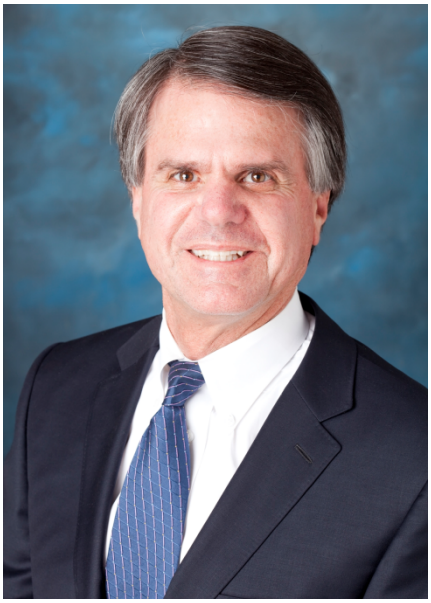

PRESIDENT'S WELCOME

Greetings.

Loyola Marymount University welcomes you to the 37th annual West Coast Biological Sciences Undergraduate Research Conference. Jesuit education has a long tradition of involving students and faculty in collaborative intellectual pursuits. So, it is particularly fitting that we host this conference as LMU celebrates its centennial.

The conference is one of the largest and longest running gatherings dedicated solely to biological research done by undergraduates. Research by student scientists epitomizes the heart of our liberal arts university, where gifted professors act as mentors, opening the eyes of students to the possibilities of a life dedicated to scientific advancement. The pursuit of new understanding is central to every university endeavor and the sharing of that knowledge is what sustains the academic community.

We are privileged to have you here. You will collaborate with faculty and students from across the country, talk about your research and enjoy the company of the people who appreciate science and intellectual gifts.

May your time here be enjoyable and enriching.

Sincerely,

David W. Burcham

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A Brief History of the Conference

The West Coast Biological Sciences Undergraduate Research (WCBSUR) Conference is one of the oldest, on-going, annual Conferences of its kind, dedicated solely to promoting undergraduate research in the biological sciences. The primary purposes of the Conference are: 1. to provide a forum for the presentation of original data generated in the fields of biology and biochemistry by undergraduate researchers; and 2. to foster inter-collegiate interactions among students and faculty who share a commitment to undergraduate research in the biological sciences.

The WCBSUR Conference was founded in the mid-70's by Dr. William Eisinger, Professor Emeritus, Biology, Santa Clara University. The first ten conferences were hosted by Santa Clara University, from 1976 through 1985. Since 1986, several institutions have hosted the Conference on an alternating basis, including Colorado College, Loyola Marymount University, Occidental College, Point Loma Nazarene University, Santa Clara University, The University of California at Irvine and the University of San Francisco.

Over 100 colleges and universities have sent student and faculty representatives to annual WCBSUR Conferences; these institutions include:

Allan Hancock College, Arizona State University, Azad University (Iran), Azusa Pacific University, Beheshti University (Iran), Biola University, Bringham Young University, California Baptist College, California Institute of Technology, California Lutheran University, California Polytechnic University at Pomoma, California Polytechnic University at San Luis Obispo, California State University at Chico, California State University at Dominguez Hills, California State University at Fresno, California State University at Fullerton, California State University at Long Beach, California State University at Los Angeles, California State University at Northridge, California State University at Sacramento, California State University at San Bernardino, California State University at Sonoma, California State University at Stanislaus, Case Western Reserve University (OH), Chaminade University (HI), Chapman University, Charles Drew Medical School, College of the Canyons, Colorado College, Creighton University (NE), Duke University (NC), Harvey Mudd College, Hiram College (OH), Humboldt State University, La Sierra University, Linfield College (OR), Louisiana State University, Loma Linda University, Loyola Marymount University, Middlebury College (VT), Mills College, Miyasaki University, Montana State University, Nebraska Wesleyan University, Northland College (WI), Occidental College, Okalahoma City University, Oregon State University, Pacific University, Pacific Lutheran University, Pepperdine University, Point Loma Nazarene University, Pomona College, Reed College (OR), Regis University (CO), San Diego State University, San Jose State University, Santa Clara University, Scripps College, Skyline College, Southwestern College, (CA), Stanford University, St. Mary's College of CA, St. Mary's University (TX), The Scripps Research Institute (La Jolla, CA),Texas S&M University at Corpus Christi, Tulane University (LA), University of Arizona, University of California at Berkeley, University of California at Davis, University of California at Irvine, University of California at Los Angeles, University of California at Riverside, University of California at San Diego, University of California at Santa Barbara, University of California at Santa Cruz, University of Colorado at Boulder, University of Hawaii at Honolulu, University of Idaho, University of La Verne, University of Louisiana at Monroe, University of Minnesota, University of Nevada at Reno, University of Nevada at Las Vegas, University of Oregon, University of the Pacific, University of Puget Sound (WA), University of Redlands, University of San Diego, University of San Francisco, University of South Australia, University of Southern California, University of Texas at Austin, University of Washington, Vanderbilt University (TN), Vanguard University, Victor Valley College, Weber State University (UT), Westmont College, Wheaton College (IL), Whitman College (WA) and Whittier College.

Plenary Speaker – Dr. Forest Rohwer

Forest Rohwer holds bachelor degrees in biology, chemistry, and history from the College of Idaho and earned his doctorate in molecular biology from the University of California, San Diego/San Diego State University Joint Doctoral Program. Rowher is a microbial ecologist and Professor of Biology at San Diego State University. Forest Rowher is a foremost expert in analysis of virus diversity in biomes ranging from coral reefs to humans. He pioneered the use of metagenomics as a means to characterize previously inscrutable viral and microbial communities. Using a combination of metagenomic and reductionistic techniques, Dr. Rowher analyzes the microbial biodiversity of coral reefs and the role of microbes in the health of this vital biome. He has authored more than 90 scientific papers and book chapters, as well as a popular science book, *Coral Reefs in the Microbial Seas*, published in 2010. Rohwer has been named a Fellow of both the American Association for the Advancement of Science (AAAS) and the Canadian Institute for Advanced Research (CIFAR). In 2008, he received the Young Investigators Award from the International Society of Microbial Ecology (ISME).

Organizers and Sponsors

CONFERENCE SPONSORS

The 37nd Annual West Coast Biological Undergraduate Research Conference has received financial support from the following:

Richard Plumb (Ph.D.), Dean of Frank R. Seaver College of Science and Engineering, Loyola Marymount University.

LMU ORGANIZING COMMITTEE

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COVER DESIGN

Wesley T. Citti (B.Sc. 08) Department of Biology, Loyola Marymount University
David Yang

A SPECIAL THANK YOU TO THE STUDENTS OF THE BIOLOGY DEPARTMENT AND THE MEMEBRS OF THE LMU CHAPTER OF TRIBETA FOR ASSISTANCE WITH MANY OF THE CONFERENCE-DAY TASKS.

Program Overview

TIME	EVENT	LOCATION
7:45 to 8:45	**Registration** Continental Breakfast	Lawton Plaza
8:45 to 10:00	Plenary Session **Welcome: Joseph Hellige** Chief Academic Officer, Loyola Marymount University **Plenary Lecture: Dr Firest Rowher** Professor Department of Biology San Diego State University ***"Viruses, Microbes and the Future of Coral Reefs"***	Hilton 100
10:00 to 10:15	BREAK	
10:15 to 11:30	**Morning Sessions** A. Ecology, Behavior, and Evolutionary Biology B. Environmental Biochemistry and Physiology C. Microbiology D. Biochemistry and Cell Biology	 Hilton 103 Hilton 107 Hilton 109 Hilton 119
11:30 to 12:30	**Poster Session I** Odd-numbered posters	Lawton Plaza
12:30 to 1:15	LUNCH	Lawton Plaza
1:00 to 2:00	**Poster Session II** Even-numbered posters	Lawton Plaza
2:00 to 3:30	**Afternoon Sessions** E. Ecology, Behavior, and Evolutionary Biology F. Genetics G. Neurobiology and Immunology H. Molecular Biology, Physiology, & Clinical Research	Hilton 103 Hilton 107 Hilton 109 Hilton 119
4:00	Concluding Remarks Awards **Reception**	Lawton Plaza

In the event of rain the poster sessions will be held in Hilton 300.

Morning seminar sessions

Session A – ECOLOGY, BEHAVIOR, AND EVOLUTIONARY BIOLOGY (Hilton 103)
Chair: Dr. Justen Whittal, Santa Clara University

S1. (10:15am) APEX PREDATORS OF COSTA RICA. Trisha Stull* (Mike Mooring). Point Loma Nazarene University, Department of Biology, 3900 Lomaland Dr., San Diego, CA 92106.

S2.(10:30am) REPRODUCTIVE BEHAVIOR OF JAGUAR IN CAPTIVITY. Hannah Green* (Robert Wiese and Mike Mooring). San Diego Zoo Global, 2920 Zoo Drive, San Diego, CA 92112 and Point Loma Nazarene University, Department of Biology, 3900 Lomaland Dr., San Diego, CA 92106.

S3.(10:45am) EFFECT OF TEMPERATURE ON AGGRESSION OF THE CONVICT CICHLID. Nathaniel Shanklin Nathaniel Bell (Dr. Ronald Coleman). California State University, Sacramento, Department of Biological Science, 6000 J Street, Sacramento, CA 95819.

S4.(11:00am) LIMBS IN TIGHT SPACES: DO FOSSORIAL MOVEMENTS FAVOR LIMB REDUCTION IN LIZARDS? Mandalyn Kautz* (Gary Gerald). Nebraska Wesleyan University, Biology Department, 5000 St. Paul Ave., Lincoln, NE 68504.

S5.(11:15am) THE CREEK TURNPIKE WETLANDS: A COMPARISON OF VEGETATIVE SURVEYS FROM 1992-1997 AND 2011. Ashley Sweeney* and Hal Reed. Oral Roberts University, Dept. of Biology and Chemistry, 7777 S Lewis Ave., Tulsa, OK 74171.

Session B - ENVIRONMENTAL BIOCHEMISTRY AND PHYSIOLOGY (Hilton 107)
Chair: Dr. Heather Watts, Loyola Marymount University

S6. (10:15am) ASSESSING BIOAVAILABILITY OF METALS IN POLLUTED ECOSYSTEMS USING RHIZOSPEHRE BIOGEOCHEMISTRY. Brianna Bernard* and Alexandria Taylor (Bonjun Koo). California Baptist University, Dept. of Natural and Mathematical Sciences, 8432 Magnolia Ave., Riverside, CA 92504.

S7. (10:30am) CADMIUM ACCUMULATION AND RESISTANCE IN *DROSOPHILA MELANOGASTER*. Austin Nguyen* and Ellie Altomare (Catharine McElwain). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045

S8. (10:45am) DIFFERENCE IN SUPERSTRUCUTRE OF HIGH-ALTITUDE AND LOW-ALTITUDE DEER MOUSE HEMOGLOBIN AS A POSSIBLE CAUSE OF INCREASED OXIDATIVE RESISTANCE IN THE HIGH-ALTITUDE SPECIES. Jake Oshlo* (Hideaki Moriyama). Nebraska Wesleyan University, Biology Department, 5000 Saint Paul Ave., Lincoln, NE 68504. University of Nebraska-Lincoln, Dept. of Biology, 3835 Holdrege Street, Lincoln, NE 68583.

S9.(11:00am) HOT NIGHT MOVES: DEVELOPMENT RATE OF A SIERRA WILLOW BEETLE DEPENDS ON TEMPERATURE AND PHOSPHOGLUCOSE ISOMERASE GENOTYPE. Margaret Mae Abercrombie* (Elizabeth Dahlhoff and Nathan Rank). Santa Clara University, Dept. of Biology, 500

El Camino Real, Santa Clara CA 95053 White Mountain Research Station, University of California, 3000 E. Line St. Bishop CA 93514

S10. (11:15am) CHANGING REPRODUCTIVE BEHAVIOR: AN ANALYSIS OF HOUSE FINCHES IN CALIFORNIA. Tauras Vilgalys*, (Heather Watts). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045

Session C – MICROBIOLOGY (Hilton 109)
Chair: Dr. Gary Kuleck, Loyola Marymount University

S11.(10:15am) EXOGENOUS ISOLATION OF MOBILE RESISTANCE PLASMIDS FROM URBAN COASTAL WETLANDS. Doug Zuill* (Drs. David E. Cummings and Eva M. Top). Point Loma Nazarene University, Department of Biology, 3900 Lomaland Dr., San Diego, CA 92106 University of Idaho, Department of Biology, Moscow, ID 83844

S12.(10:30am) AUTOTROPHIC CARBON FIXATION IN CRENARCHAEOTA FROM YELLOWSTONE NATIONAL PARK. Laura Whitmore*, Ryan Jennings, Jim Moran, Helen Kreuzer, Mark Kozubal, (William Inskeep). Montana State University, Dept. of Land Resources and Environmental Sciences, Bozeman, MT 59717 Pacific Northwest National Laboratory, Richland, WA 99352

S13.(10:45am) ISOLATION AND CHARACTERIZATION OF A MOTILITY MUTANT IN *BURKHOLDERIA UNAMAE*. Michael Onofre (Michelle Lum). Loyola Marymount University Dept. of Biology 1 LMU Drive Los Angeles, CA 90045

S14.(11:00am) THE EXTRACTION OF BIOACTIVE COMPOUNDS FROM POTENTIAL FUNGAL ENDOPHYTES. Lucas Hemmer* (Jerald Bricker). Nebraska Wesleyan University, Biology Department, 5000 St. Paul Ave., Lincoln, NE 68504

S15.(11:15am) IDENTIFICATION AND CHARACTERIZATION OF THE NOVEL BIPYRAMIDAL CRYSTAL PROTEIN GENE IN *BACILLUS THURINGIENSIS* SUBSP. *MORRISONI PG-14*. Ryan M. Oliverio* (Hyun-Woo Park). California Baptist University, Department of Natural and Mathematical Sciences, 8432 Magnolia Avenue, Riverside, CA 92504.

Session D - BIOCHEMISTRY AND CELL BIOLOGY (Hilton 119)
Chair: Dr. James Roe, Loyola Marymount University

S16.(10:15am) MEASUREMENT OF AQUAPORIN-3 EXPRESSION LEVELS IN SALT, FRESH, AND BRACKISH WATER-ACCLIMATED SAILFIN MOLLIES (*POECILIA LATIPINNA*) BY REAL-TIME PCR. Jaclyn Lange* (Gary Gerald, Therese McGinn). Nebraska Wesleyan University, Biology Department, 5000 Saint Paul Ave., Lincoln, NE 68504.

S17.(10:30am) DICOVERING PROTEINS THAT INTERACT WITH THE SMMAK16 PROTEIN FROM THE PARASITIC FLATWORM *SCHISTOSOMA MANSONI*. Megan Vanderkamp*, Tayah Kline, Daniel Shouldice, Yun-Lan Wong (Jon Milhon). Azusa Pacific University, Department of Biology and Chemistry, 675 E. Foothill Blvd., Azusa CA 91702

S18.(10:45am) SDF 1-α AND CXCR4 ARE IMPORTANT FOR POSTERIOR AXIS ELONGATION DURING *X. LAEVIS* EMBRYO DEVELOPMENT. Armbien Sabillo* (Carmen Domingo). San Francisco State University, Department of Biology, 1600 Holloway Ave., San Francisco, CA 94132

S19.(11:00am) IN VITRO ANALYSIS OF THE INTERACTION BETWEEN KAP3 OF KINESIN-2 AND ACTIN. Austin Tenney* (Matthew Berezuk). Azusa Pacific University, Department of Biology and Chemistry, 675 East Foothill, Blvd., Azusa, CA 91702.

S20.(11:15pm) ANALYSIS OF THE ROLE OF BMI-1 AND MEL-18 IN PROSTATE CANCER PROGRESSION. Lizbeth Alvarez* (Dr. Luiza Nogaj). Mount St. Mary's College, Dept. of Biology, 12001 Chalon Rd., Los Angeles, CA 90049.

Afternoon seminar sessions

Session E - ECOLOGY, BEHAVIOR AND EVOLUTIONARY BIOLOGY (Hilton 103)
Chair: Dr. Mike Mooring, Point Loma Nazarene University

S21.(2:00pm) THE ROLE OF INTRASPECIFIC VARIABILITY IN COMMUNITY ASSEMBLY PROCESSES AND SPECIES ECOLOGICAL BREADTH. Colby Sides*, Marielle Smith, Lindsey Sloat, Amanda Henderson, and Brian Enquist (Jim Ebersole). Colorado College, Dept. of Biology,14 East Cache La Poudre St., Colorado Springs, CO 80903 University of Arizona, Dept. of Ecology and Evolutionary Biology, 1041 E. Lowell St., Tucson, Arizona 85719.

S22.(2:15pm) GENETIC DIVERSITY AND POPULATION DIFFERENTIATION IN THE RARE SERPENTINE ENDEMIC, SAN BENITO EVENING PRIMROSE (*CAMISSONIA BENITENSIS*; ONAGRACEAE). Cynthia A. Dick, Julie A. Herman*, Stephanie B. Saffouri, and Ryan E. O'Dell (Justen B. Whittall). Department of Biology Santa Clara University 500 El Camino Real Santa Clara, CA 95053

S23.(2:30pm) EFFECTS OF DIETARY PHYTOESTROGENS ON PATERNAL RESPONSIVENESS AND MATURATION IN THE BIPARENTAL CALIFORNIA MOUSE.. Aaron T. Stamp*, Trey Amador, Breanna N. Harris, and Juan Pablo Perea-Rodriguez (Wendy Saltzman). University of California, Riverside, Dept. of Biology, Riverside, CA 92521

S24.(2:45pm) FEMALE BODY SIZE AND REPRODUCTIVE OUTPUT IN THE GREEN LYNX SPIDER *PEUCETIA VIRIDANS* (ARANEAE, OXYOPIDAE). Mikayla Kemp*, Kayla Murata*, Jasmin Takemoto*, Mikayla Mowzoon (Martin Ramirez). Loyola Marymount University, Dept. of Biology, 1 LMU Dr., Los Angeles, CA 90045.

S25.(3:00pm) ECOLOGICAL STRESS CAUSED BY FIRE AND ITS EFFECTS ON ORB WEAVING SPIDERS. Sophie Crinion (Martin Ramirez). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

Session F – GENETICS (Hilton 107)
Chair: Dr. David Hess, Santa Clara University

S26.(2:00pm) MAPPING FERMENTATION RATE IN DOMESTICATED STRAINS OF *SACCHAROMYCES CEREVISIAE*. Jillian Gerrity* (David Hess). Santa Clara University, Dept. of Biology, 500 El Camino Real, Santa Clara, CA 95053.

S27.(2:15pm) DEVELOPMENT OF A SYSTEM TO DEPLETE SIR2 IN ORDER TO STUDY ITS ROLE IN MAINTAINING SILENT CHROMATIN AT THE RIBOSOMAL DNA LOCUS IN *SACCHAROMYCES CEREVISIAE*. Lindsey Jones* and Rachel Jordan (Mary Bryk). Nebraska Wesleyan University, Biology Department, 5000 Saint Paul Ave., Lincoln, NE 68504.

S28.(2:30pm) PHENOTYPIC REVERSION OF FLUOROQUINOLONE RESISTANCE IN *NEISSERIA GONORRHOEAE* AFTER CESSATION OF CIPROFLOXACIN USAGE IN SAN FRANCISCO. Kiana Espinosa*, Sean Buono, Susan Phillip, Jeffery Klausner, Mark Pandori (David Hess). Santa Clara Univesity, Dept of Biology, Santa Clara, CA, 95053. San Francisco Department of Public Health Labs, San Francisco, CA, 94102.

S29.(2:45pm) MITOCHONDRIAL AND NUCLEAR DNA ANALYSIS FOR MUTATIONS AND MODIFIERS IN A LATINO FAMILY WITH DILATED CARDIOMYOPATHY. Sonia Martinez*, Simin Hakim, Van T. Hoang, Subhadra Ramanathan, and (Michael V. Zaragoza). UCI Cardiogenomics Research Program Department of Pediatrics and Biological Chemistry The University of California, Irvine, School of Medicine Irvine, CA 92697-3940.

S30.(3:00pm) MUTATIONS AND MODIFIERS IN THE MYH7 GENE: DNA ANALYSIS OF THREE FAMILIES WITH HYPERTROPHIC AND DILATED CARDIOMYOPATHY. Christine K Tran*, Simin Hakim, Van Hoang, Julia Platt, June-Anne Gold, (Michael V Zaragoza). UC Irvine Cardiogenomics Program, Dept. of Pediatrics, Division of Genetics & Metabolism, University of California, Irvine, School of Medicine, Irvine, CA USA; Loma Linda University Pediatrics/Genetics, Campus Street, Loma Linda, CA 92354.

S31.(3:15pm) CLINICAL VARIABILITY FOR NOVEL TAZ GENE MUTATION: BARTH SYNDROME WITH DIALATED CARDIOMYOPATHY (DCM) AND HEART FAILURE IN AN INFANT AND LEFT VENTRICULAR NON-COMPACTION (LVNC) IN HIS GREAT-UNCLE. Diti Ronvelia*, Jaclyn Greenwood, Julia Platt, and Simin A. Hakim (Michael V. Zaragoza, M.D., Ph.D.). University of California, Irvine, School of Medicine, Dept. of Pediatrics, Division of Genetics & Metabolism and Dept. of Biological Sciences, 2501 Hewitt Hall, Irvine, CA 92697.

Session G - NEUROBIOLOGY AND IMMUNOLOGY (Hilton 109)
Chair: Dr. Keith Garrison, Saint Mary's College of California

S32.(2:00pm) ANALYSIS OF C1Q NEURAL ANATOMY AND EFFECT ON EPILEPTIC ACTIVITY. Anu Ramachandran*, Naomi Ford, Isabel Parada (David Prince). Stanford University Dept of Neurology, Stanford, California, 94305-2004.

S33.(2:15pm) TEMOZOLOMIDE DELAYS TUMOR GROWTH BY DIMINISHING REGULATORY MACROPHAGES IN AN INNOVATIVE, INDUCIBLE, GENETIC MOUSE MODEL OF MELANOMA. Carlos Peinado*, (Bhaskar Srivastava, MD, PhD), (Susan Kaech, PhD). Yale School of Medicine, Dept. of Immunobiology, 300 Cedar St., New Haven, CT 06520

S34.(2:30pm) ANALYSIS OF INNATE IMMUNE RESPONSES OF MURINE RESPIRATORY EPITHELIAL CELLS IN RESPONSE TO INFLUENZA VIRUS INFECTION *IN VITRO*. Brittany M. Justa*, Alexander Vogel, Deborah M. Brown, and (Therese M. McGinn). School of Biological Sciences, Nebraska Center for Virology, University of Nebraska, Lincoln, NE 68583. Nebraska Wesleyan University, Biology Department, 5000 Saint Paul Ave., Lincoln, NE 68504.

S35.(2:45pm) STRATEGIES TO STUDY THE ROLE OF FAST DYNAMIC UBIQUITINATION AT SYNAPSES. Anna M. Nia*, and Anna Caputo (Felix E. Schweizer). Department of Neurobiology, David Geffen School of Medicine at UCLA, Los Angeles, California, USA.

S36.(3:00pm) EPSTEIN-BARR VIRUS INFECTED B LYMPHOCYTES AS A SOURCE OF TYPE I INTERFERONS IN SYSTEMIC LUPUS ERYTHEMATOSUS. Laura Blasnitz* (Luwen Zhang). Nebraska Wesleyan University, Biology Department, 5000 Saint Paul Ave., Lincoln, NE 68504. Nebraska Center for Virology, University of Nebraska, Lincoln, Department of Biological Sciences, 4240 Fair St., Lincoln, Nebraska 68583.

S37.(3:15pm) ALTERNATE READING FRAMES DETECTED IN CIRCULATING HIV-1 VIRAL SEQUENCE: A BIOINFORMATICS ANALYSIS. Sean Purtell*, (Keith Garrison). Saint Mary's College of California, Dept. of Biology, 1928 St. Mary's Rd. Moraga, Ca, 94556-2744

Session H - MOLECULAR BIOLOGY, PHYSIOLOGY & CLINICAL RESEARCH (Hilton 119)
Chair: Dr. Melissa Wilson, Azusa Pacific University

S38.(2:00pm) THE EFFECTS OF THIRD-HAND CIGARETTE SMOKE EXPOSURE ON THE LEVELS OF PLASMA GLUCOSE AND INSULIN IN SWISS WEBSTER MICE. R. K. Pisano*, F. Dashty*, R. Shakir, H. Torba, V. Delgado, (F. Watson and M. Thao). California State University Stanislaus, Dept. of Biology, One University Circle, Turlock, CA 95382.

S39.(2:15pm) ERRα A NEW TARGET IN ERBB2-OVEREXPRESSING BREAST CANCER: STUDIES WITH ERRA INVERSE AGONIST XCT790. Andrew Cannon*, Stetson H. Williams, Hamid Band, and (Srikumar M. Raja). Nebraska Wesleyan University, Biology Department, 5000 Saint Paul Ave., Lincoln, NE 68504. University of Nebraska Medical Center, Omaha, NE.

S40.(2:30pm) EFFECTS OF HEAVY METALS ON PROLIFERATION AND NEURONAL DIFFERENTIATION OF EMBRYONIC STEM CELLS. Circe McDonald* and Mark Gutierrez (Mohammed El Majdoubi). Dominican University of California, Department of Natural Sciences and Mathematics, 50 Acacia Avenue, San Rafael, CA 94901.

S41.(2:45pm) MOLECULAR CHARACTERIZATION OF BETA-GALACTOSIDASE IN THE UNIQUE OVINE MODEL OF GM1-GANGLIOSIDOSIS. Masis Isikbay* (Amelia Ahern-Rindell). University of Portland, Dept. of Biology, 5000 N Willamette Blvd., Portland, OR 97203

S42.(3:00pm) DOSE AND TIME DEPENDENT EFFECTS OF HDAC INHIBITORS, LBH589 AND VORINOSTAT, ON GROWTH AND SURVIVAL OF COLORECTAL CANCER CELLS: A PRE-CLINICAL ANALYSIS. Stephanie T. Kuwahara*, Shelby C. Martin and Austin D. Layton (Melissa Wilson). Azusa Pacific University Department of Biology and Chemistry 701 East Foothill Blvd., Azusa, CA 91107

Poster Sessions

Poster Session I – Odd-numbered posters, 11:30am-12:30pm, Lawton Plaza
Poster Session II – Even-numbered posters, 1:00pm-2:00pm, Lawton Plaza

P1. METHOD DEVELOPMENT FOR ISOLATION OF PHOSPHOPROTEINS USING MUTANT ALKALINE PHOSPHATASE. Dema Alniemi* and Duane Mooney (Edward Dratz). Montana State University, Dept. of Chemistry and Biochemistry, Bozeman, MT 59715.

P2. SPATIALLY CONTROLLED BIOACTIVE SIGNAL INCORPORATION TO GUIDE STEM CELL FATE IN HYDROGELS. Jacob Borrajo*, and Tatiana Segura. University of California, Los Angeles, Dept. of Chemical and Biomolecular Engineering, 5531 Boelter Hall, Los Angeles, CA 90095.

P3. EXAMINING A109 PROTEIN IN SULFOLOBUS TURRETED ICOSAHEDRAL VIRUS FROM YELLOWSTONE NATIONAL PARK. Hadeel Alniemi*1,2, (Brian Eilers)3, (C. Martin Lawrence)3 1Hughes Scholars Program, Montana State University, Bozeman, MT 2Department of Cell Biology & Neuroscience, Montana State University, Bozeman, MT 3Department of Chemistry & Biochemistry, Montana State University, Bozeman, MT. Montana State University, Dept. of Chemistry & Biochemistry, 1501 South 11th Avenue, Bozeman, MT 59715.

P4. THE EFFECTS OF KAP3 OF KINESIN-2 ON THE ORGANIZATION AND REMODELING OF THE ACTIN CYTOSKELETON IN CELL CULTURE. Danielle Hatt*, Taylor Kline* (Matthew Berezuk, Ph.D.). Azusa Pacific University, Department of Biology and Chemistry, Azusa, CA 91702.

P5. THE EFFECTS OF PROTEASE INHIBITORS ON PARATHYROID HORMONE-RELATED PROTEIN LEVELS IN LUNG CANCER CELLS. Christopher Tam*. University of California, San Diego, Dept. of Biological Sciences, 9500 Gilman Dr., La Jolla, CA 92093.

P6. COMPARATIVE PROTEOMIC ANALYSIS FOR ACQUIRED RADIATION RESISTANCE IN PANCREATIC CANCER. Kara Sunshine Robertson*, Jianhong Zhou (Yuchun Du). University of Arkansas, Dept. of Biology, Science and Engineering 528, Fayetteville, AR 72701.

P7. HIGH CHOLESTEROL DIET INCREASES FREE OXIDIZED FATTY ACIDS IN MOUSE MODELS OF CANCER. Daniel Niknam*, Taraneh Rasta*, Nika Karimi MD; Samra Vazirian MD , Maryam Shabihkhani MD, Ania Gapeleh MD, John Lotfi JD and (Greg Hough) MSc. David Geffen School of Medicine, University of California Los Angeles, 90095.

P8. CIRCULATING 15-HYDROXYEICOSATETRAENOIC ACID LEVELS ARE ELEVATED IN A MOUSE MODEL OF INFLAMMATORY DISORDERS FOLLOWING HIGH FAT DIET ADMINISTRATION.. Samra Vazirian MD, Ladan Vakili MD, Margeaux Beran, Arash Meshkat DDs MSc, Maryam Haghnegahdar MD, Mitra Owrang MD, Arezoo Rajaee MD, Roshanak Aliali MD and Greg Hough MSc.. David Geffen School of Medicine University of California Los Angeles 90095.

P9. TOWARDS THE SYNTHESIS OF ANTASCOMICIN B. Ashley Rosenberg*: David Clay: (Matt McIntosh). University of Arkansas, Department of Chemistry, Chemistry Building, Fayetteville, AR 72701.

P10. THE BEST WAY TO IMPROVE HDL, IS TO LOWER THE LDL LEVEL.. Ladan Vakili MD*,Ghazal Vakili MD, Samra Vazirian MD, Jasmine Bowers Obioha MSII, Masood Memarzadeh MSII, Foozhan Farahmand MD, Drew Huusfeldt, Tannaz Moin MD, Greg Hough MSc.. David Geffen School of Medicine at UCLA, Los Angeles, California.

P11. THE DISCOVERY OF THE MYCOBACTERIAPHAGE MEPAC. Abraham Gebreselassie and Paul (DongWoo) Chang (Gary Kuleck, Yiwen Fang, and Carl Urbinti. Loyola Marymount University, Dept of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

P12. REACTIVE OXYGEN SPECIES ARE IMPORTANT FOR PROMOTING BMP-INDUCED DENDRITIC GROWTH IN RAT EMBRYONIC SYMPATHETIC NEURONS. Charlotte Lea* (Vidya Chandrasekaran). Saint Mary's College of California, Dept. of Biology, 1928 Saint Mary's Road, Moraga, CA, 94575.

P13. EVALUATION OF THE NOVEL TUMOR SUPPRESSOR GENE, DEFENSIN-β 1, IN COLON CANCER CELLS. Austin D. Layton*, Shelby C. Martin, and Stephanie T. Kuwahara (Melissa Wilson). Azusa Pacific University Dept. of Biology and Chemistry 701 East Foothill Blvd. Azusa, CA 91107.

P14. IL-8 PRODUCTION AND NFκB INDUCTION IN CALU-3 CELLS IN RESPONSE TO QUORUM SENSING MOLECULES. Chelsey Soler*, Ashkon Banihashemi, Sam Papke, and Romina Herrera (Kathleen Tallman). Azusa Pacific University, Department of Biology and Chemistry, 701 E. Foothill Ave., Azusa, CA 91702.

P15. THE EFFECTS OF ENERGY DRINKS ON THE STRUCTURE AND FUNCTION OF EPITHELIAL CELLS AND FIBROBLASTS. Eric Shide*, (Vidya Chandrasekaran). Saint Mary's College of California, Dept. of Science, 1928 Saint Mary's Road, Moraga, CA 94556.

P16. FORMATION OF EMBRYOID BODIES IS REQUIRED FOR DIFFERENTIATION OF INSULIN-PRODUCING CELL CLUSTERS FROM MOUSE EMBRYONIC STEM CELLS. Christa D. Caneda* and Jesus Ciriza (Jennifer O. Manilay). University of California, Merced, School of Natural Sciences, 5200 N. Lake Rd., Merced, CA 95343.

P17. CHARACTERIZATION OF THE REPROGRAMMING KINETICS OF INDUCED PLURIPOTENT STEM CELLS AMONG FOUR DISTINCT DONOR CELL TYPES.. David Yao*, Chi Kent Ho, and Qiao Zeng (Yi Sun). University of California, Los Angeles, Dept. of Psychiatry and Biobehavioral Sciences, 405 Hilgard Ave., Los Angeles, CA 90095.

P18. CHARACTERIZING THE SPECIFIC MIGRATION OF MYELOID PROGENITORS INTO GLIOBLASTOMA TUMORS. Troy Kurz*, Michael Marcacci* (Mike Dorrell). Point Loma Nazarene University, Dept. of Biology. 3900 Lomaland Dr., San Diego, CA 92106

P19. OBSERVATION OF *PSEUDOMONAS AERUGINOSA* BIOFILM FORMATION ON HELA CELL CULTURE USING DAPI STAINING AND FLUORESCENT ANTIBODY LABELING. Zach Brown* and Randy Dunston* (Kathleen Tallman). Azusa Pacific University, Dept. of Biology and Chemistry, 901 E. Alosta Ave., Azusa, CA 91702.

