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DIVISION OF PHYSICAL & BIOLOGICAL SCIENCES
OFFICE OF THE DEAN
SANTA CRUZ, CALIFORNIA 95064

JACK BASKIN SCHOOL OF ENGINEERING
OFFICE OF THE DEAN
SANTA CRUZ, CALIFORNIA 95064

June 8, 2017

Dear Physical and Biological Sciences and Engineering Students, Faculty, and Guests,

It is our pleasure to welcome you to the Twentieth Annual Undergraduate Research Symposium. The undergraduate research experience in the Physical and Biological Sciences and Engineering at UCSC provides students the rare opportunity to engage in supervised research and to learn in a dynamic environment of discovery from professors who are leaders in their fields.

As you take the opportunity to view the work that has been done by the student participants, we are certain you will be impressed by the sophistication of the projects and by the accomplishments of our undergraduate students. This facet of undergraduate education is one that exemplifies the commitment to excellence in teaching and research that characterizes undergraduate education at UCSC.

To the student participants: We are extremely proud of you and the scholarly work you have undertaken. For those of you who plan to continue your academic careers in graduate school, we hope this event will provide you with the valuable experience of presenting your work in a professional scientific forum. For those who plan to enter the non-academic world, your participation in this event will be a significant addition to your resume. Our congratulations to all of you, and we wish you the best of luck in all of your future endeavors.

Our sincere thanks go out to our faculty colleagues and staff in the Division of Physical and Biological Sciences and the Jack Baskin School of Engineering, whose dedication to academic excellence has been made evident by the number and quality of the projects displayed here.

Sincerely,

Paul L. Koch
Dean, Physical and Biological Sciences

Alexander Wolf
Dean, Baskin School of Engineering

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Manolo Adrian Mejia	Oakes	MCD Biology	Jeremy Lee
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Mona Zia			Myra E Finkelstein

2017 Student Abstracts

ESTRIOL EFFECTS ON AMYLOID-BETA INDUCED PATHOLOGY IN A DROSOPHILA MELANOGASTER MODEL OF ALZHEIMER'S DISEASE

Marin Clement Alix Salomon Mazeres

Faculty Mentor: Jeremy Lee

Estriol Effects on Amyloid-Beta Induced Pathology in a Drosophila melanogaster Model of Alzheimer's Disease

Marin Mazeres
Faculty Mentor: Jeremy Lee

Alzheimer disease (AD) is a major chronic neurodegenerative disease causing memory-loss, dementia and death. It is the leading cause of dementia in the U.S. with over 5 million people affected. Patients with AD present with an accumulation of ?-amyloid plaques made of amyloid ? peptide (A?) in their brain. A? can come in a variety of different forms, of which A?42 is thought to be the most toxic. A previous study by Morinaga et al. (2011) showed that treatment of in vitro AD cells with the estrogen steroid estriol resulted in a reduction in plaque levels and in the rates of aggregation of A?.
In this study, we are determining whether estriol has an effect on A?-induced neurotoxicity in an in vivo model, Drosophila melanogaster. Our study has found no significant difference in the longevity of AD model flies treated with estriol compared to untreated AD model flies. A Western Blot protein analysis is underway to assess relative A? levels in these flies, and an estriol ELISA analysis is planned to confirm the presence of estriol in brain extracts.

A CRISPRI SYSTEM FOR INTERROGATING LONG NONCODING RNAS INVOLVED IN INFLAMMATION AND MACROPHAGE DIFFERENTIATION

Chia-Hao Andrew Chang

Faculty Mentor: Sergio Covarrubias

One of the most profound discoveries from the sequencing of the human genome is that over 85% of the genome is transcribed and yet less than 3% encodes for protein-coding exons. Long noncoding RNAs (lncRNAs) represent the largest group of RNAs produced from the genome. LncRNAs are defined as transcripts greater then 200 nucleotides in length lacking protein-coding capabilities. Only 1% of all validated lncRNAs have ascribed functions, hence this class of RNAs is greatly in need of further investigation. Current methods to characterize the function of novel lncRNAs are extremely labor-intensive, limiting the number that can be explored at one time.
The Innate Immune system provides one of the first lines of defense against infection. These responses involve complex signaling cascades that result in transient inflammation, providing protection against microbes while maintaining tissue homeostasis. Macrophages are critical effectors of this inflammatory response. Mature macrophages are derived from monocytes through a differentiation that is tightly regulated. The human monocytic cell line, THP1, is a well-established model of macrophage differentiation and inflammatory pathways. Here we establish a CRISPR transcriptional inhibition (CRISPRi) system in THP1s for screening coding and noncoding genes. We develop a fluorescence-based NFKB-reporter system for inflammatory pathway interrogation. Additionally, THP1s can be differentiated into macrophage-like cells, which allow probing into macrophage differentiation pathways. We demonstrate the ability to efficiently target candidate lncRNAs upregulated in either inflammatory or differentiation pathways. We are in the process of performing a genome-wide screen to unveil novel regulators of inflammation and differentiation.

A NEW MODEL FOR HIGH-RESOLUTION EXOPLANET TRANSMISSION SPECTROSCOPY

Zafar Rustamkulov

Faculty Mentor: Jonathan J Fortney

The recent boom in observations of exoplanet atmospheres has prompted the need for robust theoretical models to better explore their properties. High resolution infrared spectra taken by instruments such as CRIRES and ESPRESSO on the VLT, and the future MIRI and NIRSpec instruments aboard JWST, present astronomers the opportunity to study exoplanets in great detail. The properties of exoplanet atmospheres are imprinted in their transmission spectra, allowing for constraints on their structure, composition, formation, and evolution. In this study, we build a novel transmission spectrum model to characterize the properties of exoplanet atmospheres. The model expands on a previously validated opacity code and an analytic geometric path length distribution prescription to produce high-resolution spectra spanning the near- and mid-infrared range. The model's flexibility allows for rapid iterations through many atmospheric parameters to fit existing observational data, given initial pressure-temperature and abundance profiles and cloud models. The model outputs show good agreement with other models for terrestrial and Jovian planets alike. The model is applied to the planets of the TRAPPIST-1 system, and preliminary results are discussed.

ADAPTIVE OPTICS ENHANCE IN-VIVO FUNCTIONAL IMAGING OF DROSOPHILLA MELANOGASTER MUSHROOM BODIES

Jesse Cisneros Solis

Faculty Mentor: Joel Kubby

Currently non-invasive imaging technology to study neural circuits, such as functional magnetic resonance imaging (fMRI) and electroencephalogram (EEG), are limited in their spatial resolution for imaging at the cellular level. Non-linear microscopy has facilitated imaging dynamic signals of cells in a variety of model species; however, resolution and signal quality are limited by scattering and aberration introduced by refractive index heterogeneity within the tissue and optical path. We propose using adaptive optics microscopy that will provide excellent spatial and temporal resolution, allowing us to image the calcium dynamics of neurons at a biologically interesting depth within an intact organism. In this experiment we will be investigating brain wave synchronization or phase-locking in the Drosophilla melanogaster (fruit fly). Transgenic flies with the GCaMP calcium-indicator labeling in the mushroom body will allow us to image the activity of individual neurons. We will try to induce brain wave synchronization with external stimuli using LED strobe lights driven by waveform generators. Two-photon laser microscopy with adaptive optics will enable high-resolution structural and functional imaging of the mushroom bodies, structures that play a role in insect learning and memory. We have already developed a robust method for visualizing the baseline fluorescence signal in our GAL4 line. These methods will enable future experiments that probe dynamic neural activity in deep brain structures and investigations of mechanisms for learning and memory.

ANALYSIS OF LOCAL STRUCTURE IN TETRAHEDRITE USING EXTENDED X-RAY ABSORPTION FINE STRUCTURE (EXAFS) SPECTROSCOPY

Valentin Urena Baltazar

Faculty Mentor: Frank G Bridges

Tetrahedrites are a class of naturally occurring minerals with high thermoelectric efficiency. Thermoelectric materials are needed in devices aiming to convert heat to electricity directly via the Seebeck effect, and also for cooling without a refrigerant via the Peltier effect. We examine pure Cu12Sb4S13 and zinc doped Cu10Zn2Sb4S13 tetrahedrite to better understand the metal to semiconductor transition at T~95K in the pure tetrahedrite. Understanding why the transition is suppressed upon doping will shed light on the structural properties of this material. To probe the crystal structure, X-ray spectroscopy data of a sample of tetrahedrite were collected at the Stanford Synchrotron Radiation Lightsource (SSRL). The X-rays induce photoelectrons in the targeted atom whose wavefunction backscatters off neighboring atoms and interferes with itself, resulting in small oscillations in the Extended X-ray Absorption Fine Structure (EXAFS) region of the data. We use the Real Space X-ray Absorption Program (RSXAP) to analyze the EXAFS region of both the zinc and copper absorption edges. We expect to learn how the environment about the zinc atoms differs from that about Cu in the tetrahedrite and specifically how the proposed displacements of copper atoms in the pure material lead to the metal-semiconductor transition.

ANALYSIS OF MES-4 PROTEIN LOCALIZATION IN C. ELEGANS SOMATIC TISSUES

Carmen Ma

Faculty Mentor: Susan Strome

Successive generations require proper germline development and the survival of primordial germ cells (PGCs). In C. elegans, the histone methyltransferase MES-4 must be transmitted from mother germ cells to progeny PGCs in order for progeny to develop a full germline. Without transmission of MES-4, PGCs are born in larvae but eventually deteriorate, resulting in sterile adult worms. MES-4 is important for germline identity in germline tissue, but previous evidence suggests MES-4 may also confer germline identity in somatic cells: Intestinal cells underwent a soma-to-germ ‘identity’ conversion, losing its somatic programming. To understand how MES-4 drives germline identity, it is imperative to understand MES-4 localization in all tissues throughout C. elegans development. To analyze MES-4 localization, live imaging was used in MES-4::GFP endogenously tagged worms. Data obtained from live imaging shows MES-4 is enriched in germ cells and most likely present in seam cells, which are hypodermal cells that aid in elongation of the embryo. Both germ and seam cells are proliferative cells, suggesting that MES-4 function is either a cause or consequence of proliferation. Understanding localization of MES-4 will provide insight into the specific function of MES-4 in soma and its role in proliferation and germline identity.

ANALYZING THE RELATIONSHIP BETWEEN EL NIñO AND COMMON MARINE MAMMAL SPECIES STRANDINGS

Kristiana Ashlyn Davis

Faculty Mentor: Patrick William Robinson

Ocean anomalies, such as El Niño, have been known to have cascading impacts on marine ecosystems. Marine mammal strandings can be good indicator of the impacts El Niño events may have on marine ecosystems due to their role as apex predators. However, different age classes and genders of different species face unique problems that may not pertain to the other groups. Based on these differences, we investigated the potential correlations between non-El Nino year and El Niño years (using data provided by NOAA's Earth System Research Laboratory) and the standings of marine mammals of different genders and age classes. Using data from the Moss Landing Marine Labs and California Sea Otter Stranding Network, we looked at marine mammal standings that occurred between January 2006 and December 2015 of three common species found in California: sea otters (Enhydra lutris), harbor seals (Phoca vitulina), and harbor porpoises (Phocoena phocoena). There was significant difference between El Niño years and strandings of harbor seal pups ($p=0.0410$), female harbor porpoises ($p=0.0429$), sea otter yearlings ($p=0.0455$), and male harbor porpoises ($p=0.0458$). With these findings, we concluded that gender was not impacted by El Niño years for sea otters and harbor seals, but genders of harbor porpoises were affected due to similar diet and disease exposure. Sea otter yearling and harbor seal pup strandings, however, increased during El Niño years and decreased during non-El Niño years. This study provides knowledge of how oceanographic changes impacts three apex predator species and opens future studies on how other marine mammal species could be affected by El Niño as well.

APPROXIMATING DARK MATTER IN GALAXIES

Marina Huang

Faculty Mentor: Kyle B Westfall

Dark matter still largely remains a mystery. Dark matter is matter that does not interact with light and does not interact directly with anything with charges. Dark matter composes 23% of the universe, whereas atoms compose roughly 5% of the universe and dark energy composes the rest. But perhaps most importantly, it is a central piece to solving the puzzle of the universe: how it was first made and how it evolved. In this study, we use the Mapping Nearby Galaxies at APO (MaNGA) data from the Sloan Digital Sky Survey. The MaNGA data measure spectra across the face of the 10,000 nearby galaxies by using integral field units composed of optical fibers.

I propose to estimate the amount of dark matter in galaxies using measurements of the galaxy rotation velocity compared to its luminosity distribution. Dark matter is the hypothetical mass that accounts for the difference between the gravitational mass measured by the former and the mass in normal matter measured by the latter. I will be analyzing about 3,000 galaxies from the MaNGA data survey. Dark matter approximation has been around for more than 50 years, but it has not been done in the scale as big as the MaNGA survey.

ASSESSING THE ACCURACY OF PHOTOGRAMMETRY VIA AN UNMANNED AIRCRAFT SYSTEM (UAS) ON NORTHERN ELEPHANT SEALS (MIROUNGA ANGUSTIROSTRIS)

Trevor Barclay

Faculty Mentor: Daniel P Costa

Recent developments in unmanned aircraft systems (UAS) allow researchers to conduct aerial surveys more safely and at less cost than ever before. This study quantified the accuracy of morphometric measurements collected with an UAS. Photographs of northern elephant seals with empirically measured mass and size (n=14) were collected at Año Nuevo State Park during the 2017-breeding season. Photogrammetric measurements were collected and compared to direct mass and size measurements collected in the field. The accuracy of measurements collected from photographs varied between individuals, this variation was considered a result of environmental factors in the field and not an error in the process of analyzing photographs. A measurement of seals size was collected from the images and had a significant relationship with seal mass ($P<.001$ $R^2 = 0.773$ RMSE= 43kg). Mass estimation via an UAS was on average within 12% of the direct mass measurement, this level of accuracy is similar to other photogrammetric methods while causing less disturbance to study individuals. Overall as long as environmental factors in the field are accounted for morphometric measurements collected via UAS photogrammetry are accurate enough for the application of UAS as a research tool.

ASSESSING THE RELATIONSHIP BETWEEN EL NIñO AND COMMON MARINE MAMMAL SPECIES STRANDINGS

Kristiana Ashlyn Davis

Faculty Mentor: Patrick William Robinson

Ocean anomalies, such as El Niño, have been known to have cascading impacts on marine ecosystems. Marine mammal strandings can be good indicator of the impacts El Niño events may have on marine ecosystems due to their role as apex predators. However, different age classes and genders of different species face unique problems that may not pertain to the other groups. Based on these differences, we investigated the potential correlations between the severities of El Niño (using the Multivariate El Niño Index Scale data provided by NOAA's Earth System Research Laboratory) and the standings of marine mammals of different genders and age classes. Using data from the Moss Landing Marine Labs and California Sea Otter Stranding Network, we looked at marine mammal standings that occurred between January 2006 and December 2015 of three common species found in California: sea otters (Enhydra lutris), harbor seals (Phoca vitulina), and harbor porpoises (Phocoena phocoena). There was significant difference between the MEI Scale data and strandings of harbor seal pups ($p=0.0410$), female harbor porpoises ($p=0.0429$), sea otter yearlings ($p=0.0455$), and male harbor porpoises ($p=0.0458$). With these findings, we concluded that gender was not impacted by El Niño years for sea otters and harbor seals, but genders of harbor porpoises were affected due to similar diet and disease exposure. Sea otter yearling and harbor seal pup strandings, however, increased during El Niño years and decreased during non-El Niño years. This study provides knowledge of how oceanographic changes impacts three apex predator species and opens future studies on how other marine mammal species could be affected by El Niño as well.

