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"Identification of genes involved in the dual regulation control of a modified catabolite repression system in *Sinorhizobium meliloti*."

Our lab is focused on fundamental questions in biology, which can be answered by studying the genes, associated proteins, and metabolic pathways in the biologically safe system of *Sinorhizobium meliloti*, a bacteria that forms a symbiotic relationship with plants. The knowledge gained from the study of this system can be directly applied to our understanding of other bacterial systems in the mammalian pathogen *Brucella* and general mechanisms of pathogenesis of intracellular pathogens. The system regulating the bacteria-plant symbiosis is also economically important to the agricultural industry. *S. meliloti* is an intracellular bacterium that has a plant as its host, but the taxonomic relationship to intracellular animal pathogens has been well documented. In order to gain entrance to the host cell, the bacteria must exchange chemical signals with the host. Additional signals must be exchanged to prevent destruction once inside the cell. Our research focuses on the central metabolic control of a set of proteins in *S. meliloti* called Sma0113/Sma0114. This set of proteins regulates a process called succinate mediated catabolite repression, a system that allows bacteria to utilize a specific carbon source until it is exhausted, in the presence of multiple carbon sources. The study of this regulation system can lead to additional research related to preventing host sensing and utilization of carbon sources by intracellular pathogens.