

## PEPTIDOMICS ANALYSIS OF THE NITROGEN-FIXING BACTERIUM

*GLUCONACETOBACTER DIAZOTROPHICUS*

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One important application of mass spectrometry (MS) is the direct analysis of complex samples allowing the identification of small proteins and peptides in a single step. Proteomics techniques were used to characterize the major peptides expressed by *Gluconacetobacter diazotrophicus*. This bacterium, found within plants such as sugarcane and sweet potato, fixes atmospheric nitrogen, produces plant growth-promoting hormones and bacteriocins and solubilizes zinc-compounds. In the experimental setup, *G. diazotrophicus* grown in LGIP medium until exponential phase were lysed with Tris pH 11, Urea 8M, SDS 2% and DTT 200mM. Proteins were precipitated with TCA and the resulting soluble sample was dialysed in water using 1kDa membrane. Also, the culture supernatant filtered in a 0.22µm membrane was ultrafiltrated using 1 and 10kDa cut-off membranes. Both samples were concentrated in Sep-Pak C18 cartridges previously to MS analysis. Samples were analyzed in MALDI-TOF in the mass range 1.000-10.000 m/z in linear mode. The first peptidomic view of *G. diazotrophicus* PAL5 is presented herein, showing 11 major peptides in whole cell lysate of *G. diazotrophicus* cells and 13 in the culture supernatant. We identified in the MS spectra several peptides with molecular mass < 2.500Da. However, the main peaks of the lysate spectra were 5.030 and 5.162 m/z. We will further sequence these peptides by MALDI-TOF/TOF in order to elucidate their role in *G. diazotrophicus* physiology. Support: FAPERJ, CNPq and FINEP.