts, most natural proteins function at ambient temperatures, pressures and in water solvent. We describe the use of a novel PCR-based combinatorial gene-synthesis strategy for designing libraries of functionally active proteins. In this PCR-based gene synthesis strategy, many different, full-length, genes are synthesized in a single PCR tube. We have successfully synthesized a library of gene sequences with constant regions homologous to β-Lactamase and regions combinatorially varied. We have also engineered an expression system to optimize the expression and purification of the engineered proteins. The long-term value of this work is to provide the methodology for constructing libraries of novel protein sequences having interesting, useful and medically significant properties not necessarily found in nature.

P42. DNA SEQUENCING AND STORAGE BY LENGTH. Lauren K. Quezada* (Nathaniel G. Portney and Mihri Ozkan), University of California, Riverside, Dept. of Electrical Engineering, 900 University Avenue, Riverside CA 92521.

Our goal is to take a prepared cloned DNA fragment and using a computer based binary algorithm decode this fragment into a known message. We successfully cultured in a solid agar growth media several colonies of a modified *E. coli* bacterium and increased yield in a liquid culture broth. The plasmid DNA contained inside of these cells was then purified using a plasmid prep kit. Once the plasmid was deemed sufficiently pure, we could then run 17 inch, 10% TBE-Urea PAGE gels containing our undigested and digested purified plasmid and various markers. Following a Stu I digestion to extract the coded 110 bp fragment, a manual sequencing gel was then run with an Alu I partial restriction digestion of our fragment. With this, a serial dilution series was run to determine the optimal volume of Alu I to cut the fragment along all possible restriction sites. Using a non-toxic dye and a Typhoon imaging system we were able to visualize the various DNA fragments. We then quantified the separation of bands, using a factor of 4 or 8 bp to decode from binary the desired message of UCR.

P43. DISTRIBUTED ANNOTATION OF THE *D. ERECTA* CHROMOSOME 4 REVEALS A HIGH DEGREE OF SEQUENCE CONSERVATION AND SYNTENY WITH *D. MELANOGASTER* CHROMOSOME 4. N. Yu, S. Staugaard*, and K. Ahern (Dr. Gary Kuleck), Loyola Marymount University, Biology Dept., 1 LMU Drive, Los Angeles, CA 90045

Full utilization of genomic information in scientific analysis can only be realized upon the complete annotation of sequenced genomes. Elements of genome annotation can be accomplished by undergraduates who have been trained in the use of appropriate

bioinformatic tools and have gained experience in using them. To realize this goal, a Genomics Education Partnership, funded through Dr. Sally Elgin, Washington University, St. Louis through HHMI, was created including an initial pool of 15 primarily undergraduate institutions (PUI) to annotate the *Drosophila erecta* dot chromosome. The dot chromosome is the fourth and smallest chromosome. This chromosome is interesting because it is heterochromatic, replicates in late S phase, and undergoes no meiotic recombination in *Drosophila melanogaster* (a close relative to *Drosophila erecta*). Using the *Drosophila melanogaster* genome as a well-annotated guide, we constructed gene models in *Drosophila erecta* utilizing bioinformatics tools such as BLAST, ensembl, and the UCSC genome browser. We developed an efficient method of annotating genes with multiple splice variants and untranslated regions. With these techniques, we have been able to annotate 240,000 bp of the *D. erecta* chromosome 4. We will discuss the annotation process, interesting and unusual outcomes and a syntenic comparison with the *D. melanogaster* genome.

P44. MUTAGENESIS AND CRYSTAL STRUCTURE OF A METALLOENZYME RESPONSIBLE FOR THE DEGRADATION OF THE HERBICIDE ATRAZINE. Ray Uchida, Richard Warner, Bruce Howard (Charlotte Rosendahl), Southern Utah University, Dept. of Biology, 351 West University Boulevard, Cedar City, UT 84720.

Atrazine is one of the most used pesticides in the US and has recently been found to induce hermaphrodites in frogs exposed to concentrations below the EPA limit. It is therefore important to understand the way that atrazine is degraded by bacteria and the way the to optimized the enzymes used by these microorganisms to removed the atrazine. In this study we are trying to understand the structure of the active site and particular the involvement of a zinc metal in the catalysis by the TrzN enzyme in the atrazine degradation pathway. TrzN is a member of the amidohydrolase superfamily and by comparison to other members of the family, 5 amino acids have been proposed to possibly bind the metal in the active site. Progress on creating several mutants to understand the metal binding will be discussed. Optimization of the purification process of protein to be used for crystallization will also be presented.

P45. CORONARY ARTERY BYPASS GRAFT SURGERY IMPROVES FUNCTIONAL STATUS AND SURVIVAL. Farah Srichandra, Stephanie Lepionka, and Andrew Gerst (Dr. Dennis Boos), North Carolina State University, Department of Statistics, Raleigh, NC 27695.

In this study, we determined whether coronary artery bypass graft surgery (CABG) improved functional status and survival in a group of patients. *CABG* surgery creates new routes around narrowed and blocked arteries, allowing sufficient blood flow to deliver oxygen and nutrients to the heart muscles. Plaque accumulation can be accelerated by smoking, high blood pressure, elevated cholesterol, and diabetes. After CABG surgery, patients were evaluated for activities of daily living at 3 & 6 months, 1 year, and annually thereafter, at which times they were measured by the Duke Activity Status Index (DASI).

