

Personal Statement, Natasha Dhamrait

In third grade, I won my elementary school's science fair and earned an honorable mention at the county level. Although I was excited about the research itself, the entire experience put me off of science for many years. The school mispronounced my name when presenting my award and misspelled my last name on my certificate three different times. Even though I was 8 years old, I could tell that those who did well at the county level science fair were not "my people". Their projects were expensive, their names were pronounced correctly, and most notably, they were not girls of color like I was. My early experiences in science motivate me to foster diversity in science and create safe spaces for other minority scientists in academia.

I carry this goal in my current position as a PhD student at UC Davis in the Population Biology Program. I study maize domestication and the evolutionary dynamics of transposable elements using evolutionary genetics, genomics, and population genetics. Funding from the NSF GRFP will support my research and my science outreach projects aimed at making science a more diverse and inclusive field.

Intellectual Merit:

I remember sitting near the back of a dusty lecture hall on the second week of introductory genetics. The room had one of those blackboards that was more aesthetic than functional and my instructor was one of those professors who was more researcher than teacher. It was a regular day in a slightly duller than necessary class and I was not expecting anything life altering to happen. My professor lectured as I drifted in and out of focus, when he off-handedly mentioned "transposable elements", genes that can copy themselves and move around the genome. Transposable elements are ubiquitous in the genomes of organisms, representing half of the human genome and the majority of DNA in the plant kingdom. Despite identifying as a budding geneticist, I had never heard of transposable elements before, and I found myself equally intrigued and confused by the fact that most genetics studies completely ignore them. I was mesmerized by the hidden complexity that transposable elements contribute to genome evolution and over time my interest only grew. Just like that, I discovered the subject that would fuel my love for science for many years.

The next time I experienced a similar spark of inspiration was in my archeology class a few months later when I first learned about the complexity and beauty of early crop domestication. The foods we eat have been domesticated over thousands of years through a prolonged evolutionary process directed by changing human cultures, societal structures, and culinary practices. I became fascinated with learning the evolutionary history of every food I ate and every plant I grew in my kitchen garden. **My current PhD is inspired by my view that transposable elements and domestication complement each other and serve as an ideal system to study evolution.**

My research career began in undergrad when I started volunteering in research labs and later conducting independent research projects. I was in Dr. Arthur Weis' plant evolutionary ecology lab for three years. My first year I assisted a PhD student's project assessing plant responses to heatwaves. During my second and third years, I started an independent research project investigating the effect of artificial seed aging and seed storage on plant lifetime fitness across three generations. I became well versed in methods of testing and experimentation, as the procedure for artificial seed aging had never been done on my study organism before. As a result, I collaborated with researchers at the USDA to generate / test different methods.

My seed aging project was born out of an obsession with seed banks (both natural and human-made) and the idea of transgenerational stress effects. I was especially fascinated with how seed banks sat at the intersection of agriculture, science, and culture. Humans have been collecting and storing seeds for as long as farming has existed, and I loved thinking about how my research related to such an enduring aspect of the human experience. I carry this interest with me in my current work on domestication, where I analyze ancient samples of maize stored in early seed banks and use evolutionary genetics to learn more about early farming.

My first independent research project inspired me to start considering research as a career, due in no small part to the mentorship of Dr. Weis. At the time, I started mentoring fellow undergraduate students to assist in data collection, plant rearing, and methods testing for my projects. Over the three years I was in the Weis lab, I mentored 5 other undergrad students. I learned that mentor support truly has the power to completely make or break a student's experience, which has fueled my continual commitment to the mentorship of students.

My dedication to research as a career persisted throughout my undergraduate degree despite several setbacks. COVID lockdown began at the end of my third year, and the university greenhouses shut down for months. My project, which I had been working on for more than a year and a half, ended with dead third generation plants in the greenhouse, uncollected data, and a sense of loss. I faced similar issues in my fourth year thesis project in Dr. Stephen Wright's evolutionary genomics lab. My project was a computational analysis of polyploidy and subsequent gene-loss in angiosperms through comparative transcriptomic and genomic methods. By the end of the year, it was apparent that my results were non-significant. My genomics project also marked a shift in my research training from ecology to computational biology. I found the power of computational tools to explore novel hypotheses in genome biology to be unparalleled and quite thrilling. Regardless of results, the process of designing experiments, engaging with evolutionary genomics literature and theory, and presenting to academic audiences were essential for my growth as a researcher and cemented my decision to continue research as a career.

