

ANALYSIS OF GENOME EXPRESSION OF RHIZOBIUM ETLI IN FREE LIVING AND PLANT-ASSOCIATED SYMBIOTIC STATE

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Nitrogen fixation carried out by bacteria is a process by which bacteria reduce atmospheric nitrogen to ammonium. In *R. etl*, this occurs in symbiosis with *Phaseolus vulgaris* and serves as natural fertilizers in agriculture with harmless effects on the environment.

Using proteomics and transcriptomics methodologies, we identified 430 proteins and 689 genes up-regulated during nitrogen fixation. Functional composition of this set of proteins and genes ranged from enzymes participating in central metabolism. Remarkable, the significant number of proteins participating as transporters reveals the intense metabolic crosstalk between plant and bacteroid. In addition, identified proteins and/or genes participating in the regulatory mechanism in nitrogen fixation, energy transfer and cellular protection, suggesting how this proteins and genes orchestrate the metabolic activity required for nitrogen fixation.

Alternatively, we studied the extracellular proteome of *R. etli*, which is presumed to be a key element of their infection strategy and survival. Secreted proteins were analyzed in the exponential growth phase and stationary growth phases, in the exponential growth phase the most abundant group was corresponded to ribosomal proteins and in stationary phase, we found that the most abundant proteins were those with unknown function, additionally observed in *R. etli* the presence of vesicles of external membrane (OMV), and in this OMV identified proteins and other molecules, suggesting us that these structures are involved in the early stages of the process of symbiosis between bacteria and plant.

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