2019 NIH B2B PARTICIPANTS & RESEARCH

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JAVIER CABRALES (Chabot College)
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ELIANA CARMODY (Chabot College)
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MICHAEL GATHERU (Chabot College & Las Positas College)
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KARLY ORTEGA (Merritt College)
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YILDA PABLO (Merritt College)
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ANDREA SALAZAR (Chabot College)
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EDUARDO SANTILLÁN SANCHEZ (Chabot College)
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SHEWIT SIUM (Peralta Colleges)
Investigating the structural determinants for efficient co-translational folding of the model protein HaloTag using circular permutation

SHAUNA WATSON (Peralta Colleges)
The impact of sequence variation on alternative translation initiation in CEBPA

ELIANA ZAPATA (Chabot College)
Characterization of ZIM/HIM C. elegans mutants in homologous chromosomes pairing

ABSTRACTS

SARON AKALU

Kirsten Verster (PhD candidate) and Professor Noah Whiteman
Integrative Biology

Protein-level analysis of horizontally transferred genes from prokaryotes to arthropods

Horizontal Gene Transfer (HGT) is the process in which organisms ('recipients') acquire new genes from other organisms ('donors'). In the past decade, HGT has become recognized as a major driver of eukaryote evolution, but the changes that genes and their encoded proteins undergo following transitions to new cellular contexts, as well as their importance to eukaryotic fitness, are not well understood. Thus, we wanted to determine if these genes undergo predictable evolutionary adaptations at the protein level. To explore this, we examined the amino acid composition of "donor" (bacterial) and "recipient" (insect) orthologs, which is determined by the structural and functional requirements of a given protein. We mined the literature for examples of functional HGT and extracted amino acid sequences of donor and recipient lineages (n=156) in bacterial to insect HGTs. We analyzed sequences for molecular weight, isoelectric point, amino acid composition, and protein-folding motifs using Geneious. We determined that glutamate and valine tend to be more abundant in horizontally transferred orthologs of the recipient, arthropods while glycine and asparagine tend to be more abundant in orthologs from donor bacterial species. These and other differences could reflect adaptations to novel cellular contexts with different protein assembly machineries.

Saron Akalu was born in Ethiopia and raised in Oakland. She attends Berkeley City College, where she is pursuing her Associate's degrees in Anthropology and Biology. Saron hopes to transfer to the University of California, Berkeley in the Fall of 2020 to study Molecular and Cell Biology. In the future, she plans to pursue an MD or a PhD in evolutionary genetics.

ABSTRACTS

JAVIER CABRALES

Victor Reyes-Umana (PhD Candidate) and Professor John Coates
Plant and Microbial Biology

Surveying environmental samples from East Bay freshwater sources for iodate-consuming metabolisms

Iodine is an element of great biological importance with health implications for humans and other mammalian life. Iodine is primarily found in marine environments at varying concentrations, and various oxidation states such as iodide (I–) and iodate (IO3–). The distribution of nitrate and chlorate reduction are examples of anaerobic metabolisms that have been comprehensively characterized. Despite a similar molecular structure to nitrate and chlorate, the distribution of iodate reduction has not been as thoroughly characterized. Research suggests that in marine environments iodate concentrations should be elevated. Instead, the reduced form, iodide, is found at higher concentrations, suggesting iodate is being reduced to iodide. Our research focuses on whether terrestrial coastal environments harbor iodate reducing capabilities as well. To paint a more complete picture of iodine cycling in freshwater environments we collected samples from various locations across the East Bay in an attempt to grow and isolate bacteria capable of iodate reduction. In order to screen for iodate reduction we enriched sediment from these samples with iodate and organic carbon. Using ion chromatography we assessed whether iodate consumption was occurring and any samples illustrating iodate removal served as candidates harboring iodate reducing bacteria. Bacteria from promising enrichments were isolated using dilution to extinction and isolates were identified using 16S sequencing. Finally, isolates were tested for iodate reduction by growing them with acetate and iodate only. The lab will continue to collect samples from the environment and screen for isolates with iodate reducing properties. The hope is to build a collection of viable iodate reducing species and strengthen the hypothesis that these organisms are responsible for the movement of iodine in marine and coastal environments.

Javier D. Cabrales currently attends Chabot College, where he volunteers his time as a student Athletic Trainer and is a former member of Chabot's Track and Field team. He hopes to transfer to the University of California in the fall of 2020 as a Molecular and Cell Biology major. After completing his undergraduate studies, Javier plans to attend graduate school and aspires to work in orthopedics. When not studying, Javier enjoys being outdoors, spending time with his cats and stand-up comedy. Some of his passions include watching and playing sports, trail running, mountain biking and submerging himself into his artwork.

