



Biological and Agricultural Sciences

Diana Tafoya, Claudia Yañez and Jennifer Mitchell

Herbarium at Zzyzx

Faculty Mentor: Kathryn Theiss

The purpose of the study is to educate the community on the role of herbarium specimens. Herbarium specimens serve as a permanent record of the flora in a given area at a given time. This permanent record serves as a baseline which can be used to monitor changes in the flora due to climate change or habitat destruction. The desert of the Southwestern United States are an understudied area in this regard and so we focused our efforts on the Mojave National Preserve. Alan Romsper started at the Desert Studies Center in Zzyzx in 1976 and collected plants from the Mojave Desert until the mid-1980s which allows us to have a relatively complete species list for the area at this time. We produced the first formal catalog of these species and compared their diversity to that of other herbarium collections. We found that the collection at the Desert Studies Center was extremely well preserved and are not duplicated in other herbaria collections. This unique collection housed at the Desert Studies Center has unrealized potential in evaluating the effects of climate change on the Mojave National Preserve.

Funanya Uchemefuna, Precious Holley, Samantha Perez

Floral Visitors of a Tropical Milkweed

Faculty Mentor: Kathryn Theiss

Botanic gardens increase the local biodiversity within urban environments by attracting wildlife, especially pollinators. Botanic gardens often have complex community dynamics involving interactions between different species and often include a variety of both native and non-native plant species. This research aims to understand the role non-native plant species play within an urban setting. We focused on the tropical milkweed species, *Asclepias curassavica*, and this research is a continuation of previous student research. We observed floral visitors on this species at the South Coast Botanic Garden on the Palos Verdes Peninsula from September to November, 2019. We recorded the interactions various insects had with the plant such as visit duration, and the number of flowers visited by each insect. The majority of visitations observed were of the common honey bee, *Apis mellifera*, which is another non-native species. The second most common species, though much less frequent, was the monarch butterfly. We made comparisons of our data to observations from previous years to understand multi-year variation in visitation. We also provide ideas on how this type of research could be conducted with K-12 students.



Chris Navarrete, Valerie Leonard, Gloria Arellano

Population Genetics in the Pale Evening Primrose

Faculty Mentor: Kathryn Theiss

The evening primroses (*Oenothera*) are an ecologically important group who are threatened by climate change and geographic isolation. They grow across the Western United States in a variety of habitats including deserts, sand dunes, mountains, and prairies. We are particularly interested in the pale evening primrose, *O. pallida* ssp. *pallida*, which grows in low elevation sand dunes throughout the high deserts of Oregon, Washington, Idaho, and Utah. We used microsatellite markers, a common molecular tool for evaluating genetic diversity, to look at population questions related to this species. We extended the work of previous students in filling in missing data, and compared our data to other species of *Oenothera*. We first determined if missing data was due to poor DNA quality and if so, these samples were excluded from further analyses. We then reanalyzed the data with the missing values included, and found extremely high rates of genetic diversity across populations, with little genetic structuring. One of the reasons that this species has such high levels of genetic diversity across populations is that it is pollinated by the long-distance flying hawkmoths. We also provide examples of how this type of research could be incorporated into a K-12 learning environment.

Eliseo Villarreal, Brittany C. Brown-Sanchez, Juan Nuno

Characterizing the microbes in nectar carried by individual pollinators

Faculty mentor: Karin E. Kram

Milkweeds (*Asclepias curassavica*) are an important plant resource for many animals, including monarch butterflies. The animals that visit the plants deposit microbes in the nectar, which may affect the behavior of other plant visitors. Our investigation focused on characterizing the relationships of microbes to *A. curassavica* pollinators. First, we collected nectar from milkweed plants that had been visited by a single pollinator at the South Coast Botanical Garden and plated a sample the nectar on nutrient rich agar plates, allowing us to grow microbes from the nectar. We isolated each unique looking microbe, and amplified and sequenced their DNA to identify them. We were able to begin to correlate certain microbes with certain pollinators, for instance *Bacillus* species were often deposited by hover flies. We also extracted DNA from the nectar samples to characterize the entire microbial community, even those that are not culturable. We plan to identify more microbes, and determine the relationships they have with each other and with pollinator visits. These data will help us to characterize how pollinators affect the microbes in milkweeds, allowing us to use this information to form hypotheses and design experiments to test how these microbial communities might affect other pollinator interactions.