I am now a second year PhD student at The University of California, Davis in the Population Biology program. My undergraduate research in ecology, evolutionary biology, and genomics has prepared me for my current PhD in evolutionary genomics with an emphasis on quantitative methods and theory. I am a member of Dr. Jeffrey Ross-Ibarra's maize domestication and evolutionary genomics lab. My current research focuses on using transposable elements to explore the process of maize domestication and plant genome evolution. My research interests are based in transposable elements and domestication, but I am dedicated to collaboration and supportive science. Currently, I am collaborating with several labs on a project on butterfly genomics and conservation as funded by the Center for Population Biology. Post-graduation, I am interested in a career that incorporates research, science communication, and outreach.

Broader Impacts:

I decided in part to pursue graduate studies and a career in science to create a safe space for other minority scientists. While I have been gifted with excellent educators, none of them have looked like me, come from similar backgrounds as me, or identified similarly to me. Unfortunately, this is the norm for queer women of color in STEM. I have seen my educators, mentors, and leaders say anyone can succeed in STEM, despite witnessing no one like me actually doing so. This lack of representation permeates all areas of academia, forcing minorities to reconcile the gap between the perceived diversity of the student body and the actual diversity of the school faculty, researchers working in the field, and celebrated historical scientists.

I have taken every opportunity to promote diversity and inclusion in science through three different approaches: science education, science communication, and mentorship.

I am an experienced science educator and I have worked across a range of ages, from elementary school children to adults. My science education background began in highschool when I worked as a teacher's assistant for preschools. I found my love for teaching and science rejuvenated through the infectious curiosity of children who ask profound but silly questions, such as "why don't plants move?" During the summer after my first year, I was an Environmental Educator intern for the San Francisco Parks department. I designed and led school field trips to parks and natural preserves in the city. All field trips involved habitat restoration and a discussion of relevant natural history of the SF Bay Area and the park we were in. I taught children how they can improve nature in their backyard and how to feel connected to the intricate Bay Area ecosystem that is rapidly disappearing through planting native gardens, engaging with conservation work, and advocating for sustainability. Currently, I am a letter writer for the organization Letters to a Pre-scientist, which matches current scientists with middle school

children interested in science. I am also a frequent volunteer with the graduate student group, Science Says, which provides accessible science education to the general Davis community through themed tables at the local farmer's market. As a science educator, I can demonstrate that visible minorities can be successful scientists and I can teach science in a way that is accessible for those who have little to no science background.

I believe disseminating research and sharing novel science to the public are essential parts of being a scientist and I have done so through verbal, written, and visual media forms. After I graduated undergrad, I worked as an intern for one of the top 10 rated biology podcasts, Big Biology. There I researched and wrote content for bi-weekly episodes. For the past two years, I have been volunteering with the University of California Master Gardener program, a volunteer organization focused on providing research based gardening and sustainable horticulture advice to local communities. Through the Master Gardener program, I table at farmers markets, answer gardening and plant questions via email, and I solely run my County's master gardener bi-monthly newsletter on all things gardening and plants. Recently, I have started a podcast with a peer graduate student where we interview scientists who are part of the 500 queer scientists program campaign. Our goal is to improve visibility of minority scientists who are doing exciting research.

Mentorship allows me to directly improve the experience of other minority students in STEM who are interested in research and academia. Through being a mentor, I can help others combat systematic barriers, such as unequal access to research opportunities, that impede minorities pursuing careers in science. During my undergraduate, I ran the Student Leadership and Mentorship program. I trained and directly mentored more than 100 student leaders and served as a resource for the 1000+ first year students in my college. I also helped redesign the student mentorship program to be more equitable and supportive of minority students by restructuring the application process, creating long term funding opportunities for underrepresented students, and standardizing online instruction during the pandemic. When I graduated, I received the University of Toronto Student Leadership Award (2021) for my work. I am an active member of the Student Diversity Committee (SDC), which focuses on improving diversity, equity, inclusion, and justice for students in the Center for Population Biology at UC Davis. I am also involved in the SDC run Ecology and Evolutionary Biology Preview Program, designed to provide current undergraduate students, especially underrepresented students, with guidance and mentorship for applying to graduate school. I am currently directly mentoring an undergraduate student who is conducting research on transposable element diversity and dynamics through maize domestication.