P20. IDENTIFYING NOVEL COMBINATIONS OF ANGIOSTATIC THERAPIES THAT DEMONSTRATE SYNERGISTIC ANTI-TUMOR VASCULAR ACTIVITY. Jacob Tremblay*, Jack

Rusing*, Troy Kurz, Halsie Donaldson, Michael Dorrell. Point Loma Nazarene University, Dept. of Biology, 3900 Lomaland Dr., San Diego, CA 92106.

P21. STRUCTURE-FUNCTION ANALYSIS OF WDR68 IN CRANIOFACIAL DEVELOPMENT IN DANIO RERIO. Gregory Alvarado*, Yanette J. R. Peterson, Diana Doan, (Robert M. Nissen). California State University, Los Angeles, Dept. of Biological Sciences, 5151 State University Dr., Los Angeles, CA 90032.

P22. THE ANALYSIS OF GROWTH RATES IN WDR68 KNOCKDOWN CELLS AND MUTANT ANIMALS.. Ajay Bhandari* and Bingyan Wang (Robert M. Nissen). CSU Los Angeles, Dept. of Biology, 5151 State University Dr., Los Angeles, CA 90032.

P23. NEURAL ECTODERM CELLS REMAIN COMPETENT TO FORM MUSCLE FIBERS DURING *X. LAEVIS* EMBRYO DEVELOPMENT. Brigette Jong* (Carmen Domingo). San Francisco State University, Dept. of Biology, 1600 Holloway Ave., San Francisco, CA 94132.

P24. GENETIC IDENTIFICATION OF TERMITE SPECIES IN THE SAN GABRIEL VALLEY FOR USE IN DEVELOPMENTAL STUDIES. Jessica DeWitt* and Yun-Lan Wong (Jurgen Ziesmann and Joshua Morris). Azusa Pacific University, Department of Biology and Chemistry, 901 E Alosta, Azusa, CA 91702.

P25. SONG DIVERGENCE AND SPECIATION IN RED CROSSBILLS. Aaron Grossberg*, Kirsten Paasche, (Julie Smith). Pacific Lutheran University, Department of Biology, 1010 122nd Street S. Tacoma, WA 98447.

P26. POPULATION GENETICS AND IMPACT THREAT ASSESSMENT OF INVASIVE JACKSON'S CHAMELEONS IN HAWAII. Rebekah Klint*, (Brenden Holland). University of Hawaii at Manoa, Pacific Biosciences Research Center, 2500 Campus Road, Honolulu, Hi, 96822.

P27. INDIVIDUAL SIGNATURES IN VOCALIZATIONS OF CALIFORNIA MOUSE (*PEROMYSCUS CALIFORNICUS*) PUPS. Saif Hossain*, Wendy Saltzman, Sarah Rotschafer, Khaleel A. Razak, Krisitne Kaiser. University of California Riverside, Dept. of Biology, 900 University Avenue Riverside, CA 92521.

P28. PREDAWN AND MID-DAY WATER POTENTIALS TO MEASURE RESPONSE TO ALTERED PRECIPITATION REGIMES IN SOUTH COASTAL CHAPARRAL SPECIES. David Villalta*, Angelita Ashbacher (Elsa Cleland). University of California San Diego, Department of Biological Science, Ecology, Behavior and Evolution, 9500 Gilman Dr., La Jolla, CA 92093.

P29. EFFECTS OF CADMIUM ON GROWTH AND SHORT TERM PHOTOSYNTHETIC ACCLIMATION RATES TO LIGHT INTENSITY CHANGES IN RADISH PLANTS (*RAPHANUS SATIVUS* L.). Austin Nguyen and Theresa Graebener (Pippa Drennan). (Philippa M. Drennan). Loyola Marymount University, Biology Department, 1 LMU Drive, CA 90045.

P30. LA BREA TAR PITS: WHAT DO DIRE WOLF LIMB LENGTHS TELL US ABOUT PIT DATES? Genevieve Guerra*, Richard Smith*, (Wendy Binder). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

P31. TRACKING WILDLIFE MOVEMENT BETWEEN THE LOYOLA MARYMOUNT UNIVERSITY CAMPUS AND THE PLAYA VISTA RIPARIAN CORRIDOR USING MOTION SENSING CAMERAS. Courtney McCammon* (John Dorsey and Eric Strauss). Loyola Marymount

University, Biology Department, 1 LMU Drive, CA 90045.

P32. DEVELOPING GREENROOFS FOR SOUTHERN CALIFORNIA: A COMPARISON OF HEAT TOLERANCE FOR DUDLEYAS AND SEDUMS. Robert Arnold* and James McDonald* (Philippa M. Drennan). Loyola Marymount University, Biology Department, 1 LMU Drive, CA 90045.

P33. THE EFFECTS OF BENZYL BUTYL PHTHALATE (BBP) ON CRAYFISH AGGRESSION AND MEMORY. Shahid SM*, Johnson KR, Cowan AM, Gomes CS, Mehwash AI, Williams EB, Wachtarz AL, (Kaplan LAE). Quinnipiac University, Department of Biological Sciences, 275 Mount Carmel Avenue, Hamden, CT 06518.

P34. THE EFFECTS OF BENZYL BUTYL PTHALATE ON MORTALITY AND LEFT/RIGHT/NEUTRAL BIAS OF THREE SPECIES OF PLANARIA: *D. TRIGRINA*/, *D. DOROTOCEPHALA*/, AND *P. FLUVIATALLIS*/. Christofer Anderson*, Lyndsey McGlinchey, and Daniel Mascaro (Lisa A.E. Kaplan). Quinnipiac University, Dept. of Biology, 275 Mount Carmel Ave., Hamden, CT 06518.

P35. INVASION OF *ACACIA MEARNSI* ALONG THE HOLSLOOT RIVER, RAWSONVILLE, WESTERN CAPE, SOUTH AFRICA. Shane Sheets*, Duncan Katel*, (Cheryl Swift PhD). Whittier College, Depts. of of Biology & Environmental Science, 13406 E. Philadelphia St., Whittier, CA 90608.

P36. THE ROLE OF ADAPTATION DURING COLUMBINE SPECIATION. Leena McCann*, Juliana Moreno*, Cynthia A. Dick, Stephanie B. Saffouri and (Justen Whittall). Department of Biology Santa Clara University 500 El Camino Real Santa Clara, CA 95053.

P37. EFFECT OF FOOD CUES ON THE HYPOTHALAMIC-PITUITARY-GONADAL AXIS. Nikki Javier* (Heather Watts). Loyola Marymount University, Dept. of Biology, 1 LMU Drive, Los Angeles, CA 90045.

P38. SOUND TRAVELS: ORIGINS OF FRESHWATER FISHES IN THE PUGET SOUND REGION. Evan Shields* and Brianne Ankenman* (Jacob Egge). Pacific Lutheran University, Dept. of Biology, 1010 122nd St. South, Tacoma, WA 98447.

P39. EFFECTS OF BENZYL BUTYL PHTHALATE ON *FUNDULUS HETEROCLITUS* ANTI-PREDATOR BEHAVIOR. Michael MacKillop*, Matthew Stark, and Theresa Sparaco (Lisa Kaplan). Department of Biological Sciences, 275 Mount Carmel Ave Hamden, CT 06518-1908.

P40. THE EFFECT OF ACOUSTIC CUES ON AGGRESSION IN MALE PACIFIC FIELD CRICKETS, *TELEOGRYLLUS OCEANICUS*.. Yeelong Yang* and Brian Gray (Marlene Zuk). University of California, Riverside, Department of Biology, 900 University Ave., Riverside, CA 92521.

P41. LARGE MAMMAL BIODIVERISTY IN A COSTA RICAN MONTANE CLOUD FOREST. Austin Fares*, Ryan Dahl*, Caleb Bryce, (Mike Mooring). Point Loma Nazarene University, Department of Biology, 3900 Lomaland Drive, San Diego, CA 92106.

P42. USING YEAST 2-HYBRID ANALYSIS TO STUDY THE RELATIONSHIP BETWEEN PHOSPHORYLATION AND DIMERIZATION IN THE *C. ELEGANS* TRANSCRIPTION FACTOR LIN-31. Matthew Mosier*, Fernando Meza Gutierrez, and (Leilani Miller). Santa Clara University, Dept.

of Biology, 500 El Camino Real, Santa Clara, CA 95053.

P43. EFFECTS OF CADMIUM EXPOSURE AND ACCUMULATION ON OTEHR METAL LEVELS IN DROSOPHILA MELANOGASTER. Ellie Altomare*, Austin Nguyen (Cathy McElwain). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

P44. ALZHEIMER'S DISEASE IN *DROSOPHILA MELANOGASTER*: TESTING A MODEL SYSTEM. Andrew Heslin*, Anthony Wavrin*, and Theresa Graebener* (Catherine McElwain). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

P45. THE ISOLATION AND CHARACTERIZATION OF PHAGES MUUS AND CECI11. Jaee Tamhane*, Ana Lucia Fuentes*, (Gary Kuleck, Carl Urbinati, Yiwen Fang). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

P46. ALZHEIMER'S IN *DROSOPHILA MELANOGASTER*: TESTING A MODEL SYSTEM. Shannon Harringer*, Justin de Lennoy*, Shelby Chun Fat* (Cathy McElwain). Loyola Marymount University Dept. of Biology 7900 Loyola Blvd., Los Angeles, CA 90045.

P47. CONSERVATION GENETICS OF THE RED HILLS ROACH (CYPRINIDAE: *LAVINIA SYMMETRICUS* SSP). Morrell Chhay*, Tim Heyne, Jennifer O'Brien, and (Andres Aguilar). University of California, Merced, School of Natural Sciences. 5200 North Lake Road, Merced, CA 95343.

P48. MATHEMATICAL ANALYSIS OF GENE REGULATION IN *SACCHAROMYCES CEREVISIAE* IN RESPONSE TO COLD SHOCK. Nick A. Rohacz* and Katrina Sherbina* (Kam D. Dahlquist and Ben G. Fitzpatrick). Loyola Marymount University, Dept. of Biology, 1 LMU Drive, Los Angeles, CA 90045.

P49. THE EFFECT OF BENZYL BUTYL PHTHALATE ON THE EXTERNAL MICROBIAL COLONIZATION OF *FUNDULUS HETEROCLITUS*. Tanya R Swiderski*, Catherine Tobin, and Amanda Duggan (Lisa AE Kaplan). Quinnipiac University, Dept. of Biology, 275 Mount Carmel Avenue, Hamden, CT 06518.

P50. THE AMINOGLYCOSIDE ANTIBIOTIC KANAMYCIN DAMAGES DNA BASES IN ESCHERICHIA COLI: CAFFEINE POTENTIATES THE DNA-DAMAGING EFFECTS OF KANAMYCIN WHILE SUPPRESSING CELL KILLING BY CIPROFLOXACIN IN *ESCHERICHIA COLI* AND *BACILLUS ANTHRACIS*. Tina Manzhu Kang, Jessica Yuan*, Angelyn Nguyen*, Elinne Becket, Hanjing Yang, (Jeffrey H. Miller). University of California, Los Angeles Department of Microbiology, Immunology, and Molecular Genetics, UCLA, Los Angeles, CA 90095.

P51. ANALYSIS OF PLANT GROWTH PROMOTING RHIZOBACTERIA OF *LEUCANTHEMUM SUPERBUM*. Lauren Carlson and Nadhiya Govindaraj (Michelle Lum). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

P52. ISOLATION AND CHARACTERIZATION OF CELLULASE PRODUCING AND PHOSPHATE SOLUBILIZING RHIZOBACTERIA. Salma Soltani* and Maria Shibatsuji* (Michelle Lum). Loyola Marymount University, Dept. of Biology, 1 LMU Drive, Los Angeles, CA, 90045.

P53. IDENTIFYING THE PRESENCE AND EFFECTIVENESS OF PLANT GROWTH RHIZOBACTERIA IN *LONICERA HISPIDULA*. Stephen Louie (Michelle Lum). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

P54. SELF-TRANSMISSIBLE ANTIBIOTIC RESISTANCE PLASMIDS IN URBAN COASTAL WETLANDS. Michael Geiger*, Kimberly Schroeder*, Victoria Haase*, Jenna Lavenuta, and Doug Zuill (David Cummings). Point Loma Nazarene University, Dept. of Biology, 3900 Lomaland Dr., San Diego, CA 92106.

P55. THE RELATIONSHIP BETWEEN THE EXTRACELLULAR POLYMERIC SUBSTANCE (EPS) AND QUORUM SENSING MOLECULES IN *PSEUDOMONAS AERUGINOSA* BIOFILM FORMATION. Brandon Bauer* and Alex Woodrow (Kathleen Tallman). Azusa Pacific University, Dept. of Biology and Chemistry, 901 E. Alosta Ave., Azusa, CA 91702-7000.

P56. THE EFFECTS OF HEAVY METAL AND RHIZOBACTERIA ON THE GERMINATION AND GROWTH OF DUNE LUPINE. Jennifer Okonta and Michelle Lum. Loyola Marymount University, Dept. of Biology, 1 LMU Drive, Los Angeles, CA 90045.

P57. CHARACTERIZATION OF *BURKHOLDERIA TUBERUM* NODULATION MUTANTS. Marla Dallal*, Amanda Nystrom (Michelle Lum). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

P58. GENERATING AND DETERMINING THE PHENOTYPE OF AN ACYL COA DEHYDROGENASE MUTANT IN *BURKHOLDERIA UNAMAE*. Michael Carlone* (Michelle Lum). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

P59. TOWARDS IMPROVING OUR UNDERSTANDING OF BACTERIOPHAGE DIVERSITY: THE ISOLATION AND CHARACTERIZATION OF SDCHARGE11 AND THE BIOINFORMATICS ANALYSIS OF CONTAGION. Hilda Delgadillo* and Raymond Totah* (Dr. Fang, Dr. Kuleck, Dr. Urbinati). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

P60. ANTIMICROBIAL-PRODUCING BACTERIA IN TREE CANOPY SOIL: BIOLOGICAL APPROACHES. Ariel Madden* and Jenny Stein (Amy Siegesmund). Pacific Lutheran University, Department of Biology, Tacoma, WA 98447.

P61. THE AMINOGLYCOSIDE ANTIBIOTIC KANAMYCIN DAMAGES DNA BASES IN *ESCHERICHIA COLI*: CAFFEINE POTENTIATES THE DNA-DAMAGING EFFECTS OF KANAMYCIN WHILE SUPPRESSING CELL KILLING BY CIPROFLOXACIN IN *ESCHERICHIA COLI* AND *BACILLUS ANTHRACIS*. Tina Manzhu Kang, Jessica Yuan*, Angelyn Nguyen*, Elinne

Becket, Hanjing Yang, and (Jeffrey H. Miller). Department of Microbiology, Immunology, and Molecular Genetics, and the Molecular Biology Institute, University of California, and the David Geffen School of Medicine, Los Angeles, CA 90095.

P62. MUTAGENIC SPECIFICITY IN *ESCHERICHIA COLI*. Madeline Yung* and Elinne Becket (Jeffrey H. Miller). University of California, Los Angeles, Department of Microbiology, Immunology, and Molecular Genetics 405 Hilgard Ave., Los Angeles, CA 90095

P63. THE EFFECT OF DEPURATION ON MICROBIAL DIVERSITY ASSOCIATED WITH *FUNDULUS HETEROCLITUS*. McNickle LA, Muller RA, Driscoll NR, Kaplan LAE. Quinnipiac University, Biological Sciences, 275 Mt. Carmel Ave, Hamden, CT 06518.

P64. IDENTIFYING AND CHARACTERIZING THE MICROBIAL COMMUNITY OF DUNE LUPINE. Elisabeth Ferris*, Michael Pina, and Jessica Duong (Michelle Lum). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

P65. CREATION OF DELETION MUTATIONS OF *CAULOBACTER CRESCENTUS* GENES TO TEST THEIR ROLE IN GALACTURONATE METABOLISM. Meghan Garrett*, Jennifer Parker* (Dr. Craig Stephens). Santa Clara University, Department of Biology, 500 El Camino Real, Santa Clara, CA 95053.

P66. THE EFFECT OF NUCLEOTIDE POOLS ON SPONTANEOUS MUTAGENESIS IN *ESCHERICHIA COLI*. Lawrence Tse*, Alexander Cosico*, and Elinne Becket (Jeffery H. Miller). University of California Los Angeles, Dept. of Microbiology, Immunology, and Molecular Genetics and the Molecular Biology Institute, and the David Geffen School of Medicine, Los Angeles, CA 90095.

P67. USE OF HALOBACTERIUM NRC-1 AS A MODEL ORGANISM IN THE UNDERGRADUATE RESEARCH LABORATORY; GENERAL OBSERVATIONS INCLUDING ANALYSIS OF GROWTH CONDITIONS, GROWTH FACTORS, AND INHIBITORS; AND USE OF NATURAL SELECTION TO ISOLATE ANTIBIOTIC RESISTANT MUTANTS.. Christian Dove*, Matthew Christie, and Sung Shil Kim (Joe Francis) (Todd Wood). The Master's College, Dept. of Biological Science, 21726 Placerita Canyon Rd., Santa Clarita, CA 91321.

P68. ENUMERATION OF BACTERIOPHAGE AND PROKARYOTE POPULATIONS IN AN URBAN COASTAL WETLAND (BALLONA WETLANDS) IN LOS ANGELES COUNTY BY EPIFLUORESCENCE MICROSCOPY. Salman Ahmad*, Emma Kennedy*, Helena Oliveri*, Jorrel Sampana*, and James Wu* (Gary Kuleck). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

P69. DISCOVERY OF MYCOBACTERIOPHAGE "KATATTACK". Theodore Medling, Katherine Wikholm, Kat Fu (Gary Kuleck, Yiwen Fang, Carl Urbinati). Loyola Marymount University, Department of Biology, 7900 Loyola Boulevard, Los Angeles, CA 90045.

P70. DISCOVERY OF MYCOBACTERIOPHAGE CONTAGION AND COMPARING IT TO OTHER MYCOBACTERIOPHAGE. Jacob Pascual*, Vishal Bhula* (Gary Kuleck, Yiwen Fang, Carl Urbinati). Loyola Marymount University, Department of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

P71. ISOLATING BACTERIA DISPLAYING INSENSITIVITIES TO MULTIPLE ANTIBIOTICS FROM THE BALLONA WETLANDS. Nana Kufor*, Christopher Leary (Dr. Gary Kuleck, Dr. John Dorsey). Loyola Marymount University, Dept. of Biology, 1 LMU Drive., Los Angeles, CA 90045.

P72. CONTAGION: THE FRESHMAN MYCOBACTERIOPHAGE PROJECT. Paola Lockwood* (Gary Kuleck, Yiwen Fang, Carl Urbinati). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

P73. AN ANALYSIS OF BACTERIOPHAGE DIVERSITY: THE ISOLATION AND CHARACTERIZATION OF KENGEN AND ANNOTATION OF CONTAGION. Genevieve Guerra*, Lauren Magee*, and Danielle Mauch* (Dr. Yiwen Fang, Dr. Gary Kuleck, Dr. Carl Urbinati). Loyola Marymount University, Dept. of Biology, Los Angeles, CA 90045.

P74. DISCOVERY AND CHARACTERIZATION OF A NOVEL BACTERIOPHAGE THERIPPER AND BIOINFORMATIC ANALYSIS OF BACTERIOPHAGE CONTAGION. Mitchell Petredis, Wil Gendron, (Yiwen Fang, GaryKuleck). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045

P75. USING SITE-DIRECTED MUTAGENESIS AND YEAST TWO-HYBRID ANALYSIS TO STUDY DNA BINDING DOMAIN MUTANTS OF THE *C. ELEGANS* WINGED-HELIX TRANSCRIPTION FACTOR LIN-31. Amanda Dewey* and Fernando Meza Gutierrez (Leilani Miller). Santa Clara University, Dept. of Biology, 500 El Camino Real, Santa Clara, CA 95053.

P76. *SACCHAROMYCES CEREVISIAE* RESPONDS TO COLD SHOCK BY CHANGING THE EXPRESSION OF GENES INVOLVED IN NITROGEN METABOLISM. Andrew F. Herman, Alondra J. Vega, Lauren N. Kubeck, Kenny R. Rodriguez, Katrina Sherbina, Nicholas A. Rochez, Kam D. Dahlquist. Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

P77. ANTIBIOTIC RESISTANCE GENES IN BACTERIAL ISOLATES FROM THE BALLONA WETLANDS. Sarah Patno*, Samantha Hurndon*, Daniel Garcia*, Stephanie Kaweki, and Chris Leary (Dr. Gary Kuleck). Loyola Marymount University Dept. of Biology 7900 Loyola Blvd Los Angeles, CA 90045.

P78. A PUTATIVE PHYTOCHROME-LIKE PHOTORECEPTOR MAY REGUALTE THE EXPRESSION OF RED-LIGHT INDUCED PSBA RNA BINDING PROTEIN GENES IN *CHLAMYDOMONAS REINHARDTII*. Macarena Aloi*, Laura Arce and Alexander Powell (Amybeth Cohen). California State University, Fullerton, Dep. of Biological Science, 800 North State College

Blvd., Fullerton, CA 92831.

P79. DEVELOPMENTAL REGULATION OF RRNA PROCESSING IN EMBRYONIC STEM CELLS. Josue Gutierrez*, Ivy Hung, (Benjamin Yu). University of California San Diego, Department of Medicine.

P80. RETINOIC ACID (RA) REGULATES EXPRESSION OF THE VITAMIN A TRANSPORTER, STRA6, BY DIFFERENT PATHWAYS IN BREAST AND THYROID CANCER CELL LINES. Debbie Shamsian*, Sun Wook Kim, Takahiko Kogai, and (Gregory A. Brent). UCLA, VA Greater Los Angeles.

P81. AN ANALYSIS OF HEAVY METAL STRESS IN THE HYDROPONICALLY GROWN TOMATO PLANT, *LYCOPERSICON ESCULENTUM*, USING THE COMET NUCLEAR ASSAY AND ICP-MS ANALYSIS. Daniel Chu, Katherine Kimura, Howard Lin, Danielle Lee, Anthony Traboulsi, Walter Au. Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

P82. VALIDATION OF *XENOPUS LAEVIS* MONOCLONAL ANTIBODIES IN WHITE'S TREEFROG *LITORIA CAERULEA*. Adam Marentes*, Shahani Noor, (Emma Wilson, Wendy Saltzman, Kristine Kaiser). University of California Riverside, Department of Biology and Division of Biomedical Sciences, Riverside, CA 92521.

P83. LATE TREATMENT WITH ESTROGEN RECEPTOR BETA LIGAND AMELIORATES EXPERIMENTAL AUTOIMMUNE ENCEPHALOMYELITIS. Amy Wisdom*, Yuan Cao, Noriko Itoh, Rory Spence (Rhonda Voskuhl). University of California, Los Angeles Neuroscience Research Building 635 Charles E Young Drive Los Angeles, CA 90024.

P84. MONITORING THE IMMUNE RESPONSE IN TRANSGENIC ZEBRAFISH. Caitlyn McGue*, Sarah E. Schale, Bradley H. Jacobsen, David N. Pratt, Noemi Delgado, Alyssa R. Scott, Brad G. Magor, David Traver, (Dawne M. Page). Point Loma Nazarene University, Dept. of Biology, San Diego, CA; Univ. of Alberta, Edmonton, Canada; UCSD, La Jolla, CA

P85. A LINK BETWEEN NEURAL AND PSYCHOPHYSICAL INHIBITION OF RETURN. Solmaz Shariat Torbaghan, Daniel Yazdi*, Koorosh Mirpour, James W. Bisley. David Geffen School of Medicine at UCLA, Department of Neurobiology, P.O. Box 951763 Los Angeles, CA, 90095-1763.

P86. REGULATION OF SEROTONIN SYNTHESIS GENES IN THE NERVOUS SYSTEM OF THE NEMATODE *C.ELEGANS* BY WNT SIGNALING GENES. Erin Williams* (Curtis Loer). University of San Diego Dept. of Biology, 5998 Alcala Park San Diego, CA 92110.

P87. THE EFFECTS OF SECOND-HAND CIGARETTE SMOKE EXPOSURE ON THE LEVELS OF PLASMA GLUCOSE AND INSULIN USING SWISS WEBSTER MICE. R. K. Pisano*, F. Dashty*, R. Shakir, H. Torba, V. Delgado, (F. Watson and M. Thao). California State University Stanislaus, Dept. of Biology, One University Circle, Turlock, CA 95382.

P88. A NOVEL POST-TRANSLATIONAL MODIFICATION OF CORE HISTONE PROTEINS: GLUTATHIONYLATION Carl Decker*, Oscar Tello (Kathleen Weaver and Jerome Garcia). University of LaVerne, Biology Department, 1950 Third Street La Verne, CA 91750.

Abstracts

Session A – ECOLOGY, BEHAVIOR, AND EVOLUTIONARY BIOLOGY

S1. APEX PREDATORS OF COSTA RICA. Trisha Stull* (Mike Mooring). Point Loma Nazarene University, Department of Biology, 3900 Lomaland Dr., San Diego, CA 92106.

Apex predators play a critical ecological role in the Neotropics, however they face a range of threats including habitat loss, fragmentation, illegal hunting, and retaliatory killing. The decline of these top predators has been associated with loss of biodiversity, trophic cascades of herbivore and plant populations, a decline in mammalian fauna known as the 'empty forest syndrome', and ecological meltdowns. Costa Rica is of particular importance for apex predators as it represents a bottleneck through which northern and southern populations are connected. Several biological corridors are being developed to promote the movement of fauna between protected areas and forest fragments. Information on the local status of predator populations is required to make informed decisions about conservation actions, but such information is often lacking or difficult to find. There are few published journal articles on this topic, and most studies are in the form of technical reports or masters theses ('gray literature') which can be hard to access. The purpose of this project was to construct a centralized database of the current knowledge regarding mammalian predators in this region. We compiled as many studies as could be found and analyzed the results to identify general trends using graphs and maps. The data were analyzed by region and comparisons were made regarding species presence, density, activity budgets, and prey species available. Most of the reports were from the southern half of Costa Rica, with several studies from the Talamanca region and Corcovado National Park. Only one region in northern Costa Rica was investigated (Guanacaste), with three studies for that region. Most studies were based on camera traps and focused on the largest felids – jaguar, puma, and ocelot, with little information on the 3 species of small cats. Jaguar populations occurred at low densities throughout Costa Rica, but there was regional variation. It appears that coyotes are invading some areas, and may compete with the smaller felids for prey. The information from this study will be made available to the public through the internet, and can provide a valuable tool for setting conservation priorities and environmental policy in Costa Rica.

S2. REPRODUCTIVE BEHAVIOR OF JAGUAR IN CAPTIVITY. Hannah Green* (Robert Wiese and Mike Mooring). San Diego Zoo Global, 2920 Zoo Drive, San Diego, CA 92112 and Point Loma Nazarene University, Department of Biology, 3900 Lomaland Dr., San Diego, CA 92106.

The jaguar (*Panthera onca*) is the largest felid in the Neotropics and is distributed from Argentina to northern Mexico. Although studies have shown relatively high gene flow throughout this huge range, indicating a single interbreeding population, deforestation is breaking up their range into smaller habitat islands. Wild populations are threatened by habitat loss, fragmentation, illegal hunting, and retaliatory killing that may result in decreased abundance, reduced genetic diversity, and loss of connectivity between breeding populations. Because of these threats in the wild, it is important to maintain a healthy and genetically diverse captive population of jaguars to serve as a breeding pool for reintroduction of individuals into the wild. Very little is currently known about the reproductive physiology of this species, impeding captive breeding efforts of zoo populations. To resolve this knowledge gap, we conducted a study to identify reliable behavioral indicators of physiological estrus by comparing levels of reproductive hormones with behavioral trends in a female jaguar ('Nindiri') at the San Diego Zoo. We recorded behavior via continuous focal animal sampling, and measured estrogen and progesterone levels by radioimmunoassay of hormone metabolites extracted from fecal samples. During the observation period, Nindiri experienced three estrogen peaks corresponding to three estrous cycles. A sustained rise in progesterone 5 days after the third estrogen peak (indicating conception) and the birth of cubs 99 days later confirmed that breeding was successful. Mounting and vocalization by male jaguar 'Guapo' was observed at each estrous period, increasing in intensity from the first to the third estrous cycle. Associated with each estrus, we noted peaks of increased calling and scent mark investigation by 'Nindiri', as well as a sharp decline in her pacing, all occurring within 3-4 days of each estrogen peak. Successful breeding and the birth of jaguar cubs is strong evidence that these periods of changed behavior can reliably indicate physiological estrus in jaguar. Assuming these results can be replicated in other jaguar, these behavioral indicators can be used to improve captive breeding and advance jaguar conservation.

S3. EFFECT OF TEMPERATURE ON AGGRESSION OF THE CONVICT CICHLID. Nathaniel Shanklin Nathaniel Bell (Dr. Ronald Coleman). California State University, Sacramento, Department of Biological Science, 6000 J Street, Sacramento, CA 95819.

Aquarium factors often influence the health and well-being of fish. Slight changes in the environment they are kept in can drastically affect their behavior and interactions between them and other fish. We hypothesize that fish aggression can be affected by temperature and we predict that we will see more aggressive acts by fish kept in warmer temperatures. The effect of temperature on Convict Cichlids was isolated by setting up identical aquariums with contrasting temperatures of 30° Celsius and 23°. Pairs of Convict Cichlid females were placed in the tanks. Each pair consisted of a large fish (dominant) and a smaller fish (subordinate). After a 24 hour acclimation period, 30 minute observations were taken of the cichlids and the number of chases and bites that occurred were recorded. After this first observation, the pair was placed in an aquarium of the contrasting temperature. Another 24 hour acclimation period was allowed followed by another 30 minute observation period. Using these results it can be seen that fish aggression increases with increased temperature. We conclude that aquarium temperature can be used as a tool for controlling a fish's behavior and aggression, and must also be controlled for in studies of fish behavior.

S4. LIMBS IN TIGHT SPACES: DO FOSSORIAL MOVEMENTS FAVOR LIMB REDUCTION IN LIZARDS? Mandalyn Kautz* (Gary Gerald). Nebraska Wesleyan University, Biology Department, 5000 St. Paul Ave., Lincoln, NE 68504.

In vertebrates, limb reduction has occurred multiple times in different lineages and involves the gradual loss of bones of the girdles and limbs and is closely associated with body elongation. The transition from a terrestrial to a more fossorial lifestyle has been implicated as the driving force favoring this

morphological change in many of the lineages, including snakes. According to this hypothesis, limbs and more rounded bodies impede movements through the narrow passageways common in fossorial environments. To our knowledge, no study has attempted to quantify the influence of tunnel width on limb mechanics in a limb-reduced lineage. Using fire skinks (*Riopa fernandi*), we quantified the effect of decreasing tunnel width on both forelimb and hind limb kinematics and speed to test the hypothesis that limbs interfere with normal stride cycles, thereby reducing locomotor performance and decreasing locomotor efficiency in narrower passageways. Contrary to predictions, preliminary results show that hind limbs are used less frequently (i.e. more likely to be tucked to the side and dragged) than forelimbs in the most narrow tunnels. This is counter to anatomical and fossil evidence that show that lizards and snakes lose their forelimbs first over time. Variation in stride lengths and frequencies were much higher for the smallest diameter as lizards had more difficulty negotiating narrower tunnels. Though this study was conducted on a limbed lizard species, we believe this data provides valuable insight into the role fossorial movements may have had on the selection of limb reduced lizards and snakes.

S5. THE CREEK TURNPIKE WETLANDS: A COMPARISON OF VEGETATIVE SURVEYS FROM 1992-1997 AND 2011. Ashley Sweeney* and Hal Reed. Oral Roberts University, Dept. of Biology and Chemistry, 7777 S Lewis Ave., Tulsa, OK 74171.

Mitigation involves the creation or restoration of a wetland to compensate for wetlands lost due to development. The Creek Turnpike wetlands were such a mitigation and cover approximately 45 acres. The objective of this study was to reassess three sites (A, B, and C) of the Creek Turnpike wetlands, comparing them to similar surveys conducted in 1992-1997 using the Braun-Blanquet abundance scale in ground stratum and vegetative coverage. As both 1996 and 2011 were drought years, the ground stratum data showed that the percent litter coverage significantly increased in Sites B and C in 2011 as compared to 1996. The herbaceous percent coverage also decreased significantly in Site C in 2011. At Site A, the 2011 decrease in the facultative wetland (FACW) and obligate (OBL) wetland species percent cover is likely due to the 2011 drought year. The decrease in the FACW and OBL indicator groups at Sites B and C is likely indicative that the plant composition is shifting away from a wetland community toward a terrestrial community. The ecological succession of wetlands into more terrestrial ecosystems has been shown in long-term wetland surveys. Long-term studies such as this demonstrate that the likelihood of mitigated wetlands remaining wetland communities may decrease over time. Continued management and long-term monitoring should occur in mitigated wetlands in order to assess the development of a stable, functioning wetland community.

