**TITLE:** IDENTIFICATION OF DIFFERENTIAL PROTEOME IN *Herbaspirillum seropedicae*, STRAIN HRC54, GROWING IN MEDIUM WITH SUGARCANE APOPLASTIC FLUID

**AUTHORS:** Pessoa, D.D.V.<sup>a,b</sup>, Heringer, A.S.<sup>c</sup>, Vespoli, L.S.<sup>c</sup>, de Souza Filho, G.A.<sup>c</sup>, Silveira, V.<sup>c</sup>, Vidal, M.S.<sup>a</sup>, Baldani, J.I.<sup>a</sup>, Simões-Araújo, J.L.<sup>a</sup>

INSTITUTION: aUniversidade Federal do Rio de Janeiro - UFRJ. Programa de Pós-Graduação em Biotecnologia Vegetal, Centro de Ciências da Saúde (CCS). Campus Ilha do Fundão. Av. Carlos Chagas Filho, 373 - Cidade Universitária, Rio de Janeiro, RJ, Brasil. CEP: 21941-590; bCentro Nacional de Pesquisa de Agrobiologia, CNPAB – Embrapa. Laboratório de Genética e Bioquímica, Embrapa Agrobiologia, BR 465, Km 7, s/n – Pavilhão Johanna Döbereiner; Bairro Ecologia, Seropédica, RJ, Brasil. CEP: 23890-000; cUniversidade Estadual do Norte Fluminense Darcy Ribeiro (UENF), Centro de Biociências e Biotecnologia (CBB). Avenida Alberto Lamego, 2000, Campos dos Goytacazes, RJ, Brasil. CEP: 28.013-602.

## ABSTRACT:

The sugarcane is one of the most important crop in Brazil. Nevertheless, the recent data had shown a decrease of the cultivated area and consequently a decrease in yield. The use of fertilizers in order to increase the production can be harmful to the environment and elevate the production costs. One alternative to fertilizers is inoculation with diazotrophic bacteria. In this group of bacteria, the Herbaspirillum seropedicae has shown a great potential as plant growth promoter bacteria (PGPB), especially in grass plants. However, the plant-bacteria interaction molecular mechanism is not clearly understood and we need more information in order to better understand the interaction between bacteria and plant. For this, functional genomics researches assays using PGPB and plant tissues has been carried out to identify the most important metabolic pathways. The aim of this work was analyze and identify groups of differential expressed proteins in *H. seropedicae*, strain HRC54, during growth in media supplemented with sugarcane variety RB867515 apoplastic fluid, using the gel-free approach. From this assay, 383 proteins were identified, with 131 expressed differentially and 253 proteins classified as unchanged. In the expressed differentially, 73 were induced and 57 were repressed. The data analysis has shown so far that the down-regulated proteins presented, in majority, are functions of amino acid transport, chemotaxis, porin activity and outer membrane-bounded periplasmic space. On the other hand, the up-regulated proteins were related to integral component of membrane, metabolic process, oxidoreductase activity and ATPase activity. A confirmation of this data using RT-qPCR will help us to drawn and suggest a model for the plant-bacteria interaction, presenting this insight as satisfactory for this type of studies.

Keywords: Sugarcane; Diazotrophic bacteria; H. seropedicae, Proteome; Gel-free.

**Development Agency:** Conselho Nacional de Desenvolvimento Científico e Tecnológico – CNPq and Embrapa