Isolating and Mapping Suppressors of the △SMc02230 Morphologic Mutation in *Sinorhizobium meliloti*

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Specific proteins control the three-dimensional organization of cells but may behave differently in cells that are morphologically distinct. We are using two related model bacteria, *Sinorhizobium meliloti* and *Caulobacter cresentus*, to investigate how conserved proteins contribute to the synthesis and localization of specific organelles to programmed subcellular sites. In *C. crecentus*, the protein PodJ acts as a subcellular localization factor required for chemotaxis and biogenesis of polar organelles. Two homologs of the podJ gene have been identified in *S. meliloti*: SMc02230 and SMc02231. Mutants with a deletion of the SMc02230 gene form smaller swarms on soft-agar plates compared to wild-type, indicating a chemotaxis defect, and have elevated levels of exopolysaccharides. In liquid media, we observed that the △SMc02230 strain grown on M9 minimal media and in Luria Bertani broth with low salt concentrations (LBLS) display branched and aberrant morphologies. In contrast, the wild-type strain grown under the same conditions have a rod-shaped morphology. In addition, the mutant exhibits a novel defect: it is unable to grow on LBLS plates. We subsequently isolated ten colonies of the △SMc02230 mutant that were able to grow on LBLS plates, apparently due to acquisition of suppressor mutations. Using transposon mutagenesis and arbitrary PCR, we are mapping and identifying these suppressor mutations to help elucidate the defect caused by the △SMc02230 mutation. Functional comparison of conserved proteins in related species will contribute to an understanding of how cellular factors evolved to suit the particular needs of different cell types.