Session B - ENVIRONMENTAL BIOCHEMISTRY AND PHYSIOLOGY

S6. ASSESSING BIOAVAILABILITY OF METALS IN POLLUTED ECOSYSTEMS USING RHIZOSPEHRE BIOGEOCHEMISTRY. Brianna Bernard* and Alexandria Taylor (Bonjun Koo). California Baptist University, Dept. of Natural and Mathematical Sciences, 8432 Magnolia Ave., Riverside, CA 92504.

Bioremediation may be an effective and economical approach for the cleanup of metals and organic pollutants in soil and contaminated media. The approach, however, has been applied in a limited fashion, and the fundamental mechanisms regulating bioremediation processes are not well understood. The goal of this research is to gain a better understanding of these processes through the examination of key biogeochemical processes in the rhizosphere that may regulate the solubility, transport, and bioavailability of metals. We hypothesize that a dynamic association of bacteria and mycorrhizal fungi plays an important role in regulating the uptake of metals and organic pollutants by certain plants. Central to this hypothesis is the production and quality of root exudates as they serve as an energy source for microbes and can affect redox reactions of the target contaminants. This pilot study which

involved growing corn plants in plain sand medium and biosolids-treated sand medium with. These plants were irrigated with a nutrient solution that contained trace amounts of 6 heavy metals (Cd, Cr, Cu, Ni, Pb and Zn). The removal rate of the heavy metals from the growing medium was measured and the uptake of the heavy metals was also measured in the both root and shoot part of the plants over a 16 week period. Results indicate that Cd, Ni, and Zn are preferentially removed from the growing medium. Results also indicated that removed metals were more concentrated in root segments of plants and plants grown in Biosolids-treated medium removed more metals than plants grown in the non-amended sand.

S7. CADMIUM ACCUMULATION AND RESISTANCE IN *DROSOPHILA MELANOGASTER*. Austin Nguyen* and Ellie Altomare (Catharine McElwain). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045

The fruit fly, *Drosophila melanogaster*, demonstrates sensitivity to heavy metal exposure that is both variable and selectable. Our lab has demonstrated significant differences in survival of wild-type *D. melanogaster* raised on varied concentrations of Cadmium-enriched food and has measured cadmium levels in treated flies using mass spectrometry. Preliminary data from flies across eight generations of exposure indicate that descendants of flies that survived exposure to high levels of cadmium are more likely to survive high exposures, meaning that resistance is selectable. Furthermore, cadmium levels, quantified by mass spectrometry, may decline in exposed flies selected for resistance compared to sensitive flies exposed to the same concentrations of cadmium. This decrease in cadmium content may indicate a metabolic mechanism of resistance, rather than the literature-suggested sequestration mechanism. The ability of flies to develop resistance to heavy metals may have significant impact on food webs in contaminated environments and may also indicate levels of exposure to higher trophic levels. The local Ballona wetlands are contaminated with heavy metals, particularly cadmium, lead, and copper, of which the levels in flies we have begun to investigate. Interestingly, we may have also observed an influence on copper levels in flies selected for cadmium resistance, which will be an area of further investigation.

S8. DIFFERENCE IN SUPERSTRUCUTRE OF HIGH-ALTITUDE AND LOW-ALTITUDE DEER MOUSE HEMOGLOBIN AS A POSSIBLE CAUSE OF INCREASED OXIDATIVE RESISTANCE IN THE HIGH-ALTITUDE SPECIES. Jake Oshlo* (Hideaki Moriyama). Nebraska Wesleyan University, Biology Department, 5000 Saint Paul Ave., Lincoln, NE 68504. University of Nebraska-Lincoln, Dept. of Biology, 3835 Holdrege Street, Lincoln, NE 68583.

There is a significant difference in the oxygen-binding ability of the hemoglobin of high-altitude Deer Mice (*Peromyscus maniculatus*) and low altitude Deer Mice. A series of mutations, primarily in the beta chain, has been identified in the high-altitude species. This project aims to understand how the mutations affect the oxygen binding capabilities of the high-altitude species oh hemoglobin in order to better understand the mechanism of oxygen binding. With limited oxygen in higher altitude, normal cellular respiration can be hindered, which can result in a build-up of free radicals in the blood. We hypothesize that the high-altitude hemoglobin species has increased resistance to oxidative damage from the low-altitude species and that the difference is due to a difference in superstructure. To investigate the possible difference, the functionality of the heme in the hemoglobin was measured after exposure to oxidative damage. Currently, it has been shown that the high-altitude hemoglobin has a higher resistance to oxidative damage than does the low-altitude hemoglobin. Further work will be done to confirm a possible difference in the superstructures. This work was funded in part by the National Center for Research Resources (5P20RR016469).

S9. HOT NIGHT MOVES: DEVELOPMENT RATE OF A SIERRA WILLOW BEETLE DEPENDS ON TEMPERATURE AND PHOSPHOGLUCOSE ISOMERASE GENOTYPE. Margaret Mae Abercrombie* (Elizabeth Dahlhoff and Nathan Rank). Santa Clara University, Dept. of Biology, 500 El Camino Real, Santa Clara CA 95053 White Mountain Research Station, University of California, 3000 E. Line St. Bishop CA 93514

Many organisms face the threat of population decline or extinction due to climate change because environmental temperature determines their body temperature. The persistence of vulnerable ectotherm populations requires that offspring successfully develop into adults. However, determining which temperature is optimal for development is problematic. Too low of temperatures will slow development rate, increasing the chances of being preyed upon; elevated temperatures will induce stress and reduce energetic resources available for growth. I determined the optimal temperature for rapid hatching and development in Sierra Nevada populations of the willow beetle *Chrysomela aeneicollis*, a native California insect living on the edge of its habitable range. *C. aeneicollis* has a unique feature – the glycolytic enzyme locus phosphoglucose isomerase (PGI) is under temperature selection. PGI-1 is common in cool regions and PGI-4 is common in warmer regions with both alleles in relatively equal frequency in populations with a moderate climate. Previous studies have confirmed effects of PGI genotype on adult fitness without exploration of how environmental temperature affects development rate. To test the effects of maternal genotype on hatching rate, females were collected from three high elevation sites differing in thermal profile. Eggs laid in the lab by females of known PGI genotype were reared in one of three temperature treatments corresponding to maximal, minimal and mean nighttime temperatures until the clutch hatched. To test effects of nighttime temperature on larval development rate, 2nd instar larvae were collected and held at one of these same three temperatures, and growth rate was measured until pupation. I found that nighttime temperature affected development time of both the eggs and larvae; lower temperatures lead to slower development with diminished benefits at higher temperatures. Also, clutches whose mothers were homozygous for the PGI-1 allele hatched later than clutches whose mother had at least one PGI-4 allele, yet PGI heterozygote larvae experienced a slower growth rate than their homozygous counterparts. These results indicate that larvae primed to survive variable weather conditions, the heterozygotes, "pay" for their metabolic flexibility with longer development time.

S10. CHANGING REPRODUCTIVE BEHAVIOR: AN ANALYSIS OF HOUSE FINCHES IN CALIFORNIA. Tauras Vilgalys*, (Heather Watts). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045

House finches breed over a wide geographic range covering much of the United States and Mexico. Historically, this nesting has shown broad synchrony with house finches breeding from March to July. In a number of other bird species, there have been trends to breed earlier in response to changing environmental conditions over recent decades. This study undertakes a detailed examination of the breeding season of Californian house finches examining the trends in reproductive timing over time. Data were taken from historical nest records maintained at the Western Foundation of Vertebrate Zoology from 1882 to 2007. Examining the earliest and latest reported nests across decades, there is no trend in the onset of breeding. However, the breeding season has been terminating earlier in recent years. One possible explanation for this decreasing trend is the temperature inhibition of reproduction. From an analysis of historical temperature data, there is a strong trend between increasing summer temperatures and an earlier termination of breeding. Future research will directly test for an effect of temperature on reproductive termination using live birds and a more thorough comparison of nest records to historical temperature data.

Session C – MICROBIOLOGY

S11. EXOGENOUS ISOLATION OF MOBILE RESISTANCE PLASMIDS FROM URBAN COASTAL WETLANDS. Doug Zuill* (Drs. David E. Cummings and Eva M. Top). Point Loma Nazarene University, Department of Biology, 3900 Lomaland Dr., San Diego, CA 92106 University of Idaho, Department of Biology, Moscow, ID 83844

An exogenous plasmid isolation technique was adapted to capture mobile plasmids from urban wetlands in San Diego County. Triparental matings were performed with *Escherichia coli* HY842 (RifR, SmR, ZeoR) as the recipient of conjugative plasmids, *Escherichia coli* JM109 as the helper strain harboring a mobilizable resistance plasmid (pBBR1MCS) (CmR), and native bacteria from the wetlands, either the Famosa Slough or the Tijuana River Estuary, as the conjugative plasmid donors. The Famosa Slough is a wetland that is never polluted by human sewage. The Tijuana River Estuary is impacted by raw human sewage following rainstorms, and it is documented that sewage contains elevated levels of drug-resistant bacteria; many of these organisms harbor their resistance genes on mobile plasmids. Colony counts using Eosin Methylene Blue (EMB) agar confirmed the presence of fecal coliforms in Tijuana River Estuary sediments following rains. The same assay showed there were no fecal coliforms at the Famosa Slough. More transconjugants were acquired from triparental matings performed at the Estuary than at the Famosa Slough. Transconjugants were genetically confirmed to be *E. coli* HY842 using whole-cell PCR. This study was successful in adapting the triparental mating technique to exogenously isolate plasmids from highly polluted coastal environments. The captured plasmids will be analyzed for important characteristics including resistance profiles, incompatibility groups, and host range.

S12. AUTOTROPHIC CARBON FIXATION IN CRENARCHAEOTA FROM YELLOWSTONE NATIONAL PARK. Laura Whitmore*, Ryan Jennings, Jim Moran, Helen Kreuzer, Mark Kozubal, (William Inskeep). Montana State University, Dept. of Land Resources and Environmental Sciences,Bozeman, MT 59717 Pacific Northwest National Laboratory, Richland, WA 99352

Autotrophy in the archaea has recently been described as an important and under-studied source of global carbon fixation. Several archaeal species are found in ferric oxyhydroxide mats from acidic geothermal springs in Yellowstone National Park (YNP). The springs are an exceptional natural laboratory for studying microorganisms in constrained systems. However, primary productivity had not been demonstrated in these systems. The goal of this study was to confirm autotrophic growth in pure *Metallosphaera yellowstonensis*, a dominant community member in Fe(III)-oxide mats, and relate this to in situ microbial communities. *M. yellowstonensis* was grown chemolithoautotrophically, with pyrite as the solid phase electron donor, oxygen as the electron acceptor, and $^{13}CO_2$ or CO_2 as the sole carbon source. At post log-phase, biomass was harvested and analyzed using isotope-ratio mass spectrometry (IRMS) at Pacific Northwest National Laboratory (Richland, WA). The results conclusively demonstrated that *M. yellowstonensis* is capable of inorganic carbon fixation. Furthermore, the isotope fractionation value was consistent with an operating 3-hydroxypropionate/4-hydroxybutyrate cycle, which was first characterized in other Sulfolobales. Ex situ ferric oxyhydroxide mat samples were incubated with pyrite, oxygen, and $^{13}CO_2$, and then analyzed by IRMS. The data show that under limited organic carbon, these microbial communities are capable of CO_2 fixation. Currently, transcriptomics and q-rt-PCR are being utilized to confirm the expression of genes in the 3-hydroxypropionate/4-hydroxybutyrate cycle. This research was supported by the Integrative Graduate

Education and Research Traineeship (IGERT), U.S. Department of Energy (DOE), Pacific Northwest National Laboratory (PNNL), Howard Hughes Medical Institute (HHMI).

S13. ISOLATION AND CHARACTERIZATION OF A MOTILITY MUTANT IN *BURKHOLDERIA UNAMAE*. Michael Onofre (Michelle Lum). Loyola Marymount University Dept. of Biology 1 LMU Drive Los Angeles, CA 90045

Burkholderia unamae is a nitrogen-fixing species of bacteria found in endophytic relationships with crops like maize, sugarcane, and tomato. The bacteria play an essential role in converting atmospheric nitrogen into a form that can be utilized by the plant. We are studying the ability of *B. unamae* to interact with the roots of these plants, as well as the genes responsible for this association. Based on previous research, we hypothesize that motility in *B. unamae* will play a critical role in the bacteria's ability to interact with plants. We therefore screened for *B. unamae* mutants defective in motility. We introduced a transposon into *B. unamae* by using a biparental mating strategy between a rifampicin resistant
B. unamae strain and *Escherichia coli* carrying a vector that carries a transposon containing a kanamycin resistance gene. We selected for transposon- tagged mutants by selecting for colonies resistant to rifampicin and kanamycin. We then screened the mutants for defects in motility on 0.3% agar. One of the mutants, MO384, was chosen for further characterization and was confirmed to be non-motile and have an alteration in cell morphology. Molecular methods identified the mutation to be in the gene that encodes FlhC, a transcriptional activator that has been identified in other bacteria in be involved in flagellar regulation. We have performed biofilm assays and found no alteration in biofilm formation. We are currently constructing a vector to express the wild type copy of flhC in the mutant in order to complement it. Further characterization will include inoculating tomato plants to determine the role motility has in the bacterium's association with roots.

S14.THE EXTRACTION OF BIOACTIVE COMPOUNDS FROM POTENTIAL FUNGAL ENDOPHYTES. Lucas Hemmer* (Jerald Bricker). Nebraska Wesleyan University, Biology Department, 5000 St. Paul Ave., Lincoln, NE 68504

Endophytes are either fungi or bacteria that inhabit plant tissues in a symbiotic relationship that aids both species. These organisms have potential to produce novel compounds to be used as antifungal and antibiotic drugs. One such endophyte, labeled Bearnes4F1L01B, from a prior experiment proved to be promising in its primary bioassay of producing bioactive compounds that inhibit bacterial growth. Several extraction procedures were utilized until it was found that compounds produced by Bearnes4F1L01B grown on PDB media were successfully extracted with ethyl acetate. Several duplications and secondary bioassays demonstrated zones of inhibition with several various bacteria that indicate the presence of multiple bioactive compounds. Later analyses of the successful extracts could reveal novel molecules that have antibacterial potential. This work was funded in part by the National Center for Research Resources (5P20RR016469).

S15. IDENTIFICATION AND CHARACTERIZATION OF THE NOVEL BIPYRAMIDAL CRYSTAL PROTEIN GENE IN *BACILLUS THURINGIENSIS* SUBSP. *MORRISONI PG-14*. Ryan M. Oliverio* (Hyun-Woo Park). California Baptist University, Department of Natural and Mathematical Sciences, 8432 Magnolia Avenue, Riverside, CA 92504.

Bacillus thuringiensis produces insecticidal crystal proteins that are toxic to immature stages of certain

species of insect. Three major orders of target insects for these proteins are Lepidoptera (butterflies and moth), Coleoptera (beetles) and Diptera (mosquitoes and blackflies). *B. thuringiensis* subsp. *morrisoni PG-14* produces the four major mosquitocidal proteins (Cry4A, Cry4B, Cry11A and Cyt1A) synthesized by *B. thuringiensis* subsp. *israelensis* that has been used to control vector mosquitoes for over three decades. Interestingly, it produces additional 144-kDa protein that forms a quasi-bipyramidal crystal which is a typical characteristic of lepidopteran-active toxins (Cry1). When the mutant strain of *B. thuringiensis* subsp. *morrisoni* PG-14 that produces only the 144-kDa protein was constructed and characterized, it was found that this protein has the insecticidal activity against cabbage looper (*Trichoplusia ni*) larvae. To obtain the gene encoding this protein, the first eight amino acids of this protein was read (MKINAVNE) using the Edman degradation. Amino acid sequence alignments using this peptide sequence and the corresponding sequences of the Cry1 proteins indicate that the 144-kDa protein may not have the usual Cry1-type sequence although its crystal morphology is similar with Cry1's. To identify the gene(s) encoding the 144-kDa protein, PCR approach using primers designed based on the Edman degradation is under evaluation.

Session D - BIOCHEMISTRY AND CELL BIOLOGY

S16. MEASUREMENT OF AQUAPORIN-3 EXPRESSION LEVELS IN SALT, FRESH, AND BRACKISH WATER-ACCLIMATED SAILFIN MOLLIES (*POECILIA LATIPINNA*) BY REAL-TIME PCR. Jaclyn Lange* (Gary Gerald, Therese McGinn). Nebraska Wesleyan University, Biology Department, 5000 Saint Paul Ave., Lincoln, NE 68504.

Aquaporins (AQP) are integral membrane proteins that have been identified in many organismal groups and are vital for the acquisition of water and maintaining osmotic balance within cells and tissues. This study was conducted to determine plasticity in AQP-3 expression in the gills of a euryhaline fish, the sailfin molly (*Poecilia latipinna*), in three different salinities. Bioinformatic analysis has showed high nucleotide sequence conservation of AQP-3 in fish species. We hypothesized that there would be decreased amounts of aquaporins following long-term exposure to increases in salinity. Individuals were acclimated to full marine, brackish (intermediate salinity between freshwater and marine water), and fresh-water tanks for six weeks. Immediately following acclimation, gills were removed and total RNA extracted from epithelial cells using the TRIzol method. Following reverse-transcriptase polymerase chain reaction (RT-PCR), real-time PCR was performed using AQP-3 specific primers to measure AQP-3 expression levels. Published AQP-3 primer sequence of the European sea bass (*Dicentrarchus labrax*) were used in our assay because of its relatedness to the *P. latipinna*. Differences in AQP-3 expression levels among the three salinity-acclimated treatment groups will be presented.

S17. DICOVERING PROTEINS THAT INTERACT WITH THE SMMAK16 PROTEIN FROM THE PARASITIC FLATWORM *SCHISTOSOMA MANSONI*. Megan Vanderkamp*, Tayah Kline, Daniel Shouldice, Yun-Lan Wong (Jon Milhon). Azusa Pacific University, Department of Biology and Chemistry, 675 E. Foothill Blvd., Azusa CA 91702

Schistosomiasis, a disease causing significant morbidity and mortality, results from infection by parasitic flatworms from the genus *Schistosoma*. Pathology resulting from schistosomiasis and propagation of the life cycle are exclusively due to egg production by the female. Studies of schistosome adults show that the only rapidly dividing cells are those involved in egg production. Therefore, we have chosen to study the nucleolar protein SmMAK16 because it has been shown to be

involved in a key process necessary for cell cycle progression, namely ribosome biogenesis. In an attempt to determine the function of SmMAK16, it is important to establish which cellular proteins interact with it. Cellular proteins α-importin and casein kinase II-α (CKII-α) are being studied for their interactions with SmMAK16; α-importin for its potential importance to the nuclear localization of SmMAK16, and CKII-α for its involvement in phosphorylation of SmMAK16. In order to determine whether these candidate proteins interact with SmMAK16, the genes that code for α-importin and CKII-α were cloned from an adult *S. mansoni* library using PCR into the pCR2.1 TOPO-TA vector. These candidate genes will then be cloned into a pRSET plasmid so they can be expressed and purified. Likewise, SmMAK16 was cloned into a pGEX plasmid so that it too can be expressed and purified. Once purified, these proteins will be used in immunoprecipitation and/or affinity chromatography studies to determine if there are interactions between SmMAK16 and either α-importin or CKII-α.

S18. SDF 1-α AND CXCR4 ARE IMPORTANT FOR POSTERIOR AXIS ELONGATION DURING *X. LAEVIS* EMBRYO DEVELOPMENT. Armbien Sabillo* (Carmen Domingo). San Francisco State University, Department of Biology, 1600 Holloway Ave., San Francisco, CA 94132

Axis elongation is crucial to proper embryo development. This is accomplished through convergent extension cell movements as well as directed cell migration. The signaling protein SDF 1-α and its receptor CXCR4 have been shown to mediate mesoderm cell migration during gastrulation in X. laevis embryos. A subset of mesoderm cells will form transient structures called somites, which will give rise to muscle, bone, and dermis of the adult. We hypothesize that the signaling protein SDF 1-α and its receptor CXCR4 are involved in elongating the embryonic axis by contributing to the formation of somites. Our data shows that knock down of the expression levels of either SDF 1-α or its receptor CXCR4 results in a truncated axis due to the formation of fewer somites. However, explants created using CXCR4 morphant tissue reveal that convergent and extension cell movements remain normal. Using a cell transplantation approach, we show that CXCR4 morphant cells are unable to properly migrate to the dorsal region of the embryo to join the presomitic mesoderm. As a consequence, the presomitic mesoderm may not have the full complement of cells necessary to build the posterior somites, thus leading to a shortening of the axis. Collectively, our results suggest that SDF 1-α and CXCR4 mediate cell migration, but not convergent extension, to form the proper number of somites which drives the length of the anteroposterior axis.

S19. IN VITRO ANALYSIS OF THE INTERACTION BETWEEN KAP3 OF KINESIN-2 AND ACTIN. Austin Tenney* (Matthew Berezuk). Azusa Pacific University, Department of Biology and Chemistry, 675 East Foothill, Blvd., Azusa, CA 91702

Bidirectional transport along the mictrotubule cytoskeleton is necessary for many cellular processes and is coordinated by two or more oppositely directed motor proteins. The plus end directed kinesin-2 and the minus end directed dynein are two such paired motor proteins. Both kinesin-2 and dynein interact with the microtubule associate protein (MAP) dynactin, which functions to facilitate attachment of the motors to cargoes. Kinesin-2 is a heterotrimeric protein consisting of two motor subunits that directly interact with microtubules, and the non-motor, putative cargo binding subunit, KAP3. The binding of KAP3 to dynactin has been shown to involve multiple parts of dynactin including p150glued, p62, Arp1, and actin. This association is due to a central core of repeating motifs in KAP3 that bear homology to armadillo (β-catenin) repeats. It has been proposed that since kinesin-

2 and dynein have independent binding sites on dynactin, it is possible that they could bind the same dynactin molecule simultaneously. To address this hypothesis, we have designed experiments to assess the interaction of KAP3 and actin in vitro. Using seven his-tagged constructs, each containing a fragment of KAP3, we employ a metallic bead-based affinity method to see if we can isolate actin from bovine liver. Furthermore purified globular actin is used in the metallic bead-assay to determine if the his-tagged constructs will bind with the purified actin. Optimization of this technique will then allow us to address whether or not the same constructs can bind dynactin and dynein/dynactin complexes.

S20. ANALYSIS OF THE ROLE OF BMI-1 AND MEL-18 IN PROSTATE CANCER PROGRESSION. Lizbeth Alvarez* (Dr. Luiza Nogaj). Mount St. Mary's College, Dept. of Biology, 12001 Chalon Rd., Los Angeles, CA 90049

Prostate cancer is one of the leading causes of death in men. Benign types of prostate cancer can be effectively treated while the malignant types are incurable. Therefore, it is important to find molecular markers that will distinguish benign prostate cancers from the malignant ones. The Polycomb proteins (PcG) function as transcriptional repressors and are thought to prevent the transcription of tumor suppressor genes such as p16. The p16 protein is known to prevent the proliferation of cell growth and directs the cell into apoptosis. However, the mechanism of Polycomb-mediated silencing and its connection to prostate cancer progression is still not well understood. We study the role of Bmi1 and Mel-18, members of the Polycomb complexes, on the progression of prostate cancer. Our results on prostate cancer biopsies show an inverse relationship between Bmi-1 and Mel-18 levels. In malignant tumors, there is an over expression of Bmi-1 and an under expression of Mel-18 while the p16 protein cannot be detected. Based on our results from tumor biopsies, we are examining the relationships between Bmi-1, Mel-18 and p16 in vitro using immobilized template assays. These preliminary studies show that Bmi-1 and Mel-18 might be good indicators of prostate cancer progression.

Session E - ECOLOGY, BEHAVIOR AND EVOLUTIONARY BIOLOGY

S21. THE ROLE OF INTRASPECIFIC VARIABILITY IN COMMUNITY ASSEMBLY PROCESSES AND SPECIES ECOLOGICAL BREADTH. Colby Sides*, Marielle Smith, Lindsey Sloat, Amanda Henderson, and Brian Enquist (Jim Ebersole). Colorado College, Dept. of Biology,14 East Cache La Poudre St., Colorado Springs, CO 80903 University of Arizona, Dept. of Ecology and Evolutionary Biology, 1041 E. Lowell St., Tucson, Arizona 85719.

A central goal of community ecology is to explain the varying distribution and ecological breadth among species. Every species is limited by the biotic and abiotic conditions it tolerates; however, some species are capable of persisting in more diverse conditions than others. Plant functional traits determine how demographic rates and growth vary in different environments by regulating which species are filtered out of a community. In this study, we quantified intraspecific variance for more than twenty species to address two prominent hypotheses in functional ecology. 1) Along an environmental gradient, do changes in trait values within species match community-level changes in that trait? 2) Do species with greater variability have greater ecological breadth? Our results demonstrated that intraspecific shifts in trait values parallel changes in the mean community trait value; however, the rate of change of intraspecific trait values was less than the rate of change of community traits. This demonstrates that species respond

to abiotic and biotic filters across environmental gradients, but are restrained in their ecological breadth due to limited plasticity in trait values. This finding was further supported by results that demonstrated species with greater intraspecific variability in SLA had significantly larger local range sizes. Therefore, greater variability in functional traits allows species' to persist in more environmental conditions. These results support Darwin's original hypothesis in The Origin of Species that states species with more "varieties" should have greater ecological breadth, and provide evidence that functional traits can be used to quantify a species' ecological niche.

S22. GENETIC DIVERSITY AND POPULATION DIFFERENTIATION IN THE RARE SERPENTINE ENDEMIC, SAN BENITO EVENING PRIMROSE (*CAMISSONIA BENITENSIS*; ONAGRACEAE). Cynthia A. Dick, Julie A. Herman*, Stephanie B. Saffouri, and Ryan E. O'Dell (Justen B. Whittall) Department of Biology Santa Clara University 500 El Camino Real Santa Clara, CA 95053

Conservation of rare species often requires establishing new populations. During a reintroduction, every effort should be made to maintain the limited amount of existing genetic diversity in order to increase the probability of long-term species persistence. However, determining which source material to use during reintroductions depends on the distribution of genetic diversity within and among existing populations. We investigated the genetic makeup of the federally-listed threatened San Benito evening primrose (*Camissonia benitensis*), a serpentine endemic plant from the South Coast Range in central California. Historically, *C. benitensis* was thought to exist only along stream terrace habitats, but recent field surveys located numerous additional populations occupying transition zones at the edge of serpentine outcrops. We sought to determine the amount of genetic differentiation between these two distinct habitat types. Using seven microsatellite markers, we compared genetic diversity in *C. benitensis* with that of its two closest relatives, *C. contorta* (non-serpentine) and *C. strigulosa* (serpentine tolerator). Genotyping results of 317 individuals indicate that *C. benitensis* exhibits exceptionally low levels of heterozygosity (average heterozygosity = 0.146) and significant genetic differentiation between habitat types (pairwise FST = 0.0433, P *C. contorta* average heterozygosity = 0.317; *C. strigulosa* average heterozygosity = 0.489). The diminished level of genetic diversity in *C. benitensis* is consistent with its putatively self-pollinating mating system, yet pollinator observations revealed a diversity of insect visitors to these flowers. Reintroduction efforts must acknowledge the genetic distinctiveness of the two habitat types while attempting to maximize the limited amount of remaining genetic diversity.

S23. EFFECTS OF DIETARY PHYTOESTROGENS ON PATERNAL RESPONSIVENESS AND MATURATION IN THE BIPARENTAL CALIFORNIA MOUSE. Aaron T. Stamp*, Trey Amador, Breanna N. Harris, and Juan Pablo Perea-Rodriguez (Wendy Saltzman). University of California, Riverside, Dept. of Biology, Riverside, CA 92521

The California mouse (*Peromyscus californicus*) is a monogamous, biparental rodent in which fathers show strong attraction to pups while virgin males show variable paternal responsiveness. Previous studies have demonstrated that circulating testosterone enhances paternal behavior in this species via aromatization to estrogen. We tested the hypothesis that

paternal responsiveness in virgin males would likewise be enhanced by dietary estrogens (i.e., phytoestrogens, PE) from soy. Virgin males (N=16 per group) were fed commercially available diets containing high, intermediate, or low levels of PE, from the time of weaning until sacrifice in early adulthood, and behavioral responses to an unfamiliar pup, body mass, testis masses, fat-pad masses, and epididymal sperm counts were compared among the three groups. No differences were found in males' behavioral responses to a pup. Similarly, testis masses, fat-pad masses, and sperm counts did not differ as a function of dietary PE content. However, patterns of body mass over time differed significantly among groups ($P<0.001$), as mice on the high-PE diet gained more mass across the study than those on a low-PE diet ($P<0.001$); neither of these groups differed significantly from the intermediate-PE group. These results suggest that the levels of phytoestrogens in the three diets used in this study differentially affect patterns of physical growth but not paternal behavior, fat deposition, testicular development, or spermatogenesis.

S24. FEMALE BODY SIZE AND REPRODUCTIVE OUTPUT IN THE GREEN LYNX SPIDER *PEUCETIA VIRIDANS* (ARANEAE, OXYOPIDAE). Mikayla Kemp*, Kayla Murata*, Jasmin Takemoto*, Mikayla Mowzoon (Martin Ramirez). Loyola Marymount University, Dept. of Biology, 1 LMU Dr., Los Angeles, CA 90045.

In this study, we sought to determine the relationship between female size and various measures of reproductive output in the green lynx spider *Peucetia viridans*. A total of 221 *P. viridans* females were collected with their egg sacs from Kenneth Hahn Recreation Area on seven sample dates between September and December 2011. Female size [carapace width (mm)], female weight (mg), and the following egg sac parameters were recorded: egg sac mass (mg), silk mass (mg), egg mass (mg), and number of eggs. These measures were used to calculate the average egg weight; the egg sac mass per offspring; the residual index (a measure of female body condition); and the relative clutch mass (an indicator of female reproductive effort). While the analysis of the fall 2011 data is not complete, we have found that clutch mass declined through the season, probably reflecting more limited prey availability for females as fall progressed. At the same time, the percentage of silk in the egg sacs doubled near the end of the season, perhaps to provide better insulation for the enclosed eggs with the onset of winter.

S25. ECOLOGICAL STRESS CAUSED BY FIRE AND ITS EFFECTS ON ORB WEAVING SPIDERS. Sophie Crinion (Martin Ramirez). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

This study was designed to examine the effects of fire on two orb weaving spider genera, Metepeira and Cyclosa. The research site is a particular ridge on Santa Catalina Island, half of which was burned in the Two Harbors fire that occurred on May 2011. The site has been monitored since a few weeks after the fire with measurements made in both the burned area of the ridge and the unburned (control) area of the ridge. Because food availability and uptake is associated with many spider fitness indicators, we have measured aerial insect abundance every three months since July 2011. On each visit to the site we searched for orb-weaving spiders, but were unable to find enough adults to constitute a useful sample size. This project is ongoing and we plan to continue visiting the site to measure insect abundance and

search for adult spiders. Once adult females are found, weight, size, body condition and fluctuating asymmetry measures will be recorded, and reproductive output will be assessed by measuring sac and clutch mass as well as clutch size.

Session F – GENETICS

S26. MAPPING FERMENTATION RATE IN DOMESTICATED STRAINS OF *SACCHAROMYCES CEREVISIAE*. Jillian Gerrity* (David Hess). Santa Clara University, Dept. of Biology, 500 El Camino Real, Santa Clara, CA 95053.

Saccharomyces cerevisiae has been domesticated by humans over thousands of years for use in brewing and baking. This domestication involves metabolic specialization of *Saccharomyces cerevisiae*. For example, brewing strains have been specialized to ferment substrates particular to a culture or region (i.e. grape mash for wine or rice for sake) and to ferment under different conditions (temperature, fermentation length, oxygen availability, etc). Genomic analysis has shown that these domesticated fermentation species have between 30,000-90,000 single nucleotide polymorphisms (SNPs) with respect to the standard laboratory strain. Some of this natural genetic variation is responsible for the brewing strains adaptation to its particular fermentation process. This research will identify that causative genetic variation for increased ethanol production rate from glucose in a sake strain as compared to a laboratory strain. Our initial results show that the sake strain produces ethanol at a four times faster rate per cell than the laboratory strain four hours into a growth curve. Assays on the spores from a cross between the sake strain and laboratory strain demonstrate both parental and intermediate ethanol production rates. This indicates that two or more genes are responsible increased ethanol production and further experiments are underway to isolate the casual mutations of this increased ethanol production.

S27. DEVELOPMENT OF A SYSTEM TO DEPLETE SIR2 IN ORDER TO STUDY ITS ROLE IN MAINTAINING SILENT CHROMATIN AT THE RIBOSOMAL DNA LOCUS IN *SACCHAROMYCES CEREVISIAE*. Lindsey Jones* and Rachel Jordan (Mary Bryk). Nebraska Wesleyan University, Biology Department, 5000 Saint Paul Ave., Lincoln, NE 68504.