ATOMIC LAYER DEPOSITION FOR TRANSISTOR SCALING

Emmanuel Kayede

Faculty Mentor: Nobuhiko P Kobayashi

Gordon Moore's law predicts that the number of transistors per square inch on an integrated circuit will double every 18 months. Because scaling of metal-oxide-semiconductor field effect transistors (MOSFETs) and heterojunction bipolar transistors (HBTs) has reached the 10 nm and 32 nm nodes respectively, precise fabrication techniques are needed. Since modern MOSFET oxide thicknesses are <5 nm, there is significant gate leakage current due to quantum mechanical tunneling between gate and source requiring the adoption of high permittivity (k) dielectrics. Additionally, high drive current densities and stringent planarization requirements have caused new challenges for emitter metal deposition. Atomic layer deposition (ALD) has been widely used for its nanometer scale thickness control, uniform and conformal material deposition. We report ALD dielectric films of HfO2 grown with TEMAHf/H20 and ZrO2 grown with TEMAZr/H2O. For ZrO2 deposition, chamber seasoning with TEMAZr/H2O and nitrogen plasma/ TMA results in an interface thickness of 23.660 and 13.481Å respectively. Metal-oxide-semiconductor capacitors (MOSCAPs) were fabricated on 1e17 cm^-3 InGaAs/n+InP by ALD with a Ni gate metal. A ZrO2 and HfO2 based MOSCAPs were measured to have a capacitor density of 1.5 and 1.39 uF/cm^2 in accumulation at 1V for 100 Khz respectively. Initial characterization of TiN/Pt emitter metal has begun and a transmission line method process flow has been determined; details are left to future study.

BEHAVIORAL EVALUATION OF GENETICALLY INDUCED SLEEP DEPRIVATION ON ALZHEIMER'S DISEASE-LIKE PATHOLOGY IN DROSOPHILA

Manolo Adrian Mejia, Isha Amit Desai

Faculty Mentor: Jeremy Lee

Alzheimer's Disease (AD) is characterized by a shortened lifespan; cognitive impairment, including memory loss, and decreased motor and spatial abilities; and an accumulation of ABeta amyloid (A?) plaques in the brain. Clinical studies suggest that sleep deprivation may accelerate AD pathology by interfering with the clearance of neurotoxic forms of A? (Spira, et al., 2013). Our project studies the effects of sleep deprivation on the progression of AD-like pathology in model Drosophila. Drosophila showcase AD-like pathology when a transgene encoding human A? is inserted into the flies' DNA and expressed in central nervious system neurons.

We developed a Drosophila model to study the relationship between AD pathology and sleep deprivation. Our Drosophila model uses the GAL4/UAS system to express human A?-42 in the CNS, to simulate A?-42 accumulation in AD patients. We also express shRNA to knock down the Insomniac protein in our AD model Drosophila. The knockdown of Insomniac Protein inhibits normal regulation of sleep bouts and intervals, and thereby causes sleep deprivation. Our lab has previously shown that flies expressing human A?-42 with Insomniac knockdown have shorter mean life span than flies expressing A?-42 without Insomniac knockdown. Insomniac knockdown in otherwise wild type flies does not have a detrimental effect on life span. Currently, we are testing these flies with the Rapid Iterative Negative Geotaxis (RING) assay, to measure the effects of sleep deprivation on their innate negative geotaxis behavior. This will allow us to evaluate whether sleep deprivation exacerbates behavioral aspects of AD pathology, such as locomotion.

BIOCHEMICAL ANALYSIS OF U2 SNRNP ASSEMBLY

Yewande Candice Alabi

Faculty Mentor: Melissa S Jurica

The spliceosome is a large and complex ribonucleic protein (RNP) that consist of 5 small nuclear RNPs (snRNPs): U1, U2, U4, U5 and U6. These snRNPs consist of small nuclear RNAs (snRNAs) that base pair with and recognize splice site sequences in pre-mRNA. This molecular machine is responsible for the two subsequent transesterification reactions that remove non-coding regions of RNA (introns) and join the flanking coding exons together. Errors in splicing have been linked to multiple diseases and cancers, however not a lot is known about the mechanism by which splicing errors lead to disease.

It is often necessary to understand the structure of a machine in order to fully elucidate its function. The goal of this project is to use a variety of biochemical tools to determine structural features of early-assembled spliceosomes. We designed a pre-mRNA substrate predicted to form a stable complex with U2 snRNP. I have synthesized this pre-mRNA with a radiolabel and analyzed complex assembly in cell extracts via native gel assembly. Going forward, I will use an affinity tag included in the pre-mRNA to purify the complex. It will then be subject to mass spectrometry, electron microscopy and RNA probing analysis. These analyses will determine what assembly factors are present, the gross structure of the complex and the secondary structure of the snRNA components. Taken together these experiments will reveal the structural basis for early spliceosome assembly.

CHARACTERIZATION OF SPT5 MUTATIONS IN SACCHAROMYCES CEREVISIAE THAT CAUSE CRYPTIC INITIATION

Nancy Sanchez

Faculty Mentor: Grant Hartzog

During transcription elongation, accessory proteins help RNA Polymerase II transcribe through a gene by removing and reassembling physical protein barriers—nucleosomes. One accessory factor, Spt5, is a universally conserved transcription elongation factor that is essential for life in all eukaryotes. We study Spt5 in Saccharomyces cerevisiae because it is a genetically tractable model eukaryote whose gene expression machinery is closely similar to that in humans. Our hypothesis is that if Spt5 has a functional role in nucleosome dynamics during transcription elongation, we should be able to identify spt5 mutants that disrupt chromatin over transcribed sequences. One known consequence of such a disruption is activation of cryptic promoters—i.e. promoters that are normally repressed by nucleosomes. Using a yeast strain in which a well-characterized cryptic promoter was fused to the yeast HIS3 gene, we screened cells carrying randomly mutagenized spt5 for the ability to grow on media lacking histidine. The spt5 mutant plasmid candidates from yeast were recovered from His+ yeast colonies, retested for their ability to confer His+ growth in the cryptic initiation reporter strain, and screened for secondary phenotypes. The mutant plasmids were sequenced to identify the amino acid changes in Spt5 caused by the mutations. These changes clustered in a previously uncharacterized region of Spt5 and in the KOW 2, 3 and 5 domains. In the future, to test our hypothesis that Spt5 controls chromatin dynamics in transcribed regions, we will examine chromatin structure in our spt5 mutants.

CLONING THE RNA POLYMERASE OF THE INFLUENZA A VIRUS

Carolina Cuellar

Faculty Mentor: Rebecca M Dubois

CLONING THE RNA POLYMERASE OF THE INFLUENZA A VIRUS

CUELLAR, Carolina, Junior, Bioengineering major at the University of California, Santa Cruz Dr. Rebecca Dubois, Department of Bioengineering, graduate student mentor: Lena Meyer

The Influenza A virus, affecting the respiratory system, is responsible for a surge of illness every year known as ‘flu season’ which results in numerous deaths. The most effective treatment is prevention through a yearly vaccine. However, in the case of a pandemic, development of adequate quantities of a matching vaccine may take months. Consequently, the need for antivirals becomes critical. The viral RNA-dependent RNA polymerase is an excellent drug target for several reasons. This polymerase is very well conserved and because it is an RNA-dependent RNA polymerase, it is significantly different from human RNA polymerases so that any potential inhibitors have a very high chance of only targeting the influenza mechanism rather than the host organism. Lastly, this protein is essential in the reproduction of the virus ; therefore, halting it would halt its reproduction cycle in the host. The polymerase is composed of three proteins: PA, PB1, and PB2. The three genes encoding these three proteins are in the process of being cloned into a pEU plasmid in order to be expressed in an in vitro wheat germ protein expression system. This is done through the addition of restriction sites by touchdown-PCR, a restriction digest, and then ligation and transformation to create each individual construct. Currently, PB2 has been successfully cloned into pEU. Next steps include finishing cloning, expressing the protein in the wheat germ protein expression system and developing a small inhibitor assay to identify potential inhibitors.The polymerase will then be crystallized with the inhibitor to analyze the inhibition mechanism and better understand polymerase function as a whole

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CARPENTER LAB

Allyson Marie Capili

Faculty Mentor: Susan Carpenter

The immune response is critical for eliminating pathogens however; excess activation of this pathway can result in a variety of inflammatory-based diseases. For the past half-century, our understanding of how inflammation is regulated has been based on studying protein-coding genes, which we now know make up only ~1.5% of our genome. Recently, we have learned that the bulk of the genome produces a novel class of genes called long noncoding RNAs (lncRNAs). This is a fascinating group of genes of which there are approximately 16000 in the human genome. To date we only understand the function of approximately 1%. One of the strengths of my group is in large-scale screening methods. In this study we will focus on working on high throughput screening methods, which will involve knocking out all lncRNAs expressed in macrophages using Cas9/CRISPR technology. We believe that characterization of lncRNAs will lead to a more complete understanding of inflammatory pathways, which could help elucidate how these pathways are dysregulated in the context of human disease.

CHARACTERIZING SPLICING SENSITIVE DISEASE-CAUSING MUTATIONS IN EXON 6 OF THE FABRY DISEASE GENE GALACTOSIDASE A.

Nathan Bamidele, Erik Ho Mun Li, Savanna Sunflower Randi, Olivia Camille Willes, Mark David Gustincic

Faculty Mentor: Jeremy R Sanford

Precursor messenger RNA (pre-mRNA) splicing is a critical post-transcriptional process in eukaryotic cells. For each splicing event, the complex cellular machinery known as the spliceosome must assemble onto the mRNA and excise precisely the desired number of bases. This concerted process is regulated by cis-elements within the RNA, such as exonic splicing enhancers and silencers (ESE and ESS, respectively), and trans-elements such as RNA binding proteins. Approximately 10% of all disease-causing mutations affect consensus splice sites sequences, resulting in aberrant pre-mRNA splicing. However it is less well understood how missense and nonsense mutations within exons affect other splicing regulatory-elements. Recent studies conducted by the Sanford lab and others, suggest that around ~26% of disease causing missense and nonsense mutations within protein-coding genes, also interfere with splicing regulatory cis-elements (Sterne-Weiler et al. 2011).

In this project, we focus on characterizing the molecular impact of disease-causing mutations on pre-mRNA splicing within the galactosidase A (GLA) gene. The GLA gene encodes the lysosomal enzyme alpha-galactosidase A. Deficiencies in this enzyme result in Fabry disease, a debilitating disorder which causes kidney damage, heart attack, and stroke among other symptoms. Our previous studies predicted 26 putative splicing sensitive mutations within the GLA gene. We hypothesize that, these sites disrupt important functional elements involved in exon recognition by the splicing machinery. We modeled these mutations by cloning specific GLA exons and 100-200 bp of flanking intoning sequence into B-globin vectors. We used site-directed mutagenesis to create a panel of 16 mutations in GLA exon 6. The splicing reporters were then assayed by HEK293 cell transfections, total RNA isolation, RT-PCR, and end-point PCR using B-globin specific primers. For 11 out of 16 mutations within GLA exon 6, we observed a phenotypic gradient ranging from severe to moderate exon skipping. Three of the splicing-sensitive mutations resulted in creation of ESSs, whereas seven mutations resulted in loss of ESEs. Of the remaining five mutations that did not affect exon inclusion, three caused loss of ESS, one created an ESE and one disrupted an ESE. Collectively, these data suggest that at least 62% of disease-causing missense or nonsense mutations in GLA exon 6 have the potential to disrupt exon identity. We propose that GLA exon 6 is likely a fragile exon that is easily susceptible to loss of exon identity.

CHARACTERIZING SPLICING SENSITIVE DISEASE-CAUSING MUTATIONS IN EXON 6 OF THE FABRY DISEASE GENE, GALACTOSIDASE A.

Nathan Bamidele, Erik Ho Mun Li, Savanna Sunflower Randi, Olivia Camille Willes, Mark David Gustincic

Faculty Mentor: Jeremy R Sanford

Pre-mRNA splicing is a regulatory biological process, crucial for the correct expression of a vast array of protein coding genes within the human genome. The discovery of synonymous disease-causing mutations demonstrated that exonic sequences can contribute to disease phenotypes without affecting protein primary structure. This suggested that disease-causing mutations might affect other steps in gene expression, such as precursor messenger RNA splicing. Recent studies conducted by the Sanford lab and others, suggest that around ~26% of disease causing missense and nonsense mutations within protein-coding genes, also interfere with splicing regulatory cis-elements (Sterne-Weiler et al. 2011). In this project, we focus on characterizing the molecular impact of disease-causing mutations on pre-mRNA splicing within the galactosidase A (GLA) gene. The GLA gene encodes the lysosomal enzyme alpha-galactosidase A. Deficiencies in this enzyme result in Fabry disease, a debilitating disorder which causes kidney damage, heart attack, and stroke among other symptoms. Our previous studies predicted 26 putative splicing sensitive mutations within the GLA gene. We hypothesize that, these sites disrupt important functional elements involved in exon recognition by the splicing machinery. We modeled these mutations by cloning specific GLA exons and 100-200 bp of flanking intoning sequence into B-globin vectors. We used site directed mutagenesis to create a panel of 18 mutations in GLA exon 6. The splicing reporters were then assayed by HEK293 cell transfections, total RNA isolation, RT-PCR, and end-point PCR using B-globin specific primers. For 10 out of 16 mutations within GLA exon 6, we observed a phenotypic gradient ranging from severe to moderate exon skipping. Three of the mutations resulted in creation of exonic splicing silencers, including GATTAG, TACTAG, and TTAGAT. Six of the mutations resulted in loss of exonic splicing enhancer sequences including TCAGGA, GAATCA, TGGAAT and CAATCA. Of the remaining five mutations that did not affect exon inclusion, three caused loss of ESS, one created an ESE and one disrupted an ESE. Collectively, these data suggest that at least 62% of disease-causing missense or nonsense mutations in GLA exon 6 have the potential to disrupt exon identity. We propose that GLA exon 6 is likely a fragile exon that is easily susceptible to loss of exon identity.

CLEAVAGE OF PATHOLOGICAL PRION PROTEIN MUTANTS

Roman Elliott Reggiardo

Faculty Mentor: Glenn L Millhauser

The Prion protein (PrP) is an extracellular, GPI-anchored membrane protein capable of binding Copper(II) and Zinc(II) in vivo. Though lacking a well-defined native function, PrP is causally related to a host of neurodegenerative disorders. A subset of these disorders, classified as transmissible spongiform encephalopathies (TSEs), are well correlated to point mutations in the central region (CR) of PrP. This region is a potent modifier of PrP toxicity: deletion of its entirety (?CR) produces a fatal response. Additionally, ADAM metalloproteinases are known to cleave PrP within the CR. On a more global scale, the ?-helical C-terminal segment of PrP is proposed to regulate the activity of the unstructured, poly-basic N-terminus through an electrostatic cis interaction mediated by Cu2+. Cleavage in the CR may serve as a permanent off switch for this interaction and play an important role in regulating PrP activity. Cleavage reactions have been performed in vitro in the presence of both ADAM8 protease and recombinant PrP containing pathological mutations to the CR. Relative efficacy and changes in resulting peptides are being observed and quantified through mass spectrometry. Greater understanding of the effects these mutations have on ADAM8 cleavage of PrP will clarify native and pathological regulation of PrP.

CONTROL AND ESTIMATION OF SELF-BALANCING MINSEG ROBOT

Javier Matias Ruiz

Faculty Mentor: Dejan Milutinovic

A MinSeg is a small robot whose mechanics are similar to that of an inverted pendulum, with two wheels to drive the base to keep the upper mass upright. Its design causes the motor to apply torque to both the wheels and the body of the MinSeg. We wish to explore the dynamics of the system, in order to observe how to apply a controller to the system in order for it to balance on its own. To keep the MinSeg upright, we develop a model for its dynamic behavior. This model is represented as a set of differential equations derived using Lagrangian mechanics. These equations are solved using MATLAB to simulate the systems behavior. A linear quadratic regulator is then applied to the simulation, derived from the differential model around the desired equilibrium state. Testing this controller on the actual MinSeg device, however, produces unstable oscillatory performance. This could be due to certain parameters of the system being unknown. Data pertaining to the states of the system are collected during runtime to identify the parameters of the system using estimation techniques.

CONTROL OF CELL SIZE AND MEMBRANE GROWTH

Leonel Torres

Faculty Mentor: Doug Kellogg

Cell size control checkpoints ensure that the cell cycle only proceeds when sufficient growth has occurred. A hallmark of cancer cells is severe defects in cell size. A key question regarding size control concerns how cells measure how much growth has occurred during the cell cycle. Also, how do cells link cell cycle progression to growth? In budding yeast, cells that have reached the correct size in G1 produce cyclins to initiate cell cycle entry. However, we don't know how membrane growth occurs during G1 and how growth is linked to G1 cyclin production. To answer these questions, my research is investigating the requirements for growth during G1, and how growth affects key cell cycle regulators. By understanding cell size control mechanisms and how they go wrong in cancer, we can create novel therapeutics that specifically target cancer cells.

