DNA optimization of foliar fungal endophytes in *Quercus Lobata* (Valley Oak) leaves (2024)

Tawny A. Bolinas[1] and Gerald M. Cobián[2]

[1] *Biological Sciences, California State University, Chico, Chico, CA, United States*
[2] *Biological Sciences, California State University, Chico, Chico, CA, United States*

Foliar endophytic fungi (FEF) live within plant leaves without causing visible symptoms or signs of disease. These communities exhibit significant diversity, with potentially hundreds of different fungal species coexisting within a single host. While some fungi are known to play crucial roles in plant defense and adaptation to stressful environments, the functions of many others remain unknown. It is assumed that some fungi are involved in the decomposition of leaf litter once leaves have abscised. Understanding the community assembly processes involved in leaf colonization after abscission, including the influence of FEF on the colonization of decay fungi, is critical for a greater understanding of carbon cycling, as community composition is shaped by both stochastic and deterministic factors, such as priority effects. Focusing on fungal communities from green leaves through the decomposition process by investigating their roles in leaf litter decomposition and effects on the carbon cycle at Big Chico Creek Ecological Reserve, this study contributes to a deeper understanding of ecosystem dynamics. The findings can reveal how FEF shape leaf litter communities, affect nutrient cycling, and influence carbon sequestration. By tracking changes in fungal communities over time, they provide insights into ecological succession and adaptation, expanding our understanding of microbial ecology and ecosystem function. This summer's project aimed to determine the optimal type of bead matrix and the amount of lysing buffer solution required to break down plant material and extract DNA from fungal endophytes in valley oak *(Q. lobata)* leaves. Different types of lysing bead matrix (F, J, I) and varying amounts of lysing buffer solution were tested using a bead-beating machine. Extracted DNA samples were then amplified by polymerase chain reaction and visualized through gel electrophoresis. The results showed that using lysing bead matrix F with an initial 350µL of lysing solution F, followed by a 2-minute homogenization, and then increasing to 400µL with an additional 2-minutes of homogenization, led to optimal DNA amplification compared to other treatments. These findings provided valuable insights into methodologies for processing fungal DNA extractions, aiding in the study of fungal endophytes' roles in leaf litter decomposition and their influence on the carbon cycle.