ABSTRACTS

ELIANA CARMODY

Kira Mosher (Postdoctoral fellow) and Professor David Schaffer
Chemical Engineering and Bioengineering

Analyzing EphA4 activation by synthetic multivalent peptides in adult hippocampal neural stem cells

Adult mammalian neurogenesis is the process by which new neurons differentiate from neural stem cells (NSCs) and integrate into existing circuits in the mature brain. In the adult mammalian hippocampus, this process is critically involved in memory formation and maintaining plasticity. Examining the specific factors and mechanisms that promote or inhibit neurogenesis from NSCs offers important insight into the regulation of this process in the healthy and diseased brain. Moreover, these mechanisms have the potential to be harnessed to treat neurological diseases. Adult NSCs exist in specialized microenvironments, or "niches", in which they are tightly regulated and influenced by diverse signaling networks. We have recently discovered a novel role for the Eph/ephrin family in regulating adult hippocampal NSCs. Specifically, the ligand ephrin-A4 activates the EphA4 receptor on NSCs and regulates their migration and differentiation into neurons. Additionally, our lab has developed a method to synthesize multivalent peptides (MVPs) with the hope of emulating ephrin-Eph ligand-receptor binding. The goal of this study was to investigate whether MVPs, engineered to bind EphA4, can also activate EphA4 and regulate NSC function and behavior. We treated primary adult mouse hippocampal NSCs that overexpress EphA4 with four different MVPs and found that one of these peptides both phosphorylates and clusters EphA4, which are general indicators of Eph receptor activation. Additionally, we are examining whether these MVPs induce neuronal differentiation of NSCs. Our findings indicate that multivalent peptides are a novel nanoscale synthetic tool for activating EphA4 and regulating the behavior and function of NSCs.

Eliana Carmody attended Chabot College and transfers to the University of California, Davis in the Fall of 2019 as a Biological Sciences major. Eliana will continue to pursue biological research opportunities at Davis and hopes to apply to the UC Davis School of Veterinary Medicine. From a very young age Eliana has been looking forward to earning a Bachelor's degree in Biology and hopes to one day have her own veterinary practice. Eliana loves traveling, trying new foods, spending time with friends and family, and playing soccer and rugby.

ABSTRACTS

MICHAEL GATHERU

Dhruv Patel (PhD Candidate) and Professor Krishna Niyogi
Plant and Microbial Biology

Screening promoters for high light inducible gene expression to aid in photoprotection

Photosynthetic organisms rely on light for their survival. However, exposure to high light can stress photosynthetic organisms and cause an increase in reactive oxygen species (ROS) that can damage proteins and lipids in the chloroplast. To prevent this, plants employ non-photochemical quenching (NPQ) mechanisms that allow cells to dissipate excess light energy back into the environment in the form of heat. While NPQ aids in plant survival, chloroplasts sustain damage by high light conditions when exposed for long periods of time. Expression of known photoprotective genes specifically under high light may mitigate these effects. We identified and screened 7 putative high-light inducible promoters for increased production of green fluorescent protein (GFP) under varying light intensities by transient expression in Nicotiana benthamiana. A subset of the candidate promoters were tested for their ability to produce PsbS in high light conditions. An increase in PsbS is known to increase the fast-acting component of NPQ, which may aid in photoprotection. However, we failed to induce GFP and PsbS expression under the high light conditions tested. Further optimization of the conditions necessary for gene expression may inform future work and use of these promoters.

Michael Gatheru attended Chabot College and Las Positas College. He transfers to the University of California, Los Angeles in the Fall of 2019, as an Environmental Sciences major. After completing his undergraduate degree, he hopes to gain more research opportunities, specifically in environmental sciences, and possibly pursue a Master's degree in Environmental Engineering. In his free time, he enjoys cooking, painting, and listening to music.

ABSTRACTS

JESUS GONZALEZ CAMBA

Ronald Rodriguez (PhD Candidate) and Professor Sarah Stanley
School of Public Health & Department of Molecular and Cell Biology

Isolation of antibiotic-resistant mutants in a non-tuberculosis mycobacterial pathogen

