**PERSONONAL, BACKGROUND, and FUTURE GOALS STATEMENT**

Somatic mutations, traditionally regarded as errors of cellular replication, are increasingly recognized as potential biological indicators of adaptive capacity in long-lived organisms. In perennial trees such as the Oregon white oak (Quercus garryana), somatic mutations can accumulate across different branches over decades, producing intra-individual genetic variation that may contribute to resilience under environmental stress. By assessing somatic mutations as biological indicators, we can gain insight into microevolutionary processes that operate within individual trees, complementing population-level studies of genetic variation. This perspective is particularly relevant in the context of drought, a growing threat to forest ecosystems in the Pacific Northwest, where prolonged periods of water scarcity challenge the survival of keystone species like Q. garryana. Understanding the role of somatic variation in drought adaptation not only advances basic ecological and evolutionary knowledge but also has direct applications for conservation and management strategies aimed at enhancing climate resilience.

The Oregon white oak is a foundation species whose presence structures communities and supports biodiversity across its range in the Pacific Northwest. Despite its ecological importance, populations are increasingly threatened by drought, habitat fragmentation, and shifting climate patterns. Adaptation in long-lived trees is a slow process, often constrained by the timescales required for generational turnover, making it crucial to identify sources of genetic and phenotypic variation that allow trees to cope with rapid environmental change. While previous research has characterized population-level genomic diversity in oaks, the potential adaptive contributions of somatic mutations remain largely unexplored. At the same time, phenotypic plasticity—the ability of individual trees to adjust growth and physiology in response to environmental conditions—likely plays a complementary role in drought resilience. The Ten Thousand Oaks Project aims to integrate these perspectives by evaluating how standing genomic variation, somatic mutations, and phenotypic plasticity collectively shape the capacity of Q. garryana to withstand drought stress across its range.

This project is guided by four central questions. First, do individual trees accumulate distinct somatic mutations across branches, and can these mutations generate novel adaptations for drought resilience? Second, what is the relative contribution of standing genomic variation compared to phenotypic plasticity in observed drought tolerance? Third, can genomic offset analyses predict which population structures are most vulnerable under future climate scenarios? Finally, how can genomic offset analyses inform conservation strategies to enhance the climate resilience of Oregon white oak populations? Addressing these questions requires a multi-scale approach that combines fieldwork, controlled experiments, high-throughput genomic sequencing, and computational modeling.

To evaluate somatic variation, I will collect branch samples from individual trees across the species’ range, representing a diversity of climatic and geographic conditions. Partial-genome sequencing using Illumina technology will allow identification of somatic mutations, which will be mapped to functional genomic regions associated with drought tolerance. By comparing mutation patterns among branches within single trees, I can quantify intra-individual genetic heterogeneity and assess whether somatic mutations provide adaptive potential that could buffer against environmental stress. These data will provide a novel perspective on the evolutionary significance of somatic mutations in long-lived plants, positioning them as measurable indicators of an individual tree’s capacity to respond to drought.

Phenotypic plasticity will be assessed through greenhouse experiments in which seedlings from multiple populations are grown under controlled drought and well-watered conditions. Traits related to growth, water-use efficiency, and stomatal regulation will be measured to quantify plastic responses. This approach will enable the disentanglement of genetic versus environmental contributions to drought tolerance and help determine whether phenotypic plasticity can compensate for the limits of standing genetic variation. Integrating these experimental results with somatic mutation data will provide a comprehensive understanding of the mechanisms by which individual trees and populations respond to drought stress.

Genomic offset analyses will be applied to evaluate population vulnerability under projected climate change scenarios. By linking existing population genomic data with spatially explicit environmental variables derived from Geographic Information Systems (GIS), genomic offsets quantify the mismatch between current genetic variation and future climatic conditions. This approach identifies populations at greatest risk from climatic shifts and enables predictions of which genetic lineages may harbor the adaptive potential to persist. Importantly, incorporating information on somatic mutations into genomic offset models may reveal previously unrecognized sources of resilience within individual trees that could inform conservation priorities and management interventions.

The integration of high-throughput genomics, experimental phenotyping, and spatial modeling will be supported by high-performance computing resources, allowing large datasets to be processed and analyzed efficiently. This multi-disciplinary approach will produce a comprehensive view of adaptive capacity in Q. garryana, linking fine-scale somatic variation with population-level genetic structure and environmental vulnerability. By combining empirical and predictive approaches, this project will generate actionable insights for conservation management, such as identifying populations that could serve as genetic reservoirs for restoration efforts or guiding assisted migration strategies under climate change.

Expected outcomes of this research include a quantitative assessment of somatic mutation accumulation in long-lived trees, a detailed understanding of the relative contributions of standing genetic variation and phenotypic plasticity to drought resilience, and identification of populations most vulnerable to climate stress. Furthermore, this work will advance the broader application of genomic offset analyses in conservation biology by integrating intra-individual variation, which has often been overlooked in predictive models. Beyond scientific contributions, the project has broader societal implications, providing tools for forest managers, conservation practitioners, and policymakers seeking to maintain resilient ecosystems in the face of climate change.

In summary, the Ten Thousand Oaks Project seeks to illuminate the complex interplay of genetic and phenotypic mechanisms underlying drought adaptation in Oregon white oak. By treating somatic mutations as a biological indicator of adaptive potential, this research bridges molecular genetics, ecology, and conservation science. The project’s integration of field-based sampling, greenhouse experiments, high-throughput sequencing, GIS, and computational modeling provides a comprehensive framework to assess resilience across multiple scales. Ultimately, this work will enhance our understanding of how long-lived trees respond to environmental stress and inform strategies to preserve and restore keystone forest species under changing climatic conditions. By combining innovative genomics with applied conservation objectives, the Ten Thousand Oaks Project positions Q. garryana as both a model system for studying adaptation in long-lived plants and a focal point for climate-resilient forest management.