CONTROL OF CELL SIZE AND MEMBRANE GROWTH DURING G1 IN BUDDING YEAST

Leonel Torres

Faculty Mentor: Robert Sommer

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CURRENT AND HISTORIC DISTRIBUTION OF THE ENDEMIC SANTA CRUZ KANGAROO RAT, DIPODOMYS VENUSTUS VENUSTUS

Deanna Katherine Rhoades

Faculty Mentor: Gage H Dayton

Over the last century, the range of the endemic Santa Cruz kangaroo rat (Dipodomys venustus venustus) has severely contracted and may now be restricted to a single location: Henry Cowell State Park in Felton, California. Although records since 1900 support a range shrinkage of this kangaroo rat subspecies, few trapping surveys have been conducted in the past few decades, preventing accurate estimates of their current range. In order to further the survey effort for this subspecies, I live-trapped at three potential D. v. venustus habitats near Felton, California. My trapping survey found no kangaroo rats. This information, combined with past records and survey efforts, suggest that D. v. venustus may be extirpated from all but one remaining site, Henry Cowell State Park. The comparison of the D. v. venustus habitat of Henry Cowell State Park with surrounding sandhill habitats points to potential causes of the extirpation of D. v. venustus from these sites, such as reduced habitat size and proximity to residential development. Further trapping efforts and analysis of potential habitat may be necessary to confirm their extirpation outside of Henry Cowell State Park and suggest management practices to conserve this kangaroo rat subspecies.

DETERMINATION OF THE STRUCTURAL MECHANISM OF THE CDK4-CYCLIN D1-P27 COMPLEX

Katharine Leilani Bunch

Faculty Mentor: Seth M Rubin

Deregulation of the cell cycle results in over-proliferation, a hallmark of cancer. Cyclin-dependent kinase 4 (CDK4) is an enzyme that is intimately involved in regulation of the cell cycle. Its primary function is to phosphorylate and inactivate the retinoblastoma protein (Rb) whose role is to prevent premature transition into the DNA synthesis phase of the cell cycle1. Cyclin D1, a co-activator of CDK4, is overexpressed in many cancers and drives tumorigenesis. p27, an inhibitor of many other cyclin-dependent kinases (CDKs), is believed to act not only as an assembly factor for CDK4 and cyclin D1 but also as a regulator of the activity of the complex depending on its phosphorylation state. Pfizer has developed a small molecule inhibitor drug that has proven to selectively bind and inhibit the activity of CDK4-cyclin D1 in (HER2)- and (ER)+ breast cancer. Though this drug has high probability of progression-free survival upon initial use, the probability of progression-free survival is halved after 22 months 2 implying that cancer cells develop resistance to this therapeutic. The objective of this project is to solve the structure of the active CDK4-cyclin D1 complex using x-ray crystallography in order to elucidate the mechanism of resistance to breast cancer therapeutics.

DETERMINING THE FUNCTIONAL ROLE OF K1L1 OF TRANSCRIPTION ELONGATION FACTOR SPT5 IN S. CEREVISIAE

Jennifer Liu

Faculty Mentor: Grant Hartzog

During transcription, RNA Polymerase II requires the help of various accessory proteins. Two such proteins, Spt4 and Spt5, form a complex that associate with and regulate elongating RNA Polymerase II. The mechanisms by which these proteins act is poorly understood. Spt5 is universally conserved and essential for life, suggesting it plays a central role in gene expression. In eukaryotes, Spt5 is a large, multi-domain protein. Determining the functions and mechanism(s) of action of Spt5's many domains is essential to understanding RNA Polymerase II gene expression. The purpose of this study is to identify roles of Spt5 in the cell, specifically by investigating the role of the KOW1-Linker1 (K1L1) domain. Previous studies suggest a functional overlap between Spt4 and the positively charged patch (PCP) of K1L1 Spt5. spt5-PCP mutations show an elevated sensitivity to HU, suggesting a cell cycle defect. Spt4 has been shown to function in stabilizing chromatin structure at the kinetochore, which facilitates chromosome segregation. Thus, we hypothesize Spt5 may play a role in chromosome segregation, analogous to that of Spt4 in maintaining the integrity of centromeric chromatin structure. To test this hypothesis, we measured mitotic chromosome stability in spt5-PCP mutants, using a visual assay that allows us to determine chromosome transmission by monitoring chromosome stability and loss. These stabilities will be compared to spt4? and spt4? spt5-PCP mutant cells. This study has the potential to elucidate the function of the K1L1 domain of Spt5, testing the idea that the K1L1 mediates essential functions in vivo via a linkage with a mitotic pathway.

DEVELOPMENT OF MARKERLESS GENETIC EXCHANGE SYSTEM IN BSL-9

Isabella Luna Breen

Faculty Mentor: Chad W Saltikov

A markerless genetic exchange system for the bacterium Ectothiorhodospira sp. strain BSL-9 is being developed to investigate the photosynthetic arsenite oxidation genetic pathway. The BSL-9 genome contains a homolog of arxA, an arsenite oxidase enzyme which oxidizes As(III) to As(V). Development of a gene deletion method will enable detailed studies of the genetic mechanisms underlying the physiology and regulation of photoarsenotrophy in BSL-9.

In this study a new marker of sensitivity is being developed, one that employs the phosphoribosyl transferase gene (upp) and 5-fluorouracil (5-FU) toxicity, a toxic pyrimidine analog that inhibits growth and multiplication.The deletion of phosphoribosyl transferase should confer resistance to 5-FU. The genetic system involves the insertion of a plasmid into the BSL-9 genome to deliver a mutant allele of a gene targeted for deletion. This new plasmid will contain a gene that confers antibiotic resistance and the phosphoribosyl transferase gene, which will confer sensitivity to 5-FU in a phosphoribosyl transferase mutant background of BSL-9. When introduced into BSL-9, the mutant allele will recombine at either the homologous upstream or downstream regions of the targeted gene, providing the gene for phosphoribosyl transferase and reestablishing 5-FU sensitivity in BSL-9. In theory, a double homologous recombination event can be induced by exposing the resultant exconjugant to 5-fluorouracil, creating a deletion mutant.

The minimum inhibitory concentrations of 5-FU for BSL-9 were determined, and the transformed bacteria were exposed to this concentration of 5-fluorouracil to induce the development of a mutant. Work is underway on analyzing exconjugants for double homologous recombination and the loss of the phosphoribosyl transferase gene.

DEVELOPMENT OF A SPONGE METABOLITE DATABASE FOR THE RAPID IDENTIFICATION OF KNOWN SPONGE COMPOUNDS BY HIGH ACCURACY MASS SPECTROSCOPY

Allison Rose Cheney

Faculty Mentor: Phillip Crews

In order to find potential anti-cancer drug leads, novel cytotoxic compounds from marine sponges are investigated. Sponges that have been collected from all over the Indo-Pacific are extracted; the extracts are then screened against solid tumor cancer cell lines at the Josephine Ford Cancer Center. Any extracts that exhibit selective cytotoxicity towards cancer cell lines over normal cell lines are singled out. These extracts, which are a mixture of compounds, are separated into pure compounds using liquid chromatography (LC) and identified using mass spectrometry and NMR. An analytical method was developed that reduces redundant purification of sponge compounds by coupling LC-high accurate mass spectra with a database of known sponge compounds for the rapid identification of previously reported compounds. A Sponge Metabolite Database (SMD) was created that contains the accurate mass of all known sponge compounds. The sponge extracts with cytotoxic activity in the Crews lab repository were analyzed on the Orbitrap Velos Pro mass spectrometer. The accurate mass of all compounds present in the extracts was processed using the software MZMine2.2, and screened against the SMD to identify previously reported sponge compounds. A representative natural product was chosen to confirm that this database was accurate. By using this database, Agelasidine A (1) was readily identified by its accurate mass. The compound was purified by HPLC and the structure was confirmed using 1H-NMR. This allows the lab to prioritize the extracts that contain novel chemistry.

DO HISTIDINE RESIDUES IN THE C-TERMINAL DOMAIN OF THE PRION PROTEIN PLAY A ROLE IN A COPPER DRIVEN CIS INTERACTION?

Joseph Thomas-Micinski Kiblen

Faculty Mentor: Glenn L Millhauser

The prion protein (PrP) has been studied extensively due to its role in prion related diseases, which are often categorized as Transmissible Spongiform Encephalopathies. PrP is a 210 amino acid protein with a GPI anchored C-terminus as well as a non-structured N-terminus. The non-structured N-terminus which is capable of coordinating with multiple cationic divalent transition metals contains the octarepeat (OR) sequence PHGGGWGQ. The ability of histidines to chelate transition metals is a property exploited consistently for molecular protein extraction through a histidine-tag and IMAC chromatographic separation. There are 4 Histidines which are known to play a role in the N-terminal coordination with Cu(II), which is thought drive an interaction with the OR region in the N-Terminus of PrP to the C-terminus. Through analysis with magnetic resonance techniques, mutations which delete these histidines may provide insight into a mechanism for prion diseases.

DOMOIC ACID DETECTION IN THE MANTLE, DIGESTIVE GLAND, GILLS AND EXTRA ORGANS OF LOLIGO OPALESCENS AS A POSSIBLE TOXIN VECTOR TO PREDATORS AND HUMANS IN MONTEREY BAY CALIFORNIA.

Ariel Charise Boyer

Faculty Mentor: Raphael Kudela

Domoic acid (DA) is a neurotoxin produced by a genus of diatoms called Psuedo-Nitzschia. DA accumulates in the highest concentrations in filter-feeding organisms, like bivalve mussels. Research on soft bodied mollusks is minimal apart from Octopus vulgaris and Loligo opalescens

Loligo opalescens plays an important role in Monterey Bay's fishery and is a prey species for many predators. Past research on the presence of DA in Loligo opalescens has shown that DA accumulates at low concentrations. To further expand these results, specimens of Loligo opalescens were obtained and analyzed when Pseudo-nitzschia blooms were not occurring. DA was consistently found in the mantle, digestive gland, gills and extra organs of each specimen and concentrations varied from trace to 1.2 ppm. DA was tested in these organs to assess whether DA accumulates in soft bodied mollusks when Pseudo-nitzschia is not blooming. These results demonstrate DA accumulation in Loligo opalescens, suggesting that it is a possible toxin vector for predators and humans in Monterey Bay California. This study provides significant data on baseline concentrations and accumulation of DA in Loligo opalescens in Monterey Bay California and the potential for trophic transfer to marine predators and humans and the possible long term impacts.

EFFECTS OF SCOTCH BROOM (CYTISUS SCOPARIUS) INVADED SOIL ON DOUGLAS-FIR GERMINATION AND GROWTH

Stacy Wu

Faculty Mentor: Ingrid M. Parker

Invasive species often spread rapidly and change the biotic and abiotic environment. Invasive plants can impact soil conditions through chemical additions such as soil nitrogen enrichment and allelopathy, whereby chemicals produced by invasive species suppress native plants. Scotch broom, a nitrogen-fixing shrub that invades Douglas-fir clearcuts in the Pacific Northwest, increases soil nitrogen concentration and contains high concentrations of sparteine, a potentially allelopathic alkaloid. I hypothesize that these soil chemical impacts of Scotch broom may suppress Douglas-fir. I used a greenhouse experiment to test the effects of sparteine and nitrogen on Douglas-fir seed germination and seedling growth. I grew Douglas-fir in soils collected from Scotch broom invaded sites and uninvaded Douglas-fir forests and added nitrogen and sparteine to the uninvaded forest soils. The nitrogen and sparteine additions did not effect Douglas-fir seed germination or seedling growth. However, Douglas-fir seedlings grown in unammended Scotch broom invaded soils were smaller than seedlings grown in uninvaded forest soils. These results suggest that there may be other physical and chemical properties of Scotch broom invaded soils that suppress Douglas-fir growth.

ELECTRO-OPTICAL DETECTION AND CONTROL OF SINGLE MOLECULES USING SOLID-STATE NANOPORES

Mark Wyatt Harrington

Faculty Mentor: Holger Schmidt

The detection and analysis of single particles allows particle properties to be investigated in ways that are impossible when studying larger populations of those particles. To effectively study an individual particle, that particle must be isolated from other particles of comparable size, and immobilized in a location at which it can be effectively studied. The Applied Optics group has previously demonstrated solutions to some of these challenges using the optofluidic ARROW device. The liquid-core waveguide in the ARROW device allows for the study of biological particles in solution via fluorescence spectroscopy, and the integration of a nanopore in this device previously demonstrated the ability to detect single particles ranging from 1 micron beads to 100 base pair DNA fragments with various pore sizes.
In this study, we combine similar ARROW-integrated nanopores with a microcontroller gating mechanism, allowing the nanopore to be deactivated after a single particle travels through the pore, resulting in the isolation of single particles in an optical excitation volume for fluorescence analysis. Future integration of this system with an optical trapping method will allow for the creation of a biocompatible single particle analysis platform capable of studying particles over a wide size range.

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ETIOLOGY OF MUTAGENESIS VIA LOGISTIC REGRESSION OF RNA EXPRESSION DATA

Noah Aviel Dove

Faculty Mentor: Manel Camps

Different mutagenic processes produce unique patterns of base-substitution in DNA (mutation signatures). Using an innovative source separation algorithm, Alexandrov et al. identified upwards of 30 signatures in tumors in tumors. Based on a high frequency of frameshift mutations in repeat areas of the genome, four of these signatures are consistent with defective DNA mismatch repair: signature 6, signatures 15 and 20 (which are largely found in the same samples), and signature 26. Here we use logistic regression to link gene expression in tumors to the presence of MMR-related mutation signatures. Our goal is to validate logistic regression with gene expression in tumors as an approach to ascribe etiology to orphan signatures; we are also hoping to shed light on the mechanisms leading to different MMR-related signatures. Our approach admittedly ignores possible changes in gene expression in tumors relative to cells that first became precancerous, but our assumption is that some of those patterns could be maintained and even reinforced in tumors by virtue of contributing to tumorigenesis, producing a signal in our analysis. Using data from The Cancer Genome Atlas and from Alexandrov's signature identification work, produced a model that has high predictive accuracy (AUC ~~ 0.98) for MMR signatures 15 and 20 in stomach adenocarcinoma samples. Our logistic regression identified MLH1 and MSH4 as strong predictors among other DNA repair genes. MLH1 forms an essential part of cells' MMR pathway and is consistently downregulated in samples which are positive for the MMR signatures, consistent with a deficiency in mismatch repair. Such deficiencies are known to be associated with colon cancer. MSH4, by contrast, is consistently upregulated in signature 15 and 20 tumors. This Mut-S homolog is typically expressed only during meiosis, where it is thought to protect stabilize parental chromosomes during double-stranded break repair. While not a known oncogene, MSH4 is amplified in up 15% of samples for breast and prostate; it could also be partially complementing a MLH1 deficiency. Analysis of MMR signature 6 was also performed and yielded high AUC, but analysis of the variance and accumulation consistency of the bootstrapping results led to us discarding the results as the result of overfitting. Other analyses failed to produce sufficiently high AUCs. Our work demonstrates that logistic regression can be useful in investigating the etiology of long-term mutagenic processes, explores the limitations of such an approach, and identifies specific genes important to the etiology of MMR-associated stomach adenocarcinoma.

EXTENDED STUDY ON NIST/NVLAP ACCREDITED UNCERTAINTY MEASUREMENTS FOR OPTICAL COMPONENT CALIBRATION (OCC) LABORATORY

Raul Lara

Faculty Mentor: Michael Dine

Maintaining a level of uncertainty gives a confidence level to the diagnostics used at national labs. An extended study was done on the laboratory performance and accredited process to minimize and improve the uncertainty of spectral responsivity and optical density measurements in the radiometric field from 300 nm - 1100 nm. The laboratory used the Guide to Expression of Uncertainty Measurements (GUM) to define calibration uncertainties as a requirement of the scope of accreditation by National Voluntary Laboratory Accreditation Program (NVLAP) and National Institute Standard Technology (NIST) standards.