Non-tuberculosis mycobacteria (NTM) are environmental saprophytes that are capable of causing a wide variety of opportunistic human infections. Mycobacterium abscessus is one of the most pathogenic NTM species, causing various pulmonary and skin infections. These infections are incredibly difficult to treat due to its high level of intrinsic resistance to most clinically relevant antibiotics, which has portrayed M. abscessus as an "antibiotic nightmare". The genetic basis of this intrinsic resistance has been largely unexplored and identifying genes associated with this resistance can allow for the development of innovative pharmacophores. The isolation of spontaneous, antibiotic resistant mutants has identified novel genetic determinants of resistance to functionally diverse antibiotics in M. abscessus . Here, we utilized this approach to identify mutants resistant to Isoniazid (INH) and Ethionamide (ETH), two antibiotics that interfere with cell wall biosynthesis in mycobacteria. M. abscessus is highly resistant to INH and ETH, but the basis of this resistance has never been explored. Using this method, we were able to isolate mutants resistant to ETH, but not INH. Minimum inhibitory concentration (MIC) experiments revealed that the isolated bacteria grew at higher ETH concentrations compared to wild-type (WT) bacteria, approximately 4-fold greater, classifying these cells as more resistant than WT. The MIC of WT bacteria was found to be 16 µg/mL while the MIC of the resistant mutants were >128 µg/mL. To further examine resistance, a previously constructed Transposon (Tn) library in M. abscessus from the Stanley Lab was plated in the presence of inhibitory INH and ETH concentrations, which revealed viable Tn mutants. Collectively, our results have identified mutants resistant to INH and ETH. We are currently in the process of sequencing candidate genes to search for mutations that may explain the high-levels of ETH resistance observed. Future work will focus on characterizing the Tn mutants that are highly resistant to INH and ETH.

Jesus Alain Gonzalez Camba attends Chabot College and hopes to transfer to either the University of California, Berkeley or San Francisco State University, to study Molecular Cell Biology or Microbiology, in the Fall of 2020. Jesus plans to pursue research opportunities after transfer, and upon completion of his Bachelor's degree, will apply to medical school. Ultimately, he wants to join the international medical organization, *Médecin Sans Frontières*, to help underserved communities around the world. Jesus is determined to make a difference in the world, one person at a time. In his free time and during every school break, Jesus visits his family in his hometown of Puerto Vallarta, Mexico. He especially enjoys hiking in the tropical rainforest because of its rich diversity of flora and fauna, which is truly one of a kind. He also enjoys drawing with charcoal pencils as well as reading non-fiction books.

ABSTRACTS

BRITTANY KARKI

Thien Crisanto (PhD Candidate) and Professor Krishna Niyogi
Plant and Microbial Biology

UV mutagenesis screen to determine new components of non-photochemical quenching in *Nannochloropsis oceanica*

Photosynthetic organisms use light harvesting complexes proteins (LHCs) to absorb light energy. These protein networks work with photosystems to drive chemical reactions. Light absorbed by chlorophyll molecules can take one of three paths: photosynthesis, fluorescence or non-photochemical quenching (NPQ). NPQ is the dissipation of light energy as heat and occurs in excess light. This project will further examine NPQ and its components in the microalga *Nannochloropsis oceanica*. While this process has been well studied in other model organisms, its mechanisms in *N. oceanica* are still being uncovered. This microalga is particularly important because of its practical use in lipid production. Photosynthesis produces triacylglycerides (TAG), a lipid that can be used as a biofuel among other purposes. NPQ in *N. oceanica* consists of fast energy-dependent quenching (qE) and slow zeaxanthin-dependent quenching (qZ). In excess light the thylakoid lumen acidifies, and qE is activated. LHCX1, and enzyme violaxanthin de-epoxidase (VDE), have been found to contribute to the qE stage of NPQ in N. oceanica in our lab, and knockouts of lhcx1 and vde have significantly low NPQ induction. This experiment uses *lhcx1* to further understand NPQ, as well as identify other molecular components involved in qE and qZ. The *lhcx1* knockout was treated by UV mutagenesis to create double mutants in *lhcx1* and enhancers or suppressors of NPQ. Mutant NPQ phenotypes were observed using video imaging. Using pulse amplitude modulated (PAM) video imaging to create an NPQ trace, mutant phenotypes can be classified into four categories. While enhancer mutants show lower NPQ than *lhcx1*, suppressor mutants patterns are varied. One group shows wild-type level qE and qZ, the second has wild-type qE with slower qZ, and the third displays intermediate levels of NPQ.

Brittany Carole Karki attends Berkeley City College and Laney College. She hopes to transfer to the University of California, Berkeley in the Fall of 2020. Brittany plans to continue pursuing research opportunities while working toward a Bachelor's of Science in BioEngineering, with the hope of eventually attaining her PhD. In her free time, she enjoys exercising and creating different forms of art, including drawing, painting, origami, knitting, and sewing.

