

## Genomic Insights into a Desert-Adapted *Sinorhizobium* Strain from the Tunisian Sahara

R. Ben Gaied<sup>1,2</sup>, I. Sbissi<sup>1</sup>, S. Kaur<sup>3</sup>, G. C. diCenzo<sup>3</sup>, M. Tarhouni<sup>1</sup>, C. Brígido<sup>4</sup>

<sup>1</sup>Laboratory of Pastoral Ecosystems and Promotion of Spontaneous Plants and Associated Micro-Organisms, Institute of Arid Regions, University of Gabes, Tunisia

<sup>2</sup>MED – Mediterranean Institute for Agriculture, Environment and Development, Universidade de Évora, Pólo da Mitra, Ap. 94, 7006-554 Évora, Portugal.

<sup>3</sup>Department of Biology, Queen's University, 116 Barrie Street, Kingston, Ontario K7L 3N6, Canada

<sup>4</sup>MED – Mediterranean Institute for Agriculture, Environment and Development & CHANGE - Global Change and Sustainability Institute, Institute for Advanced Studies and Research, Universidade de Évora, Portugal

Email: [ccb@uevora.pt](mailto:ccb@uevora.pt)

Nitrogen fixation by rhizobia in symbiosis with legumes is essential for nitrogen cycling and sustainable agriculture and plays a critical role in the survival of native leguminous plants in the arid and Saharan environments of Tunisia. The *Sinorhizobium meliloti* strain IRAMC:0087, initially isolated from the root nodules of the Saharan shrub *Calobota saharae* in southern Tunisia, can establish nodulation with *Vachellia tortilis subsp. raddiana*, a tree well-suited to extreme desert climates, and colonize roots of *Trifolium subterraneum* endophytically. Phenotypic analyses of IRAMC:0087 demonstrate its resilience to high salinity, drought, and elevated temperatures. To further explore the genetic foundation of its adaptations, we sequenced the strain's complete genome (7.3 Mb), which comprises five replicons: a main chromosome (3,650,495 bp), a chromid pSymB (1,674,059 bp), and another large plasmid, plasmid Accessory A (1,247,198 bp), and two smaller plasmids, pSymA (597,953 bp) and plasmid Accessory B (197,378 bp), with an overall GC content of 61.94%. In total, we identified 6,558 protein-coding genes, 56 tRNAs, and 9 rRNAs, along with a prophage region of 53.3 kb showing homology with *Sinorhizobium* phage phiLM21. Gene clusters associated with rhizosphere interactions, production of secondary metabolites, plant growth promotion, and symbiosis were found within the genome. Notably, one additional plasmid encodes stress tolerance-related genes, including those for trehalose and osmoprotectant synthesis, likely enhancing the strain's capacity to withstand extreme environmental conditions. The ability of IRAMC:0087 to engage in both endophytic and symbiotic interactions with desert-adapted hosts highlights its unique adaptations. Comparative genomic studies with other rhizobial strains may uncover new genetic elements involved in symbiosis under harsh climates.

R. B.G. acknowledges the PhD mobility program supported by the University of Gabés (FSG) and the Ministry of Higher Education and Scientific Research of Tunisia, C. B. acknowledges a contract from the Individual Call to Scientific Employment Stimulus 2018 (CEEC-IND/00093/2018) from FCT. The authors thank to the Tunisian-South African project AFRITRUF and to NSERC for supporting Rhizobium research in the GCD laboratory.