

Genomic analysis of *Sinorhizobium meliloti* IRAMC:0087 an halotolerant rhizobium isolated from the Tunisian desert

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Arid and Saharan regions of Tunisia have great interest due to their endemic spontaneous legume's diversity. The strain IRAMC:0087 was isolated from root nodules of a Saharan shrub *Genista saharae* growing in Southern Tunisia. Phenotypic characterization of this strain has revealed tolerance to high salinity levels, drought and high temperatures. To investigate the basis of this, we sequenced its complete genome and compared it to the genome of the closely related strain *Sinorhizobium meliloti* NBRC 14782^T, an alfalfa (*Medicago sativa*) microsymbiont. The genome comprises 7,265,739 bp, which is comparable in size to other *S. meliloti* strains and contains a GC content of 61.94%. In total, 7536 protein-encoding sequences, 51 tRNAs and 5 rRNAs were identified. The genome encodes gene clusters supporting rhizosphere processes, secondary bioactive metabolites, plant growth-promoting activities and symbiosis. Gene distribution into COG functional categories revealed that the percentage of genes was assigned to amino acid transport and metabolism (10.92%), general function prediction (10.5%), carbohydrate transport and metabolism (9.52%), and transcription (9.21%). Despite the difference in size, IRAMC:0087 and NBRC 14782^T genomes present a similar relative occurrence of functional protein encoding genes and do not show any gross genomic alterations. Interestingly, although IRAMC:0087 contains more protein encoding genes than NBRC 14782^T (7536 vs 6696 genes), the major difference lies in the number of not functionally classifiable genes. Nevertheless, the number of genes for transposable elements (9 vs 2), for managing membrane transport (205 vs 147 genes) and for conducting iron acquisition and metabolism (41 vs 31 genes) are higher in IRAMC:0087 than NBRC 14782^T. IRAMC:0087 is an interesting strain as it 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.