ABSTRACTS

ESTHER MCCARTHY

Daniel Brauer (PhD Candidate) and Professor Matthew Francis
Chemistry

Exploring self-assembly of virus-like particle mutants

Self-assembling materials such as virus-like particles (VLPs) have attracted attention due to their well-defined, biodegradable nanoscale architecture. Therefore, these VLPs alway assemble with the same number of monomers, and thus will consistently have the same molecular weight and geometry. One promising example of this class of material is the MS2 VLP. MS2 VLPs are derived from the Bacteriophage MS2, an icosahedral virus that infects *Escherichia coli* (*E. coli*). When expressed the MS2 protein coat self-assembles into a 27 nanometer (nm) non-infectious VLP protein shell. These particles have the potential to be used in drug delivery, vaccination, and anticancer applications. For example, the Francis lab has previously covalently modified the interior of the MS2 wildtype capsid with taxol, a chemotherapeutic drug, in order to explore if this can reduce the harmful drug side effects. The Francis lab has also previously discovered a point mutation (S37P) that shifts the MS2 capsid to a smaller assembly phenotype. This 17 nm capsid has potential as an improved anticancer vehicle, since its smaller size may lead to increased accumulation in tumors. This size shift also offers an unprecedented opportunity to study the mutability of sequentially similar self-assembling particles with dramatic changes to the quaternary structure. This research aimed to discover the impact of amino acid mutations on the self-assembly properties of both the wildtype and the S37P point mutation. Results from these individual mutations can be used to inform predictive self-assembling protein models, as well as tune specific properties of capsids. We used Golden Gate Cloning to insert 10 mutated MS2 genes into a vector which was expressed in *E. coli*. Then we analyzed the capsids through Dynamic Light Scattering (DLS), Liquid Chromatography-Mass Spectrometry (LCMS), and High-Pressure Liquid Chromatography-Size Exclusion Chromatography (HPLC-SEC) to determine their mass, size, and assembly state. We successfully produced the 10 intended capsid variants as confirmed by DNA sequencing, SDS Page gel, and LCMS. Also, we confirmed the correct diameter of both the wildtype and the S37P mutation of 27 nm and 17 nm respectively. The diameter size was confirmed by through DLS and HPLC-SEC. Future work is to observe how the mutations affect physical properties such as thermostability of the MS2 protein capsid.

Esther McCarthy attends the Peralta Colleges, and plans to transfer to the University of California in the Fall of 2020 as a Chemical Biology major. After graduation, Esther hopes to attend graduate school. Esther is a member of MESA (Mathematics Engineering Science Achievement), and she is a MESA tutor at College of Alameda. In her free time, Esther enjoys baking, especially cakes and cookies, and playing video games with her siblings.

ABSTRACTS

PEARL OMO-SOWHO

Kate Morse (PhD Candidate) and Professor Elçin Ünal
Molecular and Cell Biology

Identifying factors that are important in LUTI-based repression

The time and location of gene expression affects how organisms will differentiate their cells into different lineages. Our lab studies *Saccharomyces cerevisiae* as a cellular differentiation model to understand how gene regulation affects development. Meiosis is a specialized type of cell division where a single cell divides twice to produce four daughter cells containing half the original amount of genetic information. Though translation affects the final level and localization of protein output, it is well established that transcription factors successfully passes on and coordinates gene expression during development.

In *Saccharomyces cerevisiae*, several genes are regulated through transcriptional interference and translational repression during meiosis. For these genes, a long-undecoded transcript isoform (LUTI) is expressed from a distal promoter. . LUTI mRNA expression induces a repressive chromatin state at the ORF-proximal promoter, which drives expression of the protein-coding transcript. Expression of the long isoform at the LUTI distal promoter results in cotranscriptional nucleosome repositioning at the proximal promoter, ultimately blocking transcription initiation at the proximal promoter. Furthermore, the LUTI is unable to produce protein due to the presence of repressive upstream open reading frames (uORFs) on its 5' extended region. Together, these factors prevent protein production when transcription is activated at the distal promoter. The factors responsible for nucleosome positioning changes during LUTI transcription are unknown.

To find factors important LUTI-based repression, we used a candidate-based approach to investigate chromatin remodelers known to play a role in co-transcriptional nucleosome positioning. Additionally, we are optimizing an unbiased selection approach using two LUTI reporter alleles.

Pearl Ogho Omo-sowho moved to Oakland, California in July 2016. She attended Laney College and graduated this Spring as valedictorian of her class. She transfers to the University of California, Los Angeles in the Fall of 2019 as a Human Biology and Society major, with a minor in African American studies. She aspires to attend medical school, become an obstetrics and gynecology surgeon, and bring her skills back to her home country of Nigeria. In her free time, Pearl volunteers at *Chapter 510* tutoring middle and high school students, and participates in theatre productions. She enjoys sleeping, watching movies, and reading.