The ribosomal DNA (rDNA) locus in the budding yeast *Saccharomyces cerevisiae* is a tandem array of 150-200 copies of the ribosomal RNA genes. The highly repeated rDNA locus acquires a silent chromatin conformation that protects the integrity of the rDNA locus and the yeast genome. Silent chromatin represses RNA Pol II transcription and homologous recombination, which is detected using yeast strains that have a single HIS3 reporter gene integrated into the rDNA locus. Previous experiments have shown that the level of Pol II transcription and recombination is unequal across the rDNA array. The goal of this research was to develop a system to deplete the silencing protein Sir2, which associates with the rDNA, from yeast cells in order to determine if Sir2 protein regulates the level of Pol II transcription and recombination at different positions across the rDNA array. Two approaches of depleting Sir2 protein were pursued. First, the SIR2 gene was deleted from three yeast strains that each have a HIS3 reporter gene at a different position within the rDNA array. Mapping analysis revealed that the position of the HIS3 gene had moved in each of the sir2Δ mutants, which prevented the analysis of the effect of loss of Sir2 protein on position-dependent gene expression. The second approach required placing the SIR2 gene under the control of a tetracycline-sensitive repressible promoter so that Sir2 can be depleted from the cell rapidly in the presence of doxycycline, a tetracycline analog. Sir2 depletion experiments will be

described.

S28. PHENOTYPIC REVERSION OF FLUOROQUINOLONE RESISTANCE IN NEISSERIA GONORRHOEAE AFTER CESSATION OF CIPROFLOXACIN USAGE IN SAN FRANCISCO. Kiana Espinosa*, Sean Buono, Susan Phillip, Jeffery Klausner, Mark Pandori (David Hess). Santa Clara Univesity, Dept of Biology, Santa Clara, CA, 95053. San Francisco Department of Public Health Labs, San Francisco, CA, 94102.

Within the United States, drug resistance of *N. gonorrhoeae* is monitored by the Gonococcal Isolate Surveillance Project (GISP). GISP is a CDC project that utilizes sentinel laboratories geographically separated throughout the United States for the gathering and testing of Gonococcal isolates. Data from the GISP project is used to inform treatment recommendations for gonorrhea, allowing for continuously effective medical management of the disease. Data from GISP led to the cessation of fluoroquinolone use for treatment of gonorrhea in the United States: in the year 2002 for California and in 2007 for the remainder of the United States. Working with the San Francisco Department of Public Health Laboratory, which serves as a GISP site, we sought to assess genetically the diversity of *N.gonorrhoeae* isolates in San Francisco spanning the years 2005-2009. To assess genetic diversity we utilized the NG-MAST protocol which involves sequencing two variable regions of the N. gonorrhoeae genome. During this time period, the proportion of isolates in San Francisco that were found to be susceptible to the fluoroquinolone drug ciprofloxacin increased dramatically (from 55% in 2006 to 90% in 2009). NG-MAST results from isolates across that time period revealed a rapid rate of genetic turnover in San Francisco with multiple strain types entering and exiting the city on an annual basis, implying that the shift in susceptibility seen for fluorquinolones over this time period might largely have been due to the re-establishment of susceptible strains in San Francisco rather than reversion of existing strains. We further noted that the increase in susceptibility amongst *N.gonorrhoeae* strains in San Francisco began abruptly in 2007. These data may imply that cessation of the use of a certain class of compounds can result in a return of susceptibility to those compounds locally. However these data may indicate that a local change in treatment policy may not result in phenotypic reversion until neighboring jurisdictions adopt a similar policy.

S29. MITOCHONDRIAL AND NUCLEAR DNA ANALYSIS FOR MUTATIONS AND MODIFIERS IN A LATINO FAMILY WITH DILATED CARDIOMYOPATHY. Sonia Martinez*, Simin Hakim, Van T. Hoang, Subhadra Ramanathan, and (Michael V. Zaragoza). UCI Cardiogenomics Research Program Department of Pediatrics and Biological Chemistry The University of California, Irvine, School of Medicine Irvine, CA 92697-3940.

Over 5 million Americans suffer from heart failure with a significant portion diagnosed with Dilated Cardiomyopathy (DCM), a disease that causes weakening and enlargement of the heart. In recent literature, 30-35% of DCM cases have shown to have a familial basis. In this study, we are investigating whether DNA variation, mutations and modifiers, cause and/or influence the differential expression of DCM in a Latino family with both the father (age 21) and his son (age 2) affected. We extracted the patients' DNA, PCR-amplified and sequenced TNNT2 and LMNA, nuclear DCM-associated genes and the complete mitochondrial DNA (mtDNA) to detect mutations and to determine their respective mtDNA haplogroups. Using DNA analysis software Sequencher, we found no obvious mutations;

however, the father has a homoplasmic MT-ND1 variant (13708 G>A) previously associated with an increased risk for the mitochondrial disorder LHON, Multiple Sclerosis, and cancer. As expected, we also found the father and son had different mtDNA haplogroups, L3 and C1b, respectively. Since Latino-specific haplogroups are A, B, C, or D, we were surprised by the detection of the L3, an Africa-specific haplogroup. Thus, our results underscore the importance to continue investigating both nuclear and mitochondrial DNA variation not only as potential disease-causing mutations but also as population-specific modifiers of disease phenotype including heart failure and cardiomyopathies.

S30. MUTATIONS AND MODIFIERS IN THE MYH7 GENE: DNA ANALYSIS OF THREE FAMILIES WITH HYPERTROPHIC AND DILATED CARDIOMYOPATHY. Christine K Tran*, Simin Hakim, Van Hoang, Julia Platt, June-Anne Gold, (Michael V Zaragoza). UC Irvine Cardiogenomics Program, Dept. of Pediatrics, Division of Genetics & Metabolism, University of California, Irvine, School of Medicine, Irvine, CA USA; Loma Linda University Pediatrics/Genetics, Campus Street, Loma Linda, CA 92354.

Hypertrophic cardiomyopathy, characterized as the thickening of parts in the heart, is a well-known cause of sudden cardiac death in young athletes. Dilated cardiomyopathy, characterized as the expansion of the heart, also progresses to a weakened heart that cannot pump blood efficiently. These two types of cardiomyopathy have been shown to be caused by inherited mutations in several genes including MYH7, which encodes for the myosin heavy chain beta isoform that is expressed primarily in the heart. It is our hypothesis that there are primary mutations and secondary modifiers in MYH7 that are associated with either hypertrophic or dilated cardiomyopathy and that they can be traced and followed in the family. We evaluated three unrelated families consisting of 11 individuals. DNA from each individual was extracted. We amplified and sequenced MYH7. Sequences were analyzed and variants were found by comparing the DNA sequences with a known reference. We identified three variants: Ser1491Cys, Arg858Pro, Ala1800Val. The variants in each proband were used to screen the rest of the family to verify that the mutation is cardiomyopathy associated. Data showed that two out of the three variants segregated with the disease. Database and literature review showed that two of the variants were previously reported and one was novel. Our study suggests that Ala1800Val is a disease associated mutation and that Ser1491Cys and Arg858Pro may serve as secondary disease modifiers. Our results pave a way for further research on the identified variants whether it is population studies or candidacy for genetic testing.

S31. CLINICAL VARIABILITY FOR NOVEL TAZ GENE MUTATION: BARTH SYNDROME WITH DIALATED CARDIOMYOPATHY (DCM) AND HEART FAILURE IN AN INFANT AND LEFT VENTRICULAR NON-COMPACTION (LVNC) IN HIS GREAT-UNCLE. Diti Ronvelia*, Jaclyn Greenwood, Julia Platt, and Simin A. Hakim (Michael V. Zaragoza, M.D., Ph.D.). University of California, Irvine, School of Medicine, Dept. of Pediatrics, Division of Genetics & Metabolism and Dept. of Biological Sciences, 2501 Hewitt Hall, Irvine, CA 92697.

The taffazzin gene (TAZ) is located at Xq28 and encodes a protein involved in the metabolism of cardiolipin, an essential mitochondrial phospholipid. Mutations in TAZ are associated with Barth syndrome (BTHS), an X-linked recessive condition with dilated cardiomyopathy (DCM), and left ventricular noncompaction (LVNC), a cardiomyopathy characterized by loose, trabeculated myocardium. This study investigates the clinical spectrum from BTHS with severe cardiac dysfunction in an infant to skeletal myopathy with LVNC in his great uncle through DNA analysis with the hypothesis that a common inherited mutation exists between these two individuals that explain their distinct cardiac

phenotypes. The proband is a 48-year-old male with muscle weakness and chronic fatigue since early childhood. The patient's first cardiac evaluation at age 45 showed LVNC. The proband's great nephew is a six month-old boy who at three months was admitted to the PICU with failure to thrive, lethargy and respiratory distress due to heart failure (HF). Cardiac studies revealed DCM with a spongiform trabeculated pattern of the left ventricle. At age 11 months, the patient had a heart transplant. A mutigenerational pedigree, medical records and DNA samples were obtained from the proband, his great nephew and five unaffected family members. For the two affected individuals, we conducted sequence analysis of the TAZ gene. A novel, hemizygous nonsense mutation in TAZ exon 7 (c.887G>T, p.Gly195X) was detected. We identified a novel TAZ mutation that displayed the clinical spectrum of LVNC in an adult to DCM with end-stage HF in an infant.

Session G - NEUROBIOLOGY AND IMMUNOLOGY

S32. ANALYSIS OF C1Q NEURAL ANATOMY AND EFFECT ON EPILEPTIC ACTIVITY. Anu Ramachandran*, Naomi Ford, Isabel Parada (David Prince). Stanford University Dept of Neurology, Stanford, California, 94305-2004.

Early neural development is marked by excessive outgrowth of neurons, leading to the formation of extensive networks of synapses. As development progresses, networks are selectively pruned as functional synaptic connections emerge and become prominent. This pruning mechanism is achieved by the coordinated involvement of several genes and proteins. Recently, the C1q gene, originally associated with immune inflammatory response, has been shown to be important in synaptic pruning as part of a complement cascade for synapse elimination. Errors in this mechanism have been shown to promote excessive neural signal production and epileptic activity. In a previous paper, David Prince's lab examined the effect of knocking out the C1q gene on the synaptic connectivity and resulting epileptic activity of mice. The research focused on the physiological effect of the C1q knockout through EEG recordings. It also began an anatomical analysis of axonal boutons, which have a significantly higher density in C1q KO pyramidal neurons. This project expands the scope of anatomical analysis of C1q KO pyramidal neurons, focusing on dendritic changes that occur with the knockout. Five anatomical dimensions were analyzed via confocal microscopy and neural reconstruction software: dendritic length, dendritic density, soma size, spine density and spine type. Overall, significant differences were seen - basal dendritic lengths of C1q knockouts are significantly greater than in control cells ($p < 0.05$). Spine density in C1q KO cells is also significantly higher ($p < 0.05$) than in WT. Finally, KO cells have a much higher proportion of thin-type spines than WT cells ($p<0.005$), indicating a higher proportion of immature spines on the dendritic surface. The findings of this anatomical research align with the theory that C1q plays an important role in the cascade necessary for neural pruning and spine elimination. A lack of coordinated action in this mechanism could further contribute to the irregular EPSPs and epileptic activity seen in these mice. Overall, there is strong evidence to suggest that C1q has an effect on the basal dendritic structure of pyramidal neurons in mice, and the anatomical changes associated with its absence could be capable of producing the epileptic activity shown in these mice.

S33. TEMOZOLOMIDE DELAYS TUMOR GROWTH BY DIMINISHING REGULATORY MACROPHAGES IN AN INNOVATIVE, INDUCIBLE, GENETIC MOUSE MODEL OF MELANOMA. Carlos Peinado*, (Bhaskar Srivastava, MD, PhD), (Susan Kaech, PhD). Yale School of Medicine, Dept. of Immunobiology, 300 Cedar St., New Haven, CT 06520

Current concepts regarding cancer immunoediting suggest that the immune system can inhibit or promote

melanomagenesis. For example, the CD4 and cytotoxic CD8 T cell anti-tumor immune response can mediate tumor regression when appropriately activated. On the other hand, suppression of this anti-tumor response by the same cancer cells, regulatory T cells and regulatory macrophages stimulates tumorigenesis. Optimal cancer immunotherapy, therefore, depends on appropriately activating the anti-tumor immune response while inhibiting the pro-tumor response. In fact, new therapeutics against melanoma that promote the anti-tumor response are successful in a subset of patients. Furthermore, most of these patients have previously been treated with traditional chemotherapeutics that may be conditioning this response. One of these chemotherapeutics, temozolomide, delays melanoma growth and does not appear to induce necrosis of transformed melanocytes, implying an immunomodulatory property. Therefore, we investigated this prospect using a new, inducible, genetic mouse model of melanoma. Briefly, our model relies on tumor induction by cre-mediated oncogenic changes in melanocytes that result in constitutive activation of Braf and deletion of Pten leading to increased proliferation and survival. We assessed the effect of temozolomide on the tumor immune response by treating melanoma bearing mice and assessing the immune infiltrate by flow cytometry and immunohistochemical staining of paraffin-embedded tumor sections. Surprisingly, we found a depletion of regulatory macrophages while cytotoxic and regulatory T cell infiltration was unaffected. We propose that temozolomide might act by depleting regulatory macrophages and could be combined with approaches that promote an effective cytotoxic immune response.

S34. ANALYSIS OF INNATE IMMUNE RESPONSES OF MURINE RESPIRATORY EPITHELIAL CELLS IN RESPONSE TO INFLUENZA VIRUS INFECTION IN VITRO. Brittany M. Justa*, Alexander Vogel, Deborah M. Brown, and (Therese M. McGinn). School of Biological Sciences, Nebraska Center for Virology, University of Nebraska, Lincoln, NE 68583. Nebraska Wesleyan University, Biology Department, 5000 Saint Paul Ave., Lincoln, NE 68504.

As targets for respiratory viruses, pulmonary epithelial cells are the first to recognize pathogens, and are responsible for initiating signal transduction cascades that lead to inflammatory cytokine production. A mouse model for influenza infection with the highly-pathogenic mouse-adapted strain, PR8, has been employed to investigate the role of pulmonary epithelial cells in host responses to infection. Lung tissues harvested from PR8-infected BALBc mice exhibited increased expression of IL-6, TNF-α, MIP1-α mRNA and protein, with respect to controls, at 48 hours post-infection. Separation of epithelial cells and immune cells from infected lung tissues revealed differential expression of pattern recognition receptors and innate cytokines in each cell type. Preliminary results from real time RT-PCR experiments indicated that lung epithelial cells from PR8-infected mice produced 10-fold higher levels of IL-6 and IFN-β in comparison to resident immune cells. In order to observe the unique innate signaling events and cytokine profiles of epithelial cells in the context of influenza infection, an in vitro model has been established using a mouse lung epithelial cell line (MLE-15). Initial results from real time RT-PCR experiments indicate that infection of MLE-15 cells with PR8 virus (MOI=1, 5) induced transcription of type I interferons (IFN-α/β), IL-6, and TNF-α within 24 hours. This indicates that infected epithelial cells can secrete many cytokines that initiate immune responses. This work was funded in part by the National Center for Research Resources (5P20RR016469).

S35. STRATEGIES TO STUDY THE ROLE OF FAST DYNAMIC UBIQUITINATION AT SYNAPSES. Anna M. Nia*, and Anna Caputo (Felix E. Schweizer). Department of Neurobiology, David Geffen School of Medicine at UCLA, Los Angeles, California, USA.

We are investigating the role of the ubiquitin proteasome system (UPS) in synaptic transmission. The

UPS is one of the main pathways for protein degradation in eukaryotic cells. However, protein ubiquitination does not only mark proteins for degradation, but serves as a posttranslational modification. We have previously found that inhibiting the UPS triggers a rapid increase in spontaneous neurotransmitter release. The frequency of excitatory and inhibitory postsynaptic miniature currents increase several fold within minutes of UPS inhibition while the amplitude remains constant. This suggests a rapid presynaptic function for the UPS. To identify candidate proteins that might mediate regulation of synaptic transmission, we are using proteomics, immunocytochemistry and biochemical approaches. Using synaptoneurosomes, I am investigating the ubiquitination of proteins involved in vesicle exocytosis. In particular, I am focusing on SNAP-25, a member of the SNARE complex that is responsible for vesicle fusion. SNAP-25 synaptic activity dependent turnover has been shown to depend on ubiquitination and thus represents a promising target for study as to whether ubiquitination of SNAP-25 in minutes timescale is affecting the neurotransmitter release.

S36. EPSTEIN-BARR VIRUS INFECTED B LYMPHOCYTES AS A SOURCE OF TYPE I INTERFERONS IN SYSTEMIC LUPUS ERYTHEMATOSUS. Laura Blasnitz* (Luwen Zhang). Nebraska Wesleyan University, Biology Department, 5000 Saint Paul Ave., Lincoln, NE 68504. Nebraska Center for Virology, University of Nebraska, Lincoln, Department of Biological Sciences, 4240 Fair St., Lincoln, Nebraska 68583.

Systemic lupus erythematosus (SLE), also known as lupus, is an autoimmune disease which affects the skin, joints, kidneys, and brain as well as other organs. The driving force for lupus pathogenesis are type I interferons (IFN). These proteins have a variety of functions from the activation of dendritic cells to promoting the survival and differentiation of mature lymphocytes. The primary source of IFN in the body is plasmacytoid dendritic cells (pDC). These cells are believed to be the primary source of IFN in lupus patients, yet it has been observed that the number of pDCs are declining while IFN signatures remain high in the patient's blood. Therefore, there must be an alternative source of IFN in these patients. In this research our data suggests that toll-like receptor 7 (TLR-7) activation triggers the accumulation of an Epstein-Barr virus (EBV) protein – latent membrane protein 1 (LMP-1) – in B lymphocytes. This gathering of LMP-1 primes EBV-infected B lymphocytes for IFN production and thus creates an alternative source for IFN signatures in lupus patients. Additionally, because EBV-infected cells are abundant in lupus patients we propose that primary infection of EBV may itself be a source of IFN induction. This work was funded in part by the National Center for Research Resources (5P20RR016469).

S37. ALTERNATE READING FRAMES DETECTED IN CIRCULATING HIV-1 VIRAL SEQUENCE: A BIOINFORMATICS ANALYSIS. Sean Purtell*, (Keith Garrison). Saint Mary's College of California, Dept. of Biology, 1928 St. Mary's Rd. Moraga, Ca, 94556-2744

HIV-1 alternative reading frame peptides (ARF's), coded for by reading frames outside of the main viral protein-coding reading frames have previously demonstrated strong immunogenicity. Translation of these peptides has been associated with stresses exerted on HIV-1 throughout the course of infection. ARF-specific CD8+ T Cells exert in-vitro mutational pressure and HAART may select for these specific HIV-1 variants in-vivo. We are part of a larger immunologic study to measure ARF's responses in acute and chronic HIV-1 infection. In our sub-study, thirteen identified sense ARF's were screened to eliminate sequence overlap with regions of the HIV-1 genome encoding structural or accessory proteins of the virus. However, sporadic matches between ARFs and small numbers of HIV-1 viral sequences in the NCBI database persisted. These hits, while potentially representing sequencing errors in the reports,

more likely represent incorporation of ARF amino acid sequence into circulating viral peptides in HIV1+ individuals. ARF incorporation was common in geographic regions exhibiting high instances of circulating HIV-1 recombinants, and detection was associated with recombinant events in viral genomes. If ARF sequence incorporation into viral proteins occurred randomly, we would have expected a random distribution of BLAST hits across all known HIV-1 coding regions. Accounting for the contribution that each protein-coding region makes to the HIV-1 genome and adjusting for the fraction of each main coding sequence region that is comprised of ARF sequence, we observed 58% of ARF incorporation events within the env gene region, with 24% and 18% of events incorporated into pol and gag gene regions, respectively. These results are especially interesting given that HIV-1 sequence hyper-variability is concentrated in the env region, with profound effects on host antibody neutralization of the virus.

Session H - MOLECULAR BIOLOGY, PHYSIOLOGY AND CLINICAL RESEARCH

S38. THE EFFECTS OF THIRD-HAND CIGARETTE SMOKE EXPOSURE ON THE LEVELS OF PLASMA GLUCOSE AND INSULIN IN SWISS WEBSTER MICE. R. K. Pisano*, F. Dashty*, R. Shakir, H. Torba, V. Delgado, (F. Watson and M. Thao). California State University Stanislaus, Dept. of Biology, One University Circle, Turlock, CA 95382.

Third-hand smoke (THS) consists of tobacco residue that is often smelled long after the cigarette has burned out and coats indoor surfaces where smoking has occurred such as walls, carpet and furniture. Chemicals from the residues are potentially hazardous to human health and can enter the body through inhalation of dust particles or through skin contact with contaminated surfaces. THS exposure is a relatively new area of research and its effects in animals including humans are not well studied. Mice were exposed to THS once a day, 5 days a week for 25 weeks. THS exposure was simulated by lighting a cigarette in a Plexiglas chamber lined with carpet for approximately 5 minutes. When the cigarette has completely burned, the smoke was exhausted via a ventilation system, and then mice were placed in the smoke exposed Plexiglas chamber for 5 minutes. Blood was drawn from the saphenous vein once every three weeks for plasma glucose and insulin determination. Plasma glucose was measured using a glucose meter. The level of insulin was determined using ELISA. Mice exposed to THS consumed less food and gained less weight over the 25 weeks. There was no change in the insulin level but an increase in the level of plasma glucose. Immediately after THS exposure, plasma glucose levels decreased and insulin levels slightly increased. The length of exposure time and the length of the experiment may be a determining factor on the effects of THS exposure on glucose metabolism.

S39. ERRα A NEW TARGET IN ERBB2-OVEREXPRESSING BREAST CANCER: STUDIES WITH ERRA INVERSE AGONIST XCT790. Andrew Cannon*, Stetson H. Williams, Hamid Band, and (Srikumar M. Raja). Nebraska Wesleyan University, Biology Department, 5000 Saint Paul Ave., Lincoln, NE 68504. University of Nebraska Medical Center, Omaha, NE.

Breast cancer (BC) is a leading cause of cancer deaths in women worldwide necessitating continued vigorous research efforts. While around 60% of BCs are driven by the hormone receptors (Estrogen Receptor/Progesterone Receptor; ER/PR), ErbB2-driven breast cancers constitute 20-25%, and are associated with the poorer patient outcome. Anti-Estrogens (Tamoxifen), are currently used for the treatment of hormone-dependent breast cancer whereas the ErbB2 antibody, Trastuzumab in combination with chemotherapeutics is currently the standard of treatment for ErbB2-driven breast cancers. However, intrinsic and acquired resistance to therapies continues to pose challenges. Estrogen

Related Receptor Alpha (ERRα), an orphan nuclear receptor has been shown to transcriptionally up-regulate ErbB2-expression, is therefore a potential target in the treatment of ErbB2-driven breast cancers. The purpose of this INBRE summer project study was to begin to evaluate the potential of XCT790 (a synthetic small molecule inverse agonist of ERRa) in the treatment of ErbB2-driven breast cancers. Our initial in vitro studies indicate that treatment with XCT790 resulted in dose- and time-dependent attenuation of ErbB2 protein levels in a panel of human breast cancer cell lines BT-474, SKBr3, and 21MT1 cells (western blotting). Comparison of cytotoxicity among a panel of ErbB2-high and ErbB2-low cell lines indicated that XCT790 was shown to be cytotoxic with an IC50 of around 5.0 μM, although the IC50 levels did not correlate with ErbB2-levels. Notably, the pharmacological combination of XCT790 (which transcriptionally suppresses ErbB2 expression) with the HSP90-inhibitor, 17-allylaminodemethoxygeldanamycin (17-AAG) (which leads to destabilization and degradation of ErbB2 receptor) was found to be synergistic. This work was funded in part by the National Center for Research Resources (5P20RR016469).

S40. EFFECTS OF HEAVY METALS ON PROLIFERATION AND NEURONAL DIFFERENTIATION OF EMBRYONIC STEM CELLS. Circe McDonald* and Mark Gutierrez (Mohammed El Majdoubi). Dominican University of California, Department of Natural Sciences and Mathematics, 50 Acacia Avenue, San Rafael, CA 94901.

Neurotoxic effects of heavy metals on the developing brain are a major public health concern. Because of the limitations of animal-based models and traditional cell culture models of neuronal development, the mechanisms of developmental neurotoxicity are poorly understood. In recent years, embryonic stem cell (ESC)-derived neuronal models have been developed and offer distinct advantages over traditional in vivo and in vitro model systems for investigating the effects of neurotoxins. In vitro neuronal differentiation recapitulates several critical processes involved in the development of the nervous system such as migration, differentiation, and synaptogenesis. Here, we cultured feeder-independent mouse embryonic stem cells and induced their differentiation into neurons using retinoic acid. Using this model of developing neurons, we assessed developmental neurotoxicity of four heavy metal compounds found in the environment: mercury, cadmium, lead, and manganese. Changes in cell viability, morphology, and replication rates were monitored at each step of the developmental process. The efficiency of neuronal differentiation was determined by calculating the proportions of cells that are immuno-positive for MAP-2, a cytoskeleton protein unique to neurons. Undifferentiated ESCs were generally more sensitive to higher physiological doses of all four compounds, which inhibited cell proliferation and induced apoptosis. Lower physiological doses of these compounds did not impact ESCs proliferation but did interfere with their neuronal differentiation and migration. These results are consistent with findings in animal-based models and show that the neuronal differentiation of ESCs is a useful model system for investigating developmental neurotoxicity of environmental chemicals at the cellular level. We are currently using this model to characterize developmental neurotoxicity of endocrine disruptors such as Polybrominated diphenyl ethers (PBDE).

S41. MOLECULAR CHARACTERIZATION OF BETA-GALACTOSIDASE IN THE UNIQUE OVINE MODEL OF GM1-GANGLIOSIDOSIS. Masis Isikbay* (Amelia Ahern-Rindell). University of Portland, Dept. of Biology, 5000 N Willamette Blvd., Portland, OR 97203

GM1-Gangliosidosis (GM1) is an autosomal recessive Lysosomal Storage Disorder that has been identified in sheep and is also present in numerous other mammalian species, including humans. GM1 is a fatal disease with no cure that is characterized by acute neurological degeneration. It presents with

decreased activity in beta-galactosidase (beta-gal), a protein coded for by the GLB1 gene. Beta-gal normally combines with two other proteins, alpha-neuraminidase (alpha-neur) and cathepsin A to form a Lysosomal Multienzyme Complex (LMC) that stabilizes its components. We hypothesize that the GM1-affected sheep have a mutation that alters the beta-gal structure interfering with formation of the LMC, leading to a secondary deficiency of alpha-neur that is unique to this model. We utilized protein and DNA analysis techniques to characterize beta-gal from normal and GM1-affected sheep to help elucidate the underlying genetic defect. Exons 2-16 of the GLB1 transcript were cloned from both normal and GM1 affected fibroblasts using RT-PCR and revealed the presence of possible mutations sites on the GLB1 gene. The beta-gal protein was isolated from normal and GM1-affected sheep, and analyzed using Western blotting and immunochemiluminescence. A 64kDa band was present in all samples when compared to a protein standard. Currently we are repeating RT-PCR experiments for those exons containing possible mutations, and primers have also been designed to amplify both the 5' and 3' ends of the GLB1 transcript so that the whole GLB1 cDNA may be determined.

S42. DOSE AND TIME DEPENDENT EFFECTS OF HDAC INHIBITORS, LBH589 AND VORINOSTAT, ON GROWTH AND SURVIVAL OF COLORECTAL CANCER CELLS: A PRE-CLINICAL ANALYSIS. Stephanie T. Kuwahara*, Shelby C. Martin and Austin D. Layton (Melissa Wilson). Azusa Pacific University Department of Biology and Chemistry 701 East Foothill Blvd., Azusa, CA 91107

Background: Colorectal cancer (CRC) is the second cause of cancer related deaths in the United States. Although current therapies exist, 50% of patients fail to respond to treatment, illuminating a necessity for development of novel chemotherapeutic strategies. Histone deacteylase inhibitors (HDACi) exemplify novel treatment options, with promising results in both preclinical and animal models. This study was designed to compare the dose and time dependent antiproliferative effects of two HDACi: LBH589 and vorinostat (VOR) in CRC cell lines, HCT116, HT29, and SW620. Methods: Cell lines were treated with increasing doses of LBH589 or VOR and analyzed for both growth inhibition (MTS assay) and cell survival in response to treatment at different time points. Results: Treatment with LBH589 and VOR demonstrated concentration dependent growth inhibition in CRC cells. When the potency of LBH589 was compared with VOR, lower doses of LBH589 were needed to reach the IC50 (72h) value (HCT116: 9.5nM LBH589, 1.0μM VOR; HT29: 15.3nM LBH589, 2.1μM VOR; SW620: 11.5nM LBH589, 1.6 μM VOR). Further, when growth inhibition was analyzed at 3, 6, 12, 24, 48 and 72h, LBH589 demonstrated greater potency than VOR, reaching an IC50 at 6h as compared with VOR at 24h in HCT116 CRC cells. The cell survival assay evaluating the ability of the cell to survive after initial HDACi insult, demonstrated similar results to those from the MTS assay. Conclusions: The results demonstrated that a significantly lower dose and duration of exposure was needed to reach the IC50 value for treatment with LBH589 when compared with VOR. These results indicate that LBH589 may be better suited for the translation of in vitro study results to the clinic for treatment of CRC. Future evaluation of the effects of these HDACi will evaluate the acetylation status of histones and the induction of cell death by apoptosis.

POSTERS

P1. METHOD DEVELOPMENT FOR ISOLATION OF PHOSPHOPROTEINS USING MUTANT ALKALINE PHOSPHATASE. Dema Alniemi* and Duane Mooney (Edward Dratz). Montana State University, Dept. of Chemistry and Biochemistry, Bozeman, MT 59715.

Proteomics, the study of proteins and their post-translational modifications (PTMs), is an increasingly important field of study. The most common PTM identified in cells is phosphorylation, which has been found to play a central role in a wide range of normal cellular regulation as well as in diseases such as diabetes and cancer. A new method for enrichment and isolation of phosphorylated proteins is being pursued using the E. coli alkaline phosphatase (ALP) enzyme to seek a novel and simple method for the global analysis of phosphoproteins. Wild-type ALP is a highly non-specific phosphatase that hydrolyzes the bond between a phosphate group and its attached protein. A mutation in the active site of wild-type ALP, S102L, has been made that allows the enzyme to bind the phosphate group on proteins, but prevents hydrolysis of the bond, therefore keeping the protein attached. The bead-bound ALP S102L mutant can then be used to bind phosphorylated proteins in complex biological extracts, and further, separate them from unphosphorylated proteins. After elution, the enriched phosphoproteins can be analyzed by a variety of techniques, helping researchers across many fields of study further their knowledge on the importance of phosphates, proteins, and the effects of cellular molecules on human health.

P2. SPATIALLY CONTROLLED BIOACTIVE SIGNAL INCORPORATION TO GUIDE STEM CELL FATE IN HYDROGELS. Jacob Borrajo*, and Tatiana Segura. University of California, Los Angeles, Dept. of Chemical and Biomolecular Engineering, 5531 Boelter Hall, Los Angeles, CA 90095.

Hydrogels are networks of hydrophilic polymer chains that can be used as tissue culture systems that mimic the natural stem cell niche. Because hydrogels have mechanical properties similar to natural tissues and can be modified with natural ligands, hydrogels are promising platforms to study stem cell biology. Potential applications for hydrogels include expanding/differentiating stem cells in vitro, delivering stem cells in vivo, as well as making tissue constructs. When functionalized with bioactive signals, hydrogel-based artificial niches can be used to control stem cell fate. This study aims to develop a method to spatially functionalize synthetic hydrogels with bioactive signals by using photolabile pendant moieties and enzyme-assisted bioconjugation. Such a hydrogel system allows for the photopatterning of complex biochemical patterns and gradients, which are required to imitate in vivo cell microenvironments. In this study, Arg-Gly-Asp (RGD) peptide –a bioactive adhesion motif found in the extracellular matrix (ECM) glycoprotein fibronectin– was used to enhance cell-ECM interactions and increase mouse mesenchymal stem cell (mMSC) spreading. Bioactive RGD peptides were successfully conjugated to synthetic hydrogels via enzyme-assisted conjugation. This mild and highly biocompatible process allows for controlled bioactive signal incorporation in hydrogels, and future studies will work to develop a platform to spatially program stem cell fate.

P3. EXAMINING A109 PROTEIN IN SULFOLOBUS TURRETED ICOSAHEDRAL VIRUS FROM YELLOWSTONE NATIONAL PARK. Hadeel Alniemi*1,2, (Brian Eilers)3, (C. Martin Lawrence)3 1Hughes Scholars Program, Montana State University, Bozeman, MT 2Department of Cell Biology & Neuroscience, Montana State University, Bozeman, MT 3Department of Chemistry & Biochemistry, Montana State University, Bozeman, MT. Montana State University, Dept. of Chemistry & Biochemistry, 1501 South 11th Avenue, Bozeman, MT 59715.

Sulfolobus Turreted Icosahedral Virus, or STIV, is an archaeal virus that infects the unicellular organism *Sulfolobus solfataricus*, a member of the domain Archaea. Sulfolobus thrives in hot and acidic environments, much like the hot springs in Yellowstone National Park where STIV was first isolated from. Understanding of archaeal viruses is quite limited compared to that of Bacteria and Eukarya, with only roughly 50 known archaeal viruses compared to some 2000 of the other domains. For this reason,

research with them is very important. Our goals with STIV research include learning more about archaeal viruses and their life cycles, gaining a better understanding of the requirements for life in extreme environments, and discovering more about a common ancestor from which the three domains of life emerged. Although these are large topics to explore, small scale work can be insightful to this larger picture. To learn more about STIV, the proteins making up its genome are examined. In many cases, the function of certain proteins is unknown. By determining the structure of the protein through x-ray crystallography, a corresponding function can be assigned by comparing the structure to those of known proteins in an internet database. A109 protein in STIV was the specific protein of interest. After expression of A109 in *E.coli* cells, the protein underwent purification through nickel affinity chromatography as well as both size exclusion and mono Q chromatography. Purification was followed by crystallization trials which if successful would allow for examination of protein structure. Work with A109 has reached crystallization trials. The assignment of function is the ultimate goal with regards to A109 protein in STIV. Further work would be aimed at moving beyond crystallization trials to the x-ray crystallography step and discovering the structure and function of the protein.