FINDING THEIR PATH: CHARACTERIZING THE FIRST MIGRATIONS OF WEANLING NORTHERN ELEPHANT SEALS, MIROUNGA ANGUSTIROSTRIS

Kelly Hanalei Shrader

Faculty Mentor: Patrick William Robinson

Northern elephant seals (Mirounga angustirotris) undertake expansive migrations between pelagic foraging grounds and coastal breeding grounds each year. While adult northern elephant seal migration and foraging behaviors have been well studied, little is known about the first migration and associated foraging behaviors of weanling northern elephant seals. Mother elephant seals wean their pups after four weeks of lactation then head out to sea to feed. Consequently, weanling elephant seals depart the breeding ground for the first time alone and with no known paths or experienced seals to follow. In this study, satellite tracking data from 10 weanling elephant seals and 88 adult elephant seals were analyzed to characterize weanling migration trajectories and determine any differences in transit speed across age class. We found that weanlings exhibited northbound migrations with an average latitude of 49ºN reached. Surviving weanlings reached higher latitudes than non-survivors (52ºN to 43ºN, respectively), yet this difference was not significant (p=0.0828). The average weanling transit speed was 1.377 ± 0.172 meters second-1, compared to the average adult transit speed of 1.815 ± 0.434 meters second-1. While weanling speeds were slower than those of adults, this does not represent a significant difference (p>0.05). Weanlings migrated at speeds between 1.289 and 1.509 meters second-1, which could be indicative of possible foraging behavior. More information is needed to corroborate the preliminary findings of this study, as these results have important implications to the ontogeny of northern elephant seals.

FEATHERS TO QUANTIFY LEAD EXPOSURE IN GOLDEN EAGLES

Christian Anthony Triana

Faculty Mentor: Myra E Finkelstein

Lead is highly toxic and scavenging animals, such as golden eagles, are exposed to lead when they feed on carcasses of animals shot with lead-based ammunition. Our research group has shown that sequential feather samples can be used to reconstruct a California condor’s lead exposure history during the period of feather growth and that condors have higher and more frequent lead exposures than blood monitoring shows. Thus, our research goal was to validate the use of eagle feathers to construct an eagle’s lead exposure history to better understand the frequency and magnitude of lead exposure in free-flying eagles. We analyzed sequential samples from a feather collected from six golden eagles found dead in California. All feather processing and analysis was conducted using established trace metal clean techniques under HEPA filtered air laboratory conditions and feather lead concentration were measured using inductively-coupled plasma mass spectrometry. We show that eagle feathers can illustrate an eagle’s lead exposure history over the timeframe of feather growth. Using a feather:blood conversion factor we estimated for California condors, we found that two of the eagles were exposed to lead concentrations that warrant medical treatment in condors (~35 ?g/dL), and one of these birds had lead levels considered lethal (>100 ?g/dL). The feather lead exposure profile also revealed that all the golden eagles analyzed were exposed to lead before they started growing their feathers. Eagles typically start growing their feathers in the spring and are believed to rely more heavily on carcasses in the winter months. Our results suggest that golden eagles are more likely to be lead exposed during the winter months and supports the likelihood that eagles are lead exposed when scavenging on carcasses that have been shot with lead-based ammunition.

FLUCTUATIONS IN WEDDELL SEAL DIVE DEPTH IN ASSOCIATION WITH SEASONAL CHANGES IN THE ANTARCTIC PHOTOPERIOD

Shannon Rose Bent

Faculty Mentor: Patrick William Robinson

Temporal variability in dive depth of Weddell seals (Leptonychotes weddellii) can indicate changes in the vertical distribution of prey in the water column. In Antarctica, the daily photoperiod changes between seasons, which has been shown to affect the diel vertical migration of prey. However, there has been little research looking at how Weddell seal diving metrics change in response. In this study, we used a full year of dive data collected from Time-Depth recorder tags on 8 Weddell seals near McMurdo Station to show that variations in the photoperiod are associated with changes in mean hourly dive depths across seasons. There were significant differences in mean hourly dive depth between each month (Jan-Dec) ($p<0.05$) and between noon and midnight in March ($p=0.0043$) and April ($p=0.0008$). From these results, we concluded that seals show diurnal diving patterns and have a greater range in dive depth during the austral spring (Mar-May) and fall (Aug-Oct) when there are changes in the daily photoperiod. During the austral winter (Jun-Jul) and summer (Nov-Feb), seals exhibit a low range in dive depth and no diurnal diving patterns. Future studies can be done to test for other factors that could affect daily and seasonal changes in dive depth. This study is one of the first to look at year-round diving behavior of Weddell seals in association with the variable Antarctic photoperiod. Knowledge of how the seals respond to a changing environment can give us an indication as to how they may respond to climate change in the future.

G-PROTEIN INDEPENDENT SIGNALING OF G-PROTEIN-COUPLED RECEPTORS: EXPLORING THE MELANOCORTIN SYSTEM

Ashley Tess Wong

Faculty Mentor: Glenn L Millhauser

The melanocortin signaling system is made up of five class A G-protein coupled receptors (GPCRs) that are responsible for a variety of physiological functions. The melanocortin 4 receptor (MC4R) acts as a key regulator of energy homeostasis by responding to its endogenous ligands, ?-melanocyte stimulating hormone (?-MSH) and agouti-related protein (AgRP), through the cAMP transduction pathway. This stimulation and suppression of cAMP, respectively, follow canonical GPCR signaling mechanisms. However, new research shows that melanocortin signaling cannot be explained through classical agonist/antagonist modulation of MC4R through the G?S pathway. Previous collaborative work by the Millhauser and Cone Labs has shown that there are novel accessory proteins involved in the regulation of MC4R through AgRP and ?-MSH. Namely, Kir7.1 is an inwardly rectifying potassium channel that is modulated by melanocortin ligands through MC4R, which occurs independently of G-proteins. However, the specific mechanism of this novel interaction is not understood and remains largely uncharacterized. The molecular basis of this G-protein independent interaction will be studied using cross-linking and LC-MS/MS, and will help to redefine the melanocortin signaling paradigm. Understanding the melanocortin signaling system and its accessory proteins will aid in the effort to find potent therapeutic treatments for metabolic disease and obesity.

GIRLS IN ENGINEERING DRAW A COMPUTER SCIENTIST

Huimee Valeria Sanchez, Sabrina Chengyu Tsui

Faculty Mentor: Linda L Werner

There is a large gender disparity in computing: women are underrepresented. By exposing girls to computing activities in a summer day camp, and using near-peers as teachers, we found differences in perceptions the girls held about computer scientists. We will describe the day camp program, the participants, and the activity we used to investigate the girls' perceptions of computer scientists. In order to see how the stereotypes of a computer scientist and our day camp have influenced the girls, we had them do the 'Draw a Computer Scientist' activity. The only instruction given to the participants was to draw what they thought a computer scientist looked like. We categorized many characteristics of all of the drawings in order to quantify the characteristics of each drawing. Based on our results, we believe that exposing girls to other female engineers and engaging them in age-appropriate engineering activities changed their perspectives on what a computer scientist looks like.

HIGH-THROUGHPUT FUNCTIONAL SCREEN OF SKIPPED EXONS CONTRIBUTING TO LUNG CANCER DEVELOPMENT

Maximillian Gabriel Marin

Faculty Mentor: Angela Brooks

RNA splicing is the process by which intronic regions are removed from pre-mRNA to produce mature mRNA. Alternative splicing serves as a mechanism for greater proteome and transcriptome diversity, as multiple distinct mRNA transcripts can be yielded from the same gene locus. Dysregulation of alternative splicing is understood to contribute to the development of human cancers, but identifying specific splicing events contributing to tumorigenesis has been a major challenge for researchers. Previous studies have identified and characterized an alternative splicing event in the MET proto-oncogene capable of oncogene activation. To better understand the potential of aberrant splicing to drive tumorigenesis, we are developing a high-throughput screen to assay the oncogenic potential of exon skipping events across the human genome. Skipping of candidate exons will be induced using CRISPR-Cas9 gene editing technology in primary lung cell lines, and then in vitro and in vivo functional assays will be used to measure the oncogenic potential of each exon skipping event. Through a computational analysis of DNA and RNA sequencing data of 495 lung adenocarcinoma patients, 824 putative oncogenic exon skipping events were selected as screen candidates. Candidate exon skipping events were selected based on an association with characterized splicing factor mutations, somatic splice site alterations, or an enrichment in driver negative patients. Candidate exon skipping events of highest interest were found in genes present in the Ras-Raf pathway, a frequently altered pathway in lung cancer. Identifying aberrant splicing events that are key to tumor development has the potential to lead to new therapeutic options for patients.

HOLOCENE EXPORT PRODUCTIVITY FROM BARITE ACCUMULATION IN THE EASTERN EQUATORIAL PACIFIC

Seth Mcewen Williams

Faculty Mentor: Adina Paytan

Export productivity (the fraction of total primary production exported to the deep ocean) in the Eastern Equatorial Pacific is an important component of the global carbon cycle, and is sensitive to climatic variability. Climatically driven changes in ocean circulation and nutrient transport to the area on Glacial-Interglacial time scales have been suggested as t the cause for these fluctuations. Pelagic barite ($BaSO_4$) is formed in subsurface microenvironments of the ocean by microbes that remineralize sinking organic matter. Therefore, barite accumulation rates in the sediment serve as a direct proxy of oceanic export productivity. Three sediment cores along a transect across the equator at 140°W (2°N, 0°, and 2°S) were sampled in 1cm increments for approximately 25cm down core and processed by a sequential leaching procedure to remove all non-barite material. The barite was then weighed to determine the barite weight percent compared to the original sediment mass. Barite weight percent, and therefore export productivity, has significantly increased in the two southernmost cores over the last 15,000 years. This increase is likely driven by accelerated upwelling, and/or changes in ocean circulation. The record is in alignment with broad trends previously seen at lower resolution over earlier glacial-interglacial cycles. Amid a rapidly changing climate, it is becoming increasingly important to better constrain the response and impact of ocean export productivity on the carbon cycle.

HOME RANGE TRENDS AMONG THE PUMAS OF THE SANTA CRUZ MOUNTAINS

Teng Keng Houa Moua Vang

Faculty Mentor: Christopher C Wilmers

What relationship exists between home range size and age? I hypothesized that as adult male pumas (Puma concolor) aged, their home ranges would increase significantly. The home ranges of adult male pumas in the Santa Cruz Mountains were modeled using location data obtained from GPS radio collars. The home ranges of all pumas were estimated using the local convex hull method at the 30%, 50%, 90%, and 95% contour. Using linear regression, only one puma was found to have significantly increasing home ranges ($p < .05$). Two pumas had significantly increasing home ranges only at the 50% home range ($p < .05$). The remaining pumas were not found to have home ranges increasing or decreasing significantly ($p > .05$). While my results were mixed, further analysis is needed to determine if a relationship exists among age and home range size in pumas.

IDENTIFICATION OF INDIVIDUAL SOURCES OF GENETIC VARIATION IN HIV USING A BLIND SOURCE SEPARATION ANALYSIS OF GENOMIC SEQUENCES

Jimmy Chan

Faculty Mentor: Manel Camps

Genetic variation is vital for the maintenance of HIV infections, facilitating adaptation to the immune response of the host or to exposure to antiretroviral drugs. Mutations in HIV can be caused by diverse mechanisms, including replication errors through the viral reverse transcriptase enzyme, host DNA polymerases or host RNA polymerase and also a variety of genotoxic host defense factors. The relative contribution of each of these sources of genomic variation is unknown. Here we use the unique pattern of mutations created by individual sources of mutation (mutation signatures) to identify them. HIV genome sequences, however, include the effects of selection and of genetic drift in its output, increasing the noise in our analysis.

To address these challenges, I will first remove the effects of selection by exclusively using premature stop codon-causing mutations (PSCMs) in my analysis. Given that PSCMs are deleterious, they must have occurred pre-selection and they must also be recent. Once we have identified a large number of PSCMs, we will perform blind source separation (BSS), which uses an unsupervised clustering algorithm to identify mutational patterns corresponding to distinct source of mutagenesis. Operationally, this project has three components: (1) bioinformatic handling of 454 HIV genome sequencing reads, (2) large-scale computations involving genome sequence manipulation, and (3) using pre-existing statistical packages to perform BSS. Successful identification of mutation signatures will provide new insights into the life cycle of the virus in vivo and into the impact of the genotoxic response of the host.

IDENTIFYING TYPE III SECRETION SYSTEM VIRULENCE BLOCKERS

Yongtong Lao

Faculty Mentor: Scott Lokey

Gram-negative pathogens cause millions of illnesses and death worldwide each year. Treatment of infections with antibiotics, which target all bacteria non-specifically, often gives rise to resistance and destroys healthy microbiota. Emergence of antibiotic resistance bacteria is the current issue of global public health because these bacteria cause long-lasting and epidemic infection. One promising strategy to combat the antibiotic resistant bacteria is virulence blockers, which are compounds that suppress pathogenicity without killing or inhibiting bacterial growth. Type III secretion system (T3SS), a needle-like appendage that bacteria use to inject effector proteins to the host cells to suppress host defense is an important virulence factor target for drug development. T3SS is required for virulence in dozens of Gram-negative bacteria pathogens but largely absent in nonpathogenic bacteria. We identified derivative of the natural cyclic peptide Phepropeptin that inhibit T3SS in both Yersinia and Pseudomonas through an innate immune-based high throughput screen. To further optimize the efficacy, we synthesized new derivatives with improved potency. The best compound from this series inhibits up to 90% of toxin excretion at 60?M. These peptides did not inhibit bacterial growth and did not target flagellum, a motility system structurally similar to T3SS, indicating a specific block on the T3SS. Further derivatives of Phepropeptin may lead to promising virulence blockers of several human pathogens.

IDENTIFYING NEW SUPPRESSORS OF U2 SNRNA COLD SENSITIVE MUTATIONS

Naomi Ghebrehiwet Tesfuzigta

Faculty Mentor: Manuel Ares

The spliceosome is a complex made up of more than 50 proteins and 5 small RNAs that binds to introns in eukaryotes and removes them to create coding sequences for translation. CUS1 is a gene identified to be an essential splicing protein for U2 snRNP addition in the spliceosome. It was identified to be cold sensitive for growth due to a mutation in the stem loop IIa. However, a second mutation in CUS1 was found to suppress the cold sensitive growth defect. This project focuses on identifying new suppressors of U2 snRNA cold sensitive mutations in the region of CUS1 near where the original suppressor is located. In order to identify new suppressors of U2 snRNA cold sensitive mutations CRISPR/Cas9 technology will be used used create different mutants of CUS1. The identified suppressors will be sequenced and mapped onto the structure of CUS1 in the spliceosome. These newly identified suppressors will also help to understand how the CUS1 protein functions with U2 snRNA during splicing. The project will help to better understand how U2 is positioned for binding to the intron, which a process that is often altered in lymphocytic leukemia and some cancers.

INVESTIGATING INTRONER ELEMENT TRANSPOSITION IN S. CEREVISIAE

Karla Gissel Martinez Nevarez

Faculty Mentor: Manuel Ares

While there is a lot of knowledge regarding how introns are spliced out of the eukaryotic genome, very little is known concerning where introns came from or how they are inserted into the genome. Recent discoveries have proposed mechanisms for intron transposition and have even gone as far as to suggest that they have successfully observed spliceosomal intronogenesis. While studying a strain of Micromonas pusilla, researchers came across a peculiar phenomenon where they observed that the genome of this strain of algae contained many repeating, identical sequences. The uniformity of the sequence throughout the M. pusilla genome suggested that these elements have been spliced back into the genome through some unknown mechanism. Based on these observations, the efforts of this project have been focused on investigating the mechanism behind intron transposition and the role that introner elements may play in that mechanism. More specifically, the project aims to tackle the role of introner elements in the intron transposition mechanism, if there is one. This investigation is being conducted by inducing mutations to the introner elements with the end goal of finding a mutation that strengthens the ability of the introner element to be spliced. These mutations are being cataloged and will have their effect on splicing efficiency studied through the means of copper resistance and splicing reactions. Strengthening the introner element's ability to be spliced will increase the odds that an introner transposition event will be observed. Early worked has indicated the introner elements can be spliced in Saccharomyces cerevisiae.