Future goals and Summary:

My goal in attending graduate school is to prepare for a career in research and science communication/education. To that goal, I have started volunteering at the UC Davis Herbarium for several hours a week. I assist with curation and maintenance of the herbarium samples and I facilitate research currently being conducted at the herbarium. I have started developing museum exhibits that are currently being displayed on campus and in local libraries. With public distrust in science rising, It is becoming increasingly important to effectively integrate science communication into research. As a member of both visible and invisible minority groups, I serve multiple underrepresented voices in science and education. I hope to use my unique perspectives to further shape the way we view, interact with, and apply science as a whole.

My extensive experience in evolution, genomics, and computational biology uniquely prepares me for my current research involving transposable elements and domestication. If I am funded, I will be able to continue my innovative research and work focused on fostering diversity, equity, and inclusion in science.

Maize domestication through the lens of transposable elements

Most of the foods we eat have been domesticated by humans over thousands of years through an evolutionary process that restructures genomes, radically shifts population dynamics, and alters selection pressures on large swaths of the genome. Maize (corn), *Zea mays* ssp. *mays*, was domesticated ~9,000 years ago in the Balsas River Valley of central Mexico from *Zea mays* ssp. *parviglumis* and *mexicana*, commonly known as teosinte.

Domestication is an ideal model to study adaptation, selection, and genome evolution. Due to the concise timeline of domestication, many signatures of selection are still detectable in maize and teosinte. The presence of wild relatives, like teosinte, allows for useful comparison between domesticated and non-domesticated sister taxa. The timeline and intensity of selection pressures associated with domestication are well within the range observed in natural populations, allowing for patterns observed in domesticated taxa to inform the study of natural systems¹.

In maize, transposable element (TE) rich regions of the genome control most of the genetic variation for phenotypes². TEs, or transposons, are mobile genetic elements that can change positions within the genome and increase copy number. Despite most TE activity being deleterious, TEs make up the majority of plant DNA, and more than 85% of the maize genome². TEs are highly polymorphic and differ between individuals in presence-absence, sequence diversity, genomic location, and activity level. TE composition, the collection of TEs in an individual's genome, varies greatly within and between populations but little work has been done on classifying those differences.

Since research on domestication has focused on the gene-rich regions of the genome, we know little about how domestication and adaptation has shaped and been shaped by TEs. **I will use TE composition to resolve domestication history and quantify the contribution of TEs to adaptation during domestication.**

Aim 1: How can population level differences in TE composition resolve the geography of maize domestication? Specifics of where maize was domesticated are still unknown due to confounding population structure and continual gene flow between populations. Conventional methods of studying population structure using single nucleotide polymorphisms (SNPs) are difficult in *Zea mays* ssp. since most SNPs are old and shared between all populations of maize and teosinte³. TEs mutate quicker than SNPs and can provide resolution on the recent past. TEs are also population specific within maize and teosinte^{4,5}. Population-specific TEs can refine our understanding of the geography of domestication beyond the regional scale through identification of shared and unique TEs in maize and teosinte. Identification of teosinte population with unique TEs present in all maize populations will indicate which populations of teosinte maize was domesticated from and in which geographical regions early maize domestication occurred. **Methods:** In order to compare TE composition between different populations of maize and teosinte, I will use the UC Davis high performance supercomputing cluster and repeatexplorer2, an unsupervised clustering algorithm, to detect novel TEs in 5000+ individuals from different maize and teosinte populations sequenced with short-reads^{6,7}. Most TE annotation methods are biased towards maize, but since clustering of reads and initial identification of TEs using RepeatExplorer2 are independent of pre-curated libraries, teosinte and maize TEs will be identified equally. All identified TEs will be annotated to facilitate comparison between *Zea mays* ssp. I will then compare overlap and divergence of TE clusters between populations of teosinte and maize while controlling for the age of the TE insertion and underlying population structure. **Potential Results:** Comparison of different TE clusters will allow for detection of candidate geographic regions for early maize domestication. Updating our understanding of maize domestication can inform current research on maize diversity and evolution. Once tested, this method can be applied to the identification of geographic origins of novel invaders or weedy species.