We used a statistics computer program called SAS to evaluate the data from the DASI. The results show that the groups were statistically different. Older patients received CABG with greater frequency than younger ones. Men and women received CABG with equal frequency. We found that old age and a history of chest pain were some baseline characteristics which are associated with elderly and younger patients having had CABG. When controlling for both age and chest pain, the association between CABG and death is inconclusive. Although, the elderly receive CABG with more frequency than the young and men and women receive the operation with equal frequency; these can be factors which explain mixed results. Next, we found that age and a record of chest pain are the best predictors for a need for CABG30. Specifically, the age-squared term and the age-angina interaction term—operating in a non-linear regression model—predict with a high degree of confidence. Finally, the association between people in different age groups and its direct results.

P46. STEROL REGULATORY ELEMENT BINDING PROTEIN (SREBP) EXPRESSION IN MICE LIVER AND THE GASTROINTESTINAL TRACT. Jarrod Larson* (Timothy Osborne & Tae il Jeon), University of California, Irvine, Department of Molecular Biology and Biochemistry, Irvine, CA 92697.

Sterol regulatory element binding proteins (SREBPs) are key regulatory elements involved in cholesterol regulation and fatty acid synthesis. The objective of this experiment was to determine the relative mRNA expression of multiple tissues types under various metabolic conditions. In this project eight tissue types (liver, fundus, antrum, jejunum, ileum, duodenum, tongue, and adipose tissue) were collected from seven-week-old male B6129 mice in four different feeding groups: normal diet, normal diet with Zetia and Lovastatin, normal diet followed by 24 hours of fasting, and a normal diet followed by 24 hours of fasting and then 12 hours of refeeding. SREBP-1a, SREBP-1c, and SREBP-2 genes were analyzed by isolating the RNA, making cDNA, and performing a QPCR to determine the relative mRNA expression. Additionally, two target genes for SREBP-2 were examined, HMG CoA reductase and squalene synthase. Two SREBP-1 target genes were also analyzed, fatty acyl synthase as well as ACC. In the adipose tissue samples the fasting group had very low SREBP-1c expression whereas the refeeding group had very high levels of expression, likely due to recovery mechanisms necessary for fatty acid synthesis. Among other correlations found between the tissue types it was suggested that Zetia and Lovastatin treated mice had increased SREBP-2 expression in all tissue types, with the exception of adipose tissue, providing further support of the importance of SREBP-2 in cholesterol regulation. The results from these experiments provide insight into the various regulatory mechanisms of SREBPs and their roles in cholesterol regulation and fatty acid synthesis under various metabolic conditions for a variety of tissue types.

P47. IMPLEMENTATION OF QUANTUM DOT (QD) TECHNOLOGY INTO UNDERGRADUATE RESEARCH AND TEACHING LABORATORIES
B. Russi*, A. Martin, and J. Huttenlocher (Dr. Gary Kuleck)
Loyola Marymount University, Biology Dept., 1 LMU Drive, Los Angeles, CA 90045.

Quantum dot nanocrystal technology is revolutionizing biological imaging offering superior fluorescence in very specific Gaussian distribution patterns, resistance to photobleaching, availability in a variety of size ranges with unique emission spectrum, and the capacity to be chemically coupled to a variety of macromolecules. To illustrate the potential of QD technology in teaching laboratories and undergraduate research, we have developed experimentation on the uptake and fate of QDs in protists. *Tetrahymena pyriformis*, rapidly uptakes and retains QDs at extremely low concentrations, with little apparent effect on their growth potential and morphology. Dose response experiments suggest that this bioconcentration is proportional to the concentration in solution. Ultimately, we hope to use QDs in an artificial mini-ecosystem whereby 'QD-loaded' *Tetrahymena* are fed into a trophic (food chain) with subsequent monitoring of the location and presence of the QDs. This "test" ecosystem can serve as a model for the release of nanoparticles into natural ecosystems and their subsequent bioconcentration and biomagnification. We will also discuss the utilization of QDs in an introductory bionanotechnology course, bridging between biology and engineering education at LMU.

P48. WHAT ARE THE LEARNING STYLE PREFERENCES OF PRE-MEDICAL STUDENTS COMPARED TO OTHER STUDENTS ENROLLED IN SCIENCE COURSES AT SAN FRANCISCO STATE UNIVERSITY? Pamela C. Pablico* and Huy Ngo (Jennifer Breckler), UCB/UCSF Joint Medical Program and San Francisco State University, Dept. of Biology, 1600 Holloway Avenue, San Francisco, CA, 94132.

Our study compared the distribution of learning style preferences between premedical students and non-premedical students at San Francisco State University (SFSU). We hypothesized that premedical students favor multimodal learning styles more than non-premedical students. To investigate this, we administered the VARK learning style paper/pencil questionnaire to SFSU students enrolled in undergraduate biology, chemistry, and physics courses during 2006. According to the VARK survey instrument, learning preferences can be characterized in four basic modes, i.e. V=Visual, A=Auditory, R=Read/Write, and K=Kinesthetic. Out of the approximately 1000 eligible students, 387 students completed the questionnaire. The learning style preference(s) of the 156 students who declared themselves pre-medical tended to be multimodal (61.54%) rather than unimodal (38.46%). However, there was no significant difference in multimodal learning styles between pre-med (61.54%) and non-premed (56.71%) students ($p=0.86$). This suggests that being a multimodal learner may not be unique to premedical students but is rather a general characteristic of students who attend core basic science courses. This information may prove useful to science professors at SFSU to enhance instruction. It may also provide information to medical school admissions officers about the types of learners they will encounter in the applicant pool from undergraduate universities.