Stacy Zamora, Tania Lugo, Peter Paulino, Kevin Urstadt

Examining the effects of estradiol on expression of Δ fosB and Alk mRNA after exposure to cocaine

Faculty Mentor: Philip Vieira

Substance use disorder is a chronic relapsing disease associated with alterations in the brain's mesolimbic reward pathway, and cocaine is a substance featuring such changes. Exposure to cocaine alters expression of Δ FosB, a transcription factor that reshapes neural structures in the mesolimbic pathway. These changes increase cocaine-seeking behavior and sensitivity. In contrast, the LIM-domain only 4 (Lmo4) gene encodes LIM domains that interact with DNA-binding transcription factors and attenuate sensitivity to cocaine. A third molecular switch, anaplastic lymphoma kinase (Alk), is inhibited by LMO4 and appears to promote cocaine sensitization. Sex differences in behavioral responses to cocaine have been previously observed, with estrogen/estradiol acting as a mediator. When estradiol is present in the ventral tegmental area of gonadectomized rats after exposure to cocaine, an increase in Δ FosB expression was observed – suggesting estradiol as a modulator. Bagley et al. (2017) demonstrated that estradiol increases cocaine preference and enhanced acquisition of cocaine self-administration in gonadectomized rats. This may be mediated via LMO4, as LMO4 interacts with estrogen receptor α (ER α) at the Alk promoter. Indeed, ER α knockout mice demonstrate increased cocaine sensitization with increased Alk expression in the nucleus accumbens. Since estrogen likely mediates sex differences, regulation of Alk by estrogen may be the mechanism for sex differences. Thus, this project focuses on molecular changes seen in the reward pathway in rats exposed to cocaine and estradiol, specifically the prefrontal cortex, nucleus accumbens, and major terminal areas of mesolimbic projections. Flash-frozen brains from gonadectomized male Sprague-Dawley rats exposed to 1mg/kg of cocaine and 5 μ g/0.1mL of estradiol were supplied by Bagley et al. The aforementioned areas of interest were isolated, and Δ fosB and Alk mRNA were extracted and quantified through RT-qPCR. By understanding the mechanisms and roles of estrogen and different genes in substance use disorder, sex differences can be better understood.

Treasure Porter, Mireya Abril, Alexia Mayorga

*Speciation of the Australian lizards, *Ctenotus duricola* and *Ctenotus zasticus**

Faculty Mentor: Sonal Singhal

A species is a single gene pool, which represents a group of individuals that are capable of breeding together. Studying species is important because this information is used to organize and classify different types of organisms, and it can help inform conservation differences. In this study, we are studying the Australian lizards (*Ctenotus duricola* and *Ctenotus zasticus*). *Ctenotus zasticus* has a very tiny geographic range, and they are in danger of going extinct due to construction and mining being done in their habitat. But, it is not clear if *C. zasticus* is actually a distinct species. To answer this question, we collected and analyzed over 2.5 million base pairs of genetic data across an average of 20,000 loci for 27 individuals. We then used these data to determine the number of genetic units within these species and to infer their evolutionary history. To conclude this study, we hope to discover whether the lizard species *C. zasticus* is in fact its own distinct species. This discovery could potentially help cease further destruction of their habitat and help protect them from extinction.

**Erick Galdamez Calles, Ítalo Luján pedreschi, Chez Epps***Phages from the Bay*

Faculty Mentor: Brinda Govindan

Bacteriophages are starting to become more prevalent in today's Scientific research as antibiotics are starting to lose potency with more and more superbugs being prevalent. In this study, different water samples from around San Francisco bay; Ocean Beach, Lake Merced, and Candlestick Park were obtained, filtered, then plated to observe if plaques would form. It was hypothesized that water from Candlestick Park would contain more bacteriophage when plated than water from Lake Merced and Ocean beach respectively, since bay water has more runoff from San Francisco streets which contain a broad range of bacteria and possibly bacteriophage. Each water sample was centrifuged and filtered in order to get rid of any bacteria or phytoplankton that may be in the water. Using a double agar method, the filtered phage water was then combined with E. coli (HB101) and melted top agar and plated on LB agar plates. Taking an average of each water sample that was plated, Lake Merced had the most plaque forming units(PFU's) at 12.33, while Candlestick had 9.2 PFU's and Ocean Beach with 4.2 PFU's.