P4. THE EFFECTS OF KAP3 OF KINESIN-2 ON THE ORGANIZATION AND REMODELING OF THE ACTIN CYTOSKELETON IN CELL CULTURE.. Danielle Hatt*, Taylor Kline* (Matthew Berezuk, Ph.D.). Azusa Pacific University, Department of Biology and Chemistry, Azusa, CA 91702.

Carefully controlled bidirectional transport along microtubules is required for a number of cellular processes. Bidirectional transport involves the coordination of two or more oppositely directed motors and the molecules that associate them with their desired cargo. The mechanism of motor activation and deactivation, as well as target specific association motifs is poorly understood. For one such motor, kinesin-2, it has been proposed that its non-motor subunit, KAP3, acts as a linker between the motor subunits and their target cargoes. It has been demonstrated that KAP3 Armadillo repeat fragments and intact, native kinesin-2 could co-cycle with actin *in vitro*. Being an armadillo repeat protein, it is not surprising that KAP3 could have some function in the mechanisms of the actin cytoskeleton. It is also intriguing to consider why earlier studies looking for KAP3 binding partners identified other actin binding proteins. The discovery of an interaction between kinesin-2 and filamentous actin presents an intriguing new view of how the microtubule and minifilament cytoskeletons interact and communicate with one another. However, the importance of the observed biochemical interaction at the cellular level has been left unexplored. To address this question, we have initiated the cloning of seven KAP3 fragments out of a 6X-His plasmid into a GFP vector. Future plans include using the new constructs to analyze the effects of KAP3 overexpression on kinesin-2 localization and function as well as actin cytoskeletal morphology.

P5. THE EFFECTS OF PROTEASE INHIBITORS ON PARATHYROID HORMONE-RELATED PROTEIN LEVELS IN LUNG CANCER CELLS. Christopher Tam*. University of California, San Diego, Dept. of Biological Sciences, 9500 Gilman Dr., La Jolla, CA 92093.

The prevalence of lung cancer and its serious prognosis demands research into the discovery of novel therapies. Parathyroid hormone-related protein (PTHrP) is present in roughly 2/3 of lung cancer tumors and has implications in the proliferation of the cancer. Clinical studies have shown high levels of the PTHrP peptide 1-34 (amino terminus) and low levels of 109-141 (carboxyl terminus) in tumors are associated with a decreased survival rate in patients. In order to better understand how the protein is processed, non-small cell lung cancer cell lines (BEN, H727, A549) were treated with various proteases inhibitors (Aprotinin, E64D, Pepstatin A) and 1-34/109-141 protein levels were quantified through radioimmunoassay. Aprotinin, an inhibitor of serine proteases, increased levels of lysate and media (secreted) PTHrP 1-34 levels across all cell lines. This suggests that a serine protease is most likely involved in the processing of the peptide. The E64D (cysteine protease inhibitor) produced an increase in

PTHrP 1-34 only at lower concentrations, but had no effect at higher concentrations. This suggests a possible indirect effect. Pepstatin A, an aspartyl protease inhibitor, had no effect. Future experiments done will focus specifically on understanding the interaction of the serine protease on specific cleavage sites on PTHrP. A proteolytic assay using exogenous PTHrP 1-34 combined with cell lysates will confirm that the peptide is actually being processed and inhibitors such as Aprotinin are causing an indirect effect. Synthetic androgen (R1881) will be studied as well to characterize possible sex-dependence on PTHrP levels.

P6. COMPARATIVE PROTEOMIC ANALYSIS FOR ACQUIRED RADIATION RESISTANCE IN PANCREATIC CANCER. Kara Sunshine Robertson*, Jianhong Zhou (Yuchun Du). University of Arkansas, Dept. of Biology, Science and Engineering 528, Fayetteville, AR 72701.

Pancreatic adenocarcinoma is a fatal and aggressive disease, and intrinsic and acquired resistance to chemo- or radiotherapy is one of the major contributing factors. The molecular mechanisms underlying the acquisition allowing the cancerous cell to grow are largely unknown. The objective of this study was to quantitatively examine protein expression contributing to the acquired radio-resistance in pancreatic cancer cells. For this purpose, we first established a stable pancreatic cancer cell line that differs in radiosensitivity from the parental cells. Quantitative proteomic method using stable isotope labeling was then used to systematically compare protein expression between the radio-resistant cells and the parental cells. Many proteins were found to be expressed at abnormal levels in the resistant cells. Calretinin, a calcium binding protein, was one of the proteins whose expression was up-regulated in the radio-resistant cells. Western blot tests were performed to confirm the up-regulation of the expression of calretinin. Further tests could be performed to determine the effect of the over-expression of calretinin on the radio-sensitivity of pancreatic cancer cells. In addition, EGFR, Ras, AKT/PKB, and CDK6 in the EGFR signaling pathway were found to be over-expressed and could contribute to the extended cell proliferation despite radiation treatments.

P7. HIGH CHOLESTEROL DIET INCREASES FREE OXIDIZED FATTY ACIDS IN MOUSE MODELS OF CANCER. Daniel Niknam*, Taraneh Rasta*, Nika Karimi MD; Samra Vazirian MD , Maryam Shabihkhani MD, Ania Gapeleh MD, John Lotfi JD and (Greg Hough) MSc. David Geffen School of Medicine, University of California Los Angeles, 90095.

Objective: Determination of free oxidized fatty acids following treatment with high cholesterol diet in ApoE deficient mouse model. Introduction: Inflammation is being considered a role-playing factor in many pathological conditions including cancer. High cholesterol consumption and oxidized fatty acids are known to induce inflammatory molecules. We sought to determine if a high cholesterol diet would result in elevated levels of circulating oxidized fatty acid. Methods: ApoE deficient mice (n=20 per group) were maintained on the laboratory rodent chow or on a diet containing 0.125% cholesterol (TD 18831, Harlan, Teklad) for two weeks. Mice were fasted overnight and blood was removed under anesthesia and according to UCLA ARC protocols from retroorbital sinus and was kept on ice. Plasma was separated and extreme care was taken to prevent oxidation by adding 20 μM BHT and by immediate cryopreservation. Mass spectrometry analyses were performed using a Q 4000 unit. Statistical analyses were carried out using ANOVA and StatPak Prism. Results: The levels of 9-hydroxyoctadecaenoic acid, 9-HODE and 13-HODE were significantly increased ($p= 0.013$) in mice treated with cholesterol as compared to the rodent chow diet. Conclusion: The data suggests that high cholesterol diet increases circulating levels of oxidized fatty acids in ApoE deficient mice, which could result in amplification of inflammatory molecule formation that contributes to the activation of pathways involved in cell growth regulation and balance.

P8. CIRCULATING 15-HYDROXYEICOSATETRAENOIC ACID LEVELS ARE ELEVATED IN A MOUSE MODEL OF INFLAMMATORY DISORDERS FOLLOWING HIGH FAT DIET ADMINISTRATION.. Samra Vazirian MD, Ladan Vakili MD, Margeaux Beran, Arash Meshkat DDs MSc, Maryam Haghnegahdar MD, Mitra Owrang MD, Arezoo Rajaee MD, Roshanak Aliali MD and Greg Hough MSc.. David Geffen School of Medicine University of California Los Angeles 90095.

Objective: To determine the plasma levels of the inflammatory marker 15-hydroxyeicosatetraenoic acid in ApoE deficient mouse treated with high fat diet. Introduction: 15-hydroperoxyeicosatetraenoic acid (15-HPETE) is a product of oxidation of arachidonic acid (C20:4). HPETEs are potent prooxidant molecules that can lead to stimulation of several metabolic pathways resulting in an inflammatory condition in many organs and systems. Our organism has evolved to use mechanisms to convert the potent 15-HPETE to a lesser active molecule 15 hydroxyeicosatetraenoic acid, 15-HETE. Still elevated levels of 15-HETE are undesirable in most circumstances. We sought to determine the effect of a high fat diet in an animal model of inflammation namely ApoE deficient mouse. ApoE deficient mouse is incapable of having LDL bind and be removed from circulation and thus has high LDL levels and is a model of lipoprotein oxidation in atherogenesis Methods: Three to four month old apoE deficient mice (n=20 per treatment group) were maintained on rodent laboratory chow or on a diet with 35-40 % of calories supplied by fat and containing 0.125 % cholesterol. After two weeks of treatment, the mice were fasted overnight and following UCLA ARC protocols blood was removed from retro orbital sinus, carefully protected from oxidative modification (addition of 20 μM BHT) and was immediately cryopreserved. Using SepPak columns and a Q 4000 mass spectrometer, the plasma levels of 15-HETE were determined. The data was analyzed using the software supplied by the manufacturer and statistical significance determined using ANOVA through Prism application. Results: Feeding a high fat diet amplified the circulating levels of 15-HETE ($p = 0.021$ vs. the control group), which in turn can activate pathways that produce inflammatory molecules. Conclusion: Reducing fat consumption can lead to reduced level of plasma oxidized fatty acids which in turn can help alleviate the inflammatory pressure.

P9. TOWARDS THE SYNTHESIS OF ANTASCOMICIN B. Ashley Rosenberg*: David Clay: (Matt McIntosh). University of Arkansas, Department of Chemistry, Chemistry Building, Fayetteville, AR 72701.

In a total synthesis process, it is important that each step is optimized in terms of yield, and for steps that establish a stereocenter, the stereoselectivity needs to be optimized. In a collaborative effort we are attempting the total synthesis of the natural product FKBP12 binding macrolide antascomicin B. The macrolide is shown to possess neuroregenerative properties in mouse models which may prove to be effective in treating those with Parkinson's disease. While attempting the synthesis of antascomicin B, we have focused on determining an efficient synthesis of the C29-C34 cyclohexyl moiety. The current published enzymatic method is far too lengthy at eight steps, requires a high loading of expensive enzymes, and an inability to achieve a mass scale of products. We were able to achieve a more efficient approach through asymmetric transfer hydrogenation, which allows a readily scalable approach to enantiopure alcohols. Reaction variables including sensitivity to water, and molecular equivalents of the epoxide to formic acid/triethylamine were evaluated to determine the best conditions for the reaction. The epoxy quinol was prepared on a multi-gram scale by Noyori transfer hydrogenative desymmetrization of the readily available meso-epoxy diketone. Although the intrinsic enantioselectivity was modest (82:18 er at 4% conversersion), a highly enantiopure product (99.6:0.4 er) was obtained by operation in 44% yield via kinetic resolution of the minor enantiomer with long reaction times (48 h), or in 73% yield by combination with an enzymatic resolution of 93:7 er mixture. Experiments were run in an attempt to decrease byproduct formation, increase the scale of the reactions, and increase the yield to improve the overall synthesis.

P10. THE BEST WAY TO IMPROVE HDL, IS TO LOWER THE LDL LEVEL. Ladan Vakili MD*,Ghazal Vakili MD, Samra Vazirian MD, Jasmine Bowers Obioha MSII, Masood Memarzadeh MSII, Foozhan Farahmand MD, Drew Huusfeldt, Tannaz Moin MD, Greg Hough MSc.. David Geffen School of Medicine at UCLA, Los Angeles, California.

Objective: Analyses of HDL function. Introduction: Population studies have shown that plasma levels of HDL (high density lipoprotein) inversely correlate with the prevalence of coronary heart disease (CHD). Plasma HDL levels in an individual however, does not necessarily correlate with the risk for CHD. Many patients with high HDL present with coronary events and many individuals with low HDL cholesterol do not develop coronary complications. Our group previously demonstrated that HDL composition and function could be more important than HDL levels. Under excessive inflammatory pressure unsaturated fatty acids in HDL can undergo oxidative modification. Protective enzymes including paraoxonase, LCAT and PLTP can be inactivated by oxidative modification reducing HDL's anti-inflammatory properties. This results in HDL not being able to protect LDL from oxidative modification. Methods: Fasting plasma samples from patients with documented CHD were analyzed for their ability to prevent LDL modification. Results: We demonstrated that among coronary patients over 69 percent had non protective HDL while among healthy controls 4.5 percent had dysfunctional HDL. Conclusion: While there are effective medications for lowering LDL cholesterol (namely statins) there are few or no satisfactory drugs for raising HDL levels. Therefore, it is tempting to modify our recommendation regarding low HDL cholesterol: Until there are effective medications for raising HDL, it should be clear to the public that the best way of dealing with low HDL cholesterol is lowering LDL cholesterol. After all it is the ratio of LDL to HDL that plays a role in atherogenesis and coronary heart disease.

P11. THE DISCOVERY OF THE MYCOBACTERIAPHAGE MEPAC. Abraham Gebreselassie and Paul (DongWoo) Chang (Gary Kuleck, Yiwen Fang, and Carl Urbinti. Loyola Marymount University, Dept of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

Bacteriophages are viruses that infect bacteria, and are the most abundant biological entities on the planet, and yet their diversity is underexplored, hindering our understanding of their roles in ecology and bacteria evolution. In the fall of 2011, as a part of Science Alliance Education (SEA) Phage Discovery program, a nationwide consortium of schools sponsored by the Howard Hughes Medical Institute, we began our own investigation to isolate and characterize new mycobacteriophages, phages that infect mycobacterium species like the pathogenic Mycobacterium tuberculosis. We isolated bacteriophage from soil samples collected on Loyola Marymount University. Using *Mycobacterium smegmatis* as a host, we purified a new mycobacteriophage, which we named MePac. After phage purification, we characterized it using restriction digest analysis on the genomic DNA. The results indicated that MePac belongs to the C Cluster, (myoviridae), a family of short tailed and lytic phages. In the spring, as part of a class project, we are annotating a segment of the genome of Contagion using the bioinformatics program, DNA Master. We will discuss the isolation and characterization of MePac, and our preliminary findings on the annotation of Contagion and the relevance of our research with respect to evolution and microbial ecology.

P12. REACTIVE OXYGEN SPECIES ARE IMPORTANT FOR PROMOTING BMP-INDUCED DENDRITIC GROWTH IN RAT EMBRYONIC SYMPATHETIC NEURONS. Charlotte Lea* (Vidya Chandrasekaran). Saint Mary's College of California, Dept. of Biology, 1928 Saint Mary's Road, Moraga,

CA, 94575.

Neurodegenerative diseases such as Alzheimer's disease and Parkinson's disease and the process of aging in humans are associated with changes in the neuronal morphology, specifically the retraction of dendrites. The purpose of this research study was to investigate the role of reactive oxygen species (ROS) in sympathetic neurons and to determine whether ROS are primarily harmful or beneficial to dendritic growth. ROS are types of free radicals found in cells, and they include molecules such as hydrogen peroxide, hydroxyl, and superoxide radicals. In large quantities, ROS can cause damage to DNA and kill cells, but recent research has shown that ROS production is necessary for non-cytotoxic and/or host defense functions. In this study, we first examined the effects of the antioxidants diphenylene iodinium (DPI) and nordihydroguaiaretic acid (NGA) on bone morphogenetic protein 7 (BMP-7) induced dendritic growth in cultures of sympathetic neurons from 21 day old rat embryos. In addition, since ROS are known to be produced during cellular respiration, we tested the amount and rate of oxygen consumption in neurons treated with BMP-7 using the Seahorse XF24 Analyzer. Our data suggest that ROS are produced in BMP-7 treated sympathetic neurons and are important to dendritic growth at low physiologic levels. Furthermore, different antioxidants can inhibit BMP-7 induced dendritic growth, indicating that though antioxidants are important for protective effects against excess ROS production, high levels of antioxidants may have undue damage to neurons in the form of decreased dendrite number and decreased dendritic arbor.

P13. EVALUATION OF THE NOVEL TUMOR SUPPRESSOR GENE, DEFENSIN-β 1, IN COLON CANCER CELLS. Austin D. Layton*, Shelby C. Martin, and Stephanie T. Kuwahara (Melissa Wilson). Azusa Pacific University Dept. of Biology and Chemistry 701 East Foothill Blvd. Azusa, CA 91107.

Background: Human Defensin β-1 (hBD-1) is encoded by the gene and functions as an antimicrobial peptide involved in the innate immune response. It is most often expressed in epithelial cells, including those in the colon. Previous experiments have shown that hBD-1 exhibits tumor suppressor functions in urothelial cancer cells. This study examined the presence of hBD-1 in colon cancer cells as well as examining the effect of expressing hBD-1 in colon cancer cells. Patients and Methods: A total of 18 patients' colon tissue samples were subjected to immunohistochemistry (IHC) specific for hBD-1 to examine its expression in both normal and tumor cells. To gain insight into the effects of hBD-1 expression in CRC, two CRC cell lines were transfected with pCMV6-XL4-DEFB1, alongside a control empty vector, to compare the effect of hBD-1 overexpression on cell viability at 24 and 48 hours. Results: After examining hBD-1 expression from 15 patients' colon tissue samples by IHC, results demonstrated that hBD-1 expression was present predominantly in the normal colon cells when compared to colon cancer cells. Following overexpression of hBD-1 in colon cancer cell lines, there was a significant decrease in cell number when compared to control cells indicating the role of hBD-1 in growth inhibition and induction of apoptosis. Conclusions: The results demonstrate evidence a loss of hBD-1 expression in CRC cell lines and further provide evidence for hBD-1's potential role as a tumor suppressor. Further studies need to be conducted for better understanding of the pathway that hBD-1 affects in the CRC cells' development and progression.

P14. IL-8 PRODUCTION AND NFκB INDUCTION IN CALU-3 CELLS IN RESPONSE TO QUORUM SENSING MOLECULES. Chelsey Soler*, Ashkon Banihashemi, Sam Papke, and Romina Herrera (Kathleen Tallman). Azusa Pacific University, Department of Biology and Chemistry, 701 E. Foothill Ave., Azusa, CA 91702.

Biofilms are a common defense mechanism used by many forms of bacteria. These surface-attached communities of bacteria produce measurable levels of quorum-sensing molecules. Pseudomonas aeruginosa (PA) produces two different kinds of homoserine lactone quorum-sensing molecules, N-(3-oxododecanoyl)-L-Homoserine Lactone (3OC12) and N-butyryl-L-Homoserine Lactone (C4). These molecules have been shown to induce the expression of NFκB which leads to the production of IL-8, an inflammatory cytokine of the innate immune system. NFκB induction was measured through a luciferase assay and IL-8 production was measured using an Elisa assay in response to application of 3OC12 or C4, or ratios of the two QS molecules. The impetus behind this experiment was to answer the question: does the immune system respond to quorum-sensing by itself, and if so, which lactone or combination of lactones produces the strongest response? The results showed that there is an inflammatory response raised against the quorum-sensing molecules. In the ratios of 3OC12:C4, there is a potentially additive effect seen with both IL-8 production as well as NFκB induction. However, there were some discrepancies between the Elisa and the Luciferase results for concentrations of pure 3OC12 and C4 concentrations. These are preliminary results and experiments continue to further establish the response of Calu-3 cell culture to PA quorum sensing molecules.

P15. THE EFFECTS OF ENERGY DRINKS ON THE STRUCTURE AND FUNCTION OF EPITHELIAL CELLS AND FIBROBLASTS. Eric Shide*, (Vidya Chandrasekaran). Saint Mary's College of California, Dept. of Science, 1928 Saint Mary's Road, Moraga, CA 94556.

Energy drinks and their ingredients were studied at the cellular level. Cellular effects of energy drinks were assessed on two cell types: Madin-Darby Canine Kidney (MDCK) cells and rat embryonic fibroblasts. To examine effects of energy drinks on cellular structure and function, cells were treated with Monster Energy and 5-hour Energy. It was discovered that both types of energy drinks negatively impacted cell structure and function in epithelial cells and fibroblasts. The results of the project indicate that in both kidney cells and in fibroblasts, the function of the actin cytoskeleton is disrupted without affecting the microtubule cytoskeleton. However, the underlying reason for the disrupted function is different in the two cell types. In the kidney epithelial cells, the actin cytoskeleton is disrupted, whereas the fibroblast showed a normal actin cytoskeleton but aberrant filopodia/lamellipodia formation.

P16. FORMATION OF EMBRYOID BODIES IS REQUIRED FOR DIFFERENTIATION OF INSULIN-PRODUCING CELL CLUSTERS FROM MOUSE EMBRYONIC STEM CELLS. Christa D. Caneda* and Jesus Ciriza (Jennifer O. Manilay). University of California, Merced, School of Natural Sciences, 5200 N. Lake Rd., Merced, CA 95343.

In Type 1 diabetes, insulin-producing pancreatic cells, or beta cells, are destroyed by an autoimmune response. Current clinical treatments are indefinite insulin replacement therapy or transplantation of the pancreas or beta islets. The latter two treatments are limited in available donors; a potential alternative is the use of insulin-producing cell clusters (IPCCs) differentiated from embryonic stem cells (ESCs). We hypothesize that IPCCs will reproduce the insulin-producing capacity of healthy beta cells of an adult mouse. Among several existing ESC-IPCC differentiation protocols, Blyszczuk et al. developed the most successful method to date in producing IPCCs that showed similarities to pancreatic beta cells. However, this method is time-intensive, requiring approximately 41 days. We attempted to streamline the protocol

by bypassing the formation of embryoid bodies, reducing the differentiation timeline to 27 days. At several time points during this protocol, IPCC cultures were analyzed by RT-PCR and immunofluorescence for genes and proteins expressed in pancreatic beta islet cells. The mRNA and protein expression of insulin was not observed. Furthermore, ELISA analysis detected low intracellular insulin response after challenging IPCCs with different glucose concentrations. These results reject the hypothesis that EB formation is not required for ESC-IPCC differentiation in vitro. However, it is possible that alpha cells can be differentiated, as glucagon was detected.

P17. CHARACTERIZATION OF THE REPROGRAMMING KINETICS OF INDUCED PLURIPOTENT STEM CELLS AMONG FOUR DISTINCT DONOR CELL TYPES.. David Yao*, Chi Kent Ho, and Qiao Zeng (Yi Sun). University of California, Los Angeles, Dept. of Psychiatry and Biobehavioral Sciences, 405 Hilgard Ave., Los Angeles, CA 90095.

The utility of the induced pluripotent stem cell (iPSC) system has been well-established, with applications ranging from disease modeling, developmental studies, and tissue-specific regenerative therapies. However, many of the molecular mechanisms underlying cellular reprogramming to an embryonic cell-like state, especially changes in transcription networks, have not been well defined. Such alterations may explain the differences in the rate and efficiency of reprogramming among various cell types. In order to identify the genes that regulate cell-type specific reprogramming kinetics, four different cell types - keratinocytes (Kerat), human foreskin fibroblasts (hFF), amniotic fluid-derived cells (AFDC) and adipose-derived stem cells (ADSC) - were reprogrammed by retroviral transduction with the OSKM four factors: OCT4, SOX2, KLF4, and c-MYC. Based on their individual reprogramming kinetics, Kerat and hFF were categorized as slow- reprogramming iPSCs, and AFDC and ADSC as fast-reprogramming iPSCs. These results, and future transcriptomics and epigenetic profiling assays between these two groups will be analyzed to identify genes with putative roles in determining the kinetics of cellular reprogramming.

P18. CHARACTERIZING THE SPECIFIC MIGRATION OF MYELOID PROGENITORS INTO GLIOBLASTOMA TUMORS. Troy Kurz*, Michael Marcacci* (Mike Dorrell). Point Loma Nazarene University, Dept. of Biology. 3900 Lomaland Dr., San Diego, CA 92106

Purpose: Prior research and observation have suggested that certain Macrophage sub-populations actively migrate with high selectivity toward tumors. Understanding this attraction may shed light on methods to target tumors in treatment. This project's goal was to develop reproducible methods for studying and characterizing the migrating cells. Methods: We adapted the *ex ovo* Chick Chorionallantoic membrane (CAM) model to study the migration of a sub-population of mouse myeloid progenitors towards 9L (rat) glioblastoma tumor cells. On the CAM, myeloid progenitors were placed adjacent to tumor onplants and the percent migration of cells into the tumor onplants were compared to non-tumor, control onplants. Cells that migrated into the tumors were then isolated and quantified using Flow cytometry. Another model was developed using 96-well chemotaxis plates. 9L glioblastoma tumor cells were placed in microplate wells and myeloid progenitors in suspension on the opposite side of the filter. Migration was observed and quantified using a fluorescence plate reader. Various conditions were tested to identify optimal conditions. Results: Specific migration from the heterogeneous CD44hi bone marrow collection toward 9L rat cancer cells was observed in both models. The CAM model was reproducible and provided a natural, vascularized, environment in which to study migration, but proved to be too slow and biologically variable for efficient, initial cell characterization. The ChemoTX system demonstrated far greater resolution and was considerably faster, but does lack many of the benefits of the more relevant, CAM model. Conclusion: Our results verify these two models as a means to study and characterize the

tumor-specific migration of myeloid progenitor cells. Future studies can use these models to study the molecules and cytokines involved in cellular targeting, and identify / characterize the specific-specific targeting cells. The chemotaxis model allows for higher throughput and less biological variability, while the ex ovo CAM model provides the opportunity for more specific studies in a physiologically relevant system.

P19. OBSERVATION OF PSEUDOMONAS AERUGINOSA BIOFILM FORMATION ON HELA CELL CULTURE USING DAPI STAINING AND FLUORESCENT ANTIBODY LABELING. Zach Brown* and Randy Dunston* (Kathleen Tallman). Azusa Pacific University, Dept. of Biology and Chemistry, 901 E. Alosta Ave., Azusa, CA 91702.

Pseudomonas aeruginosa (PA) is a disease-causing bacterium commonly associated with respiratory tract infections of cystic fibrosis (CF) patients. *P. aeruginosa* adapts to the host's defense by forming mucoid biofilms – a collection of bacteria inside a matrix-enclosed capsule that offers protection from immune cells and antibiotics. In previous experiments, the PA strain PA01 formed black plaques when grown on HeLa cell cultures. The PA strain PAK did not form the characteristic plaques. Biofilms are not all alike; some are flat and some form large pillar-shaped structures. It is possible that each type of biofilm requires different treatment strategies. Are these black plaques produced by PAO1 on HeLa cells biofilms? If yes, what type of biofilm do they form? The hypothesis is that the black plaques represent pillar-shaped biofilms, and the surrounding microcolony of PAO1 represent a flat biofilm. To investigate this further, HeLa cells were grown atop polylysine-coated cover slips. PAO1 was added to the HeLa cell cultures at 500 cfu/ml. Plaque formation occurred around 5 to 6 days. To analyze biofilm formation, cultures were stained with 4,6-diamidino-2-phenylindole dihydrochloride (DAPI) to identify nuclei of remaining HeLa cells or DNA in bacteria. Biofilms were labeled with a FITC- HHA antibody that binds to the mannose component of biofilms. Confocal microscopy was used to examine cultures and analyze the three-dimensional structure of any biofilms present. Preliminary results indicate that small three dimensional biofilms are formed in PAO1 cultures of HeLa cells. The implication for potential treatment of biofilms in human disease is not yet understood.

P20. IDENTIFYING NOVEL COMBINATIONS OF ANGIOSTATIC THERAPIES THAT DEMONSTRATE SYNERGISTIC ANTI-TUMOR VASCULAR ACTIVITY. Jacob Tremblay*, Jack Rusing*, Troy Kurz, Halsie Donaldson, Michael Dorrell. Point Loma Nazarene University, Dept. of Biology, 3900 Lomaland Dr., San Diego, CA 92106.

Purpose: Tumor angiogenesis is critical for the growth and progression of cancer and thus, blocking tumor vascularization is an important potential treatment modality for cancer. However, angiostatic monotherapies have had limited success in clinic. Recent studies in our lab have shown the synergistic effects of specific combination angiostatic therapy (Dorrell et al., PNAS 2007), but unfortunately the angiostatics used in this proof-of-concept study are years away from FDA approval. Our current studies focus on finding synergistic combinations of angiostatics that are clinically approved or within phase III of clinical trials, to find novel combinations that confer similar synergistic activity for potent retardation of tumor vascularization. Methods: Using the ex ovo Chick Chorioallantoic membrane (CAM) model, we studied tumor vascular growth into U87 (human) or 9L (rat) glioblastoma tumor onplants. Dosing information for individual angiostatics in the CAM model were first determined in order to identify the maximum doses with no effect. These monotherapies were then used in various combinations to determine which monotherapies demonstrated exponential potency in combination. Blood vessel growth into the tumor was observed and quantified using confocal fluorescence microscopy. Results: After testing several monotherapies, our results have demonstrated that angiogenesis in glioblastoma tumors

was significantly reduced with the use of a double combination therapy consisting of Avastin and Torisel whereas each monotherapy showed little effect. Conclusion: Our results verify the possible synergistic effects of combination therapy against blood vessel growth. While not all combina tions demonstrate synergistic activity, if specific combinations of approved drugs are found, these may provide a novel treatment modality for patients with glioblastoma. We will continue to screen for synergistic combinations, specifically focusing on the addition of a third drug to the Avastin – Torisel combination with the goal of conferring even higher potency.

P21. STRUCTURE-FUNCTION ANALYSIS OF WDR68 IN CRANIOFACIAL DEVELOPMENT IN DANIO RERIO. Gregory Alvarado*, Yanette J. R. Peterson, Diana Doan, (Robert M. Nissen). California State University, Los Angeles, Dept. of Biological Sciences, 5151 State University Dr., Los Angeles, CA 90032.

Wdr68 is a 343 amino acid WD40-repeat domain containing protein required for craniofacial development in the zebrafish *Danio rerio*. The Wdr68 protein physically interacts with two members of the Dual-specificity tyrosine-regulated kinase (Dyrk) family, Dyrk1a and Dyrk1b. Both Dyrk1a and Dyrk1b possess Nuclear Localization Signals (NLSs) and the subcellular localization of Wdr68 mirrors that of its interaction partners. Consistent with a functional requirement in the nucleus, a derivative of Wdr68 that is unable to localize to the nucleus is also incapable of supporting craniofacial development. Wdr68 and Dyrk1b are important for the expression of several signaling molecules involved in craniofacial development and Dyrk1b can inhibit the function of a transcriptional co-repressor, HDAC5. Consistent with a direct role in the regulation of gene expression in vivo, it was previously found that while a fusion between the Cebp1 transcriptional activation domain and Wdr68 can restore jaw cartilages in a wdr68 mutant zebrafish RNA rescue assay, a fusion between the Mad1 repression domain and Wdr68 failed to rescue wdr68 mutant animals. Taken together, these findings suggest a nuclear Dyrk1b-Wdr68 complex with transcriptional co-activating functions. A series of Wdr68 deletions that fail to interact with Dyrk1a were recently reported. Utilizing this data, we constructed two Wdr68 deletions that remove sequences outside the WD40-repeats, 19C lacks amino acids at the N-terminus (1-18), and N336 lacks amino acids at the C-terminus (337-343). While located outside the WD40-repeats, these regions are among the most conserved in Wdr68. Because we expect that physical interaction with Dyrk1 family members is required for Wdr68 function, it was hypothesized that both N and C termini are required for Wdr68 function in zebrafish craniofacial development. Interestingly, we also present data indicating that the recessive wdr68hi3812 retroviral insertion mutant allele is temperature sensitive. This finding is unusual because the retroviral insertion is located within the first coding exon after the codon for amino acid N44.

P22. THE ANALYSIS OF GROWTH RATES IN WDR68 KNOCKDOWN CELLS AND MUTANT ANIMALS. Ajay Bhandari* and Bingyan Wang (Robert M. Nissen). CSU Los Angeles, Dept. of Biology, 5151 State University Dr., Los Angeles, CA 90032.

Wdr68 is a 343 amino acid WD40 repeat domain protein that is highly conserved across diverse organisms. Wdr68 can physically interact with some members of the dual-specificity tyrosine-regulated kinase (Dyrk) gene family, such as Dyrk1b. Recent findings indicate that Wdr68 couples an upstream Ras-MAP3K signal to downstream kinases such as Dyrk1b. While the relationships between canonical Ras-MAPK signaling and growth control are well characterized, little is known about the role Wdr68 might play in the regulation of cellular growth. In zebrafish, Wdr68 and Dyrk1b are important for craniofacial development and establishment of left-right asymmetry. Dyrk1b is also required for Myogenin (Myog) expression in the mouse myoblast differentiation model cell line C2C12. In COS7

cells, wdr68 knockdown (wdr68-KD) impairs cell growth. Both in zebrafish and C2C12 cells, we found that Wdr68 is also required for Myog expression. In this study, we are further analyzing the necessity of Wdr68 in C2C12 cell growth by comparing the growth of wdr68-KD and dyrk1b knockdown (dyrk1b-KD) cells to non-target (NT) control cells over a four-day period. These three samples will be grown over the same period of time and counted to analyze the potential differences in cell number. We hypothesize that growth will be delayed in C2C12 cell wdr68-KD in comparison to NT control cells. Additionally, wdr68-/- zebrafish mutant animals have significant growth defects in lateral body length in comparison to wild-type age-matched animals. Growth defects of wdr68-/- animals are only localized in the craniofacial region until nine days post fertilization (grown at 28oC), possibly indicating when maternal wdr68 levels are exhausted during embryonic development. To further analyze when wdr68 is required during development, wdr68 heat shock-inducible transgenic zebrafish lines will be constructed. This study will further characterize the roles of Wdr68 in cellular and embryonic growth with potential implications for regenerative medicine and the treatment of cancer.

