

I fell in love with science before I started my undergraduate career when taking community college classes that introduced me to the world of research. Through a wide assortment of research opportunities, I have gained a passion for research in mechanisms and systems of gene regulation. I wish to continue to learn and discover more in the field of epigenetics and transcriptomics. I like to think of the field of gene regulation to be looking into the ancient language of genetics and how we can understand the words (genes) of life, but now need the grammar (gene regulation) to gain a better understanding of biological systems that can lead to great strides in both medical and agricultural tools. Furthermore, I believe that the University of Washington, Seattle's Genome Sciences Ph.D. program matches the work ethic and experience I have gained in my undergraduate career and can give me the training I desire to contribute to the field of gene regulation.

When starting at UCR, I was a Neuroscience major. I later decided to major in Cellular, Molecular, and Developmental Biology to gain an in-depth view of the different levels of genetics that affect living organisms. I added a minor in Applied Statistics later to understand the data pipeline of research. Determined to gain more experience, I looked outside UCR and applied to several NSF-funded Research Experiences for Undergraduates (REU). I was accepted into the Genome Science Summer Research program at The University of Washington, funded by the NSF REU program. During the summer of 2019, I worked in Dr. David Hawkins's lab. In his lab, I worked on a project dealing with the functional conformation of cis-regulatory elements in human t-cells and macrophages that either has enhancer activity (increase gene expression) or silencer activity (decrease gene expression). I investigated these regulatory elements by using a vector that had a weak promoter and inserted two different libraries of fragmented human DNA in a Massively Parallel Reporter Assay (MPRA). The libraries generated included one for possible enhancer regions and the other for possible silencer regions. Data collection and analysis looked at the ratio of gDNA to cDNA in each region tested by using High-throughput Sequencing to observe if any had enhancer (higher cDNA count than gDNA) or silencer activity (higher gDNA count than cDNA). Understanding these cis-regulatory elements can lead to a better understanding of how certain diseases function, with the disease not simply being a genetic issue but a regulatory issue such as immune-mediated diseases. Learning and understanding how impactful gene regulation is from Dr. Hawkins's lab inspired me to strive to learn more.

This experience gave me perspective on my desire for a career in the sciences and pushed me to work towards graduate school. As a result, I asked for guidance at UCR's Graduate Division and asked what I should work towards for graduate school. I was told about the UC Leadership Excellence Through Advanced Degrees (UC LEADS) program I qualified for. I applied directly after and was chosen as a member. At the time, I was also very involved in possibly one of the most impactful communities in my career choice, the Louis Stokes California Alliance for Minority Participation (CAMP). CAMP gave me opportunities to receive funding, allowing me the freedom to gain further research experience during my school years, and provided an important support group on my journey navigating the world of academia. Since I believe strongly in its goal of making research approachable and affordable for people in underrepresented communities, I decided to run for a leadership position. I joined the STEM program's board of officers my sophomore year of college and later became the acting president my junior year to help other students find their path in science.

During my time as President of CAMP, I ensured that we stayed fully functional during the online world the Covid -19 Pandemic created. I decided that our main goal for the 2020 - 2021 school year was to give as much information on career development in STEM as possible. The primary way I wanted to accomplish this goal was by inviting different experts from different areas of science to come and talk about their path in science. We invited UCR faculty to speak about their experiences in STEM and had speakers from industry to talk about what other careers are available in science. To further prepare members, we had a panel of previously graduated CAMP alumni come to answer questions students have about graduate school and give advice to students interested in following a career in academia.

Driven by my curiosity about gene regulation, I was excited to start in Dr. Xuemei Chen's lab as part of CAMP Scholars, a program to help students with funding research during their school year. Her lab investigates the role of micro-RNA in gene regulation and the mechanisms of RNA noncanonical capping in *Arabidopsis thaliana*. The main project focus was to look into non-canonical RNA end-caps in *Arabidopsis thaliana* that are characterized as other substrates acting as the 5' end-cap of RNA other than the canonical 5' m7G cap. I began by reviewing the current literature on enzymes possibly functioning as a decapping mechanism with common non-canonical RNA end-caps, such as the redox cofactor NAD-capped RNA. Later during the summer of 2021, I participated in UC LEADS summer research program, where I designed experiments for investigating the subcellular localization of these enzymes that possibly decap non-canonical RNA. More specifically, I was interested in finding enzymes that localize in the mitochondria of plants since many of the substrates that can act as end-caps are associated with metabolism. This incredibly excited me since it was interesting to think about how there could be a connection between energy production and gene regulation. To observe these enzymes, I transiently expressed them in *Nicotiana benthamiana* each fused with a fluorescent marker and co-infiltrated with a mitochondrial fluorescent marker to observe under a confocal microscope. After the Summer of 2021, I continued working on this project for two more quarters, funded by the CAMP Scholars program. Now, I am focusing on optimizing better visualization techniques and creating an effective mitochondrial marker. Working on this project has been the most impactful on my development as a researcher. It has challenged me to continuously push forward to find solutions to problems and constantly improve my lab techniques.

I was able to further use and develop my research aptitude in the summer of 2022 when I was funded by UC LEADS to participate in UC San Francisco's Summer Research Training Program. During my time at UCSF, I worked in Dr. Yin Shen's neurobiology lab. During my time there, I investigated the evolution of the human brain from the perspective of gene regulation. The main focus of the project was looking at the most evolved region of the human genome, called the Human Accelerated Regions (HARs). During this time, I was able to utilize all my experience in research to leverage RNA-seq to investigate if the HARs can humanize chimpanzee cells if inserted into induced pluripotent stem cell-derived two-week excitatory neurons. Working on this project gave me the final boost in confidence I needed to solidify my resolve to apply to graduate school and confirm my passion for the field of epigenetics.

With my experience and intellectual interest aligning with the University of Washington, Seattle's Genome Sciences Ph.D. program, I believe I could grow as a researcher and contribute to research in gene regulation. My time in Seattle was by far one of the most impactful times in my scientific career, and being able to continue it with all the outstanding faculty I am already familiar with would be an honor.