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INVESTIGATING SATB2'S ROLE IN THE DEVELOPMENT OF LATER-BORN CORTICAL PROJECTION NEURONS

Casey Christina Stockel, Sonja Lorean Plasil

Faculty Mentor: Bin Chen

The mammalian cerebral cortex is essential for our most complex sensory, motor and behavioral experiences. Within the developing neocortex, proper neuronal migration and morphology is crucial for overall cognitive function. Special AT-rich sequence-binding protein 2 (satb2) is a DNA binding protein required for the development of callosal neuron identity, and recently has been shown to be involved in subcerebral axon development. Haploinsufficiency of SATB2 in human patients leads to severe intellectual disability, speech impairment, and abnormal cleft development. Besides regulating cortical neuron identity, the function of Satb2 in regulating cortical neuron migration and differentiation remains unknown. The overall goal of this project is to validate that Satb2 regulates soma spacing and upper-layer neuronal migration in the cerebral cortex

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INVESTIGATING IF TARGETED CLEAVAGE AT SPECIFIC POSITIONS RELATIVE TO SPLICING SITES LEADS TO UNIQUE PHENOTYPES IN CANCER EVOLUTION

Dominic John Schenone

Faculty Mentor: Angela Brooks

Alternative splicing is a widespread process contributing to structural transcript variation and proteome diversity. Aberrant transcripts contribute to essential phenotypes associated with cancer and tumor development. Data mining and analysis was done in order to determine if targeted cleavage or mutations generated at specific positions relative to splicing events relate to the presence of specific phenotypes in cancer evolution. Previously published data from a genome-wide CRISPR screen in mice used a genome-scale library with 67,405 single-guide RNAs(sgRNAs) to identify tumor-suppressor genes. This project focused on the annotation and calculation of each of these sgRNAs positions relative to splicing sites throughout the mm10 mouse genome. Each of these sgRNAs was accompanied by normalized counts detailing the presence of each sgRNA after plasmid creation, initial lentiviral infection, and early and late tumor phases. From the initial 67,405 sgRNAs, 2897 were within the cleavage and mutation range of either the 3p or 5p ends of a splicing site. The majority of these sgRNAs were at the 5p-2 and 5p-3 positions, with many of the 5p-2 having enrichment at the early and late tumor stages, potentially linking these positions to enrichment. Further in-depth analysis will be done to determine if there is a clear relationship between the 5p-2 position and enrichment.

INVESTIGATING THE ROLE OF CLOCK EXON 19 IN REGULATING THE CIRCADIAN TRANSCRIPTION FACTOR COMPLEX CLOCK:BMAL1 ACTIVITY

Ivette Perez

Faculty Mentor: Carrie L. Partch

Most living organisms are governed by an internal molecular clock that ensures temporal homeostasis throughout the ~24-hour solar day. Within the suprachiasmatic nucleus (SCN) of the hypothalamus exists a circadian transcription factor complex known as CLOCK:BMAL1, which drives the transcription of the core-clock genes known as Cry and Per. In turn, the transcriptional activity of the CLOCK:BMAL1 is negatively regulated by PER and CRY proteins to complete the feedback loop that makes up the circadian clock. One other negative regulator of interest is Clock-Interacting Protein Circadian (CIPC). CIPC inhibits the CLOCK:BMAL1 transcriptional activity by binding to CLOCK Exon 19, a 51 amino acid region of CLOCK. Clock ?19 is a mouse mutant allele characterized by the deletion of Exon 19 and it is known to greatly deplete the production of circadian rhythms. Through size exclusion chromatography, we were able to determine that CIPC and CLOCK Exon 19 form a stable complex. Using x-ray crystallography, we aim to solve the structure of the CLOCK Exon 19-CIPC complex, which will help us gain mechanistic insight into the functional role of CLOCK Exon 19 in circadian rhythms.

INVESTIGATING THE EFFECTS OF STROMAL ANDROGEN RECEPTOR ON PROSTATE CANCER PROGRESSION.

Joshua Stefanson

Faculty Mentor: Zhu Wang

Stromal androgen receptor (AR) plays an important role in both prostate development and prostate cancer. Although the function of stromal AR during development is widely known, its role in prostate cancer progression is unclear and highly controversial. In order to solve this problem, inducible mouse models were used to conditionally knockout stromal AR in adulthood to mimic a homogenous microenvironment in which prostate cancer disease ordinarily advances in. Using an inducible smooth muscle cell-specific Cre-recombinase mouse line, stromal AR was conditionally knocked out in adulthood. Our preliminary results suggest that this Cre-driver is extremely efficient. In addition, the deletion of stromal AR leads may lead to increased proliferation. Thus, we can inquire that stromal AR may play are a role as a growth inhibitory factor during adulthood in these conditions.

INVESTIGATING THE INTERACTIONS BETWEEN KRAB-ZINC FINGERS AND TRANSPOSABLE ELEMENTS

Joshua Shueng Gu

Faculty Mentor: David Haussler

KRAB Zinc Fingers (KZNFs) are a large family of regulatory proteins that have evolved to battle against transposable elements (TEs) and protect the genome. However, little is known about the current KZNF-TE interactions. In my thesis project, I investigated the interactions between KRAB-Zinc fingers (KZNFs) and transposable elements. Throughout evolution, different KZNFs have emerged to battle invading TEs, leading to primate specific KZNF-TE interactions. Even though chimpanzee, the closest relative to a human, have similar protein encoding genes, they have different TE insertions. I hypothesize that KZNF-TE interactions cause species specific differences.

In order to determine which KZNFs interact with which TEs, I cloned a library of 146 KZNFs in order to determine their activities in stable TE cell lines. The KZNFs were cloned into a FLAG tagged lentiviral construct before being introduced to 293FT human cells using a lentivirus packaging system. The resulting lentivirus are being used to infect mESC lines engineered with a single instance of a primate-specific TE reporter. My work establishes a powerful platform to study how KZNF-TE interactions have influenced human-specific biology.

INVESTIGATION OF THE INFLUENCE OF MICROBIOME ON DAPHNIA MAGNA MERCURY TOLERANCE

Peter Chanseyha

Faculty Mentor: Marilou Sison-Mangus

Mercury pollution is a global concern and can impacts human and ecosystem health. Mercury toxicity can cause damage to the nervous system and eventually lead to death in human and aquatic animals. We recently isolated a clone of Daphnia magna from Yolo-Bypass, California (hereafter referred as CAY) where elevated mercury concentration has been reported. D. magna has been used as a model organism in ecotoxicology, making this organism an ideal model to investigate host responses to environmental stresses, including mercury toxicity. While there are limited studies reporting host responses to mercury toxicity in Daphnia, the roles of microbiome in influencing host's responses are unknown. Here, we characterize host responses under mercury stress in D. magna CAY and the Iinb1 clone isolated from Germany, and report differences in terms of survival and fecundity between the two Daphnia clone. We also isolated microbiota from D. magna CAY and Iinb1, and characterize antibiotic resistance, mercury tolerance, as well as identification of the presence of mercury biotransformation genes.

LEAF EXTRACT EFFECTS ON CULTIVABLE BACTERIA

Sophia Andrea Mahoney

Faculty Mentor: Nader Pourmand

Microbes have numerous applications for the production of valuable commercial products and in carrying out chemical transformations. One of the most vital applications of bacteria and other microorganisms is the production of antibiotics that help treat many bacterial infections. Antibiotics have been difficult to obtain because it is approximated that only one percent of microorganisms have been cultivated in labs due to the diverse conditions and unique resources present in every habitat. Most currently used antibiotics have come from soil microbes because of the many nutrients and resources that are provided in these environments due to the decaying matter around it and the symbiotic relationships often formed between the bacteria and the plant's rhizosphere. The most effective way to grow microbes is to mimic the conditions and resources of the environment from which the microbe was native to.

In this study, the conditions of soil environments was recreated to try to supplement the growth of more bacteria by using plant-specific leaf extract that would normally be found decaying around the plant. Rhizosphere soil and leaf extract were obtained from two plants, Sword Fern (Polystichum munitum) and Wavyleaf Silktassel (Garrya elliptica) to compare the diversity and quantity of colony forming units on soil plated with and without respective leaf extract. The composition of the leaf extract was analyzed using HPLC to determine the components that supplement the growth of the microbes.

MAPPING OF SENSITIVE SITES IN DROSOPHILA MELANOGASTER USING CONSTRUCTED INVERSION BREAKPOINT ANALYSIS

Maria Victoria Serrano

Faculty Mentor: Russell Corbett-Detig

The Drosophila melanogaster genome boasts upwards of 500 reported naturally occurring chromosomal inversions. As in other taxa, these inversions, particularly those spanning larger sections of the genome, act to suppress local recombination in heterozygotes, with ever larger inversions acting to suppress recombination in ever larger regions. This trend is not universal, however, because inversions with breakpoints near so called "sensitive sites" appear to extend their suppressive effect beyond what would be predicted by comparison to non-sensitive site inversions. These sensitive sites are not well characterised, and our aim is to map them by measuring the resultant recombination rates when we manually create pericentric inversions spanning chromosome 2, first broadly throughout the chromosome and then with fine mapping in the vicinity of detected sensitive sites. Recombination will be confirmed via cytology and phenotyping, as successful inversion will, upon heat shock treatment, reconstruct the mini-white gene. Once successful inversion has been confirmed, recombination rates will be assessed via progeny mortality. This research will further elucidate a long known but little investigated feature of the D. melanogaster genome.

MARINE MAMMAL TAPHONOMY: OBSERVATIONS AT THE AñO NUEVO BREEDING COLONY OF THE NORTHERN ELEPHANT SEAL (MIROUNGA ANGUSTIROSTRIS)

Meghan K Yap-Chiongco

Faculty Mentor: Patrick William Robinson

Taphonomy is an important field in paleoecology, linking the processes between the death and the burial of an organism. Research in this field uses extant species to study the degradation process to make inferences about how an organism enters the fossil record. The taphonomic processes affecting marine mammal decomposition, however, have remained relatively unstudied. The beaches of Año Nuevo State Park provide a dynamic environment in which to study these processes due to the presence of a Northern elephant seal (Mirounga angustirostris) breeding colony. Here, the effects that species composition, behavior, and environment have on the locality and abundance of bone assemblages is analyzed through asking the following questions: first, does bone assemblage reflect the diversity and species composition of the living fauna at Año Nuevo? Second, what is the distribution of the bones and vertebrate remains? And lastly, what is the effect of the colony and shoreline environment on bone assemblages? Using direct observation of the superficial bone record at Año Nuevo, 410 bones and 33 carcasses were found along Año Point. Most elements were from Northern elephant seal pups, reflecting the species composition of Año Nuevo and the high mortality rates of pups during the breeding season. This research is one of the first to understand how marine mammals enter the fossil record, and how representative those bones are of the living fauna.

MODELING POWER ELECTRONIC CIRCUITS WITH COMPUTER SIMULATION SOFTWARE FOR RENEWABLE ENERGY SYSTEMS

Carlo Martin Figueroa

Faculty Mentor: Joel Kubby

Renewable energies are energy sources that are replaced on a regular bases. Examples of these energy sources include wind, solar, geothermal, and hydro power. There are incentives such as tax credits and rebates for the use of these energy sources. In addition, a number of states have plans and goals to readily utilize them. For instance, California has the Renewables Portfolio Standard(RPS) that states by 2020, 33% of electricity must sales come from renewable sources. Technology has been developed to harness these energy sources. The most well known are wind turbines that harness wind and photovoltaics (PV) which uses solar radiation. To make use of these energy sources, power electronic circuits must be used. These type of circuits convert DC (direct current) to AC (alternating current) and vice versa. They can also increase or decrease AC and DC voltages. Using circuit simulation software, a mock renewable energy system was made using mostly analog components. Starting with an DC source, an inverter was used to convert it to AC. This is due to renewable energy technology producing a DC voltage with the renewable source. The DC then must be converted to AC to be usable. Last, a circuit was developed to either increase or decrease the initial DC in case it proved to be too much or too little. This is to prevent blackouts and protect hypothetical infrastructure from being damaged if too much power is produced. The simulation proved to be successful, but a physical model must be built to test viability.

MOLECULAR MECHANISMS REGULATING EXOPOLYSACCHARIDE PRODUCTION IN VIBRIO CHOLERAE

Elise Rose Brown

Faculty Mentor: Seth M Rubin

Vibrio cholerae(VC) is a species of bacteria responsible for development of a diarrheal disease known as cholera. The ability of VC to sustain itself in the human host long enough to infect the host is a result of the pathogen's ability to form a biofilm. Biofilms are surface- attached microbial communities composed of microorganisms and an extracellular matrix composed mainly of macromolecules. The major component of the VC biofilm matrix, accounting for about 50% of its composition, is vibrio polysaccharide(VPS), a carbohydrate synthesized inside the cell and secreted to the extracellular matrix. The putative tyrosine kinase VPSO was found to be an important protein in the pathway for synthesis of VPS. Genetic studies have shown that a knockout of VPSO inhibits formation of the biofilm. The goal is to identify the role of VPSO in the VPS synthesis pathway through determination of its structure and interactions with other identified VPS proteins and second messenger molecules. We hypothesize that interactions between VPSO and other synthesis proteins are inhibited in its autophosphorylated state and that its activation stimulates VPS synthesis. To date, we have expressed and purified VPSO from E.coli, evaluated some kinase activity and tested interactions with VPSU, the predicted phosphotyrosine phosphatase identified as part of the VPS gene cluster. Elucidation of how phosphorylation state affects VPSO activity will help give insight into the VPS synthesis pathway for therapeutic targeting against VC.

MORPHOLOGY AND EVOLUTION OF SUBLIMATION PITS ON PLUTO

Nadim Abu-Hashmeh

Faculty Mentor: Francis Nimmo

Pluto's Sputnik Planitia region hosts a geologically young surface of nitrogen ice that exhibits striking pitted terrain. These pits are most likely formed by sublimation due to incident sunlight (similar to the southern polar cap of Mars); however, their evolution over time has resulted in unique morphological characteristics. Motivated by this, we used the high-resolution mosaic strips captured by New Horizons' Long Range Reconnaissance Imager (LORRI) to map sublimation pits in the southernmost region of Sputnik Planitia. Statistical data shows pit orientations appearing North-South dominant; their morphology also indicates extensional evolution along the major axis caused by further sublimation and contact-coalescence processes. Qualitative analysis of the region yielded clues for an evolutionary path for individual pits that coalesce into each other and exhibit an elongated end-stage. Additionally, densely-pitted regions generally appear to correlate with regions containing longer pits, implying that coalescence may be an important process for elongation. We also model the evolution geometry through competing effects of diffusion (viscous relaxation) and retreat (sublimation). The model demonstrates single-pit and coalescing-pit evolutions that influence overall length, as well as a potential ability for the pit to move in space while evolving.

NANOCELL: SIMPLE NANOPORE SENSOR WITH SMARTPHONE INTERFACE

Alexander Phillip Martin-Ginnold

Faculty Mentor: Kevin Karplus

Solid-state nanopores and accompanying biochemistry can be used as a versatile sensor capable of detecting genetic diseases or mutations, viruses, proteins, enzymes, or any number of other molecules found in biolog- ical samples. Solid-state nanopore technology is still in its youth, but its versatility and stability paints a promising picture for its use as a next generation biosensor. Original methods for studying data from a solid-state nanopore were incredibly costly, using expensive amplifiers built for studies on ion flow in neurons. Recently, cheaper amplifier methods have been developed, but what they lost in price they gained in complexity, adding on board computing power.

In this project, I produced a device that reduced cost and complexity over current nanopore sensing methods by taking advantage of standard features of smartphones. This cost reduction makes nanopore sensing much more accessible, requiring only a sub-20 dollar device and a smartphone.

