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Plasmid profile of two isolates of *Sinorhizobium meliloti* isolated from different soil areas in Basrah/ Iraq

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Abstract. Genetic diversity of two isolates of *Sinorhizobium meliloti* grown in different soil samples were investigated. The results showed that two isolates of *S. meliloti* were different in their plasmid profile .One of these isolates was containing one large megaplasmid with molecular weight (1.6Mb) and the other isolate was containing two large megaplasmid with molecular weight (1.6Mb and 1.3Mb). pSymA and pSymB in *S. meliloti* are involved in the formation and functioning of nitrogen-fixing root nodules. Genes located on pSymA are necessary for nodulation and nitrogen fixation, while those located on pSymB are involved in exopolysaccharide synthesis and uptake of various nutrients.

Key words: ***Sinorhizobium meliloti*** **,** Plasmid profile, Genetic diversity.

Introduction

The symbiosis between legumes and N_2-fixing bacteria (rhizobia) is of huge agronomic benefit, allowing many crops to be grown without N_2 fertilizer. It is a sophisticated example of coupled development between bacteria and higher plants, culminating in the organogenesis of root nodules (7). There have been many genetic analysis of rhizobia, notably of *Sinorhizobium meliloti* (the symbiont of alfalfa), *Bradyrhizobium japonicum* (soybean), and *Rhizobium leguminosarum*, which has Biovars that nodulate peas and broad beans (Biovar *viciae*), clovers (Biovar *trifolii*), or kidney beans (Biovar *phaseoli*).

Genomes of the plant-associated bacteria are still larger. The genome of *Agrobacterium*. *tumefaciens* is about 5.6 Mb, with one circular and one linear chromosome, plus two native plasmids (10, 28). To date, three rhizobial genomes have been sequenced. *S. meliloti* 1021 has a 3.5 Mb chromosome plus two megaplasmids, namely pSymA and pSymB, with the former having genes for nodulation (*nod*) and symbiotic N_2 fixation (*nif* and *fix*)(8). In contrast, the symbiosis genes of *Mesorhizobium loti* MAFF303099 (which nodulates *Lotus*) and of *B. japonicum* USDA110 are on chromosomal 'symbiosis islands', with the chromosome of the latter (9.1 Mb) being among the largest yet known in bacteria(14, 15). *nif* and *fix* genes are present on chromosome in *Rhizobium loti*, *Bradyrhizobium* spp. And *Azorhizobium* spp. These genes are located on asymbiotic plasmid in *S. meliloti*, *R. leguminosarum* and *Rhizobium* spp. NGR234 (25) *Rhizobium leguminosarum* has yet another genomic architecture: one circular chromosome and several large plasmids, the plasmid profile varying markedly among isolates in terms of sizes, numbers, and incompatibility groups (18, 24). The subject of the present study, *R. leguminosarum* biovar *viciae* (Rlv) strain 3841 (a spontaneous streptomycin-resistant mutant of field isolate 300 (9, 13), has six large plasmids; pRL10 is the pSym (symbiosis plasmid). It is very