Aim 2: To what extent do TEs contribute to adaptation in maize? We know of several traits where TEs regulate expression of a gene selected for during domestication, such as *tb1* and *gt1*, which allowed for denser planting of maize, and *ZCN8*, where a change in flowering time allowed maize to grow in

temperate areas^{8,9,10}. However, general patterns of how often TEs are under positive selection and contribute to adaptation are unknown. **Methods:** To identify regions of the maize genome that have been under selection during domestication, I will run a genome scan on long-reads using selscan¹¹. I will quantify how often TEs are present within or around 10kb of those sweeps and present-absence variation of those TEs across 100+ fully assembled maize and teosinte genomes. Using genome-wide association studies (GWAS), I will investigate the association of the TE genotype with the domestication phenotype to connect TEs to adaptation. I will utilize other available transcriptomes, epigenetic sequencing, and recombination maps to compare the association of TEs to phenotype across methylation type, expression level, and genomic region. **Potential Results:** With estimates of TEs associated with selective sweeps, I can describe patterns of how often TEs are under selection and the amount of genetic variation that is explained by TEs.

Intellectual Merit: The history of maize has societal and cultural impacts for the indigenous peoples of the Americas. Studying domestication aids our understanding of our past and protects our future as we continue to grow and consume maize. Domestication informs adaptation and evolution in the natural world through the application of domestication as a model system. Understanding the evolution of TEs is essential for studying genome evolution, especially in maize where TEs are the majority of the genome. Methods used to identify geographic origins of evolutionary complex populations will be developed into a pipeline and made publically available on GitHub for collaborators. I will present this work through two publications and at various conferences, including the annual Maize Genetics Meeting and Evolution.

Broader Impacts: I am committed to mentorship and science outreach through my professional career. Currently, I am mentoring an undergrad student in TE evolutionary dynamics and I have plans for future undergrad projects involving comparisons of TE contributions during different phases of domestication. I am developing a series of traveling display boxes to educate the public about maize domestication and evolutionary biology. I am working in collaboration with local libraries, the UC Master Gardener program, and the director of exhibit development at the Exploratorium, a science and art museum in San Francisco. Once completed, the traveling display boxes will be available for check out by anyone in Yolo County, California. Work will be completed by winter 2024. This project is an extension of a previous display case I created which is currently on display at UC Davis, that details the history, biology, and cultural importance of maize domestication. In collaboration with my lab and a science communication agency, I consult on the development of a video game for elementary schoolers on maize domestication and interdisciplinary plant science research. The game will be publicly available for any educational institution to be used as an extension to science instruction and guides students through archeology, genetics, and plant science research. The game will be completed by summer 2024.

References: 1. Purugganan, M.D. and Fuller, D.Q. *Evol.*(2011) 2. Engelhorn J. et al. *BioRxiv* (2023) 3. Sellinger T, Johannes F, Tellier A. *BioRxiv* (2023) 4. Xue W et al. *J. Genet.* (2019) 5. Shujun O. et al. *BioRxiv* (2022) 6. Novák P. Neumann P. Macas J. *BMC Bioinform* (2010) 7. Tittes S. et al. *bioRxiv* (2021) 8. Studer A, Zhao Q, Ross-Ibarra J, Doebley J. *Nat Genet.*(2011) 9. Wills DM et al. *PLoS Genet.*(2013) 10. L. Guo, et al. *Curr. Biol.*(2018) 11. Szpiech Z. Hernandez R. *Mol. Biol. Evol.* (2014).

