

**EXECUTIVE SUMMARY [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.

Microbe-host interactions are ubiquitous on earth and can range from mutualistic (benefiting both partners) to pathogenic (disease-causing). For example, in the rhizobia-legume symbiosis, bacteria such as *S. meliloti* live inside cells of the legume plant and supply the plant with fixed nitrogen in return for carbon sources. These rhizobia-legume symbioses are ecologically and agriculturally important since they produce over half of the earth's biologically fixed nitrogen and form the basis for crop rotation. In contrast, residence of *Brucella* bacteria inside mammalian host cells causes brucellosis, a costly animal and human disease prevalent in developing countries. *Brucella* has also been classified by the CDC as a potential bioterrorism agent. Although *S. meliloti* is a plant symbiont and *Brucella* is a mammalian pathogen, both share a requirement for the ExoS and ChvI genes for successful interaction with their hosts. ExoS-ChvI are known to control gene expression together, but most of their target genes are still unknown. Recently, we used genomics to identify a new set of genes that are likely controlled by ExoS-ChvI in the model rhizobial species *S. meliloti*. Here, we aim to clarify the relationships between these potential target genes, symbiosis, and ExoS-ChvI. The insight gained by studying these evolutionarily conserved genes vital for microbe-host interactions will be applicable to the improvement of agricultural productivity and to the prevention and treatment of brucellosis, a possible bioterrorist threat.