

Structural Modifications on *Herbaspirillum rubrisubalbicans* Lipopolysaccharides Show no Effect on Maize Root Colonization

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Bacteria of the genus *Herbaspirillum* are found in association with the main economically important grasses such as wheat, maize, rice and sugar cane. The association brings benefits to these plants since *Herbaspirillum* species are able to produce auxins, gibberellins and are also able to perform biological nitrogen fixation, lowering the demand for nitrogen-containing chemical fertilizers, and reducing the environmental impact of these monocultures. The lipopolysaccharides (LPS) found on the outer membrane of Gram-negative bacteria are structurally complex molecules, important to cell adhesion in different surfaces, including plant roots. LPS show a highly conserved moiety (ECA) and an extremely diversified portion (O-antigen), also known as a pathogenicity factor in many bacteria. In order to understand the importance of LPS on the plant-*Herbaspirillum* interaction, three mutants have been constructed for genes related to LPS biosynthesis in *H. rubrisubalbicans*, namely *rmIB*⁻ (dTDP-glucose-4,6-dehydratase), *waaL*⁻ (O-antigen ligase) and *wecB*⁻ (UDP-N-acetylglucosamine-2-epimerase). The phenotypic profile of LPS extracted from these mutants has been analyzed, as well as the adhesion and colonization abilities, and resistance to chemical stress. The results have been compared to those found for strain M1 of *H. rubrisubalbicans*, showing that LPS is not essential for maize root colonization, but structural modifications of these molecules cause a decrease in biofilm formation and resistance to SDS and salicylic acid, besides altering *H. rubrisubalbicans* competitiveness against other bacteria. In summary, the structural modifications on the LPS caused by mutations on the biosynthesis these molecules did not affect colonization of maize roots.

Keywords: plant-bacterium interaction, lipopolysaccharide, nitrogen fixation

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