

Genome Sequence of *Azospirillum brasiliense* CBG497 and Comparative Analyses of *Azospirillum* Core and Accessory Genomes provide Insight into Niche Adaptation

Florence Wisniewski-Dyé 1,* , Luis Lozano 2, Erika Acosta-Cruz 1, Stéphanie Borland 1, Benoît Drogue 1, Claire Prigent-Combaret 1, Zoé Rouy 3, 4, Valérie Barbe 4, Alberto Mendoza Herrera 5, Victor González 2 and Patrick Mavingui 1

1. Université de Lyon, UMR 5557 CNRS, USC 1193 INRA, VetAgro Sup Ecologie Microbienne, Villeurbanne 69622, France
2. Centro de Ciencias Genómicas, Universidad Nacional Autónoma de México, AP565-A Cuernavaca, Morelos 62210, México
3. Laboratoire d' Analyse Bioinformatique en Génomique et Métabolisme CNRS UMR8030, France
4. Institut de Génomique, CEA, Génoscope, 2 rue Gaston Crémieux, 91057 Evry, France
5. Centro de Biotecnología Genómica, Instituto Politécnico Nacional, 88710 Reynosa, Tamaulipas, México

Abstract:

Bacteria of the genus *Azospirillum* colonize roots of important cereals and grasses, and promote plant growth by several mechanisms, notably phytohormone synthesis. The genomes of several *Azospirillum* strains belonging to different species, isolated from various host plants and locations, were recently sequenced and published. In this study, an additional genome of an *A. brasiliense* strain, isolated from maize grown on an alkaline soil in the northeast of Mexico, strain CBG497, was obtained. Comparative genomic analyses were performed on this new genome and three other genomes (*A. brasiliense* Sp245, *A. lipoferum* 4B and *Azospirillum* sp. B510). The *Azospirillum* core