

Organization, Regulation, and Distribution of Genes Responsible for the Utilization of Deoxyfructosyl Glutamine an Amadori Opine

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Dfg is an Amadori opine found in plant tumors induced by chrysopine-type strains of Agrobacterium tumefaciens. Cosmid clones responsible for utilization of dfg from genomic library of pAtC58 were isolated. Characterization of the cosmid clones indicated that a 6.2-kb BglII (Bg2) region is essential for utilization of dfg. This region contains five ORFs-socRABC and D. SocR negatively regulates the expression of socR itself and socABCD. SocA and SocB are ABC-type transporters responsible for transport of dfg and MOP. SocC and D could be responsible for enzymatic degradation of dfg, being homologs of sugar oxidoreductases and an amidoriase from Corynebacterium sp., respectively. The repression of soc operon by SocR was relieved when cells contain a mocC clone and also MOP was supplied, suggesting that dfg or other catabolic intermediate of MOP is an inducer. By Southern hybridization analyses, various Agrobacterium and related soil-bacterial collections in the family Rhizobiaceae were examined for the presence of homologs of socD and mocD in the genomes, which are essential for degradation of dfg in the two gene sets responsible for the catabolism of dfg. It appears that mocD homologs are specific to Ti plasmids in agrobacterial species, and socD homologs are present in non-Ti plasmid episomes in Agrobacterium, and also present in some of Rhizobium and Sinorhizobium spp. examined. All of the Agrobacterium strains and some of the Rhizobium strains containing socD homologs were able to utilize dfg as sole carbon source. Based on results of Southern hybridization and dfg-utilization traits, Agrobacterium isolates examined could be divided into seven groups.