Natalya Cardona*The impact of climate heterogeneity in niche evolution and diversification of Encelia in Western North America*

Faculty Mentor: Sonal Singhal

Closely related species can rapidly diversify across different environments, leading to large phenotypic differences between species. One example is the species in the Encelia genus, a genus of perennial desert shrubs. The species in this genus evolved within the last five million years and rapidly radiated throughout North American deserts to inhabit a spectrum of niches. Ecological niche modelling (ENM) uses geographic and environmental information to characterize the niche of species. These models can then be used to study niche evolution and its relation to speciation. Here, we use environmental data (climatic & soil composition data) and species occurrence records mined from online databases to construct ENMs. We then integrate these with a species-wide phylogeny to test models for divergence or conservatism of niche across species diversification. Our study seeks to understand the environmental variables driving niche evolution and radiation of Encelia across the deserts of California & Mexico. Doing so will allow us to understand the impact of climate heterogeneity in rapid species radiation. In particular, we test if closely-related species have divergent or conserved niches. If we find closely-related species have divergent niches than expected under a null model of niche evolution, environmental factors (change in climate) significantly impact niche divergence and is a driver of speciation. If we find species have more conserved niches, then environmental factors might not have a significant impact in niche evolution and is not a significant driver of speciation. More generally, our work will characterize the effects of historical climate change in evolution.



Annette Zaragoza

Night Puppies are Man's Best Friend, Too!

Faculty Mentor: Ashish Sinha

The aim of this research project was to study the bat population in Northern California, and its declining rate due to White-nose Syndrome. In doing so, the various difficulties the current population encounters were considered, such as increasing environmental temperatures, and decreased fertility. In addition to understanding the mechanisms for bat population decline, a continued effort aims to progress the association between a declining populations with a rise in mosquito-borne illnesses. Purposefully, the research will highlight areas of overlap between the two factors in an attempt to illustrate the impact a bat population has on the general health of humans. When there is a rise in the mosquito population, statistically there is an increased chance of contracting a mosquito-borne illness; bats help regulate mosquito populations. The overall knowledge of these creatures remains unfulfilled due to their elusive nature and difficult study sites. I plan to utilize secondary data and research to develop an insight into the relationship between bats and mosquito-borne illnesses. Overall, the plan is to enlighten the general public of the important eco-services bats provides, hopefully inspiring an increased conservation effort.

Gabriel Angulo

Geographic Information Systems for invasive species research and better communication with stockholders.

Faculty Mentor: Parveen Chhetri

The most common contributor to past human-caused species extinction is invasive species. They are only second to land cover and use changes caused by humans. California is significantly affected by the existence of invasive species. California is densely populated, has diverse topography, soil, and climate, which make it favorable for a wide range of invasive species. Like islands, which are especially susceptible to invaders, California is isolated from other terrestrial areas by ocean, mountains, and desert (Dowell and Gill 1989, Bakker and Slack 1971). A research gap exists when it comes to the work being done on invasive species and landscape management. Differences between scientific theory and application have typically limited opportunities for model-based knowledge to reach the stakeholders responsible for problem-solving (Tonini and Shoemaker 2007). This is what is known as a knowing-doing gap, where science fails to communicate their findings properly, or management fails to use the resources provided by research. I gathered data on invasive species of flora that exist in Southern California that are ranked by the National Forestry Service as requiring immediate treatment response due to a combination of invasiveness, high site susceptibility or values, and/or with high spread potential. Doing so will test the potential for Geographic Information Systems (GIS) to bridge the knowing-doing gap.. I used tabular data gathered from the United States Forestry Service, and US Federal Data for topography of Southern California. I manipulated tabular data by exporting selected attributes in the GIS platform. I used the Aggregate polygons tool to create new features for ecosystems in Southern California. Maps were developed using GIS. GPS data gathered from Cal flora was used to create polygons representing Invasive flora. Final outcome of this project is a possibility for becoming a user-friendly tool to bridge the knowing-doing gap.