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OBSERVATIONS OF TIDALLY INDUCED SEISMICITY AT THE GROUNDING ZONE OF THE WHILLANS ICE PLAIN

Tyler Grant Paladino

Faculty Mentor: Susan Y Schwartz

West Antarctica’s Whillans Ice plain is home to many interesting seismological as well as glacial phenomena. The Whillans Ice Plain is part of the greater Whillans Ice Stream, a fast-moving ice sheet that, like other Antarctic ice streams, help to drain ice from the south polar cap and into the greater hydrologic cycle. As such, it is important to understand the mechanics behind these ice sheets. Previous studies of the area noticed a large asperity, or “sticky spot" near the center of the plain, which was found to be the cause of large double couple style moment magnitude 7 seismic events. These events are tidally modulated, occurring at both high tide and low tide. Researchers also found an area near the grounding zone of the Whillans ice plain and the Ross ice shelf, which was previously believed to be another sticky spot where seismic energy could nucleate. Here, we will argue that this second sticky spot is uncoupled from the main area, while still being tidally modulated. By utilizing beamforming techniques as well as Rayleigh-Love wave analysis, it was discovered that this area is seismically very complicated, with possible seismic source mechanisms that include crevassing and double couple movement, as well as a combination of both. After further analysis, double couple motion was ruled out, and basal crevassing is now the most likely mechanism. That being said, Further seismic and glaciological research is necessary to better understand this area and verify the mechanism behind these events.

ORGANIC CARBON SOURCING THROUGH THE MID-LATE HOLOCENE IN A MANGROVE DOMINATED LAGOON

Christopher James Vigil

Faculty Mentor: Kyle Houston Broach

Tropical mangrove ecosystems are important contributors to the global carbon cycle with coastal habitats accounting for 14% of carbon sequestration by the world's oceans. In equatorial regions the standing biomass of mangrove forests are often comparable to tropical rainforests. Furthermore, mangrove forests provide essential resources such as nursey grounds for wildlife, depocenters for sediment and carbon, and provide some degree of protection from coastal erosion. Anthropogenic forces are responsible for the disappearance of approximately 50% of global mangrove forests over the past 50 years. Understanding how these ecosystems vary through the long-term is essential to predict how they will respond to future climate shifts and how that response will impact the global carbon budget. We use carbon isotopes to trace sources to the sedimentary organic matter pool in Celestun lagoon in the Yucatan Peninsula, Mexico, in order to determine the dominant vegetation source (mangrove forests, seagrass beds, and particulate matter) and how they may have changed over the last 5,000 years. Downcore analysis of ?^13 C near upper lagoon revealed a range of values between -24.7 & -21.5 with an average value of -23.73 and a strong trend toward positive values at around 90cm in depth. Surface material sampled near the middle lagoon ranges from -23.50 to -21.10 with an average of -22.75. We interpret these results as mixing between vegetation endmembers with a dominant mangrove signal and an infiltration of seagrass both downcore and trending N-S along the lagoon. High resolution sediment cores sampled near the upper, middle, and lower segments of Celestun lagoon may provide insight into natural variability in organic matter sources within the habitat and long-term change in the carbon sequestration budget of this mangrove site.

PHOSPHORYLATION OF VPSU IN VIBRIO CHOLERA

Jacqueline Osorio

Faculty Mentor: Seth M Rubin

Vibrio Cholera is a pathogenic bacteria that causes the disease cholera. It has the ability to form biofilm matrices that allow it to survive in natural ecosystems and in the host. If we understand how these biofilms are formed, we may be able to inhibit the process, creating antibacterial surfaces and drugs. The protein phosphatase VPSU is implicated in the signaling pathway that results in production of the biofilm matrix polysaccharide. Understanding the structure and activity of this protein is the first step towards understanding its role in the signaling pathway. Phosphate assays, with p-nitrophenyl phosphate as a substrate, activity were measured to help characterize the enzyme activity.

POROUS CARBON FROM REDWOOD BARK AS AN EFFECTIVE CATALYST FOR ORR

Forrest Matthew Nichols

Faculty Mentor: Shaowei Chen

Thermal treatment of redwood tree bark (RB) yields porous carbons with apparent electrocatalytic activity towards the oxygen reduction reaction (ORR), a reaction that has been recognized as a major bottleneck limiting fuel cell performance. Various experimental parameters (pyrolysis temperature, activating agents, additives) have been controlled for a systematic manipulation of the carbon structures. RB, KOH, and urea mixed at a 1:1:1 weight ratio and heated to 900 ?C for 3 hours exhibits the highest catalytic activity of all tested samples. This facile chemical treatment method provides a detailed structural understanding of the catalytic origin of carbon based electrocatalysts, and provides a framework for their optimization, allowing for their advancement toward commercial applications.

PRESENCE AND PREFERED THERMAL RANGE OF CHYTRID FUNGUS PATHOGENS IN UCSC'S FOREST ECOLOGY RESEARCH PLOT (FERP)

Kylie Nichole Sullivan

Faculty Mentor: Barry Sinervo

Many scientists believe we are in Earth's sixth mass extinction event (Wake D.B. & Vance 2008). Global climate change causes deviations in ecosystem characteristics (i.e. temperature and precipitation) (Karl & Trenberth 2003). Extreme fluctuations in these characteristics facilitate higher susceptibility to insect or pathogen outbreak in forest communities (Dale et al. 2001). Batrachochytrium dendrobatidis, a fungal pathogen commonly known as Bd, is responsible for massive decline of amphibian populations around the globe (Pounds et al. 2006). Batrachochytrium salamandrivorans (Bsal), is a species of chytrid that is specific to salamanders and newts. Amphibians are bioindicators of the health of an ecosystem; tracking population status is vital to their communities.North America has the highest salamander biodiversity in the world- making Santa Cruz an acceptable case study site. This investigation sought to answer the following questions: Is there a presence of Bd and Bsal on UCSC's Forest Ecology Research Plot? What temperature ranges are associated with the presence of Bd and Bsal in this area? We sampled UCSC's Field Ecology Research Plot (FERP) for both Bd and Bsal using coverboard methodology. Bd and Bsal tested negative for all subjects: California slender salamander (Batrachoseps spp.), Yellow-eyed ensatina (Ensatina eschscholtzii xanthoptica), and the Rough-skinned newt (Taricha granulosa). Thermal analysis of salamander locations, under coverboards and parallel "natural cover", the likelihood of salamander presence increases with higher mean temperatures. Conversely, cover items with higher average daily maximum temperatures were less likely to have salamanders present.

PROBING DIMERIZATION INTERACTIONS OF HUMAN PLATELET 12-LIPOXYGENASE

Angel Ray Baroz

Faculty Mentor: Ted Holman

Human platelet-type 12-lipoxygenase (hp-12LOX) are highly regulated enzymes that catalyze the hydroperoxidation of polyunsaturated fatty acids (PUFA) to forms oxylipins such as leukotrienes and lipoxins, which are signaling components of the inflammatory responses in our bodies. Unregulated or excessive inflammation is linked to numerous disease processes, such as psoriasis, hypertension, diabetes and cancer. To aid in drug development against hp-12LOX, studies are needed to advance the explanation of structure & function and thus, to enact rational drug design. Previous theoretical molecular modeling and experimental data has established that hp-12LOX is active as a dimer, and we further probed the nature of this association.

Using site directed mutagenesis and size exclusion chromatography (SEC), we explored two models of interactions: ? – ? interactions between surface aromatic residues and interactions between leucine-hydrophobic residues thought to be leucine zipper motif. We have generated three mutants to test the aforementioned models, focusing on one mutant, which eluted as a monomer confirmed by SEC, that disrupts the leucine zipper. In order to gain further insight, we conducted steady state kinetic experiments to analyze the different substrate specificity against six essential fatty acids: arachidonic acid (AA), dihomo-?-linolenic acid (DGLA), eicosapentaenoic acid (EPA), ?-linolenic acid (ALA) and docosahexaenoic acid (DHA).

PROTEIN EXPRESSION OF OVERLAPPING READING FRAMES OF MYCOBACTERIOPHAGE VIOLET

Kevin Nsikan Ekanem

Faculty Mentor: Grant Hartzog

Bacteriophage, viruses that infect bacteria, are the most numerous organisms and one of the greatest sources of genetic diversity on the planet. With greater than 1000 sequenced genomes available, mycobacteriophage, which infect mycobacteria, are the best characterized class of bacteriophages. Comparison of these genomes has shown that each mycobacteriophage is unique and that the mycobacteriophages frequently exchange small portions of their genomes with their hosts and other mycobacteriophage. This extensive exchange prevents construction of conventional phylogenies but mycobacteriophage with similar genomic structures can be grouped in one of 27 clusters. We are studying Violet; a mycobacteriophage isolated at UCSC that is a member of cluster A1. Interestingly, gp57 of Violet is encoded by a 1.5kb nucleotide sequence that appears to be completely unique to the A1 cluster. A BLASTx search showed that this sequence has the potential to encode protein in two different reading frames. The first appears to encode a protein whose N- and C-termini resemble a DNA methyltransferase and whose central region is unique. The second reading frame, which roughly overlaps the unique domain in the first open reading frame, encodes an HNH nuclease. Interestingly, mass-spectrometry of phage Violet suggest that both reading frames are expressed. We will discuss hypotheses and strategies to explain the genesis and functions of this interesting gene.

QUALITATIVELY ANALYZING ADHESION OF VIBRIO CHOLERAE BIOFILMS

Reem Basel Rashid

Faculty Mentor: Ahmet Ali Yanik

The purpose of this project was to quantitatively analyze adhesion forces of pathogenic vibrio cholerae biofilms, which are complex communities of microorganisms that attach to surfaces, using a microfluidic device. Microfluidics is an attractive alternative to traditional methods, such as adhesion assays, as it offers high-throughput performance and its simplicity in experimental setup and use. In addition, by using microfluidics we can create one device that will generate different shear stresses acting on the sample by changing the dimensions of the channel allowing us to test multiple conditions simultaneously. Fabricating these devices using soft lithography ensures a fast turnaround for device design. Polydimethylsiloxane (PDMS), the polymer used to create the devices, is optically transparent allowing for the use of real-time microscopy to explore cell behavior. The adhesion of the bacteria was quantified by taking images and counting the number of bacteria attached at different points in the channel, which correspond to different shear stresses. The significance of this project comes from evidence that nearly all bacteria form biofilms as a strategy for survival. Microorganisms on catheters and implants causing persistent infections are examples of biofilms with important implications in public health. The adhesion of different mutations of vibrio cholerae were explored to see how the absence or presence of certain proteins affects surface adhesion of the biofilm and to show the versatility and the potential of using microfluidics to study biological behavior. It was found that adhesion of bacteria did indeed depend on the shear stress acting upon it.

SAGA, H2B DEUBIQUITINATION AND CHROMATIN ACCESSIBILITY

Evelyn Estelle Suva

Faculty Mentor: Grant Hartzog

In eukaryotes, DNA is wrapped around a complex of eight proteins called histones to form a nucleosome; this repeating unit is the major component of chromatin, a complex of proteins and DNA found in a cell's nucleus. While nucleosomes allow for the compact storage of DNA, they also act as a barrier to transcribing RNA polymerase, which requires physical access to the underlying DNA. Many studies have observed that actively transcribed genes are still associated with nucleosomes, suggesting that cellular factors are removing nucleosomes ahead of a transcribing RNA polymerase and subsequently reassembling nucleosomes in its wake. How these nucleosome dynamics are coordinated during transcription is not well understood. My project focuses on understanding how a large, multi-functional protein complex, SAGA, regulates chromatin structure during transcription. My focus is on the DUB module, a subcomplex of SAGA that removes ubiquitin from histone H2B. Ubiquitination of H2B is associated with actively transcribed chromatin. We hypothesize that targeting different protein components of the SAGA complex will lead to either more tightly wound chromatin or more permissible chromatin, through histone H2B ubiquitination. To investigate this hypothesis, we are using a genetic reporter assay to isolate and characterize the composition and activities of defective SAGA complexes from mutants in which its Ada1 subunit is defective. Our goal is to determine which components of SAGA are required for its ability to maintain chromatin structure. This will be followed up by measuring histone H2B ubiquitination levels in these mutants.

SF3B1'S ROLE IN INTRON RECOGNITION

Alia Renee Edington

Faculty Mentor: Melissa S Jurica

The spliceosome is a dynamic molecular machine found in the nucleus of cells that has a critical function in gene expression. The spliceosome is composed of ribonucleoproteins (snRNPs) complexes made from five U-rich snRNAs: U1, U2, U3, U4, U5, and U6. The spliceosome cuts out non-coding regions of a mature RNA, conventionally referred to as introns, and ligates the remaining coding regions known as exons. The newly spliced product is further translated to produce proteins for a multitude of functions for the cell.

The purpose of this project is to understand the role of the U2 snRNP splicing protein, SF3B1, in intron recognition. Mutated SF3B1- such as those frequently found in malignant myelodysplastic syndrome (MDS)- will be tested against different substrates in its ability to recognize and discriminate between a "decoy" branch point of alternating strength placed upstream of the normal branch point. The spliced products will then be analyzed by their size to determine if proper recognition has occurred, and SF3B1 inhibiting drugs will be tested in a similar fashion to determine if they function like a mutated SF3B1 protein.

SCREENING PIPELINE FOR BACTERIAL TYPE III SECRETION SYSTEM INHIBITORS

Jocelyn Makalia Delgado

Faculty Mentor: Victoria Auerbuch Stone

Antibiotic resistance is a rising concern amongst bacterial pathogens. An emerging strategy in decreasing the rate of bacterial resistance and bringing new antimicrobials to the market involves inhibiting bacterial virulence factors. The type three secretion system (T3SS) is a molecular syringe that injects toxic effector proteins into the cytosol of host cells. When the T3SS is genetically rendered non functional, most T3SS possessing pathogens become avirulent, making the T3SS an excellent molecular target for novel antimicrobial drugs. Many T3SS inhibitors have been discovered over the last decade but very little is still known about their mechanism of action. Our lab aims to develop a screening pipeline capable of characterizing the basic activity of T3SS inhibitors, using enteropathogenic Yersinia as a model T3S-expressing pathogen. Based on the tight regulation and hierarchical process of T3SS assembly and secretion, our pipeline determines the activity of T3SS inhibitors at specific stages of type III secretion. Specifically, this work focused on the first two phases of type III secretion: T3SS basal body formation, as monitored by a fusion between the fluorescent protein mCherry and YscV, a protein component of the T3SS C-ring and T3SS needle polymerization, assessed by immunohistochemistry against the T3SS needle subunit YscF. While there appears to be a difference in YscF puncta between DMSO and the inhibitors, no statistical significance can be concluded. Understanding the function and regulation of the T3SS will allow for the opportunity to explore and improve potential therapeutics, while providing insight on the basic characterization of the T3SS.

SCREENING FOR T3SS INHIBITORS IN MARINE INDONESIAN SPONGES

Gavin Christopher Jared Smith

Faculty Mentor: Phillip Crews

Tropical marine sponges are known to be a source of natural products that may be useful for treating human diseases including cancer and bacterial or viral infections. The purpose of this project is to identify, isolate, and elucidate the structures of compounds in marine Indonesian sponges that may act as inhibitors to the type three secretion system (T3SS), a commonly employed virulence factor among Gram-negative bacteria. The current extract being analyzed, from a Theonella albino (95574F), was separated into seven pre-fractions, F0-F6, via HPLC before being sent to the UCSC screening center and the Josephine Ford Cancer Center (JFCC) to test for activity against the T3SS and cancer cell lines. While the data from the UCSC screening center and JFCC indicated little activity against the T3SS and cancer cell lines, the chromatography of the 95574F F2 fraction—obtained via liquid chromatography mass spectrometry (LCMS)—indicated the presence of two abundant compounds designated H12 and H14. After obtain mass spectrometry data and NMR data from the H12 and H14 fractions, H12 was identified as Cyclolithistide A. The chromatographic and mass spectrometry data suggest that H14 is the potentially novel, di-chloro analog of Cyclolithistide A. The primary objective now is to obtain enough material of the H14 fraction in order to carry out the NMR experiments necessary to elucidate the structure of this novel compound and identify the location of the second chlorine atom.