P23. NEURAL ECTODERM CELLS REMAIN COMPETENT TO FORM MUSCLE FIBERS DURING *X. LAEVIS* EMBRYO DEVELOPMENT. Brigette Jong* (Carmen Domingo). San Francisco State University, Dept. of Biology, 1600 Holloway Ave., San Francisco, CA 94132.

As the embryo develops, cells become committed to specific fates and form all the tissue types found in the adult. During *X. laevis* gastrulation, the three embryonic germ layers form: the endoderm, mesoderm, and ectoderm. The endoderm forms the primitive gut, the mesoderm gives rise to muscle, and the ectoderm differentiates into neural tissue. Previous studies suggest that neural ectoderm cells retain a level of plasticity that is distinct from cells of the other germ layers. To determine this range of plasticity, we transplanted fluorescently-labeled neural ectoderm cells into the prospective muscle region of a host embryo. By varying the developmental stage of donor cells, we were able to identify the stages during which neural ectoderm cells remain competent to form muscle fibers. We found that neural ectoderm cells become competent to form muscle during gastrulation, but that this plasticity is lost by the onset of neurulation. These results offer new insights into the plasticity of embryonic cells to give rise to different cell types.

P24. GENETIC IDENTIFICATION OF TERMITE SPECIES IN THE SAN GABRIEL VALLEY FOR USE IN DEVELOPMENTAL STUDIES. Jessica DeWitt* and Yun-Lan Wong (Jurgen Ziesmann and Joshua Morris). Azusa Pacific University, Department of Biology and Chemistry, 901 E Alosta, Azusa, CA 91702.

Although the genetics of insect eye development has been well studied over the last thirty years, most of the advances have come via one model organism: *Drosophila melanogaster*. While work in this holometabolous insect has allowed us to gain valuable insight into the genetics of insect eye development, recent studies have suggested that many of these discoveries may not apply to the more primitive arm of the clade: the hemimetabolous insects. Therefore, in an attempt to identify new hemimetabolous model organisms for use in development genetic studies, we collected termite colonies from various locales in Southern California. Termites were chosen because in preliminary studies of visual system development unique, previously un-described features were observed. While the colonies collected were preliminarily

classified based upon morphology, we found it necessary to confirm this identification through genetic analysis. Identification was achieved through sequencing a portion of the 16s rDNA locus from each colony and then comparing the data with published examples from each candidate species. Comparison was performed using the BLAST algorithm and through use of Neighbor Joining Analysis. Most of the termite colonies were identified as the drywood termite Incisitermes minor, confirming the previous morphological classification.

P25. SONG DIVERGENCE AND SPECIATION IN RED CROSSBILLS. Aaron Grossberg*, Kirsten Paasche, (Julie Smith). Pacific Lutheran University, Department of Biology, 1010 122nd Street S. Tacoma, WA 98447.

Over 150 years ago, Darwin posed the question: how do new species arise? A prominent hypothesis is that divergent natural selection causes phenotypic divergence and promotes reproductive isolation (Schluter 2000). Red Crossbills (*Loxia curvirostra* complex) in North America are a group of incipient bird species for which we know much about the ecological conditions favoring morphological divergence and specialization on alternative resources yet less is known about the nature of behavioral reproductive isolation (Smith and Benkman 2007). North American Red Crossbills are divided into nine groups referred to as call types which show a high degree of reproductive isolation with levels of mixed pairing between sympatric call types less than 1%. We examined whether song divergence may function as a behavioral isolating mechanism. We recorded the songs of wild male type 2 and type 9 crossbills and quantified the nature and extent of differences between songs of the two call types. The syllable repertoires of type 2 and type 9 songs differ substantially with only 5% syllable overlap between call types. There were also differences in structural characteristics between the songs of the call types. Type 2 songs have longer syllables and more time between syllables. They also have higher maximum and minimum frequencies, and greater frequency range than type 9 songs. Our findings suggest that the songs of the call types differ and that song may function as a pre-mating isolating barrier.

P26. POPULATION GENETICS AND IMPACT THREAT ASSESSMENT OF INVASIVE JACKSON'S CHAMELEONS IN HAWAII. Rebekah Klint*, (Brenden Holland). University of Hawaii at Manoa, Pacific Biosciences Research Center, 2500 Campus Road, Honolulu, Hi, 96822.

Several dozen Jackson’s chameleons (*Chamaeleo jacksonii xantholopholus*) were introduced to Oahu from Africa by a pet importer in 1973. A recent study demonstrated that Jackson’s chameleons prey on native invertebrates, including critically endangered tree snails, in pristine Hawaiian forests. The University of Hawaii Tree Snail Conservation Laboratory has begun a series of investigations to determine the level of threat posed by this invasive reptile, including molecular studies to evaluate genetic diversity of chameleon populations in Hawaii. Population genetics theory predicts that introduced species with low genetic diversity will not thrive in novel habitats due to an inability to adapt, however, chameleons are established and thriving on all major islands of Hawaii. We hypothesize that chameleons have done well in the Hawaiian Islands despite low genetic diversity, contrary to theoretical predictions. Current molecular research involves the collection of Jackson’s chameleons by hand from native Hawaiian forests and generation of mtDNA sequences (ND4-Leu). In collaboration with researchers in Eastern Africa and Australia, African haplotypes collected from the natural range in Kenya were compared to those of Hawaiian chameleons using phylogenetic trees and haplotype networks. Preliminary data show low genetic variance within Hawaiian chameleons; only four haplotypes were found among 52 Hawaiian chameleons with Kenyan sequences differing by just a few basepairs. Our hypothesis is supported by preliminary results, and sampling is ongoing. Threat assessment and population genetic studies of predators such as Jackson’s chameleons contribute to the efforts to conserve and maintain the

integrity of Hawaiian forests and associated endemic biodiversity.

P27. INDIVIDUAL SIGNATURES IN VOCALIZATIONS OF CALIFORNIA MOUSE (*PEROMYSCUS CALIFORNICUS*) PUPS. Saif Hossain*, Wendy Saltzman, Sarah Rotschafer, Khaleel A. Razak, Krisitne Kaiser. University of California Riverside, Dept. of Biology, 900 University Avenue Riverside, CA 92521.

Many species of animals use vocalizations for parent-offspring communication. Vocalizations can contain information about the caller, and unique call signatures can be used to determine a caller's age, sex, and identity. This study focused on pup vocalizations produced by the California mouse, *Peromyscus californicus.* The California mouse is an altricial, biparental species, as pups are dependent on both parents for survival. Studies investigating individual signatures in California mouse pup vocalizations, and in biparental mammals in general, are lacking. We recorded vocalizations from 15 pups in 5 litters, for 3 minutes each on days 1, 5, 9, 13 and 17 of age. Calls were analyzed for a suite of frequency, duration, and amplitude parameters. We used stepwise discriminant function analysis to identify model variables, and a discriminant function analysis to determine if these variables permit reliable distinction among individuals, litters, and sexes. Preliminary analyses suggest that signatures exist that permit discrimination among litters and among individuals, but not between sexes. The data also show that litters and individuals are more distinguishable as pups mature. Though more data need to be collected, these initial results suggest that California mouse parents may be able to distinguish their litters from other litters and to identify individual pups within their litters based on calls alone. This work will enhance our understanding of parent-offspring interactions in the California mouse.

P28. PREDAWN AND MID-DAY WATER POTENTIALS TO MEASURE RESPONSE TO ALTERED PRECIPITATION REGIMES IN SOUTH COASTAL CHAPARRAL SPECIES. David Villalta*, Angelita Ashbacher (Elsa Cleland). University of California San Diego, Department of Biological Science, Ecology, Behavior and Evolution, 9500 Gilman Dr., La Jolla, CA 92093.

The chaparral of Southern California is predicted to encounter a climate shift toward increased drought, in addition to higher interannual variation in rainfall. We sought to determine how native chaparral species will respond to these climate shifts by evaluating their ecophysiological responses to experimentally altered precipitation regimes. To do this we applied 0, 50, 100, 150, or 200% of ambient precipitation in a randomized block design over 30 experimental plots (3.4m x 3.7m). We hypothesized that we would find the lowest soil water availability in the drought plots, but that adult shrubs with deeper roots would be less influenced the experimental treatments. To test these hypotheses we measured pre-dawn and mid-day water potentials for each species. Using a pressure chamber, we evaluated the water status of plants when at equilibrium with the soil (pre-dawn) as well as their tolerance to water stress while photosynthetically active (mid-day). Surprisingly we found that both adult and juvenile shrubs encountered lower soil moisture availability under lower precipitation treatments, evidenced by more negative predawn water potentials ($p=0.006$). We found that juvenile shrubs exhibited higher mid-day water-stress than adults, but while mid-day water stress was greatest for adults of all species under the lowest precipitation treatment (most negative mid-day water potentials) adult mid-day water stress was not significantly different under the other conditions. These results confirm that chaparral species are extremely drought tolerant, but that juvenile stages are more sensitive, such that multiple low rainfall years could prevent establishment and initiate long-term changes in species composition.

P29. EFFECTS OF CADMIUM ON GROWTH AND SHORT TERM PHOTOSYNTHETIC

ACCLIMATION RATES TO LIGHT INTENSITY CHANGES IN RADISH PLANTS (*RAPHANUS SATIVUS* L.). Austin Nguyen and Theresa Graebener (Pippa Drennan). (Philippa M. Drennan). Loyola Marymount University, Biology Department, 1 LMU Drive, CA 90045.

The effects of heavy metals and other human contaminants have become an important consideration for environmental restoration and conservation. The effects of cadmium on growth and photosynthetic acclimation rates were investigated in the radish plant, *Raphanus sativus* L. Plants were raised post-germination on nutrient solutions containing various concentrations of cadmium (0, 10, 20 μM CdCl2) in sand culture. Plant height and leaf area were measured throughout growth. Cadmium-treated plants were observed to have stunted growth rates in early exposure to cadmium, with higher growth in later vegetative stages. Leaf areas, measured at 20 days post-germination, were insignificantly largest in the lower cadmium concentration, likely due to a biostimulatory phenomenon, hormesis. Cadmium contents in the root and shoot systems were analyzed by mass spectrometry to investigate accumulation and transport of this heavy metal. Light response curves of plants from each cadmium concentration showed a decreased photosynthetic saturation as cadmium exposure increased. Cadmium was observed to significantly reduce photosynthetic acclimation rates in both concentrations of cadmium versus the controls by fourfold in the first change of light conditions from 600 to 400 μmol/m^2s, and twofold in the second transition from 400 to 200 μmol/m^2s. This reduction of acclimation may have detrimental effects on survival of plants in variable environmental conditions. Furthermore, location of sequestration of cadmium, whether in the roots or leaves, will influence the effect of transferring cadmium up trophic levels to predators.

P30. LA BREA TAR PITS: WHAT DO DIRE WOLF LIMB LENGTHS TELL US ABOUT PIT DATES? Genevieve Guerra*, Richard Smith*, (Wendy Binder). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

Dire wolves (*Canis dirus*), a wolf species that became extinct approximately ten thousand years ago, are the most common vertebrate species found at the Rancho La Brea tar pit collection at the Page Museum. Wolf bones have been collected from various pits, which are asphalt seeps that contain a collection of fossils, some of which have been radiocarbon dated to a distinct time period. A recent study of dire wolves focused upon changes in limb lengths over time (along with other measures) of bones from each of the many excavated pits. Due to extreme data sets collected from Pit 13, including unusually short limb lengths, it has long been thought that Pit 13 contains anomalous data. Our research, involving comparisons of measurements from Pit 3 data, which dates from before Pit 13, but substantially overlaps with Pit 13, indicates a strong degree of concordance in measurements between Pits 3 and 13, and shows a similar pattern between these and earlier and later pits. This suggests that Pit 13 follows expected patterns from stratification analysis, and is not just an anomalous collection.

P31. TRACKING WILDLIFE MOVEMENT BETWEEN THE LOYOLA MARYMOUNT UNIVERSITY CAMPUS AND THE PLAYA VISTA RIPARIAN CORRIDOR USING MOTION SENSING CAMERAS. Courtney McCammon* (John Dorsey and Eric Strauss). Loyola Marymount University, Biology Department, 1 LMU Drive, CA 90045.

The upland border habitats of urban wetland systems are likely critical areas that support remnant populations of both native and introduced species of mammals. Loyola Marymount University is situated in a wildlife corridor lying southwest of the Ballona Wetlands, offering resources they would not otherwise be available to resident species. The exploitation of the University's campus suggests a resilient behavior pattern of resident animals and the possibility of the campus serving as an ecological sink. The

study area includes Loyola Marymount University, the adjacent bluff, and the constructed Riparian Corridor on the Playa Vista property beneath LMU. The aim of this study was to characterize the animal movement patterns onto LMU's campus and in the surrounding bluff habitat in preparation for future radio-telemetry studies. Presence-absence data were gathered using motion-sensored cameras with infrared technology. There were four different "areas" being sampled (University Hall, the Riparian Corridor, LMU trail, and Cabora Road) with three strategically placed cameras in each area. Cameras were placed on or around game trails leading to the university's campus and onto the adjacent bluff. GPS locations were taken of animal trails and holes in the LMU fence in order to find a relationship between trails and entrance onto LMU's campus. Results showed a range of mammals (coyotes, foxes, raccoons, possums, feral cats, skunks) moving on and off campus, providing insight to LMU's relationship with the local wildlife. This study also highlights the importance of wildlife corridors within heavily urbanized areas, providing a knowledge base for future wildlife research at LMU.

P32. DEVELOPING GREENROOFS FOR SOUTHERN CALIFORNIA: A COMPARISON OF HEAT TOLERANCE FOR DUDLEYAS AND SEDUMS. Robert Arnold* and James McDonald* (Philippa M. Drennan). Loyola Marymount University, Biology Department, 1 LMU Drive, CA 90045.

Green roofs provide a wide range of ecological benefits in urban settings by increasing energy efficiency, preventing stormwater runoff, and reducing urban heat island effects through evapotranspiration. In developing greenroofs for southern California it was found that the native dudleyas had greater survival during the summers than the industry-standard sedums. This study further investigated the response of both dudleyas and sedums to heat-stress. Whole pieces of tissue collected from plants in greenroof mesocosms at LMU were subjected to dry heat from 20°C to 55.6°C for 1 hour. Tissue samples were subsequently cut into 3-cell-thick sections and placed in 1% neutral red solution in a 7.5 pH 0.2M phosphate buffer (w/v) for 10 minutes and then rinsed in buffer for 10 minutes. Stained cells were counted using a bright-field microscope. The ratio of stained cells to unstained cells showed the reaction of each species to increased temperatures and heat-stress. Neutral red is a vital stain and is not taken up by dead cells. At temperatures below 40°C both showed very high staining ratios. As the temperatures were increased above 40°C a decline in the number of stained cells was observed. At temperatures above 52°C both dudleyas and sedums showed a marked decline in cells stained as only a few cells survived. The sedums showed a steeper decline of stained cells than the dudleyas. The sedum tissue had fewer cells stained at each temperature interval between 40°C and 52°C. This suggested that the dudleya cells can withstand higher temperatures and heat stress.

P33. THE EFFECTS OF BENZYL BUTYL PHTHALATE (BBP) ON CRAYFISH AGGRESSION AND MEMORY.. Shahid SM*, Johnson KR, Cowan AM, Gomes CS, Mehwash AI, Williams EB, Wachtarz AL, (Kaplan LAE). Quinnipiac University, Department of Biological Sciences, 275 Mount Carmel Avenue, Hamden, CT 06518.

Chemical and behavioral signals resulting from previous battle victories is said to enhance crayfish aggression in subsequent interactions. To determine if benzyl butyl phthalate (BBP) impacted this relationship, crayfish (N=92) were initially paired and their behaviors (striking, pushing, approaching, threatening, displacement, holding, and avoiding) were evaluated to categorize individuals as winners or losers. Following BBP exposure (0.1ppm for14 days), control winners (CW) were paired with control losers (CL), dosed winners (DW), and dosed losers (DL). DW were paired with DL and CL. As anticipated, control and BBP winners were more aggressive and engaged in more interactions than losers (P=0.001). In CW/CL pairings, CL won 25% of the interactions. In DW/DL pairings, however, DL won

60% (P=0.0001). DL were also more successful than CL in pairings with CW (70% vs. 25%, P=0.0001). Thus, BBP may function by altering pathways that the impact memory of previous crayfish losses rather than past victories.

P34. THE EFFECTS OF BENZYL BUTYL PTHALATE ON MORTALITY AND LEFT/RIGHT/NEUTRAL BIAS OF THREE SPECIES OF PLANARIA: *D. TRIGRINA*/, *D. DOROTOCEPHALA*/, AND *P. FLUVIATALLIS*/. Christofer Anderson*, Lyndsey McGlinchey, and Daniel Mascaro (Lisa A.E. Kaplan). Quinnipiac University, Dept. of Biology, 275 Mount Carmel Ave., Hamden, CT 06518.

This study utilized two toxicological end points (mortality and left/right/neutral bias) to assess the impact of the plasticizing agent benzyl butyl phthalate (BBP) on the planaria *Dugesia trigrina*/, *Dugesia dorotocephala*/, and *Procotyla fluviatallis*/. Initial left/right/neutral bias was determined using a Y-maze. Following BBP exposure (0.1, 0.01, or 0.001 ppm BBP administered every 48 hours for four doses), left/right/neutral bias was re-assessed. BBP exposure shifted the left/right/neutral bias significantly among the planaria species tested. Both *D. trigrina*/ and *P. fluviatallis*/ exhibited the same dose-response threshold (0.01 ppm BBP), while *D. dorotocephala*/mthreshold appeared to be much lower (0.001 ppm BBP). BBP-induced mortality differed among *D. dorotocephala*/i (65%), *P. fluviatallis*/i(58%), and *D. trigrina/* (40%). Planaria responded to BBP in a dose-dependent manner, thus confirming the use of these endpoints in BBP toxicity assessment. Studies to delineate additional endpoints and clarify the observed genus/species differences are in progress.

P35. INVASION OF *ACACIA MEARNSI* ALONG THE HOLSLOOT RIVER, RAWSONVILLE, WESTERN CAPE, SOUTH AFRICA.. Shane Sheets*, Duncan Katel*, (Cheryl Swift PhD). Whittier College, Depts. of of Biology & Environmental Science, 13406 E. Philadelphia St., Whittier, CA 90608.

The invasion of alien plants in natural ecosystems has become a serious environmental problem that threatens the sustainable use of benefits derived from the natural ecosystem. Specifically in South Africa, over 180 alien species have invaded ten million hectares of land. The cost of the impacts of the invasive species is significant, reducing the value of the ecosystems immensely. One common invasive plant is *Acacia mearnsii* or commonly known as Black Wattle. This alien plant species is listed as one of the top hundred worst invasive species according to the Global Invasive Species Database and threatens the native habitat by competing with indigenous vegetation, replacing communities, reducing native biodiversity and increasing water loss from riparian zones. The primary focus of this study was to analyze the effects on species composition between native and non-native species in relation to elevation from thalwag to gain a better understanding about disturbance levels in the riparian environment and its effect on distribution. This research was undertaken along the Holsloot River in Rawsonville, Western Cape, South Africa. Through interpretation of results, although there is a greater amount of non-native individuals then that of native individuals, there is a greater basal coverage by the native species. This provides insight into characteristics of the individual species as well as age demographics of the population. Also, in relation to elevation, it can be seen that Brabejum, a native species in comparison, has an increase in number of individuals further from the thalwag or at higher elevations while *Metrosideros*, another native species in comparison, clusters at lower elevations. Black Wattle was found to take advantage of the intermediate elevations. This can be contributed to tolerance of the individual species to various disturbance levels caused by changes in stream flow as a result of drought or flood. This project will contribute to the academia of this topic by shedding light on the condition of the problem currently in order to gain a better understanding of the intimate interaction between native and invasive flora to draw conclusions about species composition and overall ecosystem health.

P36. THE ROLE OF ADAPTATION DURING COLUMBINE SPECIATION. Leena McCann*, Juliana Moreno*, Cynthia A. Dick, Stephanie B. Saffouri and (Justen Whittall). Department of Biology Santa Clara University 500 El Camino Real Santa Clara, CA 95053.

Adaptation and speciation have been central concepts in evolutionary biology since Darwin's original discoveries, yet the role of natural selection during speciation is hotly debated. In order to study the role of natural selection during speciation, one can look to sympatric speciation where reproductive isolation evolves through diversifying selection in the face of gene flow. Sympatric speciation is the process in which one species forms two distinctive species while living in the same geographic area. Adaptation of plants to unique soil types, like serpentine soils in California, provides a window into the process of sympatric speciation since plants often evolve from adjacent non-serpentine habitats. In southern San Francisco Bay Area, two species of columbines (*Aquilegia formosa* and *A. eximia*) can be found growing adjacent to each other. One of these species (*A. eximia*) has recently adapted to survive on serpentine soil and flowers later in the season than the non-serpentine species (*A. formosa*). We first determined whether these two species are uniquely adapted to their soil types by comparing the first stages of growth in a reciprocal transplant experiment involving both serpentine and non-serpentine soils. Although there was very little difference in germination rates of the two species on the different soil types, we found that all *A. formosa* individuals died when planted on serpentine soil. *Aquilegia eximia* was capable of growing on both soil types. We are continuing to examine the role of adaptation to these unusual soils in a common garden experiment, while simultaneously examining the role of pollinators and gene flow between these two species.

P37. EFFECT OF FOOD CUES ON THE HYPOTHALAMIC-PITUITARY-GONADAL AXIS. Nikki Javier* (Heather Watts). Loyola Marymount University, Dept. of Biology, 1 LMU Drive, Los Angeles, CA 90045.

Organisms have evolved to assume reproductive readiness when conditions are opportune for breeding. This timing is achieved by physiological responsiveness to environmental cues such as temperature, water, and social cues. Specifically, environmental cues can stimulate the hypothalamic-pituitary-gonadal (HPG) axis in preparation for reproduction. In the first part of this study, we conducted a literature review to evaluate the extent to which mammals and birds are responsive to food cues to stimulate reproductive development. Our review indicates that changes in food availability (either quality or quantity) can affect luteinizing hormone (LH) secretion and gonad size across taxa. It is hypothesized that food cues are transduced to the HPG axis via their effects on the GnRH system, as is the case for photic cues. However, we found no studies that had examined the effects of food cues on the gonadotropin-releasing hormone (GnRH) system of the hypothalamus. Therefore, in the second part of this study we utilize immunocytochemistry to evaluate GnRH response to a food cue in a songbird, the pine siskin (*Carduelis pinus*). Here, we focus on female pine siskins, which show greater gonadal development in response to a preferred food (seeds) compared with a control diet.

P38. SOUND TRAVELS: ORIGINS OF FRESHWATER FISHES IN THE PUGET SOUND REGION. Evan Shields* and Brianne Ankenman* (Jacob Egge). Pacific Lutheran University, Dept. of Biology, 1010 122nd St. South, Tacoma, WA 98447.

Geological events have the ability to play a major role in shaping species distributions. The goal of our

project was to investigate the role glacial events played in shaping the distribution patterns of freshwater fishes in the Puget Sound region of Western Washington, an area covered by ice as recently as 15,000 years ago. We tested competing hypotheses of dispersal from a Chehalis River refugium, a Columbia River refugium, or the marine environment to explain the dispersal of freshwater fishes into Puget Sound associated rivers following glacial retreat. To test these hypotheses, four co-distributed freshwater fish species native to Western Washington were collected from river systems across the region. Intraspecific relationships among populations were reconstructed using phylogenetic analyses based on sequence data from the mitochondrial gene cytochrome b. Results indicate that one of the species, the Coastrange Sculpin (*Cottus aleuticus*), likely dispersed from a marine environment; two of the species, the Longnose Dace (*Rhinichthys cataractae*) and the Riffle Sculpin (*Cottus gulosus*), likely dispersed from the Chehalis River refuguim; and the dispersal pattern of one species, the Torrent Sculpin (*Cottus rhotheus*), was ambiguous. Collectively, these results indicate that a Chehalis River refugium and the marine environment, not a Columbia River refugium, were the primary origins of freshwater fish dispersal into Puget Sound rivers.

P39. EFFECTS OF BENZYL BUTYL PHTHALATE ON *FUNDULUS HETEROCLITUS* ANTI-PREDATOR BEHAVIOR. Michael MacKillop*, Matthew Stark, and Theresa Sparaco (Lisa Kaplan). Department of Biological Sciences, 275 Mount Carmel Ave Hamden, CT 06518-1908.

Fundulus heteroclitus, a euryhaline fish, tends to associate with individuals of similar length and body weight. Size-assortative shoaling is an adaptive behavior utilized as anti-predator mechanism. In our previous study, shoaling was negatively influenced by a four-week exposure to benzyl butyl phthalate (BBP), a synthetic chemical used to increase the flexibility of plastics and a suspected endocrine disruptor. In this experiment, *F. heteroclitus* (N=400) were collected from Long Island Sound, depurated, and exposed to 0.1 ppm BBP daily for four weeks (N=40). Another 40 large fish served as an unexposed control group. Three-compartment test aquaria, containing a shoal of large fish on one side, a shoal of small fish on the other side, and a center focal fish compartment were used to assess fish behavior each week. Single large focal fish were placed in the central compartment, and focal fish head position was recorded in 30-second intervals for ten minutes. No difference in shoal choice was observed between control and treated fish groups during the first two weeks of BBP exposure. There was, however, an observed shoal choice difference between control and BBP exposed fish during the third and fourth weeks of exposure. BBP exposed fish were three times less likely to pick the large shoal by week four as compared to the previous three week exposure and exhibited a maladaptive shoal choice (neutral or small fish shoal) 1.4 times more often than control fish. Treated fish exhibited greater agitation as compared to control in exposure weeks two (16.2%), three (31.4%) and four (50.4%). Thus, a four-week exposure period of 0.1 ppm BBP appeared to produce the greatest disruption in both shoaling and non-circumspect behavior (agitation) among *F. heteroclitus*.

P40. THE EFFECT OF ACOUSTIC CUES ON AGGRESSION IN MALE PACIFIC FIELD CRICKETS, *TELEOGRYLLUS OCEANICUS*.. Yeelong Yang* and Brian Gray (Marlene Zuk). University of California, Riverside, Department of Biology, 900 University Ave., Riverside, CA 92521.

Population density is an important factor that affects behavior and development in many animal species. Some species use direct physical contact and interactions to determine population densities, but in solitary species, direct contact is limited and infrequent. Members of these species may utilize acoustic, chemical, and/or visual cues to estimate population density. By taking advantage of a natural mutation, flatwing, that keeps males from producing sound, I tested how acoustic cues alter perception of population density. In crickets, population density affects levels of aggression. I reared male crickets in different acoustic environments: song, to simulate an environment with a higher population density, and no song, to

simulate an environment with a low population density, and measured levels of aggression in pairwise interactions. Results of this study will be discussed.

P41. LARGE MAMMAL BIODIVERISTY IN A COSTA RICAN MONTANE CLOUD FOREST. Austin Fares*, Ryan Dahl*, Caleb Bryce, (Mike Mooring). Point Loma Nazarene University, Department of Biology, 3900 Lomaland Drive, San Diego, CA 92106.

Mammalian biodiversity in the Neotropics is threatened by past and present deforestation from human activities, such as agricultural expansion. In particular, tropical montane cloud forests are extremely species-rich, highly threatened, but poorly studied by the scientific community. Such is the case in the Costa Rican montane cloud forests of the Talamanca Cordillera, perhaps the most important region of the country for the conservation of large predator and prey species. Ecotourism is an economic alternative to deforestation that maintains forest ecosystems and its inhabitants, but may have unknown effects on animal activity and behavior. Our study examined species presence, activity patterns, and the impact of tourists on mammal diversity in the Savegre Valley and Quetzal National Park of Costa Rica. We employed camera trapping and other non-invasive techniques to survey medium to large-sized mammals from lower montane forest to alpine páramo. A network of 31 cameras was deployed on trails ranging from 2100 to 3300 meters in elevation, which we regularly hiked to monitor the cameras. From our camera trap data we confirmed the presence of 20 predator and prey species that varied from 1-250 kg. Of the predators, capture frequency was high for puma and coyote, lower for small cats, and rarest for jaguar. A surprising number of photos were taken of oncilla, perhaps the rarest felid in Costa Rica. Common prey species included collared peccary, found at middle elevations, and tapir and brocket deer at high elevations. Daily activity budgets suggest that coyote, tapir, and paca are highly nocturnal, while puma, peccary, and coati are more diurnal. Human presence on the trails had a negative impact on the abundance of some species, but did not appear to influence others. Our survey documents a healthy population of large predators and their prey, implying a healthy ecosystem and indicating the advantages of ecotourism as a land use alternative. Future work will expand our camera traps into other regions of the Talamanca mountain range and incorporate new techniques such as fecal genetic analysis and scent stations. The large population of coyotes should be monitored since, as an invasive species, they are a potential competitor with the smaller felids.

P42. USING YEAST 2-HYBRID ANALYSIS TO STUDY THE RELATIONSHIP BETWEEN PHOSPHORYLATION AND DIMERIZATION IN THE *C. ELEGANS* TRANSCRIPTION FACTOR LIN-31. Matthew Mosier*, Fernando Meza Gutierrez, and (Leilani Miller). Santa Clara University, Dept. of Biology, 500 El Camino Real, Santa Clara, CA 95053.

The goal of this ongoing research project is to determine the specification of vulval cell fate in the model organism *Caenorhabditis elegans*. LIN-31, a transcription factor in a conserved RTK/Ras/MAP kinase signaling pathway, is required for proper vulval development in *C. elegans*. In the current model, when LIN-31 heterodimerizes with another transcription factor, LIN-1, it promotes non-vulval cell fates. When LIN-31 is phosphorylated through a signal transduction process, the dimer is disrupted and the individual LIN-31 protein can then promote a vulval cell fate in vulval precursor cells. While LIN-31 protein

contains four MAP kinase consensus phosphorylation sites (referred to as M1, M2, M3, and M4), it is unknown which of these sites are actually phosphorylated. It is also unknown which sites need to be phosphorylated in order to disrupt the LIN-31::LIN-1 heterodimer. Using PCR-based site-directed mutagenesis, each of the four MAP kinase consensus sites have been eliminated singly and in various combinations. Also, the effects of constitutive phosphorylation have been mimicked by replacing a threonine in the consensus site with a negatively-charged acidic amino acid. A yeast 2-hybrid (Y2H) system has also been developed to study the various effects on the binding affinity between LIN-31 and LIN-1. The Y2H system has already yielded very interesting results providing insight into the relationship between phosphorylation and dimerization. Currently, we are in the process of switching the binding and activation domains in our Y2H system in order to verify the results of our initial results.

P43. EFFECTS OF CADMIUM EXPOSURE AND ACCUMULATION ON OTEHR METAL LEVELS IN *DROSOPHILA MELANOGASTER*. Ellie Altomare*, Austin Nguyen (Cathy McElwain). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

The fruit fly, *Drosophila melanogaster*, demonstrates sensitivity to heavy metal exposure that is both variable and selectable. Flies raised on cadmium-enriched food have been analyzed by mass spectrometry to quantify levels of a variety of heavy metals in flies exposed to cadmium as larvae and in flies that have developed resistance to cadmium over as many as nine generations of exposure. We have observed a number of trends in cadmium and other nutrient levels. The higher the level of cadmium exposure in the first generation, the higher the level of cadmium found in the fly body. This may be attributed to a mechanism of sequestration in the gut lining, discussed by previous literature. After selection for resistance, however, cadmium content decreases in flies. This suggests a metabolic mechanism of resistance rather than sequestration. Cadmium also influences other nutrient and metal levels in flies. Increasing first-generational cadmium exposure inversely correlates with copper levels in fly bodies. This may suggest cadmium interference with uptake and/or transport of copper in exposed flies. These effects across generations will also be investigated, along with cadmium's possible effects on other element levels in the fly body. These effects of cadmium on other metals may impact metabolic and survival activity in flies, transcending to fitness of flies in contaminated environments.

P44. ALZHEIMER'S DISEASE IN *DROSOPHILA MELANOGASTER*: TESTING A MODEL SYSTEM. Andrew Heslin*, Anthony Wavrin*, and Theresa Graebener* (Catherine McElwain). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

The extensive genetic tools available in *Drosophila* make it an attractive system for studying human disease. In mammals, Alzheimer's syndrome is correlated with the appearance of aggregating Aß42 polypeptide in the brain. Our collaborator at Loyola Marymount University has isolated a polypeptide that prevents aggregation *in vitro*. We are working to test this polypeptide in vivo in *Drosophila melanogaster*. The Alzheimer's model in *Drosophila melanogaster* compares survival of flies carrying two alternative artificial genes that encode for the aggregation of the polypeptide (Aß42) and a non-aggregating control polypeptide (Aß40). The Aß42 flies have reduced life spans and activity levels compared to the control lines, both those expressing Aß40 and expressing a transmembrane form of the protein, C99. As a first step to demonstrating effects of the artificially constructed polypeptides in vivo, we have attempted to demonstrate the Aß42 effects in *Drosophila melanogaster* that were reported in other labs. In our hands the Aß42 expressing flies showed only a slight shortening of life span compared to C99 control lines and both lines began to die much earlier and died more rapidly than reported. Over the summer, we adjusted our experimental parameters. In this paper, we report on experimental

conditions, which extend the survival of both the experimental and controls. Under these conditions, the "Alzheimer's flies," those expressing the Aß40, show a significant decrease in survival. We are now in a position to test the polypeptides in vivo.

