

## DIFFERENTIAL PROTEOME OF *GLUCONACETOBACTER DIAZOTROPHICUS* UNDER SUGARCANE INFLUENCE

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*Gluconacetobacter diazotrophicus* (GD) is a micro-aerobe *bacterium* able to fix atmospheric nitrogen. Its presence was demonstrated living in the apoplastic fluid and the xylem of sugarcane plant. The interaction between host and bacteria has been studied *in vitro*. Some sugarcane genes involved in this communication have been depicted. Here, we aimed to understand this interaction at the point of view of bacteria throughout differentially expressed proteins when bacteria is grown in the presence (vs.,-plant) and absence of sugarcane (control cells) using proteomics techniques. Two-dimensional gel electrophoresis, MALDI-TOF-TOF mass spectrometry analysis and protein identification by Mascot search in non-public GD data bank were used. The gel images of replicated experiments were matched and the protein spots were statistically evaluated by two samples *t*-test. The majority of proteins present in both conditions belonged to genetic information processing, cellular motility, signaling, transporter and general metabolism. The differentially expressed control cell proteins were different isoforms present in both samples. The vs.,-plant differentially expressed proteins were different isoforms present in both samples and proteins involved in signaling, oxidative metabolism as well as others proteins not commonly involved in energy production and conversion. These results suggest that this is a robust biological system, i.e., is resistant to drastic environmental changes and is regulated at metabolic level. Financial support: CAPES, CNPq and Faperj