SONIC HEDGEHOG PATHWAY REGULATES GSX 2, OLIG 2, AND PAX 6 EXPRESSION IN THE CORTEX

Jessica Arozqueta Basurto

Faculty Mentor: Bin Chen

Neuronal stem cells (NSC) and their progenitors control early brain development via a signaling transduction cascade, one of which is achieved through the sonic hedgehog (Shh) signaling pathway. In the central nervous system (CNS) there is a graded concentration of Shh that causes the activation or repression of transcription factors (TFs), thus resulting in specification of particular brain regions. These TFs help dictate gene expression in particular brain region, and help signal for cell differentiation. We hypothesize that that the Shh pathway regulates lineage progression of NSCs. Through the loss of function and gain of function of the Shh we can denote what TFs are present in this pathway and to what level are they affected. Generating two transgenic mouse lines, one that over activated and another that suppressed the Shh, TFs Pax 6, Gsx 2, and Oligo 2 were found to have altered cell production. These TFs are among the earliest to be expressed in neuronal progenitors and are involved in early embryonic development. Oligo 2 helps drive the production of oligodendrocytes and specific types of neurons. Pax 6 helps generate projection neurons and Gsx2 is required for early specification of lateral ganglionic eminence (LGE) progenitor cells. In loss of function of the Shh pathway there was a decreased in cell production and in gain of function there was an increase in cell proliferation, all pertaining to each of the previously stated TFs. The subventricular-zone (SVZ) was the cortex region where cell proliferation had the greatest change.

STRUCTURAL STUDIES TO UNDERSTAND EVASION OF AN ASTROVIRUS SEROTYPE-2 SUBTYPE TO A POTENT NEUTRALIZING ANTIBODY

Edmundo Ismael Perez

Faculty Mentor: Rebecca M Dubois

A new human astrovirus strain HastV-2-Oxford, part of a largely variable HAstV-2 serotype, was found to be resistant to a potent neutralizing antibody PL-2. The HastV-2-Oxford capsid spike protein (Spike-2-Oxford) was recombinantly expressed in E. coli and purified using Talon batch purification followed by size exclusion chromatography. X-ray crystallography allowed determination of the three dimensional structure of Spike-2-Oxford and identification of structural differences compared to its wild type countertype Spike-2-CDC-Spain. Programs such as Coot and Phenix were utilized to reach a well-validated structure. The structure revealed that a mutation from Serine463 to Proline463 in loop1 that forms part of a crucial Spike/antibody contact region was responsible for the antibody neutralization resistance. Proline locked the Spike-2-Oxford's loop 1 in one conformation, leading to the clashing of antibody residues. The heavy chain of the scFv is predicted to clash with residues of the loop 1 region in the Spike-2-Oxford protein, allowing the virus to avoid being neutralized. An scFv was then engineered to delete the heavy chain using site directed mutagenesis. The scFv was expressed using the S2 insect cell system to bind this new strain. The engineered scFv deemed to be "sticky" and so site directed mutagenesis was once again performed but on Spike-2-Oxford to revert the proline to its wild type amino acid, serine. This was done to confirm if the amino acid change is enough to avoid neutralization.

SYMBIOTIC ALGAE VARIABILITY IN CARIBBEAN CORALS UNDER AN IN-SITU OCEAN ACIDIFICATION EXPERIMENT

Eva Jason

Faculty Mentor: Adina Paytan

Due to increased anthropogenic carbon dioxide emissions, Earth's oceans have experienced a drop in pH levels, a process called ocean acidification. As the carbon dioxide concentration in the atmosphere increases, it dissolves into the ocean and forms carbonic acid. The acidic conditions make it difficult for corals and other marine organisms to build their skeletons from calcium carbonate. The goal of this work is to estimate the effect of ocean acidification on three coral species. Corals were collected at low pH springs and control sites from the Mesoamerican reef in Quintana Roo, Mexico and transplanted into natural low pH settings as well as ambient sites. We monitored the overall health of the corals after two years of exposure to low pH seawater by determining the cell concentration of symbiotic algae living in the coral tissue. Once the study is complete we hope to find out if corals are adapting to the more acidic environment. We anticipate that this study can give insight into long term effects on corals as Earth's oceans become more acidic.

SYNTHESIS AND BIOPHYSICAL TECHNIQUES FOR ALZHEIMER'S A?42 PEPTIDE

Diana Laura Lucas Baca

Faculty Mentor: Luis Alejandro Rodriguez

Alzheimer's disease is a neurodegenerative disease that causes memory loss and worsens in its later stages causing the patient to live a complicated life. Alzheimer's usually affects people over the age of 60 but it can also develop in younger people in the age of 40 and 50. Two neuronal proteins, amyloid beta (A?) that is extracellular and tau that is intracellular, are a part of the pathological aspect of Alzheimer's that leads to the death of the neuron. We are interested in the A? protein, which consist of 42 amino acids, its short sequence allows us to synthesize the protein in the lab. Once the peptide has been synthesized, it is then purified through High Pressure Liquid Chromatography (HPLC) in order to be used in the following experiments revealing its biophysical behavior. Circular Dichroism (CD) spectroscopy allows us to monitor the protein's folding and the duration it takes to reach a ?-sheet confirmation which then forms into oligomers. In the oligomeric stage of the A? peptide, it is found to be the toxic component that leads Alzheimer's disease. Furthermore, Photochemically Induced Crosslinking of Unmodified Proteins (PICUP) is used to crosslink the oligomers, following gel electrophoresis to further examine the A? oligomers. Finally, the usage of Thioflavin T (ThT) allows us to record the peptide's ability to form fibrils. Through these experiments we will be able to better understand the protein structure and unveil its toxicity.

TBR1 REGULATES CELL FATE SPECIFICATION OF CORTICOTHALAMIC NEURONS

Tejaswini Chowdhary Cherukuri

Faculty Mentor: Bin Chen

The cerebral cortex is a thin, layered structure located on the outermost portion of the mammalian brain. It is essential for higher functions such as sensory perception, spatial reasoning, and motor command. The cortex is generated in an inside-out fashion, with the deepest layers being formed first, and the more superficial layers being produced later. Each layer is associated with a predominant neuronal subtype, characterized by gene expression profiles and axonal targets. Defects in the generation of these layers, and their subsequent axonal projections, leads to severe neurodevelopmental disorders. The research performed in the Chen lab focuses on the underlying molecular mechanisms that regulate the developing neocortex.

T-box Brain 1 (Tbr1) is a transcription factor that plays an essential role in the development of the neocortex. Tbr1 has recently been identified as a high confidence Autism Spectrum Disorder gene (hcASD) and has been shown to regulate other hcASD genes. When mutated, neurons fail to migrate to their correct laminar positions, leading to aberrant axonal projections. Previous work in our lab showed that mutations in Tbr1 cause a complete loss of corticothalamic neurons, and an increase in subcerebral neurons. Thus, we hypothesize that Tbr1 directly regulates the cell fate specification of corticothalamic neurons by upregulating corticothalamic genes and repressing subcerebral genes. To test this, we will use state of the art mouse genetics, RNA-seq, and chromatin immunoprecipitation followed by high-throughput sequencing (ChIP-seq). Through this research, novel information about Tbr1 in the developing neocortex will be elucidated. This knowledge will help build a foundation for the future research of ASD.

THE DIVERSITY AND DISTRIBUTION OF MACROFUNGI IN COASTAL MIXED EVERGREEN FOREST

Samuel C Castro

Faculty Mentor: Gregory S. Gilbert

Fungal diversity varies with plant community composition and the abundance of plant species, as well as environmental factors. Because the structure and dynamics of plant communities vary with different combinations of species, monitoring the diversity and distribution of fungi in many distinct communities allows us to gain insight into the dynamics of plant-fungi relationships. In this study, we surveyed a grid of eighty-one, 28 m2 plots on the UC Santa Cruz Forest Ecology Research Plot and identified fungal species encountered in each plot during 9 sampling days spaced at two week intervals between October 2016 and March of 2017. We compared fungal spatial data with that of woody plant species to examine the relationship between the abundance of woody plants and the diversity and distribution of fungal species. Fungal diversity was not correlated with the diversity of woody species, but was negatively correlated with the density of both Corylus cornuta and Morella californica. Nine fungal species were found to correlate with the abundance of individual woody species. Two fungi were found to correlate with common pairings of woody plants. This study establishes a baseline and a standard protocol which may be used to determine how the diversity and distribution of fungal species change as the forest responds to changing climate and community composition.

THE EFFECTS OF VANGL2 AND PRICKLE2 ON MAMMARY DUCTAL SIZE

Melawit M Tekeste

Faculty Mentor: Lindsay Hinck

Breast cancer is one of the leading diseases among women in the United States and can arise from mutations in developmental pathways. One process that controls cell behavior across organs is the planar cell polarity (PCP) pathway, which orients cells in the sheet of epithelium. To study how the PCP pathway affects mammary ductal size, we analyzed mammary glands isolated from mice deficient in VANGL2 and PRICKLED2, which are two core PCP proteins, and quantified the area of individual ducts along their length. Results from these experiments showed wild-type ducts maintain a constant area while VANGL2 and PRICKLED2 mutant ducts display two phenotypes: an overall larger area and one that rapidly increases and decreases across the duct. These results suggested that the PCP pathway, specifically VANGL2 and PRICKLED2, functions to maintain ductal size. Our studies will provide insight into the function of this mechanism in mammary gland patterning in order to better understand their disruption during disease.

THE EFFECTS OF THE NORTH PACIFIC WARM TEMPERATURE ANOMALY ON NORTHERN ELEPHANT SEAL DIVING BEHAVIOR

Emily Corinne Nazario

Faculty Mentor: Patrick William Robinson

Over the past decade there has been increasing concern about climate change and the effects that rising atmospheric temperatures may have on the world's oceans. It is currently understood that the North Pacific Ocean has been directly affected by a specific warming event nicknamed the “blob”. The effects of these higher than normal water temperatures on oceanic ecosystems are difficult to measure due to a number of variables. However, selecting a species such as the Northern Elephant Seal (Mirounga angustirostris), a top predator who spends a majority of its life in the water, can represent how pelagic ecosystems have been influenced by the blob. In this experiment, tagged elephant seals recorded sea surface temperatures, bottom temperatures, dive duration, dive depth, and satellite location.

Seals were tagged using the Robinson et al. (2012) method and a total of 49 were used for this study. Only data collected within the area of 30-70ºN and 125-160ºW was used, and the post-molt and post-breeding migrations were analyzed separately. Dive depth and duration were expected to decrease as water temperatures increased, however, only dive depth and surface/bottom temperatures were proven to be statistically significant between blob and non-blob years. This change in dive behavior can be representative of a changing oceanic ecosystem and can be used to study how other organisms may be affected. This information may then be used as a line of evidence to further the understanding of climate change’s effects on the marine ecosystem.

THE FORMATION OF THE LYSOSOME/VACUOLE: THE ROLE OF THE RAB-7 GTPASE

Masuda Sharifi

Faculty Mentor: Barry J Bowman

Lysosomal activity in animal cells and vacuolar activity in fungal cells aid in similar processes for the degradation and recycling of intracellular materials. Lysosomal/vacuolar compartments contain hydrolytic enzymes that ensure the maintenance of an acidic internal environment. Neurospora crassa, a filamentous haploid fungus that has complementary genes to humans, served as the model organism to investigate the function of the vacuolar compartments. The formation of vacuoles was visualized by RFP tagged vacuolar membrane proteins (VMA-1). Using confocal microscopy, a cluster of vesicles were shown to reside in the hyphal tip. These ring-like organelles also showed localization of the VMA-1, which suggest that these were immature vacuoles or prevacuolar compartments (PVC). The RAB-7 GTPase, an enzyme essential in the transportation of proteins to specific destinations and in late endosome-vacuole membrane fusion signaling, was found to associate with the PVCs. Therefore, we hypothesize that PVCs play a similar role as endosomes during intracellular protein trafficking. In order to gain better insight into the role of PVCs in vacuole/lysosome formation, we aim to knock out RAB-7 using CRISPR-Cas9 genome engineering technology. We will observe any phenotypic abnormalities in the absence of RAB-7, which will further indicate if RAB-7 is essential in the formation of the vacuole/lysosome.

THE GENE EXPRESSION OF A BACTERIA-DEPRIVED DAPHNIA

Lon Jason Blauvelt

Faculty Mentor: Marilou Sison-Mangus

It is now an accepted tenet that host-associated microbiomes play an important role in the biology and physiology of the eukaryotic host. For instance, the lack of microbiota in many host taxa results in various developmental and physiological impairments, the effects mostly seen on nutrient processing, and mucosal immune system. In the freshwater crustacean model Daphnia magna, we observed a significant reduction in growth, loss of fecundity, and high mortality when the daphnid host was grown without its associated microbiome. To understand the molecular mechanisms that underpin the interaction of microbiota and the daphnid host, we analyzed the differences in the gene expressions of bacteria-free and conventional Daphnia magna using RNA-seq.

We found that 30% of the organism's gene expression was significantly (p-value < 0.1) affected by this lack of microbiome (3145 genes upregulated; 3057 genes downregulated). Preliminary results from some of the top proteins affected corroborated some of the effects seen in our previous findings, revealing a down-regulation of the host's immune system and an up-regulation of viral proteins. Cuticle-forming proteins, necessary for growth, were similarly detrimentally affected, along with a broad range of other proteins necessary for fitness, revealing the unseen detriments and benefits of these symbiotic microorganisms to the daphnid host.

THE ROLE OF ALTERNATIVE SPLICING REGULATION IN THE INNATE IMMUNE RESPONSE

Pratibha Jagannatha

Faculty Mentor: Angela Brooks

The innate immune system is our first line of defense against infection. Initiation of the innate immune response involves a coordinated system of signaling pathways which results in an inflammatory response. While inflammation is important, chronic inflammation can lead to a variety of diseases. A number of these diseases are highly prevalent and currently incurable. Further study is required to identify better targets for more effective treatments.

The goal of our study is to take a systematic high-throughput approach to rapidly identify genes that are critical for controlling inflammation. Our study specifically focuses on the role of alternative splicing regulation through the activation of specific pathways upon induced inflammation in macrophage cells. It involves stimulating macrophage cells with molecules that are recognized by toll-like receptors (TLRs) located in the membranes of macrophage cells. We analyze RNA-seq data from this experiment using DESeq2, to identify differentially expressed genes, and we use JuncBASE to identify differential splicing changes. Based on this data, we then identify candidate genes that show significant changes in gene expression and alternative splicing after induced inflammation.

Overall, the majority of the significant events were categorized into the alternative first exon event type. Using RT-PCR, we were able to validate all four selected genes: AMPD3, TNIP1, RCAN1, and NCOA7. We are currently investigating whether these alternative first exon changes affect translation efficiency using polyribosomal profiling. Through this process, we will learn more about the different layers of gene regulation in the context of chronic inflammation.

THE ROLE OF ASTRAL MICROTUBULES IN ACENTRIC CHROMATID SEGREGATION

Hannah Marie Vicars

Faculty Mentor: William Sullivan

Normal mitosis requires that chromosomes are equally separated into newly formed daughter cells. This is achieved by forming bipolar attachments between microtubules and the kinetochore located at the centromeric regions of each chromosome. However, the presence of an unrepaired double stranded DNA break (DSB) during mitosis would lead to the generation of acentric chromosome fragments lacking a kinetochore. Consequently, acentrics would be expected to be incapable of attaching to microtubules and segregating poleward. Unexpectedly however, live imaging of mitosis in Drosophila neuroblasts reveals that acentric chromosome fragments efficiently segregate to daughter nuclei during anaphase. The goal of my research is to determine the mechanisms that drive acentric poleward segregation. Insight into this process comes from our finding that acentric chromosomes are tightly embedded in microtubule bundles along the cell periphery as they travel from the metaphase plate toward the poles in anaphase. This suggests that a subset of peripheral microtubules, known as astral microtubules, may play a key role in acentric segregation. To test this idea, we are visualizing acentric segregation in centrosomin (cnn) mutant background. The same combination of cell biological and genetic approaches will be used to test the role of other microtubule-associated proteins in acentric segregation.

THE ROLE OF CHD1, A CHROMATIN REMODELER, IN TRANSCRIPTION.