ABSTRACTS

KARLY ORTEGA

Sarah Leinwand (Postdoctoral fellow) and Professor Kristin Scott
Molecular and Cell Biology, Helen Wills Neuroscience Institute

Neurodevelopment and maturation of learning and memory

As children develop and mature so does their learning and memory. How adult behavior matures and the underlying neurodevelopment changes are still unknown. We used the fruit fly, *Drosophila melanogaster*, as a model system because it provides us with a numerically simpler nervous system and powerful genetic tools. The *Drosophila* mushroom body (MB) offers a well-researched area of the brain with a specific function in learning and memory. The cells in this area of the brain are called Kenyon cells (KC). KC are then subdivided into different neuron classes αβ, α′β′, and γ. We are interested in α′β′ neurons as they are important for memory consolidation and the Scott lab has found a decrease in neural activity in early adult development, specifically in α′β′ cells. We track early adult development for a week. Young adult flies are considered to be at Day 0-1 (the same day as eclosion). Flies are considered to be mature adults at 7-8 days after eclosion.

We hypothesize that changes in neural activity during early adult development are correlated with anatomical changes of α′β′ cells over the first week of adulthood. We established a system using immunostaining to quantify changes in shape, branching and synapse numbers of individual α′β′ cells from young day 1 and mature day 7 flies by activating two UAS reporters with heat shocks. When these two UAS reporters are activated the expression will label the neurons' membranes with green fluorescent protein and the presynapses with a red fluorescent protein (mStrawberry) tagged BRP protein. Specifically, BRP is a protein known to be located at the presynapse. The presynapse is the site where the axon comes into contact with other cells and transfers information. These points of contact are known as synapses. I have found heat shock conditions that label only one or a few cells. This then allows us to quantify changes in shape, branching, and number or location of presysnapses to determine if there are differences with age. This will provide insight into how cells required for learning and memory mature in early adulthood. Studying these neurodevelopmental processes will ultimately provide us with a better understanding of mechanisms for brain development and the maturation of learning and memory.

Karly Ortega attends Merritt College and is majoring in Biology with a minor in Latin American Studies. She will be transferring to a university in the Fall of 2020. After earning her undergraduate degree she plans to attend medical school to pursue pediatrics. Currently, Karly teaches introductory entomology K-12, at a San Francisco non-profit called *SaveNature*. Apart from her academic and work life Karly enjoys gardening, drawing, camping and reading. A few of her favorite authors and poets are Ursula K. Le Guin, James Purdy, and Federico Garcia Lorca.

ABSTRACTS

YILDA PABLO

Jessica Tucker (Postdoctoral fellow) and Professor Britt Glaunsinger
Molecular and Cell Biology; Plant and Microbial Biology

The gammaherpesvirus MHV68 increases RNA polymerase III transcription during infection

Gammaherpesviruses, including human Kaposi Sarcoma Associated Herpesvirus (KSHV) and murine gammaherpesvirus 68 (MHV68), are viruses that are known to lead to cancer. These viruses manipulate the gene expression of their hosts in order to create a cellular environment that supports viral replication. Studying the virus's ability to manipulate host gene expression will help us learn more about the process of transcription in human cells. RNA polymerase III (RNAPIII) transcribes noncoding RNAs essential for cell growth, including transfer RNAs (tRNAs) utilized in protein synthesis. The transcription of RNAPIII genes goes up during infection with many DNA viruses, a phenotype shared with transformed and cancerous cells. To discover if the gammaherpesvirus MHV68 also induces RNAPIII activity, we examined how the virus activates expression of model RNAPIII genes with a type II promoter structure. We cloned a tRNA gene (tRNA-Arg from *D. melanogaster*), a retrotransposon gene (B2 SINE from mouse) and a viral RNAPIII gene (VAI from adenoviruses) into plasmids and expressed these genes in human HEK293T cells. We infected cells with MHV68 to compare RNAPIII gene expression in the presence and absence of viral replication. We measured gene expression using reverse transcription polymerase chain reaction (RT-qPCR) and found that transcription of Pol III genes increases during infection with MHV68. These results will inform future studies that will investigate the mechanism of RNAPIII upregulation during MHV68 infection and provide insight into RNAPIII dysregulation in cancer.

Yilda Pablo attends Merritt College and is majoring in Biology. She plans to transfer to a university in the Fall of 2021. Yilda enjoys spending time with family and listening to folklore shared by her father. She also likes exploring new places. Yilda strives to stay healthy by balancing her diet, playing sports, and exercising. In the future she would love to spend time helping others live a healthy holistic lifestyle and watching them grow by accomplishing their goals.