P45. THE ISOLATION AND CHARACTERIZATION OF PHAGES MUUS AND CECI11. Jaee Tamhane*, Ana Lucia Fuentes*, (Gary Kuleck, Carl Urbinati, Yiwen Fang). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

Bacteriophages, viruses that infect bacteria, are one of the most copious microorganisms available for research. Although their population numbers are exponentially large, little is known about their ecological functions and roles in natural settings. In order to broaden our knowledge about their role in natural environments, we are involved in HHMI Science Education Alliance Phage Program to isolate and characterize new bacteriophage. We isolated two distinct lytic mycobacteriophages on the host M. smegmatis, Muus and Ceci11, from two individual soil samples on the Loyola Marymount University campus in the fall of 2011. Using polymerase chain reaction (PCR) and gel electrophoresis, we categorized the phages into the B Cluster, a group of phage characterized by distinctive molecular and morphological features. For the spring, isolated a third phage, Contagion and E Cluster phage, which as a group, we collectively sequenced its genomes and annotated its genes with the aid of bioinformatics tools like DNAMaster, GeneMark, BLAST, etc. We will present the results on Muus and Ceci11, B Cluster phage, from the fall and our preliminary progress in gene discovery and annotation in Contagion and discuss how we will use these findings for comparative genomic analysis for evolutionary and ecological purposes.

P46. ALZHEIMER'S IN *DROSOPHILA MELANOGASTER*: TESTING A MODEL SYSTEM. Shannon Harringer*, Justin de Lennoy*, Shelby Chun Fat* (Cathy McElwain). Loyola Marymount University Dept. of Biology 7900 Loyola Blvd., Los Angeles, CA 90045.

The extensive genetic tools available in *Drosophila melanogaster* make it an attractive system for studying human disease. The Alzheimer's model in *D. melanogaster* compares various characteristics of flies carrying two alternative, artificial genes that encode for the aggregating polypeptide (Aß42) and a non-aggregating control polypeptide (C99). These flies have reduced viability, activity and also reduced learning and memory. We are currently working to develop the system for testing this loss of learning and memory. In mammals, Alzheimer's syndrome is correlated with the appearance of aggregating Aß42 polypeptide in the brain. Our collaborator, Dr. David Moffet at Loyola Marymount University has isolated a polypeptide that prevents aggregation *in vitro*. Our lab is working to test this polypeptide in vivo in *D. melanogaster*. As a first step, we have attempted to demonstrate the Aß42 effects in D. melanogaster that were reported in other labs. Specifically, we are in the early stages of testing reduced learning and memory in Aß42 expressing flies as it pertains to exposure to quinine. Both the Aß42 flies and the controls will be introduced to a small dose of quinine and then tested later to see if they learn to avoid the adverse stimulus. It has been previously demonstrated that control flies show a higher level of memory than do Aß42 flies. We hope to replicate these results in our lab. This will allow us to test the effects of Aß42 expression on a supplemental parameter that can be assayed earlier in the life span without killing the flies.

P47. CONSERVATION GENETICS OF THE RED HILLS ROACH (CYPRINIDAE: *LAVINIA*

SYMMETRICUS SSP). Morrell Chhay*, Tim Heyne, Jennifer O'Brien, and (Andres Aguilar). University of California, Merced, School of Natural Sciences. 5200 North Lake Road, Merced, CA 95343.

The Red Hills roach (*Lavinia symmetricus* ssp) is a narrow-range endemic sub-species of the more widespread California roach complex (*L. symmetricus*). It is found in headwater streams in the Red Hills region, which is located in the Sierra Nevada foothills approximately 60 kilometers east of Modesto, California. Previous morphological and phylogenic studies on the Red Hills roach have determined that it is in fact a distinct lineage. The goals of this study are to determine levels of within-site genetic variation and fine-scale genetic structure among known 'populations' of the Red Hills roach. We hypothesize that populations of the Red Hills roach should have a low amount of diversity in mitochondrial and nuclear DNA due to their small sizes and isolations. We targeted one mitochondrial gene: Cytochrome B (Cyt B) and six microsatellite loci for our analysis. The Cyt B sequence data confirmed the uniqueness of the Red Hills roach. Analysis of population structure, based on mitochondrial DNA and microsatellites, indicated high levels of gene flow among sites, with one genetically distinct location. We hypothesize that these high levels of gene flow are the result of a complex metapopulation structure for these populations. Future work will be aimed at understanding colonization and dispersal dynamics in this system.

P48. MATHEMATICAL ANALYSIS OF GENE REGULATION IN *SACCHAROMYCES CEREVISIAE* IN RESPONSE TO COLD SHOCK. Nick A. Rohacz* and Katrina Sherbina* (Kam D. Dahlquist and Ben G. Fitzpatrick). Loyola Marymount University, Dept. of Biology, 1 LMU Drive, Los Angeles, CA 90045.

DNA microarray technology was used to measure the effect of cold shock on gene expression within *Saccharomyces cerevisiae*, budding yeast. To determine which transcription factors control the response to cold shock, total RNA was purified from the wildtype strain and strains deleted for the CIN5, GLN3, HMO1, and ZAP1 transcription factors during growth at 30ºC (t0); at 15, 30, and 60 minutes into cold shock at 13ºC; and at 90 and 120 minutes during recovery at 30ºC. Four to five replicates were performed for each strain and timepoint. A total of 103 DNA microarrays were competitively hybridized with RNA from the t0 timepoint, labeled with the Cy3 dye, and mixed with RNA from each of the other time points labeled with Cy5 dye. Spatial and intensity biases present in the microarray data because the two dyes have different properties were corrected using Loess normalization and median absolute deviation scaling performed with R Statistical Software. We then tested for significant changes in gene expression using a modified ANOVA test. Because we performed hypothesis tests for thousands of genes, we used the Bonferroni and Benjamini and Hochberg corrections to minimize the false positive rate. We found that 1686 genes showed differential expression for at least one timepoint in the wild type strain at a corrected $p < 0.05$. However the strain deleted for HMO1 had only 39 genes that showed significant differences in expression, suggesting that the absence of HMO1 seriously disrupted the cell's ability to respond to cold shock.

P49. THE EFFECT OF BENZYL BUTYL PHTHALATE ON THE EXTERNAL MICROBIAL COLONIZATION OF *FUNDULUS HETEROCLITUS*. Tanya R Swiderski*, Catherine Tobin, and Amanda Duggan (Lisa AE Kaplan). Quinnipiac University, Dept. of Biology, 275 Mount Carmel Avenue, Hamden, CT 06518.

Microbial diversity associated with fish scales may be an important factor to consider when assessing benzyl butyl phthalate (BBP) toxicity. *Fundulus heteroclitus* scales and water samples were taken weekly from control and BBP treated groups (0.1 ppm BBP daily, 30 consecutive days). Bacterial morphological

data supported an anticipated concomitant decline in colony color among control isolates from scales (70%) and ambient water (73%). As compared to control, a greater and more precipitous decline in colony color was observed among BBP scale isolates (90%), and no difference observed in BBP water isolates (73%). After 30 days, BBP scale isolates were all gram-negative while controls were all gram-positive. The Sunflower-yellow that dominated initial scale and water isolates was significantly reduced in control and disappeared from BBP isolates. Thus, BBP had a demonstrable effect on microbial colonization of *F. heteroclitus* scales. Further studies to identify the microbes and their xenobiotic capabilities are planned.

P50. THE AMINOGLYCOSIDE ANTIBIOTIC KANAMYCIN DAMAGES DNA BASES IN ESCHERICHIA COLI: CAFFEINE POTENTIATES THE DNA-DAMAGING EFFECTS OF KANAMYCIN WHILE SUPPRESSING CELL KILLING BY CIPROFLOXACIN IN *ESCHERICHIA COLI* AND *BACILLUS ANTHRACIS*. Tina Manzhu Kang, Jessica Yuan*, Angelyn Nguyen*, Elinne Becket, Hanjing Yang, (Jeffrey H. Miller). University of California, Los Angeles Department of Microbiology, Immunology, and Molecular Genetics, UCLA, Los Angeles, CA 90095.

The distribution of mutants in the KEIO collection of *Escherichia coli* gene knockouts that display an increased sensitivity to the aminoglycosides kanamycin and neomycin indicates that damaged bases resulting from antiobiotic action can lead to cell death. Strains lacking one of a number of glycosylases (e.g. AlkA, YzaB, Ogt, KsgA) or other specific repair proteins (AlkB, PhrB, SmbC) are more sensitive to these antibiotics. Mutants lacking AlkB display the strongest sensitivity among the glycosylase- or direct lesion removal-deficient strains. This perhaps suggests the involvement of ethenoadenine adducts, resulting from reactive oxygen species and lipid peroxidation, since AlkB removes this lesion. Other sensitivities displayed by mutants lacking UvrA, PolV, or components of double-strand break repair indicate that kanamycin results in damaged base pairs that need to be removed or replicated past to avoid double-strand breaks that saturate the cellular repair capacity. Caffeine enhances the sensitivities of these repair-deficient strains to kanamycin and neomycin. The gene knockout mutants that display an increased sensitivity to caffeine (dnaQ, holC, holD, priA) indicate that caffeine blocks DNA replication, ultimately leading to double strand breaks that require recombinational repair from functions encoded by recA, recB, and recC among others. Additionally, caffeine partially protects cells of both *Escherichia coli* and *Bacillus anthracis* from killing by the widely used fluoroquinolone antibiotic ciprofloxacin.

P51. ANALYSIS OF PLANT GROWTH PROMOTING RHIZOBACTERIA OF *LEUCANTHEMUM SUPERBUM*. Lauren Carlson and Nadhiya Govindaraj (Michelle Lum). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

In this experiment, we isolated and analyzed bacteria from the root of *Leucanthemum superbum* in order to determine the presence of Plant Growth Promoting Rhizobacteria (PGPR). Three isolates were chosen for further analysis and subjected to testing of several PGPR properties, including auxin production, phosphate solubilization, and cellulase production. All three isolates tested positive for at least two of the tests. The Polymerase Chain Reaction, gel electrophoresis, and DNA sequencing were all performed on the 16S rDNA, and the three isolates were determined to be *Pseudomonas* sp., and *Sphingobium* sp. These isolates were tested for actual plant growth promotion; tomato seeds were grown with solution of each isolate and root lengths were measured and analyzed statistically. The results of the test did not show a statistically significant difference; however, there was a noticeably smaller mean root length on seeds grown with the Pseudomonas species solutions, so we are repeating the experiment to determine whether the two isolates may actually be plant growth inhibiting bacteria. We are currently planning on testing the

three isolates for siderophore production and testing for plant root and shoot growth on *Leucanthemum* seeds for more definitive results. We will also be testing the effects of the heavy metal Zinc on isolates at increasing concentrations and on *Leucanthemum* seeds with heavy metal to determine if they are able to promote plant growth through bioremediation.

P52. ISOLATION AND CHARACTERIZATION OF CELLULASE PRODUCING AND PHOSPHATE SOLUBILIZING RHIZOBACTERIA. Salma Soltani* and Maria Shibatsuji* (Michelle Lum). Loyola Marymount University, Dept. of Biology, 1 LMU Drive, Los Angeles, CA, 90045.

Bacteria are often associated with the roots of plants, and those that are beneficial to plants are referred to as plant growth promoting rhizobacteria (PGPR). We are interested in identifying novel rhizobacteria that may have potential as biofertilizers. Bacteria were isolated from the roots of *Iris* sp. and *Taraxacum officinale* and tested for properties characteristic of PGPRs. 75 of our isolates have been screened for phosphate solubilization, siderophore production, cellulase activity, and auxin production. We chose six isolates that showed cellulase activity and/or phosphate solubilization for further study and inoculated them on switchgrass in order to further determine their potential as PGPRs. We are currently in the process of repeating this step of the experiment because our original results were inconclusive due to the fact that several of the seeds failed to germinate. We have already amplified the DNA of these isolates and ran a gel electrophoresis. We utilized the sequencing of the 16S rDNA gene to identify these isolates. Through further characterization of the isolates' morphology and biochemical characteristics, we seek to isolate plant growth promoting rhizobacteria with potential for agricultural applications, such as looking into the use of these PGPRs instead of chemical fertilizers.

P53. IDENTIFYING THE PRESENCE AND EFFECTIVENESS OF PLANT GROWTH RHIZOBACTERIA IN *LONICERA HISPIDULA*. Stephen Louie (Michelle Lum). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

Besides the essentials such as air, water, and sunlight, many plants require additional minerals and nutrients that they cannot obtain through conventional means. To achieve these ends, plants will establish relationships with Plant Growth Promoting Rhizobacteria (PGPR). PGPR are unique in that they can either produce or acquire certain nutrients necessary for the plant or indirectly control plant pathogens. The objective of this study was to isolate and characterize bacterial strains from the rhizosphere of *Lonicera hispidula* (California honeysuckle) to observe if they exhibit any PGPR properties. In addition, a molecular analysis of each bacterium was performed. The 16s rDNA of each bacterium was amplified by the polymerase chain reaction. The products were sequenced and compared to the 16S rDNA database to deduce the identity of each isolate. We identified one of the isolates as *Rhodococcus* sp. PGPR properties such as phosphate solubilization were also observed. Verification of the isolates' identities and characterization of the various PGPR properties will be discussed in greater detail.

P54. SELF-TRANSMISSIBLE ANTIBIOTIC RESISTANCE PLASMIDS IN URBAN COASTAL WETLANDS. Michael Geiger*, Kimberly Schroeder*, Victoria Haase*, Jenna Lavenuta, and Doug Zuill (David Cummings). Point Loma Nazarene University, Dept. of Biology, 3900 Lomaland Dr., San Diego, CA 92106.

Bacterial resistance to clinical antibiotics is threatening to undermine our ability to fight many common infections. While much attention has been rightly given to the spread of antibiotic resistance in the clinical setting, very little work has been done to understand the roles of resistant bacteria and mobile resistance genes in the natural environment. In this study, we are attempting to shed light on the nature of self-transmissible resistance plasmids in urban wetlands of southern California. Previous work in our lab has shown that fluoroquinolone resistance genes are deposited and accumulate in the sediments of two San Diego wetlands during winter storm events. In some cases, these genes persist through the dry season. We are using enrichment and mating (conjugation) techniques to induce the transfer of resistance plasmids from wetland bacteria to laboratory strains where the plasmids can be isolated and studied. Plasmid pLNU.11 (ampR, tetR, doxR, sxtR) was isolated from a multidrug-resistant strain of Citrobacter freundii that was selectively enriched on ampicillin and nalidixic acid. Plasmid pTRE.P11 (ampR, pipR, ticR, tetR, doxR, strR, sxtR) was isolated by biparental mating with wetland bacteria as plasmid donors, Pseudomonas putida KT2442 as recipient, and tetracycline to select for transconjugants. Finally, plasmid pTRE.Ec2 (encoding no readily identifiable resistances) was isolated by triparental mating with wetland bacteria as plasmid donors, E. coli JM109 (pBBR1MCS, cmR) as the intermediate recipient, and *E. coli* HY842 (rifR, strR, zeoR) as the final recipient. In addition to these three, dozens of other plasmids have been isolated and are currently being characterized for their antimicrobial phenotypes. Our results demonstrate the utility of these methods for shedding light on the antibiotic resistance plasmid metagenome in natural wetlands, and support the notion that urban wetlands act as reservoirs of mobile antibiotic resistance genes.

P55. THE RELATIONSHIP BETWEEN THE EXTRACELLULAR POLYMERIC SUBSTANCE (EPS) AND QUORUM SENSING MOLECULES IN *PSEUDOMONAS AERUGINOSA* BIOFILM FORMATION. Brandon Bauer* and Alex Woodrow (Kathleen Tallman). Azusa Pacific University, Dept. of Biology and Chemistry, 901 E. Alosta Ave., Azusa, CA 91702-7000.

Pseudomonas aeruginosa (PA), a gram negative bacillus, is the most common bacterium found in nosocomial and life threatening infections of immune compromised patients and has proven to be a leading cause of cystic fibrosis (CF) respiratory infections. The success of PA is often attributed to its ability to evade immune response and antibiotics by forming biofilms, sessile communities of bacteria irreversibly attached to a surface or to each other and embedded in a matrix of extracellular polymeric substance (EPS). Biofilm formation is driven by quorum sensing molecules released by bacteria. Comparisons of biofilms grown in the laboratory and those from the sputum of CF patients reveal that biofilms have different structures and different ratios of quorum sensing molecules. Some biofilms are flat, some develop small three-dimensional structures, and some develop large mushroom-shaped pillars. Previous research in this laboratory developed a method to grow PA biofilms with two distinct phenotypes, referred to as mucoid and non-mucoid. The goal of this study is to use a FITC HHA-lectin antibody and DAPI nucleic acid staining to examine the biofilms in these two phenotypes using confocal microscopy. DAPI is traditionally used to stain the nuclei of eukaryotic cells; it is not commonly used for bacteria, especially gram negative bacteria with thick cell walls. It is hypothesized that the mucoid phenotype will produce a three-dimensional, mushroom-shaped biofilm, whereas the nonmucoid phenotype will produce a flat biofilm. Preliminary data indicate that the double label technique is working and ready to be used in examining the biofilms.

P56. THE EFFECTS OF HEAVY METAL AND RHIZOBACTERIA ON THE GERMINATION AND GROWTH OF DUNE LUPINE. Jennifer Okonta and Michelle Lum. Loyola Marymount University, Dept. of Biology, 1 LMU Drive, Los Angeles, CA 90045.

Urban run-off is a source of heavy metal contamination and one of the many negative consequences of our growing and developing cities. Not only does it affect the oceans, beaches, and wildlife, but it can also have a major impact on plants. The purpose of my study is to find out how heavy metals and the root-associated bacterium, *Variovorax* sp., affect *Lupinus chamissonis* (dune lupine) growth. This particular nodulating legume can be found near Loyola Marymount University at the sand dunes of El Segundo and at the Ballona wetlands. Different root assays and germination experiments have been conducted. *Lupinus chamissonis* seeds treated with 250 μM ZnSO4 or inoculated with *Variovorax* were found to have higher germination rates than untreated seeds. However, I found that higher concentrations of zinc (0.5 – 1.0 mM) inhibited root growth. Future studies will investigate whether *Variovorax* influences the impact high concentrations of zinc have on dune lupine growth.

P57. CHARACTERIZATION OF *BURKHOLDERIA TUBERUM* NODULATION MUTANTS. Marla Dallal*, Amanda Nystrom (Michelle Lum). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

The symbiotic relationship between the family Rhizobiaceae, alpha-proteobacteria, which include many species of rhizobia, and plants of the Leguminoceae, has been well-studied and had been the only known bacteria with the capability of forming nodules. Under nitrogen-limiting conditions, capable plants form a symbiotic relationship with a host-specific strain of rhizobia. Rhizobia cause the formulation of nodules on legume plant roots inside which the bacteria can convert atmospheric nitrogen to ammonia, a form that is readily utilized by plants. In return, rhizobia receive organic nutrients such as, carbohydrates and sufficient oxygen, from the plants. Recently it was demonstrated that *Burkholderia tuberum*, a member of the beta-proteobacteria, can nodulate some legumes. A library of transposon tagged mutants of *B. tuberum* was generated and screened for exopolysaccharide mutants. Two *B. tuberum* mutants, discovered to be defective in EPS were determined to have mutations in the genes coding for glutamate synthase (Bt-3) and trigger factor (Bt-5). With these mutants, further investigation will be carried out as to their ability to nodulate plants and form biofilms, both processes of which EPS is involved. The mutants were complemented by expression of the wild-type copy of the genes. Cowpea and cow bean plants were inoculated with both the Bt-3 and Bt-5 mutants and it was observed that no nodules appeared on the plants inoculated with Bt-3, while those inoculated with Bt-5 did produce nodules. Polymerase chain reaction was carried out to amplify the wild-type and cloned into a pJET vector. The genes were sub-cloned into a pLAFR vector and mated with *B. tuberum* mutants. If complementation has occurred, the wild-type, EPS producing phenotype should be observed. The complemented mutant can then be used as a control in subsequent studies of nodulation and biofilm formation.

P58. GENERATING AND DETERMINING THE PHENOTYPE OF AN ACYL COA DEHYDROGENASE MUTANT IN *BURKHOLDERIA UNAMAE*. Michael Carlone* (Michelle Lum). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

Burkholderia unamae is a nitrogen-fixing bacterium associated with plant roots and known to promote plant growth. *B. unamae* was mutated by introduction of a transposon by conjugation. The transposon-tagged mutants were then screened for defects in exopolysaccharide biosynthesis by looking for a non-

mucoid phenotype. From this process, we were able to isolate the mutant MC093, which molecular methods revealed contains a mutation in the Acyl CoA Dehydrogenase gene. Acyl CoA Dehydrogenase is an enzyme that is responsible for the metabolism of fatty acid chains in bacteria. Though this is a relatively common enzyme, mutations of the gene have not been well characterized phenotypically. Further characterization of the phenotype of MC093 is being done, including additional analysis of exopolysaccharide production and biofilm formation.

P59. TOWARDS IMPROVING OUR UNDERSTANDING OF BACTERIOPHAGE DIVERSITY: THE ISOLATION AND CHARACTERIZATION OF SDCHARGE11 AND THE BIOINFORMATICS ANALYSIS OF CONTAGION. Hilda Delgadillo* and Raymond Totah* (Dr. Fang, Dr. Kuleck, Dr. Urbinati). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

Bacteriophages infect and consequently lyse (rupture of host's cell membrane to release the new viral particles) their host, bacteria. These bacteriophages are acquiring more attention in research due to the growing awareness of their importance in ecology and evolution. The target of this research is to discover novel phages through the Howard Hughes Medical Institution Science Education Alliance (HHMI SEA) Phage Discovery Program at Loyola Marymount University. In the fall of 2011 we collected, isolated, purified, and characterized numerous bacteriophages. One of these collected phages was SDcharge11 , a lytic phage (ability to only lyse bacterial host) and member of the B1 sub-cluster. This virus is capable of infecting *Mycobacterium smegmatis*, an exemplary microorganism in exploring phage, and was found on the campus of Loyola Marymount University. Currently, in the spring of 2012, we began collectively analyzing, through division of groups, a single bacteriophage named Contagion due to its large amount of DNA. Furthermore, in our present research, we are deciphering its genomic DNA using numerous sources such as DNA Master, BLAST, and GeneMark. We will present our preliminary findings from our fall and spring research as a contribution to the understanding of bacteriophages' evolutionary process and their potential role within our biosphere.

P60. ANTIMICROBIAL-PRODUCING BACTERIA IN TREE CANOPY SOIL: BIOLOGICAL APPROACHES. Ariel Madden* and Jenny Stein (Amy Siegesmund). Pacific Lutheran University, Department of Biology, Tacoma, WA 98447.

The rise of antibiotic-resistant pathogens is one of the looming challenges to global public health. Our research turns to the endemic microbial communities of the tree canopy of the temperate rainforests of Washington as untapped troves of new natural products possessing biological activity. Previous work by Nadkarni and Auman provide evidence of the comparison of ground and tree canopy soils in this bioregion leading to differentiated microbial communities. Initial studies have been focused on the culture and identification of bacterial strains present in canopy soil samples. Kirby-Bauer disk diffusion assays were used to locate strains possessing antimicrobial activity against *Escherichia coli*, *Pseudomonas aeruginosa*, and *Staphylococcus aureus*. After larger-scale culture of the most highly active microbes, pH-based extraction enabled the isolation of crude extracts which were then further purified by flash column chromatography on silica. Current studies focus on the characterization of the isolated antimicrobial compounds by NMR and LC/MS techniques.

P61. THE AMINOGLYCOSIDE ANTIBIOTIC KANAMYCIN DAMAGES DNA BASES IN *ESCHERICHIA COLI*: CAFFEINE POTENTIATES THE DNA-DAMAGING EFFECTS OF

KANAMYCIN WHILE SUPPRESSING CELL KILLING BY CIPROFLOXACIN IN *ESCHERICHIA COLI* AND *BACILLUS ANTHRACIS*. Tina Manzhu Kang, Jessica Yuan*, Angelyn Nguyen*, Elinne Becket, Hanjing Yang, and (Jeffrey H. Miller). Department of Microbiology, Immunology, and Molecular Genetics, and the Molecular Biology Institute, University of California, and the David Geffen School of Medicine, Los Angeles, CA 90095.

The distribution of mutants in the KEIO collection of *Escherichia coli* gene knockouts that display an increased sensitivity to the aminoglycosides kanamycin and neomycin indicates that damaged bases resulting from antibiotic action can lead to cell death. Strains lacking one of a number of glycosylases (e.g. AlkA, YzaB, Ogt, KsgA) or other specific repair proteins (AlkB, PhrB, SmbC) are more sensitive to these antibiotics. Mutants lacking AlkB display the strongest sensitivity among the glycosylase- or direct lesion removal-deficient strains. This perhaps suggests the involvement of ethenoadenine adducts, resulting from reactive oxygen species and lipid peroxidation, since AlkB removes this lesion. Other sensitivities displayed by mutants lacking UvrA, PolV, or components of double-strand break repair indicate that kanamycin results in damaged base pairs that need to be removed or replicated past to avoid double-strand breaks that saturate the cellular repair capacity. Caffeine enhances the sensitivities of these repair-deficient strains to kanamycin and neomycin. The gene knockout mutants that display an increased sensitivity to caffeine (dnaQ, holC, holD, priA) indicate that caffeine blocks DNA replication, ultimately leading to double strand breaks that require recombinational repair from functions encoded by recA, recB, and recC among others. Additionally, caffeine partially protects cells of both *Escherichia coli* and *Bacillus anthracis* from killing by the widely used fluoroquinolone antibiotic ciprofloxacin.

P62. MUTAGENIC SPECIFICITY IN *ESCHERICHIA COLI*. Madeline Yung* and Elinne Becket (Jeffrey H. Miller). University of California, Los Angeles, Department of Microbiology, Immunology, and Molecular Genetics 405 Hilgard Ave., Los Angeles, CA 90095.

Mutation detection and analysis systems have been an invaluable resource for investigating the specificity of mutagens and from mutators resulting from inactive DNA repair proteins. Previous identification in our laboratory of 79 base substitutions in the rpoB gene, resulting in rifampicin resistance in *Escherichia coli*, has created a rapid and practical system of mutational analysis. However, this system needs to be complemented with a second system to verify the generality of its findings. We have therefore developed more fully the gyrA/nalidixic acid resistance system. We have detected 12 base substitutions spread over 8 sites within a 350 base pair stretch of the gyrA gene and an additional base substitution at a different part of the gene that results in nalidixic acid resistance in Escherichia coli. The mutagens 5-bromodeoxyuridine and 2-aminopurine, as well as mutS, mutL, and mutT mutators, all display their expected mutational specificity in this system. Further analysis reveals that the sequences surrounding a hot spot at 260 bp in the gyrA gene has a striking similarity to a hot spot at bp 1547 in the rpoB/Rifr system.

P63. THE EFFECT OF DEPURATION ON MICROBIAL DIVERSITY ASSOCIATED WITH *FUNDULUS HETEROCLITUS*. McNickle LA, Muller RA, Driscoll NR, Kaplan LAE. Quinnipiac University, Biological Sciences, 275 Mt. Carmel Ave, Hamden, CT 06518.

The effect of depuration on external microbial colonization of *Fundulus heteroclitus* was examined. It

was anticipated that depuration would impact equally the microbial diversity associated with ambient water and fish scales. Fish scales and ambient water samples were collected from Long Island Sound (Fall 2011) and transported back to the laboratory. Over the course of a fifteen-week depuration, bacteria were isolated from scales and water. By the end of depuration, bacterial colony color diversity diminished from thirteen colors to predominately one (cream) among fish scale isolates, and Gram stain results shifted from mostly Gram-positive to Gram-negative. Similar trends were observed among microbes isolated from water: colony color decreased from ten to one (light eggshell) and Gram stain shifted from predominantly positive to negative. These results indicate that depuration dramatically impacts the bacteria found on and around *F. heteroclitus*. Experiments are underway to identify the genera of the persistent bacteria.

P64. IDENTIFYING AND CHARACTERIZING THE MICROBIAL COMMUNITY OF DUNE LUPINE. Elisabeth Ferris*, Michael Pina, and Jessica Duong (Michelle Lum). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

Lupinus chamissonis (dune lupine) is a nodulating species of the legume family present in the Ballona wetlands and El Segundo sand dunes near Loyola Marymount University. Legumes such as dune lupine have symbiotic relationships with nitrogen-fixing soil bacteria (Rhizobia) that reside in special root structures called nodules. We are interested in characterizing the bacteria that reside in these nodules as it is the first step towards screening for plant growth promoting bacteria (PGPR) that could be useful in restoration efforts. Nodules were isolated from roots of dune lupine, surface sterilized, crushed, and plated on selective media. To identify the bacterial isolates, the polymerase chain reaction (PCR) was performed on the 16S ribosomal DNA and the products were sequenced and compared to the BLAST database. Five bacteria were identified as *Bradyrhizobium japonicum*, *Rhizobium lusitanum*, *Variovorax paradoxus*, *Methylobacterium tardum*, and *Mesorhizobium* sp. Strains were screened for plant growth promoting properties such as cellulase activity, phosphate solubilization, and ACC deamination. *R. lusitanum* tested positive for both cellulase activity and phosphate solubilization, *V. paradoxus* tested positive for cellulase activity and ACC deamination, and *Mesorhizobium* sp. tested positive for cellulase activity and phosphate solubilization. Sterile plants were inoculated with both individual strains and in combination to determine which bacteria were able to induce nodulation in plants. From this, it was determined that only *B. japonicum* is able to induce nodulation independently while the other bacteria colonize nodules but do not nodulate when inoculated without *B. japonicum*. In addition, genes controlling nodulation and nitrogen fixation are currently being isolated using PCR.

P65. CREATION OF DELETION MUTATIONS OF *CAULOBACTER CRESCENTUS* GENES TO TEST THEIR ROLE IN GALACTURONATE METABOLISM. Meghan Garrett*, Jennifer Parker* (Dr. Craig Stephens). Santa Clara University, Department of Biology, 500 El Camino Real, Santa Clara, CA 95053.

The oligotrophic freshwater bacterium *Caulobacter crescentus* is able to utilize many different as carbon and energy sources, including galacturonate and glucuronate. The CC_1487-1492 gene cluster is necessary for glucuronate and galacturonate metabolism via the hexuronate isomerase pathway. Included in this cluster is a transcription factor known as HumR (CC_1489), which regulates the expression of the uxaA operon (CC_1487 and CC_1488) and uxaC operon (CC_1490, CC_1491, and CC_1492). Previously, mutations had been generated in all of these genes using plasmid integration, an approach which carries the risk of polar effects. In order to test the functions of each gene independently, deletion mutants were created by homologous recombination with engineered plasmids. The mutants strains were

then tested for their ability to metabolize various sugars, including glucuronate and galacturonate, as well as other sugar as controls. Our results show that all 5 of these genes are important for galacturonate metabolism in *Caulobacter*. Future goals include directly assaying for other enzymes involved in sugar metabolism in *C. crescentus*, including galacturonate isomerase and pectate lyase.

P66. THE EFFECT OF NUCLEOTIDE POOLS ON SPONTANEOUS MUTAGENESIS IN *ESCHERICHIA COLI*. Lawrence Tse*, Alexander Cosico*, and Elinne Becket (Jeffery H. Miller). University of California Los Angeles, Dept. of Microbiology, Immunology, and Molecular Genetics and the Molecular Biology Institute, and the David Geffen School of Medicine, Los Angeles, CA 90095.

Spontaneous mutations, while crucial for evolution, can have detrimental consequences on human health, leading to complications such as cancer and drug resistance. However, many of the sources of spontaneous mutations have yet to be characterized. Thus, we sought to elucidate pathways leading to these mutations. To do so, mutagenesis assays were conducted in various *E. coli* knockout mutants using three different mutation detection systems. These assays were additionally performed in the presence and absence of 5-bromodeoxyuridine (5BdU), a highly mutagenic uridine base analog. From these experiments, we discovered that the activity of an exoribonuclease contributes to mutagenesis in response to 5BdU and in the absence of mismatch repair (MMR), as shown by the reversal of mutagenesis in both conditions in the absence of this exoribonuclease. We discovered that while every other mutagen has its own unique mutational spectrum, 5BdU has the same spectrum as a strain that is defective in MMR. This suggests that 5BdU does not cause its own specific mutations, but rather exacerbates mutations normally repaired through MMR. The role that this exoribonuclease plays in spontaneous mutagenesis makes its human homolog a possible target in cancer therapy.

P67. USE OF HALOBACTERIUM NRC-1 AS A MODEL ORGANISM IN THE UNDERGRADUATE RESEARCH LABORATORY; GENERAL OBSERVATIONS INCLUDING ANALYSIS OF GROWTH CONDITIONS, GROWTH FACTORS, AND INHIBITORS; AND USE OF NATURAL SELECTION TO ISOLATE ANTIBIOTIC RESISTANT MUTANTS.. Christian Dove*, Matthew Christie, and Sung Shil Kim (Joe Francis) (Todd Wood). The Master's College, Dept. of Biological Science, 21726 Placerita Canyon Rd., Santa Clarita, CA 91321.