John Coulston

Investigating Zebrafish Gut Microbiome Dynamics throughout Development

Faculty Mentor: Fang Wang

Human health heavily depends on our own microbiomes. Imbalances in one's microbiome have recently been connected to multiple health conditions such as obesity and diabetes. However, host-microbiome interactions have not been well understood. Since zebrafish live for about three years in a controlled laboratory environment, we can study and record their microbiome over the course of their entire life. There are numerous genetic, molecular, and cellular tools readily available for zebrafish as well; enabling us to conduct functional analyses and manipulation. In particular, we utilized DNA metabarcoding and Next Generation Sequencing to isolate microbial DNA and identify which microbial phylums are present, as well as their relative proportions. We have collected gut microbiome samples from 4 month old, 6 month old, and 13 month old male and female wildtype zebrafish. The microbial DNA was isolated and barcoded using 16sRNA V4 primers. The DNA was then sequenced using Illumina MiSeq (a Next-Generation Sequencer) and was then analyzed using software USEARCH. Upon analyzing the results, it was found that while the 13 month old male and female zebrafish microbiomes were rather similar. However, the four month old mixed gender zebrafish contained a noticeably different distribution. The 4 month old zebrafish gut microbiomes contained a much larger proportion of unidentified OTUs. Most interestingly, 6 month old male and females have noticeably different proportions. Both microbiomes had relatively the same abundance of Proteobacteria. However, males had a large percentage of Tenericutes while females had a large percentage of Firmicutes. We will be collecting more samples from 6 month old zebrafish to confirm this trend, and look into possible influences as to why this would happen.

Taylor Wright

The Prevalence of n-Nitrosodimethylamine in Our Produce

Faculty Mentor: Shannon Roback

This study focuses on the N-nitrosamine known as N-nitrosodimethylamine (NDMA) which is regularly found in treated drinking and wastewater. We further wanted to focus on the possible prevalence of NDMA in water used in crop production. All samples were collected from a farm in Monterey, California. The methods used for sampling included collecting vegetables, soil, and water. Collected vegetables included broccoli, brussel sprouts, celery, and spinach, which were all collected in replicates of three. Samples of soil were collected from each of the six different sites on the farm where the vegetables were grown, also in replicates of three. Water samples were gathered from the local water sanitation plant that supplies water to the farm, in replicates of two. After all samples were collected and properly cleaned, they were stored in ice chests on dry ice, and shipped overnight to the University of Wisconsin-Madison. Researchers at the University of Wisconsin-Madison are working as our partners, and testing for levels of NDMA that may possibly be present in the crops collected, as well as the water used to grow the crops. The data for this study is forthcoming and will be presented during student research day.



Raul Gutierrez, Erik Martinez

Identifying Genes That Play a Role in Long-Term Stationary Phase in Escherichia coli

Faculty Mentor: Karin Kram

Escherichia coli can adapt to live in an environment without any additional nutrients for long periods of time. When *E. coli* grows in an environment where nutrients are scarce, they enter long term stationary phase (LTSP). We can use this phase in the lab as a proxy for a more natural environment and observe how cells adapt to these conditions. In order to identify nonessential genes that play a role in survival during LTSP, we competed cells in the KEIO collection with wild type (WT) *E. coli* cells. The KEIO collection is a set of *E. coli* strains, each with a single-gene deletion of a nonessential gene, representing all non-essential genes. We performed competitions with WT cells during ten days of incubation, into LTSP. After screening the entire collection, we identified 101 gene deletions that affected the cell's ability to compete with WT. While some of the identified strains did not show a difference in growth once competitions were in tubes versus the 96-well plates used for screening, we were able to confirm that some of the strains did have a difference in growth compared to WT cells. Several strains, including those missing *carB* (encodes enzyme for amino acid metabolism), *fpr* (involved in redox reactions in central metabolism), *mprA* (produces a regulator involved in antibiotic resistance and efflux), *gor* (helps maintain sulfur groups for storage) or *hdfR* (regulates transcription of operon that encodes protein for flagella synthesis) were outcompeted by WT cells during LTSP, indicating that these genes are essential for survival in long-term cultures. Overall, we have identified several genes that are important for survival in LTSP and can begin to determine why these genes play a role in survival into LTSP by determining their function in long-term cultures.

