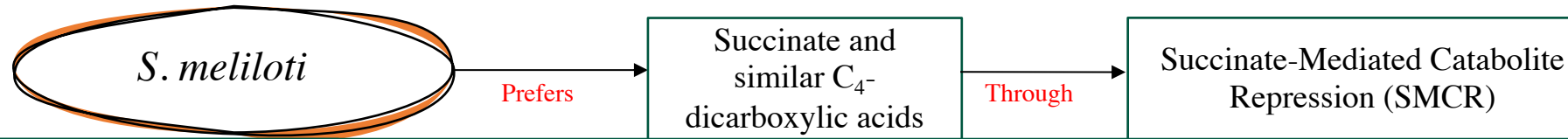


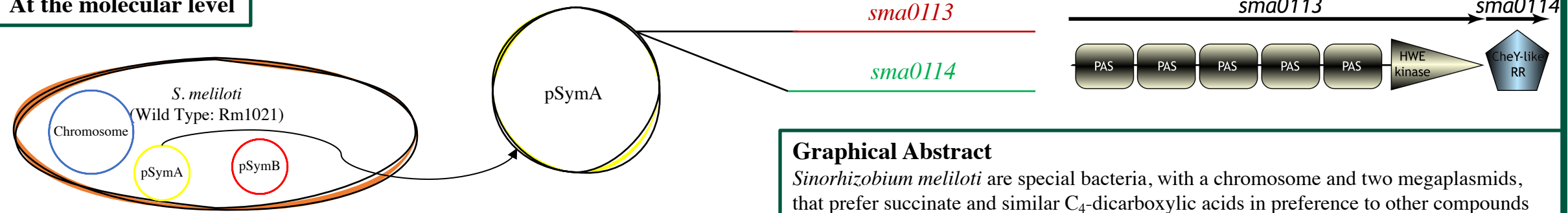
Dual Regulation in the Signal Transduction System of *Sinorhizobium meliloti*

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Overview

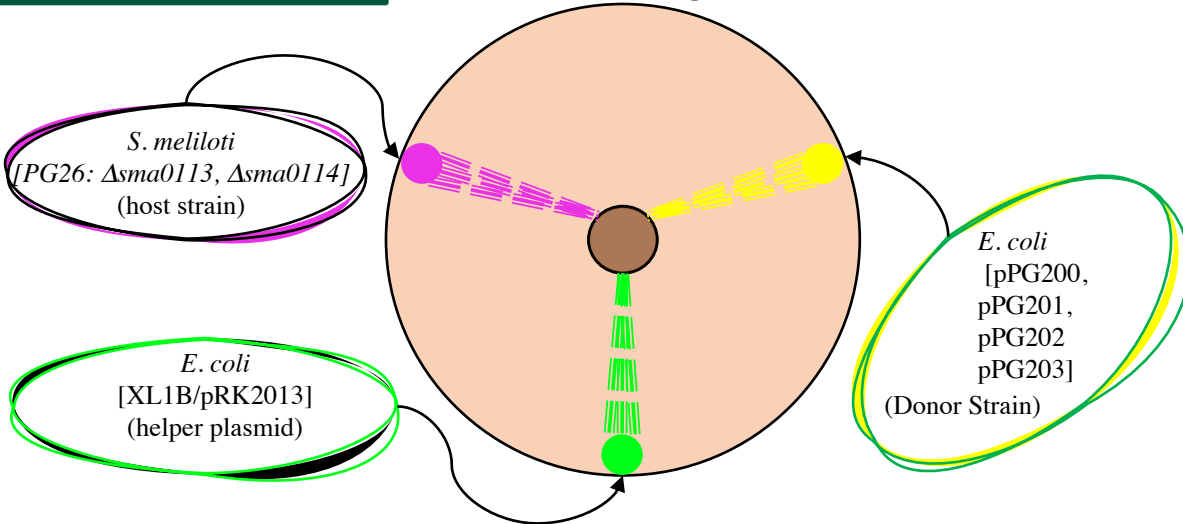


At the molecular level



Current Study

3° Mating



Graphical Abstract

Sinorhizobium meliloti are special bacteria, with a chromosome and two megaplasmids, that prefer succinate and similar C₄-dicarboxylic acids in preference to other compounds through a process deemed SMCR. In addition, these bacteria use the dicarboxylate transport system A (DctA) to transport the preferred compounds and establish catabolite repression. Most bacteria, like *E. coli* and *B. subtilis*, use the phosphotransferase system (PTS) to transport glucose. Recently, a mutation in the gene *sma0113*, which codes for an HWE-Kinase, resulted in a relaxation of SMCR. The neighboring gene, *sma0114*, codes for a response regulator and was also chosen to be further studied. Based upon predicted functionality and encoded protein sequence, cross regulation is possible. Using MiST, phylogenetically related HWE- Kinases and response regulators were identified and targeted (*smb20515*, *smc01504*, *smc01507*, and *smc01953*). PG26 is a variant of *S. meliloti* which lacks both the *sma0113* and *sma0114* genes. Then, triparental mating was performed with PG26, *E. coli* containing a helper plasmid, and *E. coli* containing a non-replicating plasmid with truncated versions of the identified genes (donor strain). Successful integration will then be confirmed using selective media and PCR. The goal of the study is to identify the dual regulation system of *S. meliloti*, involving the PTS and HWE-Kinases (including their respective response regulator), in hopes of a better understanding between catabolite regulatory pathways and global gene regulation.