ABSTRACTS

ANDREA SALAZAR

Catherine Hernandez (PhD Candidate) and Professor Britt Koskella
Integrative Biology

Bacteriophages as an alternative disease management strategy for bacterial speck on tomato seedlings

With increasing global human populations, the demand for adequate resources continues to rise. Agriculture is no exception to this growing crisis. Although agricultural industries can fulfill current needs, the demand for crops will soon expand past this point. Such concerns have heightened research to investigate alternative disease management strategies in plants. Previous research has been done testing bacteriophage (phage) therapy as a possibility for treating and preventing bacterial plant diseases. Phages are viruses that infect bacteria and have a more limited range of impact than antibiotics. Early trials beginning in the mid-1920s had some promising results, but success was mixed partly due to the limited understanding of bacteria-phage interactions on plants. Given the rise in antimicrobial resistance, and the development of new technology and methods, interest has been revived in phage as a disease management strategy.

We investigated the interactions between lytic phages and the bacterial plant pathogen *Pseudomonas syringae*, which causes "bacterial speck" and infects a wide variety of agriculturally-important plants. We developed a high-throughput method for repeatable screening of phage-mediated lysis of *P. syringae* on tomato seedlings, which require less space and preparation time than adult plants. Seedlings grown from surface-sterilized seeds were inoculated by flooding with bacteria and phage. The cotyledons (seed leaves) were examined daily to record disease progression over a seven-day period. Each seedling was homogenized to quantify bacteria and phage densities at the end of the seven days. Our experiment consisted of two trials. The first investigated a low phage to bacteria ratio and the other tested a high phage to bacteria ratio. Our first experiment revealed that bacterial densities were not significantly decreased by the presence of phage, but phages did replicate. Our second trial showed that phages again replicated, but in contrast to our initial trial, bacterial densities were either significantly decreased or completely eliminated by phage. These results were also reflected in the disease progression of phage-treated seedlings. They exhibited fewer disease symptoms compared to non-phage treated plants, including minimal to no bacterial speck and prolonged life spans. From our work, we found that phage application on tomato seedlings using our methods can significantly reduce pathogen growth and disease symptoms, suggesting that this could be an effective disease management strategy for *P. syringae*. Future work will involve isolation of novel phages from field-grown tomato plants to determine if wild isolates are more effective than our lab strains. Development of less invasive plant protection methods can be beneficial for plants grown in various ways, including in agriculture, ecological restoration projects, or even community gardens. Our experiments will pave the way for studying alternative disease management techniques that could be applied around the world.

Andrea J. Salazar attends Chabot College. She is a proud resident of culturally-rich Hayward, nestled in the heart of the Bay. There she finds herself at the intersection of passionate communities. Most of her work is dedicated toward building unity, equity, social justice, and empowerment of underrepresented communities. Some of her accomplishments include co-founding the Indigenous Peoples Club at Chabot and collaborating with community leaders to organize events which focus on thinking critically to encourage cooperative action. She is currently pursuing an Ecology major and Ethnic Studies minor. Her mission is to cultivate environmental justice for indigenous communities across the globe. The inclusion of indigenous perspectives on environmental policies and efforts is essential for promoting a sustainable planet. Through the practice of ecosystem restoration and the integration of native wisdom and knowledge she hopes to pave the way for a more diverse science community. When she is not busy, Andrea is at an open mic, hiking trail, or music jam session.

ABSTRACTS

EDUARDO SANTILLÁN SANCHEZ

Santiago Yori (PhD Candidate) and Professor Andreas Martin
Molecular and Cell Biology

Modification of the 26S Proteasome for substrate trapping and identification

The removal of proteins is an important cellular process. Proteins are an essential group of macromolecules involved in thousands of cellular processes, such as cell signaling and replication. Some proteins are regulated through their degradation and failure to remove them can result in disease. Proteins may also become misfolded and lose their functions, these misfolded proteins can become toxic to the cell and are normally sequestered and degraded. In eukaryotic cells, the molecular machine responsible for degradation and protein homeostasis is the 26S proteasome. The proteasome's role is to housekeep the cell's proteome, however we do not have a complete picture of the variety of substrates processed by the proteasome. Our mission is to identify the behavior of the proteasome and its conformational changes after post-translational modifications, as well as indexing the cell's degradome - the entire set of a cell's degraded substrates. In order to prevent degradation of substrate for identification, we altered the base's structure to covalently trap the substrate at the hexameric AAA+ unfoldase of the proteasome. Once trapped, we can use mass spectroscopy to identify proteins commonly degraded in the cell. We are also able to determine the specificity of the proteasome for specific substrates in varying conditions. With these findings, we hope to further understand the function of the proteasome in eukaryotic cells.