Intellectual Merit Criterion

Overall Assessment of Intellectual Merit

Very Good

Explanation to Applicant

The applicant has a strong research record despite the pandemic related interruptions to her research. She showed a lot of initiative and independence in a two year research project on seed banks, and even though the experiment was shut down in the middle due to COVID, the results already collected were interesting and are being writing into a manuscript on which she is co-first author. Her current research is on transposable elements in maize, but she fosters collaborative science and is collaborating with several other labs in their research. The proposal was very well written with a succinct but very informative introduction to set the context and two well developed aims. The level of detail in the methods make it clear that this project is feasible and will be completed and I appreciated the potential results, although they could have been elaborated a bit more along with a final description of how the anticipated results would directly answer the proposed question.

Broader Impacts Criterion

Overall Assessment of Broader Impacts

Excellent

Explanation to Applicant

The applicant highlights three pillars of broader impacts that are important to her: science education, science communication, and mentorship. She has a strong history of excelling in all of those areas and has concrete plans to continue to grow in each area. I am impressed by the diversity of different ways that she plans to connect to the broader community, taking advantage of different media to reach students through letters, general public through a podcast, the local community through farmers markets, video games for elementary schools, display boxes with local museums and libraries, etc. She has a history of mentoring and clearly recognizes the importance of a mentor on shaping an student's experience. She ran the Leadership Mentorship program and helped redesign it to make it more equitable and supportive of minority students, for which she received the University of Toronto Leadership award. She also mentored 5 other undergraduates while she was an undergraduate. As a graduate student she is working with the Student Diversity Council, in particular for the preview program for underrepresented minority students applying for graduate school and is already directly mentoring an undergraduate student and plans to mentor additional students.

Summary Comments

Intellectual Merit Criterion

Overall Assessment of Intellectual Merit

Excellent

Explanation to Applicant

strengths: excellent applicant with previous research experience, awards, honors. The applicant has 3 years experience working in an academic lab during which gained extensive experience in evolution, genomics, and computational biology, but also experience mentoring students, leadership roles, and working with USDA on projects. The personal statement is very well written and makes the applicant transpire as mature individual. The scientific proposal is extremely well and clearly written, although in non a canonical way in terms of hypothesis, it is clear what the goal, rationale, methods, possible problems and results are. weaknesses: no real critiques, only that although an overall hypothesis is missing, it seems that aim specific hypothesis are framed as questions. it would have been better to be clearly state aim specific hypothesis.

Broader Impacts Criterion

Overall Assessment of Broader Impacts

Excellent

Explanation to Applicant

strengths: academic activities that the applicant has engaged previously span from broadening participation of underrepresented groups into science, education, outreach through different media including novels and radio. The applicant will engage in helping underrepresented students, as well as scientific outreach. Very interesting methods for outreach through expo and games that, although not explicitly stated, delineate what are the broader impacts of the research project and impact on society. weaknesses: none

Summary Comments

Excellent proposal, very nicely and clearly written. There are no big critiques besides having a more traditional way of stating what are hypothesis that will be tested.

Intellectual Merit Criterion

Overall Assessment of Intellectual Merit

Excellent

Explanation to Applicant

This is an extremely solid proposal. It is well-written, it is clearly structured, the research aims are easy to follow, the methods are clear and there are clear outcomes from this research. The student has access to the resources needed to complete this research. I have identified no weaknesses. The student is currently investigating the domestication of maize using transposable elements. TEs have the advantage of having a higher mutation rate than SNPs, so their analysis should be able to infer relationships not apparent by other means. The student proposes using a comparative approach using Zea and Teosinte. Potential problems such as the bias of the databases are considered and an approach to solve it is described. The number of samples included in the analysis for which the student has sequencing data, over 5000, is staggering. The second aim focuses specifically on the role of transposon in domestication, by analyzing their effect on genes with known effect in domestication.

Broader Impacts Criterion

Overall Assessment of Broader Impacts

Excellent

Explanation to Applicant

The student has already completed several outreach activities including education at different levels, including environmental education activities, letters to a pre-scientist, and volunteer activities in local farmer markets. The student has a track record in science communication and divulgation. In addition, the student has participated in multiple mentoring activities in their current and former institution that were recognized were relevant awards. The student plans to continue with their role in the community and specific actions are listed in the proposal (completing museum displays, and educational video games).

Summary Comments

This application has been a pleasure to read. Extremely solid science and broad impacts.

--