

**EXECUTIVE SUMMARY [NON-CONFIDENTIAL, NON-TECHNICAL ABSTRACT FOR PUBLIC INFORMATION OR PROGRAM PROMOTION]:** State in layman's terms the application's broad, long-term objectives and specific aims, making reference to the potential public benefits of the project relevant to California. Do not include proprietary or confidential information. This may be distributed before the funding decision has been finalized.

Plants have multiple defenses against a variety of foes, including herbivores and pathogenic microbes. Although expression and regulation of plant defenses is complex, it is currently an area of biotechnology research. Ultimately, we hope that genetic engineering can help plants best utilize defense pathways, increasing crop productivity and reducing dependence on pesticides.

However, little is known about the impact of plant defense gene expression on soil microbiota, which are intimate partners with plant roots and improve soil fertility and sustainable agriculture practices. Plant defense gene expression can potentially secrete compounds that may alter soil and root-zone bacterial populations, including both beneficials and pathogens. Finally, when crops are tilled into the soil after harvest, other gene products may be released during decay, again affecting soil microbial populations.

Here, we propose to study the impact of plant defense gene expression on soil microbiota by comparing *Arabidopsis thaliana* mutants that constitutively express several defense pathways with wild-type and non-inducible mutants. We will grow plants over their 6-week life cycle, measuring defense gene expression and determining the genetic 'fingerprint' of root-zone bacterial populations. We will then till plants into the soil and track soil microbiota genetic diversity as plants decay. This project will serve as the basis for one master's thesis, help train graduate students in advanced molecular biology techniques, and provide data for future proposal efforts.