A proteome reference map for *Gluconacetobacter diazotrophicus* PAL5

Lery, LMS[1,5]; Medeiros, MS[2,5]; Santos, MF[3,5]**;** Santos, EO[2,5], Mortera, P[1,5]; von Kruger, WMA[1,5], Domont, GB [3,5]; Teixeira, KRS[4,5]; **Coelho, A**[2,5], Bisch, PM[1,5]

[1] Unidade Multidisciplinar de Genômica - UFRJ, [2] Departamento de Genética - UFRJ,
[3] Departamento de Bioquímica-IQ-UFRJ, [4]EMBRAPA Agrobiologia, [5]Rede de Proteômica do Estado do Rio de Janeiro

G. diazotrophicus is a nitrogen-fixing bacteria found as an endophyte in roots, stems and leaves from sugar cane, coffee plant, sweet-potato and pineapple. *G. diazotrophicus* is of great interest not only due to its capacity to assimilate N_2, but also because it is a good model to study symbiosis of the bacterium with plant. Moreover, besides its economical importance to increase crop productivity, a better understanding of its physiology will allow the development of more efficient methods for its inoculation into vegetal species and others biotechnological approaches. Physiological proteomics requires 2D reference maps, on which most of the main proteins are identified. We present a reference map for *G. diazotrophicus* proteins, which contains about 450 spots and more than 200 identified proteins (through MALDI TOF and MALDI TOF/TOF analysis), corresponding to the products of 171 genes, with isoeletric points between 4 and 7 and molecular masses between 10 and 120 kDa. Several of the spots corresponded to the same protein, as found for various proteomes. These isoforms may be due to post-translational modifications. The results were obtained from gels run on 18 cm immobilized pH gradient strips and 12,5% SDS polyacrylamide gels, representatives of *G. diazotrophicus* cells at the stationary phase of a pH controlled growth curve. Identified proteins were grouped into 20 different categories and 26 metabolic pathways. Most of identified proteins were categorized as members of energy and aminoacid metabolism and protein synthesis. Surprisingly, hypothetical proteins accounted for only 11% of identified proteins. Functions such as toxin production, resistance and adaptation were also represented. Many detected pathways, such as nitrogen, glutamate and amino groups metabolism and urea cycle are involved in nitrogen metabolism and they could suggest routes for nitrogen fixation in this bacterium. A first version of the genome sequence of *G. diazotrophicus* was made available for protein identification (RioGene project - in progress). It is important to note that the determination of complete genome sequence will contribute to a better proteome annotation and study of proteins from the point of view of their structure and expression.