

**EFFECT ON RHIZOBACTERIAL COMMUNITIES AND SPATIAL
DISTRIBUTION OF *AZOSPIRILLUM BRASILENSE* CBG-497 STRAIN IN
RHIZOSPHERE OF CONVENTIONAL AND GENETIC MODIFIED MAIZE**

Lourdes Vital L.^{1*}; Ma. Antonia Cruz H.¹; Eyra L. Ortiz P.¹; Luz E. de-Bashan²; Juan C. Segoviano R.³ and Alberto Mendoza H.¹

1 Centro de Biotecnología Genómica-Instituto Politécnico Nacional, Laboratorio de Interacción Planta-Microorganismo, Boulevard del Maestro s/n Esq. Elías Piña, Col. Narciso Mendoza, C.P. 88730 Cd. Reynosa, Tamaulipas, México Tel y Fax: 01(899) 925-1656 y 925-3996.

2 Centro de Investigaciones Biológicas del Noroeste, S. C., Laboratorio de Microbiología Ambiental, Av. Instituto Politécnico Nacional 195, Col. Playa Palo de Santa Rita Sur, La Paz Baja California Sur, C.P. 23090, México.

3 Centro de Investigación y Desarrollo en Ciencias de la Salud (CIDICS). Unidad de Bioimágen. Av. Dr. Carlos Canseco esquina Gonzalitos, Col. Mitras Centro sin número Monterrey, Nuevo León, C.P. 64460, México.

Maize crop is affected by various factors (diseases, insects, pests, etc.) that reduce their productivity. The transgenic plants were created to improve agronomic traits (insect resistance, herbicide tolerance, etc.); the key benefits perceived by the agricultural producer through simplification in the management, increased yields and decreased production costs. However, studies show that the adoption of these crops are having questions about the use and marketing of them. Thus, the transgenic plants are very useful tools for scientific research. The aim of this study was to determine possible effects on the structure of rhizobacterial communities in rhizosphere of genetically modified maize which was transformed with a gene that it confers resistance to herbicide glufosinate, compared to the non-transgenic line (hybrid conventional). PCR-single strand conformation polymorphism (SSCP) profiles generated from conventional and transgenic maize rhizospheres revealed that the transgenic maize did not affect in the structure of bacterial communities under greenhouse conditions. Furthermore, fluorescence *in situ* hybridization (FISH) analysis showed association with the Plant Growth Promoting Bacteria *Azospirillum brasilense* on roots of transgenic maize. Our results indicated that the genetic modification of maize had not effect on the structural composition of the bacterial communities, which shared similar species bacterial and the association of *A. brasilense* was highly similar at zones of root and density bacterial under *in vitro* conditions. In general, the impact of plant traits on the interactions was not significate between both types of maize plants. This work was the first approach to assess bacterial communities and the interaction of *A. brasilense* on transgenic plants.