Maria Fernanda Gonzalez

Faculty Mentor: Robert Ian Shelansky

Transcription is the cellular process of encoding RNA from DNA. This is a complex process that requires transcription factors, activators, chromatin remodelers and many other components. These factors perform a wide variety of functions such as recognizing the gene or recruiting other factors or changing chromatin structure. Yet it's still not completely understood how chromatin plays a role in regulating transcription. To best study transcription the PHO5, a highly active gene, in S. cerevisiae was used. Observations made using an electron microscope show that Chd1 changes the chromatin structure of PHO5. Furthermore, FISH analysis measured decreased levels of transcription in ?chd1 cells. But what is the mechanism by which Chd1 is affecting chromatin in PHO5? To answer this question, we used the two-reporter assay where the body of PHO5 is replaced with either YFP or CFP genes in diploid S. cerevisiae cells. From this experiment, we will gain insight into transcription levels and cellular noise levels. In a ?chd1, we expect lower levels of transcription and a change in the cellular noise profile. The results from this study will increase our understanding of transcription and Chd1's function in it.

THE ROLE OF RAB-5 AND RAB-7 GTPASES IN THE BIOGENESIS OF VACUOLES

Sofia Estefani Romero

Faculty Mentor: Barry J Bowman

Neurospora crassa (N.crassa,) a filamentous fungus, was used to investigate proteins involved in the biogenesis of vacuoles/lysosomes. Like mammalian lysosomes, fungal vacuoles contain hydrolase enzymes that serve in the degradation of macromolecules. Previous studies have identified a high concentration of unidentified organelles to congregate in the hyphal tip of N. crassa; characterized by Bowman et al. as prevacuolar compartments (PVC.) Confocal microscopy of fluorescently tagged rab-7, a small Rab GTPase involved in the endocytic pathway, revealed to strongly localize on PVCs, tubular vacuolar networks, and on mature vacuole membranes suggesting that the PVCs are associated with the vacuole. Thus, we hypothesize that the PVCs can act similarly as late endosomes/multi-vesicular body (MVB) in the transportation of proteins to vacuoles mediated by rab GTPases. In Addition, Rab-5 is a GTPase protein that primarily localizes on early-endosomes that exchanges for RAB-7 as early-endosomes mature to late-endosomes. Therefore, to support our hypothesis, rab-5 and rab-7 were fluorescently tagged by PCR and imaged via confocal microscopy to observe the co-localization of rab proteins. Confocal microscopy reaffirmed the localization sites of RAB-7, however, RAB-5 only marginally localized on PVCs while a significant number of smaller vesicles decorated the hyphae. Surprisingly, preliminary co-localization analysis showed that RAB-5 and RAB-7 do not evenly localize on the PVCs and only slightly co-localize on the tubular vacuoles. The observations indicate that rab-5 is associated with vacuoles, however, additional co-localization analysis is necessary to better identify the significance between PVC and rab proteins in vacuole synthesis.

THE EFFECT OF SHIPPING LANES ON CALIFORNIA SEA LION'S (ZALOPHUS CALIFORNIANUS) BEHAVIOR

Sandra Elaine Traverso

Faculty Mentor: Patrick William Robinson

The effect of shipping lanes on California sea lion's (Zalophus californianus) behavior

Sandra Traverso
Faculty mentor: Patrick Robinson

Abstract

Several studies have been done on the interactions between shipping lanes and marine mammals. In particular, this has been well studied in Cetaceans. There is evidence that the noise associated with shipping lanes causes an increase in the stress of right whales (Rolland, 2012). In Southern California a major shipping lane transits between the the Channel islands and the mainland, through the Santa Barbra Channel. The southern most Channel island, San Nicolas island is breeding colony for the California sea lions. The Northern Channel islands and the coastal area ranging from San Luis Obispo Bay down to Malibu are known foraging areas (Mchuron, 2016). As the marine mammals most common patient, it is crucial to understand if this shipping lane is having an effect on the at sea behavior of the California sea lion. Primarily, we wanted to know if sea lions spend time and if they are diving in these areas. Adult female sea lions (n=31) were tagged, the GPS location and dive behavior data was acquired from 2005 to 2008. The sea lions showed a significant difference in time spent within 5 km of the shipping lane when compared to outside the lane. Dives within 5 km of the shipping lane as compared to outside the also showed a significant difference. Further investigation is required to determine why sea lions are not utilizing this area.

References

McHuron, E.A., Robinson, P.W., Simmons, S.E. et al. Oecologia (2016) 182: 995. doi:10.1007/s00442-016-3732-0

Rolland, R. M., Parks, S. E., Hunt, K. E., Castellote, M., et al. (2012) Evidence That Ship Noise Increases Stress in Right Whales. Proceedings of the Royal Soc'y B.

THE EFFECT OF SHIPPING LANES ON CALIFORNIA SEA LION'S (ZALOPHUS CALIFORNIANUS) BEHAVIOR

Sandra Elaine Traverso

Faculty Mentor: Patrick William Robinson

The effect of shipping lanes on California sea lion's (Zalophus californianus) behavior

Sandra Traverso
Faculty Mentor: Patrick Robinson

Abstract

Several studies have been done on the interactions between shipping lanes and marine mammals. In particular, this has been well studied in cetaceans, and falls short in pinnipeds. There is evidence that the noise associated with shipping lanes causes great stress in right whales (Rolland, 2012). In Southern California a major shipping lane transits between the Channel islands and the mainland, through the Santa Barbra Channel. The southern most Channel island, San Nicolas island, is breeding colony for the California sea lions. The Northern Channel islands and the coastal area ranging from San Luis Obispo Bay down to Malibu are known foraging areas (Mchuron, 2016). As the marine mammal centers most common patient, it is crucial to understand if this shipping lane is having an effect on the at sea behavior of the California sea lion. Our primary question, is whether the sea lions spend time in the lane, and if they are diving in these areas. Adult female sea lions (n=31) were tagged, the GPS location and dive behavior data was acquired from 2005 to 2008. The sea lions showed a significant difference in time spent within 5 km of the shipping lane when compared to outside the lane. Dives within 5 km of the shipping lane as compared to outside the also showed a significant difference. These results show that sea lions are not utilizing this area. This could mean this area of is little importance, and their prey simply isn't present, or the disturbance associated with the shipping lane is too great. Further investigation is required to determine why sea lions are not utilizing this area, and to ensure that it is not due to the disturbance from the shipping lane.

References

McHuron, E.A., Robinson, P.W., Simmons, S.E. et al. Oecologia (2016) 182: 995. doi:10.1007/s00442-016-3732-0

Rolland, R. M., Parks, S. E., Hunt, K. E., Castellote, M., et al. (2012) Evidence That Ship Noise Increases Stress in Right Whales. Proceedings of the Royal Soc'y B.

TO IDENTIFY TYPE III SECRETION SYSTEM VIRULENCE BLOCKERS

Yongtong Lao

Faculty Mentor: Joshua Allen Schwochert

Gram-negative pathogens cause millions of illnesses and death worldwide each year. Treatment of infections with antibiotics, which target all bacteria non-specifically, often gives rise to resistance and destroys healthy microbiota. Emergence of antibiotic resistance bacteria is the current issue of global public health because these bacteria cause long-lasting and epidemic infection. One promising strategy to combat the antibiotic resistant bacteria is virulence blockers, which are compounds that suppress pathogenicity without killing or inhibiting bacterial growth. Type III secretion system (T3SS), a needle-like appendage that bacteria use to inject effector proteins to the host cells to suppress host defense is an important virulence factor target for drug development. T3SS is required for virulence in dozens of Gram-negative bacteria pathogens but largely absent in nonpathogenic bacteria. We identified derivative of the natural cyclic peptide Phepropeptin that inhibit T3SS in both Yersinia and Pseudomonas through an innate immune-based high throughput screen. To further optimize the efficacy, we synthesized new derivatives with improved potency. The best compound from this series inhibits up to 90% of toxin excretion at 60?M. These peptides did not inhibit bacterial growth and did not target flagellum, a motility system structurally similar to T3SS, indicating a specific block on the T3SS. Further derivatives of Phepropeptin may lead to promising virulence blockers of several human pathogens.

TREETRONIC MOISTURE DENSITY SCANS OF TANOAKS EXPOSED TO SUDDEN OAK DEATH

Haley Morgan Burrill

Faculty Mentor: Gregory S. Gilbert

Sudden Oak Death, caused by plant pathogen Phytophthora ramorum, is wiping out tanoaks in the mixed evergreen forests of California. The disease is known to cause cankers within the tree cambium, girdling water transport within the tree. We tested the Treetronic electrical impedance tomogram's efficacy of detecting moisture density on two Quercus individuals by comparing moisture density of wood samples. We then used the Treetronic on twenty Notholithocarpus densiflorus individuals of varying health statuses to detect internal moisture density. We found tanoaks more visibly diseased to have lower moisture density, consistent with our expectations of the cankers' effects on tanoak trees.

TUNA CONSUMPTION BEHAVIORS OF UCSC STUDENTS AND MERCURY CONCENTRATIONS IN TUNA SERVED AT THE UCSC DINING HALLS

Yasuhiko Murata, Mona Zia

Faculty Mentor: Myra E Finkelstein

Tuna is a popular food choice and served daily at the UCSC dining halls. However, tuna can contain high levels of methylmercury which is of concern for people that consume tuna on a regular basis. The goal of our study was to assess if UCSC students were consuming tuna at levels that would warrant concern given the EPA reference dose of mercury consumption of 0.1 ug/kgbw /day. We also investigated if students who stated tuna consumption could be harmful to their health ate tuna less frequently than students who did not think tuna consumption was harmful to their health. A random sample of UCSC students who use the dining hall was asked if they would like to participate in the survey, of the 168 students asked, 92 agreed to take the survey (acceptance rate of 55%). Out of the 92 student surveys, 29 reported they ate tuna; 14 of them reporting they ate tuna more than once a week at the dining halls. Of the 29 students who eat tuna, 3 of them (~10%) thought that the amount that students eat does not matter. We also found a large amount of variation between the subjects' answers with respect to how often tuna could be consumed before concern is warranted from mercury exposure, with values ranging from 1 to 100 times per week. In conclusion, 32% of students reported that they eat tuna at the dining hall, while 15% of students reported that they ate tuna more than once a week. We found that tuna served at the UCSC dining hall contains about 0.06 µg/g mercury thus a 63 kg student who consumes tuna > 2 times per could be exceeding the EPA mercury reference dose of 0.1 ug/kgbw/day.

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Tuna is a popular food choice and served daily at the UCSC dining halls. However, tuna can contain high levels of methylmercury which is of concern for people that consume tuna on a regular basis. The goal of our study was to assess if UCSC students were consuming tuna at levels that would warrant concern given the EPA reference dose of mercury consumption of 0.1 ug/Hg per kg body weight/day. We also investigated if students who stated tuna consumption could be harmful to their health ate tuna less frequently than students who did not think tuna consumption was harmful to their health. A random sample of UCSC students who use the dining hall was asked if they would like to participate in the survey. Out of 92 student surveys, 29 reported they ate tuna; 14 of them reporting they ate tuna more than once a week at the dining halls. For the students who eat tuna, 3 of them thought that the amount that students eat don't matter. We also found a large amount of variation between the subjects answers with respect to how much tuna can be consumed before concern is warranted from mercury exposure. 47% of surveyed students also agreed to submit a hair sample for hair mercury level analysis. In conclusion, 32% of students reported that they eat tuna at the dining hall, while 15% of students reported that they ate tuna more than once a week.

UNDERSTANDING THE EFFECTS OF TEMPERATURE ON SEX RATIO IN A SEXUALLY DIMORPHIC FISH SPECIES

Devin Chance

Faculty Mentor: Eric Palkovacs

The proportion of males to females in any given population is expected to be in equilibrium around 1:1. However, there are cases in nature of extremely skewed sex ratios. Several studies have suggested temperature to be associated with these skewed sex ratios. Here, I examined the relationship between sex ratio and temperature in the globally invasive mosquitofish. Mosquitofish exhibit sexual dimorphism, with females sometimes doubling males in body size. Following predictions from the temperature-size rule, smaller body sizes are expected at warmer temperatures. I therefore predict that hotter temperatures lead to an increase in the fraction of males. To test this prediction, I collected mosquitofish from geothermal ponds and streams in California and New Zealand. I examined the relationship between sex ratio and temperature. As predicted, I found that hotter sites had a greater proportion of males. My results show that temperature may be an explanation for skewed sex ratios in species showing sexual size dimorphism, such as mosquitofish. Results also suggest that increasing temperatures may cause sex ratios to change in nature, with potentially important ecological and evolutionary consequences.

USE OF 87SR/86SR DATA DURING THE EOCENE TO RECONSTRUCT PALEO-OCEAN CHEMISTRY

Carolyn E Brady

Faculty Mentor: Adina Paytan

Carolyn Brady
Faculty Member: Adina Paytan

Pelagic barite (BaSO4) is formed in in the oceanic water column within micro-environments composed of sinking organic matter. In paleoceanography, barite (BaSO4) accumulation rates are used as a proxy for export production the fraction of primary productivity fixed carbon that is transported to the deep ocean. During formation, barite incorporates the chemical signature of the surrounding water in which it is formed; hence it also serves as an excellent resource for reconstructing paleo-ocean chemistry. In this study, BaSO4 will be used to obtain oceanic radiogenic 87Sr/86Sr data during the Eocene (35 – 60 Ma) to reconstruct changes in paleo-weathering rates, which are the driving force behind the carbon cycle over geologic time. Although data regarding this relationship during the Eocene is readily available, there is significant scatter and more research can be done to better corroborate existing data. We hypothesize that this study's data will confirm some of the previously published findings for the Eocene – resulting in a fairly consistent ratio from ~40 – 60 Ma but will reveal some fine structure in the trends.

VISUALISING AND SIMULATING PLANETARY FORMATION IN 3D

Robert Luke Naylor

Faculty Mentor: Douglas N C Lin

Planetary Formation is a little understood process. One of the reasons for this is the lack of confirmed observations of systems caught in the act. To understand what such a system would look like, we have undertaken 3D hydrodynamical simulations using the Fargo3D code. We have then visualised the simulation results using the 3D animation software Blender using a number of different methods. Major features include large spiral density waves that emanate from any forming planet embedded in the protoplanetary disc. These waves protrude from the disc plane, creating "mountain tops" that are directly exposed to stellar radiation. We have written python codes to calculate the absorption and reprocessing of radiation within these features and we have also visualised these in 3d. We have made promising comparisons to observations (e.g. of the LkCa 15 system). In the future we want to combine this 3d analysis with spectral synthesis code, which will give us details on observation such as hydrogen alpha emission.

20th Annual

Undergraduate Research Poster SYMPOSIUM

Jack Baskin School of Engineering Courtyard
Thursday, June 8, 2017
2:00 - 4:00 PM

APPLICATION AVAILABLE ONLINE
Deadline: MAY 31, 2017.
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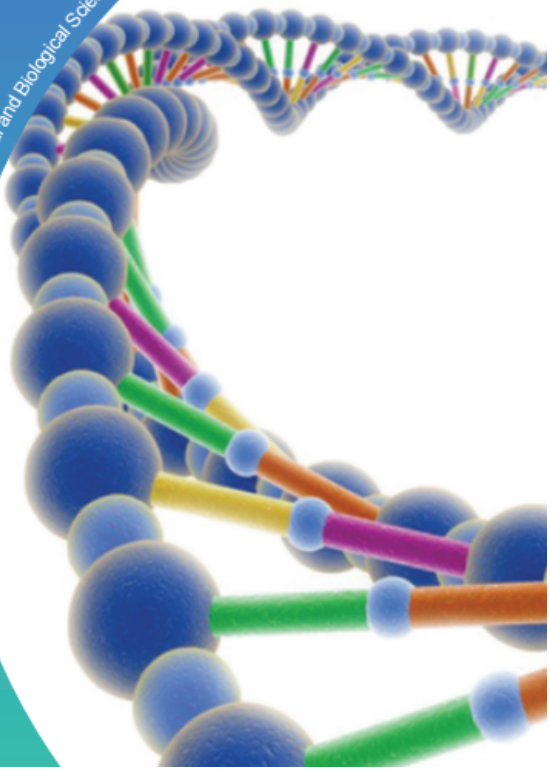
Hosted by the Physical and Biological Sciences Department and Jack Baskin School of Engineering



This event will recognize and promote the outstanding undergraduate science and engineering research that is being carried out at UCSC while providing students with the experience of presenting their research results in a professional setting.