Halobacteria NRC-1 thrive on high concentrations of salt, allowing undergraduate researchers the ability to grow and analyze these bacteria without contamination of cultures by microbes commonly found in the undergraduate microbiology laboratory. In our laboratory we have discovered a new antibiotic, PVPCA, a chemical commonly found in the pharmaceutical and cosmetic industries. In a previous study, we have shown that PVPCA inhibits several different Halophile bacteria, but not common laboratory strains of bacteria such as E.coli (1). We have recently examined PVPCVA for its effects on the moderate halophile *Vibrio alginolyticus*; concentrations of PVPCVA which inhibit halobacteria have not been detected to inhibit *V. alginolyticus*. In fact, our general observations suggest that certain concentrations of the inhibitor might enhance growth of *V. alginolyticus*. As a first step towards determining the mechanism of PVPCA antibiotic function we have attempted to isolate antibiotic resistant halobacteria. Paper disks infused with the PVPCVA antibiotic create zones of inhibition of halobacteria growth on salt agar. Micro-colonies of halobacteria growing in or near these zones of inhibition have been detected and isolated. The isolated bacteria do not show antibiotic resistance when replated on salt agar plates in the presence of antibiotic. In our current laboratory research, we are developing an induced natural selection process in which broth cultures of Halobacteria NRC-1 are exposed to long term various concentrations of the antibiotic. Progress toward mutant isolation will be reported. (1) Chambers C., et.al., Identification of a

Novel Polymeric Archaeostatin. 35th Annual WCBSCUR, April 24, 2010, Santa Clara University, Santa Clara California.

P68. ENUMERATION OF BACTERIOPHAGE AND PROKARYOTE POPULATIONS IN AN URBAN COASTAL WETLAND (BALLONA WETLANDS) IN LOS ANGELES COUNTY BY EPIFLUORESCENCE MICROSCOPY. Salman Ahmad*, Emma Kennedy*, Helena Oliveri*, Jorrel Sampana*, and James Wu* (Gary Kuleck). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

In understanding population dynamics of microbial populations, it is necessary to be able to directly count the number of viruses, bacteria, and other microorganisms from environmental samples. The environmental samples we are working with are from the Ballona Wetlands. To our knowledge, this is the first study of its kind which explores bacteriophage and other microbe temporal and spatial dynamics in a natural, urban coastal wetlands system. This is a method-development project in which we are modifying and improving a previously published procedure to work with samples from a wetland environment. Serial-diluted samples fixed with a formaldehyde solution and mounted onto a Anodisc membrane were stained with SYBR Green I and mounted onto glass slides. They were examined and enumerated using a confocal microscope. We hope to develop this as an efficient way to accurately estimate the relative numbers of microorganisms in the various environmental niches within the Ballona Wetlands so that the flux in abundance ratios of viruses to bacteria, as well as eukaryotes can be compared. It is anticipated that this project will reveal fundamental information that is a foundation to examining and understanding microbial population dynamism in an urban coastal wetlands ecosystem. We intend to present preliminary findings on the effectiveness of the methods we developed as well as preliminary enumeration data and its significance in the Ballona Wetlands.

P69. DISCOVERY OF MYCOBACTERIOPHAGE "KATATTACK". Theodore Medling, Katherine Wikholm, Kat Fu (Gary Kuleck, Yiwen Fang, Carl Urbinati). Loyola Marymount University, Department of Biology, 7900 Loyola Boulevard, Los Angeles, CA 90045.

Research in the most abundant life-form on Earth, bacteriophage, a virus that infects bacteria, is essential to understanding their role in evolution of bacteria. Phages have numerous applications in food processing and phage therapy. However, as significant as their role is in bacterial evolution, relatively little research has been done on bacteriophages. As a result, we are undergoing a yearlong research project to investigate the characteristics of a specific phage within Loyola Marymount University's campus. In fall 2011, a mycobacterial phage, named "KatAttack" was isolated and purified from its host bacterium, *Mycobacterium smegmatis*. This was done using plaque streaking, PCR, gel electrophoresis, and restriction digest. Currently, our research focus has shifted from purifying the phage to analyzing a specific phage's genomic DNA. Analyzing the pattern of bands seen in the gel electrophoresis of genomic DNA cut by certain restriction enzymes we categorized our phage into Cluster A. Bioinformatic analysis of the phage's genome allows us to identify the encoded genes as well as the relationship between our phage and those in the phage genome database. Using specialized programs such as BLAST and DNA Master, we can take a more intimate approach into the purpose and function of bacteriophage genes. We will be describing our progress in deciphering the genomic content of "KatAttack" and evaluate its evolutionary importance and role in ecology.

P70. DISCOVERY OF MYCOBACTERIOPHAGE CONTAGION AND COMPARING IT TO OTHER MYCOBACTERIOPHAGE. Jacob Pascual*, Vishal Bhula* (Gary Kuleck, Yiwen Fang, Carl Urbinati). Loyola Marymount University, Department of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

Bacteriophage are the most abundant life form on the planet and are of great significance because of their role in many genetic and evolutionary processes. It is difficult to even find two phage that are nearly identical in gene content and genome structure. Due to their abundance, diversity, and relatively small genomes, an analysis of their genomes can reveal a great deal about genetic evolution. Despite their abundance , however, relatively little genomic analysis has been undertaken. To expand our understanding of mycobacteriophage, bacteriophage that infect mycobacteria, we, as a part of the Howard Hughes Medical Institute (HHMI) Science Education Alliance (SEA) Phage Program , began a year-long research project to isolate and purify a single phage, from soil samples collected at LMU. During the fall, we isolated and characterized the phage Zoolander, which we discovered to be lysogenic, incorporating its own DNA into the bacterial host's genome. We also isolated and characterized Zoolander's DNA, and identified it as a C cluster phage based on enzyme restriction mapping. After one semester, we selected one of the group's phage, Contagion, a lysogenic E cluster phage, for sequencing over the winter break. Now, as part of a class project, we are collectively using bioinformatics and algorithms, such as GeneMark, and BLAST, to begin a comparative genomic analysis of Contagion's genome and gain further understanding of phage DNA and the phage's role in ecology and evolution. We will discuss the isolation and characterization of Zoolander and our bioinformatic analysis of Contagion.

P71. ISOLATING BACTERIA DISPLAYING INSENSITIVITIES TO MULTIPLE ANTIBIOTICS FROM THE BALLONA WETLANDS. Nana Kufor*, Christopher Leary (Dr. Gary Kuleck, Dr. John Dorsey). Loyola Marymount University, Dept. of Biology, 1 LMU Drive., Los Angeles, CA 90045.

Antibiotic resistant bacteria and genes have been increasingly recognized as biological pollutants with impacts on public health and ecosystem vitality. Water quality research in the Del Rey Lagoon, and initial sampling in the adjacent Ballona Wetlands demonstrated the presence of multi-antibiotic resistant (MAR) bacteria. These aquatic communities receive input of contaminated runoff from Ballona Creek that drains the highly urbanized Ballona Creek Watershed. To determine if the Wetlands act as a sink or source for MAR bacteria, a study was initiated in 2011 to characterize species MAR bacteria entering and leaving the wetlands during tidal flood and ebb flows. A second site was added in Ballona Creek above the tidal prism to determine the structure of the MAR bacterial assemblage in pure runoff that would be diluted in the Ballona Estuary prior to entering the Wetlands on flood tides. Our hypothesis is that natural wetland processes will alter the composition of MAR bacteria between flood and ebb flows. Water samples were collected during eight sampling events in the wetlands and four in the Creek. Bacteria were initially isolated using heterotropic plate spreads followed by replicate plating on TSA infused with clinical concentrations of eight antibiotics. Resistances were confirmed using Kirby- Bauer disk testing. Preliminary results will be presented comparing the percentage of bacteria resistant to each of the antibiotics, and multiple antibiotics, during the flood and ebb flows in the Wetlands and runoff in the Creek.

P72. CONTAGION: THE FRESHMAN MYCOBACTERIOPHAGE PROJECT. Paola Lockwood* (Gary Kuleck, Yiwen Fang, Carl Urbinati). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

Bacteriophages are running rapid in this world and very few people stop to admire them. They are double-stranded DNA viruses that attack bacteria, and have an estimated population of 10^{31} (Hatfull). With such an extensive population diversity is sure to follow. With this diversity bacteriophages are potentially useful in the fields of bioinformatics and genetic engineering. The Howard Hughes Medical Institute (HHMI) Science Education Alliance (SEA) Phage Program sponsored this undergraduate research project to dig into the world of phages and see what we could learn from a phage and its host *Mycobacterium smegmatis*. I, along with my classmates, isolated, purified, cultivated, and examined our own phages; mine being Contagion, which was found on the LMU campus. Our class could only sequenced one phage, Contagion, which we then, from sequencing, gained insight into its genetic structure and functions. This phage characterization resulted from cluster determination, restriction enzyme patterns, and morphotype. Contagion belongs to Cluster E with a myoviridae morphology. Contagion was then chosen to be further analyzed in our second semester with bioinformatics programs such as DNAMaster, GeneMark, and Glimmer. The use of these bioinformatics tools permitted us to annotate and confirm Contagion's genome through the comparison of its genes with those of other known phages. This was valuable research because of its contribution to the growing database of mycobacteriophages and the importance of this knowledge in future attempts of unlocking the mycobacteriophage world.

P73. AN ANALYSIS OF BACTERIOPHAGE DIVERSITY: THE ISOLATION AND CHARACTERIZATION OF KENGEN AND ANNOTATION OF CONTAGION. Genevieve Guerra*, Lauren Magee*, and Danielle Mauch* (Dr. Yiwen Fang, Dr. Gary Kuleck, Dr. Carl Urbinati). Loyola Marymount University, Dept. of Biology, Los Angeles, CA 90045.

While bacteriophage, the viruses that infect bacteria, are the most abundant life form in existence, comparatively little research has been done on them. The study of their abundance and diversity could provide important insights into evolution, microbial ecology and their applications in medicine. To increase the number of phage under study, we have joined the Howard Hughes Medical Institute (HHMI) Science Education Alliance (SEA) Phage Program, which focuses on discovering and isolating new mycobacteriophage for individual and comparative analysis. We collected soil samples from around the LMU campus during the fall to isolate, purify, and characterize an individual mycobacteriophage, KenGen. We conducted molecular analysis and electron microscopy imaging to determine that KenGen is a lysogenic phage belonging to the A2 cluster of the siphoviridae family. As part of a class project, one phage, Contagion, was selected for sequencing over the winter break, and, in the spring of 2012, we are carrying out bioinformatics analysis using DNAMaster software to annotate and describe the genes present in the phage genome. In this report, we will discuss the isolation and characterization of KenGen and review our preliminary findings on the bioinformatics analysis of Contagion. Based on comparison to other similarly classified phages' genomes, we will consider the impact of our research on a better understanding of mycobacteriophage structure and function.

P74. DISCOVERY AND CHARACTERIZATION OF A NOVEL BACTERIOPHAGE THERIPPER AND BIOINFORMATIC ANALYSIS OF BACTERIOPHAGE CONTAGION. Mitchell Petredis, Wil Gendron, (Yiwen Fang, GaryKuleck). Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

Mycobacteriophage are viruses that infect mycobacteria and in particular the model host, *Mycobacterium smegmatis*. Although bacteriophage are the most abundant entities on the planet, relatively little research has been conducted on them, even though the study of their diversity may reveal useful insights into evolution and microbial ecology. Through the Howard Hughes Medical Institutes' Science Education Alliance (HHMI SEA) Program, we were able to purify, isolate, and characterize a single, unique phage, named TheRipper from the soil of the Loyola Marymount University – Westchester campus in the fall of 2011. To categorize this phage, we used an electron micrograph, PCR, and restriction enzymes to determine that TheRipper is a B4 cluster phage, whose members are lysogenic siphoviridae with cloudy plaques and non-contractile tails. Currently, as part of group project we are conducting bioinformatic analysis using programs such as BLAST, DNAMaster, and Phamerator to accurately map the genetic structure of the bacteriophage Contagion and carry out comparative analysis with other known phage genomes. We will discuss the isolation and characterization of TheRipper and describe our preliminary bioinformatics findings with Contagion in the context of its significance to evolution and microbial ecology.

P75. USING SITE-DIRECTED MUTAGENESIS AND YEAST TWO-HYBRID ANALYSIS TO STUDY DNA BINDING DOMAIN MUTANTS OF THE *C. ELEGANS* WINGED-HELIX TRANSCRIPTION FACTOR LIN-31.. Amanda Dewey* and Fernando Meza Gutierrez (Leilani Miller). Santa Clara University, Dept. of Biology, 500 El Camino Real, Santa Clara, CA 95053.

LIN-31, a winged-helix transcription factor, acts as an effector of the conserved RTK/Ras/MAP kinase signaling pathway and is required for vulval development in the nematode *C. elegans*. In the current model, LIN-31 plays two roles in vulval development: 1) it heterodimerizes with another transcription factor, LIN-1, to promote non-vulval cell fates and 2) when the dimer is disrupted due to signaling events, it promotes a vulval cell fate. While the interaction between LIN-31 and LIN-1 was revealed through co-immunoprecipitation experiments, this interaction is not observed in yeast two-hybrid (Y2H) assays when full length LIN-31 is used. Previous experiments in our lab have shown that LIN-31 and LIN-1 do interact in a Y2H experiment when the LIN-31 DNA binding domain is removed. Because LIN-31 belongs to a large family of winged helix proteins with a highly conserved DNA binding domain, we hypothesize that when the LIN-31 protein is fused to the GAL-4 DNA binding domain in a Y2H experiment, the LIN-31 winged-helix domain may direct DNA binding somewhere else in the yeast genome, preventing transcription of the Y2H reporter genes. The goal of this specific project is to confirm this hypothesis by performing yeast two-hybrid assays using LIN-1 and full length LIN-31 with specific mutations in the DNA binding domain that are known to disrupt DNA binding. Two sites within this domain have been altered using PCR-based site-directed mutagenesis (SDM), including QuickChange SDM. These mutations will then be sub-cloned into full-length lin-31 cDNA fused to the GAL-4 binding domain, for Y2H analysis. Based on these results, investigations of the interactions between LIN-31 and other proteins and its effect on cell-fate specification, can move forward.

P76. *SACCHAROMYCES CEREVISIAE* RESPONDS TO COLD SHOCK BY CHANGING THE EXPRESSION OF GENES INVOLVED IN NITROGEN METABOLISM. Andrew F. Herman, Alondra J. Vega, Lauren N. Kubeck, Kenny R. Rodriguez, Katrina Sherbina, Nicholas A. Rochez, Kam D. Dahlquist. Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., 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 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 environmental stress response (ESR) genes, but less is known about the early response genes and which transcription factors regulate them. We have characterized 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. Results were analyzed using the program GenMAPP to determine which biological processes were activated in response to cold shock and recovery. We found that genes involved in nitrogen metabolism change expression during cold shock. The transcription factor Gln3p is an activator of genes regulated by nitrogen catabolite repression. We found that a strain of yeast in which the GLN3 gene was deleted has impaired growth at 15°C. We then performed a cold shock and recovery DNA microarray experiment on the Δgln3 strain to determine the effect of Gln3p on the transcriptional network that responds to cold shock. Analysis of the data indicates that fewer Gln3p target genes change expression due to cold shock in the deletion strain than in the wild type strain. In particular genes involved in nitrogen metabolism due to cold shock are particularly regulated by Gln3p.

P77. ANTIBIOTIC RESISTANCE GENES IN BACTERIAL ISOLATES FROM THE BALLONA WETLANDS. Sarah Patno*, Samantha Hurndon*, Daniel Garcia*, Stephanie Kaweki, and Chris Leary (Dr. Gary Kuleck). Loyola Marymount University Dept. of Biology 7900 Loyola Blvd Los Angeles, CA 90045.

Antibiotic resistance genes (ARGs) have been classified as a biological pollutant, which poses both a public health risk and environmental threat. The presence of these genes in coastal wetlands in Southern California has been documented but determining the extent of their influence on human health and ecosystems depends on an assessment of their presence, persistence and dissemination properties as well as the host bacteria which harbor them. As a first step in assessing whether they pose a threat in the Ballona Wetlands, we conducted studies to quantitatively measure their relative abundance. Using replica-plating techniques, six thousand bacteria colonies were screened for multiple-antibiotic insensitivities resulting in approximately 150 strains with 5 or more antibiotic insensitivities being isolated for further molecular probing. Since these strains are more likely to carry ARG, we developed qualitative molecular methods to detect the presence of ARGs within our isolates of interest. A library of different validated tetracycline ARG primer pairs has been constructed to screen DNA from the isolates and a number of strains have been shown to carry different tetracycline resistance genes. We will report on the results of our testing these isolates, the progress in creating libraries for other common antibiotic resistances and the identification of possible human pathogens harboring multi-drug resistance genes.

P78. A PUTATIVE PHYTOCHROME-LIKE PHOTORECEPTOR MAY REGUALTE THE EXPRESSION OF RED-LIGHT INDUCED PSBA RNA BINDING PROTEIN GENES IN *CHLAMYDOMONAS REINHARDTII*. Macarena Aloi*, Laura Arce and Alexander Powell (Amybeth Cohen). California State University, Fullerton, Dep. of Biological Science, 800 North State College

Blvd., Fullerton, CA 92831.

Chlamydomonas reinhardtii is a fresh-water, unicellular, green alga that is readily used as a model organism for the study of photosynthesis. Our research focuses on the regulation of a set of nuclear-encoded genes (rb38, rb47 and rb60) in this alga, whose protein products direct the translation of the chloroplast-encoded psbA mRNA to the D1 protein, which plays a pivotal role in the light reactions of photosynthesis. We have shown that the rb38 and rb60 genes, and the nuclear-encoded psbO gene (encodes the Oxygen Evolving Enhancer I protein), are induced by red light. The rb47 gene is constitutively expressed. These results are novel, as very few red light-induced processes have been characterized in *C. reinhardtii*, and no red light photoreceptor has been identified. Red-light induction of the rb38, rb60 and psbO genes was reversed by far-red light; the hallmark of a phytochrome-regulated response. Currently, genomic PCR and Southern blot analyses are being performed in order to isolate the phytochrome-like gene in *C. reinhardtii*. The results obtained should elucidate the nature of the genomic sequence for this novel red light photoreceptor, aiding in the construction of a signal-transduction pathway for the expression of the rb and psbO genes.

P79. DEVELOPMENTAL REGULATION OF RRNA PROCESSING IN EMBRYONIC STEM CELLS. Josue Gutierrez*, Ivy Hung, (Benjamin Yu). University of California San Diego, Department of Medicine.

Stem cells must balance between cell growth and cell division so that they can maintain their cell identity (self-renewal) so as to propagate differentiated progenies (differentiation). ESCs, cycling very rapidly, may have substantial metabolic and synthetic needs that must be met to forecast future cell growth. An important aspect of regulation on cell growth must rely on ribosome production and we hypothesize that this event may be subjected to regulation upon differentiation signals to forecast future cell growth. With this assumption, we decided to investigate ribosome production and in particular rRNA maturation during the course of differentiation. We employed qPCR technique and FISH (fluorescent in situ hybridization) analysis to detect rRNA levels and patterns as a measurement of ribosome production. Surprisingly, we observed that mESCs under accumulate mature 28S rRNA when compared to differentiated cells. To further understand mechanistically how this occurs, we investigated expression levels of 47S pre-rRNAs in mES cells and found that this nucleolar pre-rRNA accumulates at higher level in mES cells. These results suggest that there is a potential regulation on rRNA processing in ESCs and such event may coordinate with differentiation cues to trigger production of mature ribosome needed for cell lineage specification. To address this point, we decided to artificially alter rRNA processing kinetics by over-expression of two rRNA processing factors: fibrillarin and dyskerin, and assay for effects on mESCs. To analyze functional consequences of over-expression of rRNA processing factors, we introduced them in to mESCs by a transient transfection method. We then investigated potential changes on accelerated rRNA processing as well as several targeted gene expressions by qPCR analysis. We found that 47S pre-rRNA was further processed into mature 28S rRNA with a concomitant reduction of a stem cell-specific gene expression (i.e. Oct), indicating loss of pluripotency of ESCs. Meanwhile, some early cell lineage-specific gene expressions increase correspondingly. Taken together, these data suggest a functional involvement of rRNA processing in roles with mESC pluripotency maintenance and differentiation.

P80. RETINOIC ACID (RA) REGULATES EXPRESSION OF THE VITAMIN A TRANSPORTER, STRA6, BY DIFFERENT PATHWAYS IN BREAST AND THYROID CANCER CELL LINES. Debbie Shamsian*, Sun Wook Kim,Takahiko Kogai, and (Gregory A. Brent). UCLA, VA Greater Los Angeles.

STRA6 is a retinol-binding protein receptor, which mediates retinol uptake in brain, retina, placenta, testis, and other tissues. A derivative of retinol, retinoic acid (RA), induces differentiation and inhibits cell proliferation in many types of cancer cells, including breast cancer and thyroid cancer. STRA6 has been initially identified as a gene up-regulated by RA treatment. I compared the regulation of STRA6 gene by RA in MCF-7 breast cancer cells, BHP 2-7 human thyroid cancer cells and FRTL-5 rat thyroid cells. I found that RA induces STRA6 mRNA in both MCF-7 cells and BHP 2-7 cells, but not FRTL- 5 cells. And that inhibition of both MEK and PI3K significantly reduced STRA6 expression in BHP 2-7 cells. In MCF-7 cells on the other hand, inhibition of PI3K, but not MEK, abolished tRA-induced STRA6 expression.

P81. AN ANALYSIS OF HEAVY METAL STRESS IN THE HYDROPONICALLY GROWN TOMATO PLANT, *LYCOPERSICON ESCULENTUM*, USING THE COMET NUCLEAR ASSAY AND ICP-MS ANALYSIS. Daniel Chu, Katherine Kimura, Howard Lin, Danielle Lee, Anthony Traboulsi, Walter Au. Loyola Marymount University, Dept. of Biology, 7900 Loyola Blvd., Los Angeles, CA 90045.

Increasing levels of the heavy metal, zinc, in plants induces oxidative stress causing overt damage at the molecular and cellular level and severe imbalances in ion distribution in plant tissues. We have developed a hydroponic system using tomato plant, *Lycopersicon esculentum*, to analyze the impact of heavy metal stress. To quantitate the effect of increasing concentrations of zinc, we have modified and utilized an in vitro assay, the comet nuclear assay. This assay involves the isolation of nuclei from plant tissues and the detection of DNA breakage and membrane damage using confocal microscopy. To quantitate the tissue specific levels of zinc in experimental plants, we have used a spectroscopic technique, inductively coupled plasma gas chromatography (ICP-MS). This technique measures the content of 28 different ions in the tissues, allowing us to monitor the absolute levels of zinc and the impact of zinc concentration on other ion species. Our preliminary findings indicate that a) plant growth is increasingly inhibited at higher zinc concentrations; b) nuclear damage occurs when plant roots are exposed to 50 µM zinc; c) the levels of zinc in all three tissues tested (roots, shoots, leaves) is strongly correlated with zinc concentrations in the media; and d) increasing levels of zinc dramatically impact the levels of iron and manganese. Collectively, these results demonstrate the critical impact that heavy metal exposure has on plant growth and development. We will discuss these findings and ongoing progress in examining oxidative stress in plants.

P82. VALIDATION OF *XENOPUS LAEVIS* MONOCLONAL ANTIBODIES IN WHITE'S TREEFROG *LITORIA CAERULEA*. Adam Marentes*, Shahani Noor, (Emma Wilson, Wendy Saltzman, Kristine Kaiser). University of California Riverside, Department of Biology and Division of Biomedical Sciences, Riverside, CA 92521.

Amphibian populations have been declining across the globe for decades. Many of these declines have been attributed to emerging infectious diseases such as chytridiomycosis, a fungal skin infection, suggesting that a greater understanding of amphibian immune function is necessary. To better characterize the amphibian immune response, we used monoclonal antibodies (mAb) to determine what membrane-bound proteins are expressed among the population of immune cells extracted from frog spleens. Available mAb for amphibians are raised against the model species *Xenopus laevis* presenting a conflict for researchers working with other amphibian species. Despite species specificity, mAb cross-reactivity among taxa is not uncommon. Thus, we set out to determine whether *X. laevis* mAb will label immune cells in White's treefrog, *Litoria caerulea*. Preliminary data suggest that a treatment of 100 µL of

mAb can label immune cells in the *L. caerulea* spleen, facilitating further studies into immune function and immunosuppression in White's treefrog.

P83. LATE TREATMENT WITH ESTROGEN RECEPTOR BETA LIGAND AMELIORATES EXPERIMENTAL AUTOIMMUNE ENCEPHALOMYELITIS. Amy Wisdom*, Yuan Cao, Noriko Itoh, Rory Spence (Rhonda Voskuhl). University of California, Los Angeles Neuroscience Research Building 635 Charles E Young Drive Los Angeles, CA 90024.

Multiple Sclerosis (MS) is an autoimmune disease characterized by inflammation and neurodegeneration. Current MS treatments focus on treating the inflammatory component of the disease and do not directly target neurodegeneration. Estrogen has well-documented neuroprotective effects in many disorders of the CNS, including experimental autoimmune encephalomyelitis (EAE), the most commonly used mouse model of MS. Treatment with an estrogen receptor beta (ERβ) ligand has been shown to be effective at ameliorating clinical disease and providing neuroprotection in EAE. However, the protective effects of this ERβ ligand have only been demonstrated when administered prior to induction of disease. Therefore, we tested whether ERβ ligand treatment could still provide clinical protection and neuroprotection when treatment was initiated after onset of disease. We found that treatment administered both before and after disease induction was effective in ameliorating EAE. In case treatment paradigm, ERβ ligand treatment did not affect the peak level of early disease, but promoted recovery during the chronic phase of disease. Our findings suggest that therapeutically administered ERβ ligand can successfully treat EAE, which could eventually translate into an effective treatment for MS. Since most adverse effects of high dose estrogen treatment are mediated through ERα, not ERβ, novel use of ERβ ligands as neuroprotective agents would likely have a very good safety profile.

P84. MONITORING THE IMMUNE RESPONSE IN TRANSGENIC ZEBRAFISH. Caitlyn McGue*, Sarah E. Schale, Bradley H. Jacobsen, David N. Pratt, Noemi Delgado, Alyssa R. Scott, Brad G. Magor, David Traver, (Dawne M. Page). Point Loma Nazarene University, Dept. of Biology, San Diego, CA; Univ. of Alberta, Edmonton, Canada; UCSD, La Jolla, CA

Zebrafish make ideal models for immunology research because they possess many of the same cell lineages as mammals, their genome has been fully sequenced, and many transgenic models already exist for these fish. However, no transgenic models that specifically labeled B cells previously existed, and therefore we created reporter lines that label IgM+ B cells with eGFP. These lines were validated by flow cytometry and qPCR. GFP+ and GFP- cells were sorted from the lymphoid fraction of various organs and analyzed for gene expression. The GFP+ cells expressed IgM but not IgZ (another B cell lineage) or Lck (a T cell marker). To monitor the immune response, and specifically the presence of B cells, IgM:eGFP zebrafish were injected with either a T-cell dependent or a T-cell independent antigen. The kidney, spleen, peritoneal exudates, and gut were then removed and analyzed by flow cytometry. The numbers of B cells increased in these organs, including antigen-specific B cells. Future research will focus on determining the most ideal secondary response.

P85. A LINK BETWEEN NEURAL AND PSYCHOPHYSICAL INHIBITION OF RETURN. Solmaz Shariat Torbaghan, Daniel Yazdi*, Koorosh Mirpour, James W. Bisley. David Geffen School of Medicine at UCLA, Department of Neurobiology, P.O. Box 951763 Los Angeles, CA, 90095-1763.

Inhibition of return is thought to help guide visual search by inhibiting the orienting of attention to previously attended locations. In the psychophysical domain, this is seen as a slowing in reaction time (RT), but in the modeling and neural domains this is represented by a decrease in activity on saliency or priority maps. To test whether these 2 views are related, we trained 3 animals to perform an RT version of a foraging task in which they visually searched for a target, but had to rapidly respond to a probe if it appeared. We found that RTs varied depending on what stimulus was present in the probed location. These RTs could be modeled based on neural activity collected previously, but only when habituation was incorporated into the model. Due to the complex relationship between RTs and neural activity, we conclude that inferences about the state of the brain should only be made from RTs in simple, well controlled tasks.

P86. REGULATION OF SEROTONIN SYNTHESIS GENES IN THE NERVOUS SYSTEM OF THE NEMATODE *C.ELEGANS* BY WNT SIGNALING GENES. Erin Williams* (Curtis Loer). University of San Diego Dept. of Biology, 5998 Alcala Park San Diego, CA 92110.

In the nematode *C. elegans*, the Scr/Hox5-like homeotic complex gene lin-39 is necessary for correct development of many cells in the central body, including neurons. In mutants lacking the LIN-39 transcription factor, six male-specific ventral nerve cord neurons called CPs no longer make the neurotransmitter serotonin. We have found that CP neurons in lin-39 mutant worms fail to express four different genes required for making and using serotonin. For example, the cat-4 gene encodes an enzyme required for making biopterin, a cofactor essential for serotonin synthesis. Whereas most males expressed a cat-4::GFP reporter fusion in all 6 CP neurons, only 10% of lin-39 mutant males expressed cat-4::GFP in 1 or more CP neurons. To find other genes that function like lin-39 in serotonergic neuron development, we are using RNA interference (RNAi) to knock down genes during larval development when CP neurons are specified. In RNAi controls using cat-4::GFP, 92% of males expressed the transgene in 6 CPs in our negative control (empty vector), whereas 54% expressed cat-4::GFP in $\leq$ 5 CP neurons in our positive control (lin-39 RNAi). We have found that knockdown by RNAi of the genes hmp-2, sys-1, and sem-4 also reduces serotonin synthesis gene expression. Both hmp-2 and sys-1 function in Wnt/MAPK signaling - hmp-2 encodes a β-catenin and sys-1 encodes a β-catenin-like protein. The sem-4 gene encodes a zinc-finger protein previously shown to interact with lin-39 in vulval development in the central body.

P87. THE EFFECTS OF SECOND-HAND CIGARETTE SMOKE EXPOSURE ON THE LEVELS OF PLASMA GLUCOSE AND INSULIN USING SWISS WEBSTER MICE. R. K. Pisano*, F. Dashty*, R. Shakir, H. Torba, V. Delgado, (F. Watson and M. Thao). California State University Stanislaus, Dept. of Biology, One University Circle, Turlock, CA 95382.

Second-hand smoke (SHS) is the smoke given off by the burning end of a cigarette or exhaled by the smoker. SHS contains more than 4,000 chemical substances, 50 of which are known carcinogens in humans and animals. In general, cigarette smoke exposure affects carbohydrate metabolism and in humans is linked to insulin resistance and diabetes. Insulin is a hormone that stabilizes plasma glucose to prevent hyperglycemia. The objective of this project was to determine the effects of SHS exposure on levels of plasma glucose and insulin in Swiss Webster Mice. Mice were randomly divided into experimental and control groups. The experimental mice were exposed to the smoke from a lit cigarette once a day, 5 days a week, for 25 weeks. The animals were fed and weighed daily. Blood was drawn from

the saphenous vein every third week for plasma glucose and insulin determination. Plasma glucose was measured using a glucose meter. The level of insulin was determined using ELISA. Mice exposed to SHS consistently consumed less food and gained less weight over the 25 weeks. Plasma glucose levels significantly decreased while levels of insulin remain the same with chronic SHS exposure. Following immediate SHS exposure, plasma glucose and insulin levels both increased. The increased plasma glucose level is the result of sympathomimetic effects of nicotine on the nervous system. Increase in plasma glucose is a concern because it may lead to insulin resistance and diabetes.

P88. A NOVEL POST-TRANSLATIONAL MODIFICATION OF CORE HISTONE PROTEINS: GLUTATHIONYLATION Carl Decker*, Oscar Tello (Kathleen Weaver and Jerome Garcia). University of LaVerne, Biology Department, 1950 Third Street La Verne, CA 91750.

The modification of core histone proteins plays an essential regulatory role in gene transcription, as their structural conformation directly affects the expression of the DNA material coiled around them. Therefore, a better understanding of histone modifiers is critical in gaining further insight into several maladies associated with dysfunctional gene expression, including cancer and neurodegeneration. Aligned with this premise, the objective of this study was to determine if core histone proteins could be modified by glutathione disulfide (GSSG), a tripeptide with known protein interaction capabilities. Core histones were extracted and isolated from a culture of SHSY5Y human neuron cancer cells, and treated with 0.01mM, 0.025mM, 0.05mM, 0.1 mM, 1.0 mM, and 5.0 mM concentrations of GSSG. Histone isolates were then processed through a western blot analysis and visualized via chemiluminescent detection. Subsequently, all core histones (H2A, H2B, H3, and H4) were shown to be glutathionylated in a positive, dose- dependent fashion. To both expand these data and address the limitations of our chemical model, we are now investigating the relationship of nitric oxide (NO) and hydrogen peroxide (H_2O_2) oxidative stress with SHSY5Y histone glutathionylation under an in- vitro paradigm.

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