Albert Barrios

Insulin Receptor Isoform IRA/IRB Expression in Breast Cancer Cell Lines

Faculty Mentor: Douglas Yee

Breast cancer cells express both Insulin-like Growth Factor Receptor Type 1 (IGFR1) and Insulin Receptor (IR) that promote the growth and survival of tumors. IR are composed of two different insulin receptor isoforms; IRA and IRB. We utilized IR isoform specific primers in quantitative reverse transcriptase PCR (qRT-PCR) that was validated using IRA and IRB overexpressing clones of MCF7 cells and normal human tissues. Over 40 breast cancer cell lines and ER+ patient tumor samples, were studied to determine IRA, IRB, total IR, IGFR1, IRS1, and IRS2 expression in cell lines and patient samples. Across the ATCC breast cancer cell lines and ER+ patient tumors, heterogeneity was found between all targeted genes. However, one group of cell lines like ZR-75-30, MDA-MB-468, and HCC1806 commonly expressed low expressions of IFGR1, but high expressions of total IR, where IRA isoform is predominantly expressed. It was also shown that some cell lines like MDA-MB-134-VI, HCC1500, and BT-483 expressed highly throughout all targeted genes, but significantly in both IGFR1 and total IR. In ER+ patient samples, it was commonly found gene expressions levels were comparable between IRS1, IGFR1, and IRA, while some patient samples expressed IRB more than IRA. Utilizing these genes can serve to screen patients for targeted therapy. Some ER+ patients, u11-13031 and k11-1608, can be revisited for further clinical trials to observe if treatments are effective by targeting IGFR1, IRS1, and IRA. Using CRISPR technology, IRS1 was knocked out completely for one clone, and it was confirmed via western blot and qRT-PCR analysis, which resulted in the inhibition of ligand-stimulated growth of cells. In Tamoxifen Resistant MCF7 and Long Term Estrogen Derived Cells MCF7 lines, it was shown that IGFR1 gene expression was absent, and IRS1 expression in low levels. However, further analysis is needed to characterize any prominent cell lines.



Juana Alcocer Infante

NMR studies of the HIV-1 p17 heparan sulfate binding

Faculty Mentor: Kari Pederson

Human immunodeficiency virus (HIV) destroys the immune system by attacking and destroying white blood cells. HIV has an efficient life cycle that helps it replicate and spread throughout the body. Modern medicine only helps to block HIV at different stages of the life cycle. Evidence shows that HIV protein p17 plays a critical role in the retrovirus life cycle. HIV-1 p17 binds to heparan sulfate and regulates its bioavailability. The present study is long term, focusing on the binding strength of heparan sulfate ligand to p17 in HIV. First, it is necessary to optimize the expression of p17. HIV-1 p17 is expressed by inserting a short DNA sequence into E. coli, growing E. coli, chemically inducing protein production and purifying the protein. Optimization is carried out by varying the length of time and temperature of the E coli growth procedure. Maximizing the yield of p17 is necessary in order to have concentrated samples for future NMR experiments to study the binding interactions.

Jocelyn Molina-Mancio

Metabolic changes in adipose tissue in response to Chronic Electronic Cigarette Exposure

Faculty Mentor: Jorge Espinoza-Derout

Tobacco use is a leading cause of preventable death in the United States. In recent years, electronic cigarettes (e-cigarettes) use by youth has augmented at a disturbing rate. Nicotine can induce lipolysis in adipocyte tissue, leading to increased serum free fatty acids (FFA). Chronic increase of FFA has been shown to contribute to the development of insulin resistance and metabolic syndrome. In adipocytes, decreased levels of Sirtuin 1 (SIRT1) are associated with metabolic syndrome. Our laboratory has shown that chronic e-cigarette exposure induces cardiac dysfunction, atherosclerosis and hepatic steatosis in the ApoE knockout (KO) model. In this study, we investigated the role of adipocyte tissue in the metabolic changes associated with e-cigarette exposure. We developed a mouse e-cigarette exposure model system that delivers nicotine in mice that is equivalent to that in human e-cigarette users. ApoE KO mice were exposed to saline, e-cigarette without nicotine [e-cigarette (0%)] and e-cigarette with 2.4% nicotine [e-cigarette (2.4%)] aerosol for 12 weeks. We observed increased serum FFA levels in mice treated with e-cigarette (2.4%). Western blot analyses showed that mice treated with e-cigarette (2.4%) had decrease levels of SIRT1 when compared to with control mice. The increased levels of serum FFA and SIRT1 depletion may suggest a role of adipocyte tissue in the metabolic effects produced by e-cigarettes. Understanding the consequences of e-cigarette use on metabolic disease is directly relevant to the development of policies related to e-cigarette use.