Eduardo Santillán attends Chabot College. He intends to transfer to the University of California in the Fall of 2020 as a Biochemistry major. He plans to pursue pharmaceutical and medicine manufacturing or work in research, developing treatments for autoimmune diseases. Eventually, he hopes to teach at a community college level. Aside from learning, Ed enjoys playing the guitar, going to raves, playing video games with his friends, and spending time with his girlfriend.

ABSTRACTS

SHEWIT SIUM

Shawn Costello (PhD Candidate) and Professor Susan Marqusee
Molecular and Cell Biology

Investigating the structural determinants for efficient co-translational folding of the model protein HaloTag using circular permutation

Protein folding is a physical process by which a polypeptide chain folds to its native 3D structure, which is key to determining function. Protein folding is a very sensitive process that can be affected by external factors including temperature, pH, and ionic strength. These factors can affect the ability of protein to fold into their correct form or structure. Misfolded proteins, or proteins that fail to fold correctly, are often inactive or toxic and cause disease. One external factor that is of great interest is the proximity of the ribosome and vectorial synthesis. Most protein folding studies monitor the folding of full length protein, however proteins are translated by the ribosome and can begin folding as they are being synthesized. This process is called co-translational folding and several studies have shown that this process can result in folding that is faster and more efficient than folding off the ribosome. In this study we are using circular permutation to investigate the structural determinants for efficient co-translational folding of the model protein HaloTag. Circular permutation changes the linear arrangement of structural regions in a protein, and because translation is vectorial this will change the order of synthesis and possibly the co-translational folding pathway. To create circular permutants we performed Gibson assemblies. We then expressed the circular permutants in E.coli and purified the protein using ion exchange and gel filtration chromatography. We then used circular dichroism and fluorescence polarization techniques to determine the circular permutant stability, folding rate and co-translational folding efficiency which we compared to wild-type HaloTag. We found that our circular permutant 59 is prone to misfolding both in cells and during in vitro translation, while circular permutant 195 was able told fold well during both processes. These results along with data from other circular permutants will allow us to identify the structural effects for the efficient co-translational folding of HaloTag.

Shewit Sium attended the Peralta Colleges and transfers to the University of California, Riverside in the Fall of 2019 to pursue a degree in Microbiology. After completing her undergraduate degree, she wants to pursue a career in a health profession. During her free time she enjoys reading, traveling and swimming.a

ABSTRACTS

SHAUNA WATSON

Samantha Fernandez (PhD Candidate) and Professor Nicholas Ingolia
Molecular and Cell Biology

The impact of sequence variation on alternative translation initiation in CEBPA

Proteins are responsible for important functions carried out within a cell, from building structures to supporting immune health, making protein synthesis essential to living organisms. Translation initiation dictates which proteins are expressed within cells and recent evidence suggests that this process is much more complex than previously realized. We now know that alternative translation initiation occurs on mRNAs to not only regulate protein expression but to produce new protein isoforms. One such protein that undergoes alternative initiation is human CCAAT Enhancer Binding Protein Alpha (CEBPA), a transcription factor that controls the expression of specific genes. Initiation occurs at two alternative start codons in CEBPA's mRNA to produce either a long or short protein isoform. The long isoform activates transcription while the short isoform lacks a critical activation domain, rendering it incapable of activating transcription. This provides these isoforms with the ability to predetermine the fate of the cell. CEBPA has an evolutionary conserved upstream open reading frame (uORF) contained in its 5' untranslated region (UTR) that is an important component for alternative translation initiation. Using a dual-color reporter assay, we can measure the relative abundance of the two isoforms. Considering the importance of the 5'UTR for modulating start site selection, we pursued defining which area in CEBPA's 5' UTR that regulates this choice. To do so, we first leveraged the natural sequence variation in CEBPA to ascertain which part is responsible for the differences in isoform expression. We cloned the 5'UTRs from three homologs of human CEBPA upstream of our dual color reporter and measured the expression of the two isoforms by flow cytometry. Preliminary results found that specific homologs increased the expression of the long isoform relative to the short isoform whereas others increased the expression of both isoforms. These results suggest that the 5'UTR of CEBPA is critical in regulating its alternative initiation and proposes that the relative expression of the two isoforms has been fine-tuned over evolutionary time.

