Genomic analysis of a *Sinorhizobium* strain isolated from the Tunisian desert

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The N_2-fixation by rhizobia in symbiosis with legumes is critical to global nitrogen cycling and sustainable agriculture[1] and for survival and prevalence of endemic spontaneous legume's in Arid and Saharan regions of Tunisia. The strain *Sinorhizobium meliloti* IRAMC:0087 was originally isolated from root nodules of a Saharan shrub *Calobota saharae* growing in the Saharan regions of Southern Tunisia. IRAMC:0087 can nodulate *Acacia tortilis* var. *raddiana*, a plant-tree adapted to extreme climatic conditions, and endophytically colonize *Trifolium subterraneum* roots. Phenotypic characterization of this strain has revealed tolerance to high salinity levels, drought, and high temperatures. To further investigate the molecular basis of this strain´s behavior, we sequenced its complete genome. The genome comprises 5 replicons, a chromosome (3,650,495 bp), the p*SymA* and p*SymB* (1,247,198 and 1,674,059 bp) replicons, and two additional plasmids (597,953 and 197,378 bp) with a GC content of 61.94%. In total, 6,558 protein-encoding sequences, 56 tRNAs and 9 rRNAs along with an intact prophage of 53.3 kb with similarity to *Sinorhizobium* phage phiLM21 were identified. The genome encodes gene clusters supporting rhizosphere processes, secondary bioactive metabolites, plant growth-promoting activities and symbiosis. Interestingly, one of the additional plasmids encodes several genes and gene clusters related to stress tolerance, namely trehalose and osmoprotectant biosynthesis, which may contribute to the adaptation of this strain to severe conditions. IRAMC:0087 exhibits an endophytic and symbiotic behavior with hosts adapted to extreme climatic conditions. Comparative genomic analyses with other rhizobial strains have the potential to reveal novel factors mediating symbiosis under those conditions.

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References

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