Shauna Watson is originally from Oakland and has lived all over the Bay Area, although she considers herself settled in Oakland since moving back 4 years ago. She was an Analyst in IT for 10 years prior to returning to school at the Peralta Colleges in 2017. Currently, Shauna is majoring in Statistics with an end goal of gaining a Master's in BioStatistics. She loves being a math tutor for Laney College and providing private in-home tutoring. Shauna plans to transfer to the University of California in the Fall of 2020. In her free time she enjoys soaking up as much time as possible with her husband Sean and her 4-year-old, Shani.

ABSTRACTS

ELIANA ZAPATA

Gina Caldas (Postdoctoral fellow) and Professor Abby Dernburg
Molecular and Cell Biology

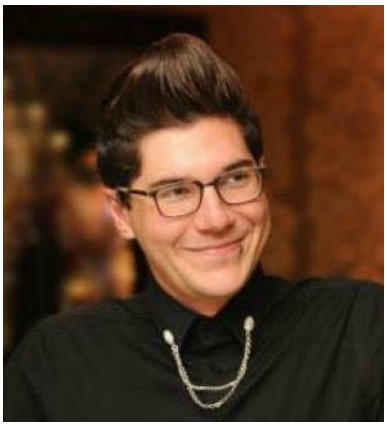
Characterization of ZIM/HIM C. elegans mutants in Homologous Chromosomes Pairing

Meiosis is an essential process for sexual reproduction. During Meiosis, germ cells give rise to haploid cells, which later mature into an egg or sperm. C. elegans have large germlines in which the different steps of meiosis are organized in a spatial and temporal manner, making them an ideal model system for investigating different aspects of meiosis. One of the first events upon meiosis entry is recognition and pairing between homologous chromosomes. Specifically, maternal and paternal chromosomes of the same class find each other and pair. Pairing is later stabilized by the synaptonemal complex (SC), which forms along homologs. Correct homolog pairing is necessary for later crossover formation and recombination, which is essential for proper gamete formation and a genetically diverse offspring. However, how homolog chromosomes are able to accurately recognize each other upon meiosis entry is a fundamental question that has yet to be answered.

At one end of C. elegans chromosomes, there are regions called “Pairing centers” which are enriched for DNA motifs that recruit the zinc-finger ZIM/HIM proteins. Previously, it was shown that absence of these proteins result in defects in homolog pairing, demonstrating the important role of ZIM/HIM proteins in this process. By mapping the architecture of chromosomes at early meiotic stages, our lab has recently discovered the existence of chromatin loops at the pairing center regions. The bases of these loops occur at the ZIM/HIM motifs, suggesting that ZIM/HIM proteins may serve as loop anchors. A reasonable hypothesis is that ZIM/HIM proteins promote loop formation, and loops are required for recognition and pairing between homologs. To test this hypothesis, we seek to characterize a C. elegans strain in which two of the ZIM/HIM genes have been removed (Dzim-3; Dhim-8), and map chromatin architecture in absence of these proteins. My contribution to this project will be to characterize pairing defects in Dzim-3; Dhim-8 animals, developmentally and cytologically, and to generate a Dzim-3; Dhim-8 strain that can be manipulated for enrichment of early meiotic nuclei, which is necessary to investigate chromatin architecture in early meiosis. Results from this work will be important for future studies on the role of ZIM/HIM proteins in homologous recognition.

Eliana Zapata attends Chabot College in Hayward, the city where she was born and raised. She plans to transfer to a four-year university in the Fall of 2020 to pursue a Bachelor’s degree in Psychology. Eliana loves reading fiction, painting with her sister, and traveling with her friends. Being a part of the NIH B2B program has opened her eyes to many different career paths and inspired her to explore what she wants to do after acquiring her degree.

IN MEMORIAM



CRIS ALVARO (1988–2018)

In memory of Cris Alvaro, Ph.D., our first Summer Coordinator, who was instrumental in shaping our Summer Research program and in changing the lives of the students with whom they worked.

Cris identified as trans and non-binary, and used the pronouns they/them/theirs. They were passionate about creating an inclusive environment in science, an environment where diversity—of race, ethnicity, gender, class—would be embraced.

The programming that supports our students during their summer experience all began with Cris. From creating a safe space for students to be vulnerable at the program orientation, to decoding what it means to be a "scientist", to organizing and facilitating weekly community-building dinners, to individually mentoring each student, to helping each student prepare their final research poster, to addressing any issues or problems that arose, to re-envisioning the process we use for selecting mentors (and the support that we provide the mentors), Cris did it all.

But most of all, Cris provided support, encouragement, and empathy to our students, and helped them to see that they, too, belonged in science.