



Acclimation of microorganisms to harsh soil crust conditions: Experimental and genomic approaches

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Biological soil crusts (BSC) are formed by the adhesion of sand particles to cyanobacterial exo- polysaccharides and play an important role in stabilizing sandy desert. Its destruction promotes desertification. These organisms cope with extreme temperatures, excess light and frequent hydration/dehydration cycles; the mechanisms involved are largely unknown.

With the genome of newly sequenced *Leptolyngbya*, isolated from Nizzana BSC, we conduct comparative genomics of three desiccation tolerant cyanobacteria. This yield 46 unique genes, some of them similar to genes involved in sporulation of the gram positive bacteria *Bacillus*.

In order to understand the molecular mechanisms taking place during desiccation we built an environmental chamber capable of simulating dynamic changes of environmental conditions in the crust. This chamber allows us to perform repetitive and accurate desiccation/rehydration experiments and follow cyanobacterial physiological and molecular response to such environmental changes.

When we compared fast desiccation (less than 5 min) of isolated cyanobacteria to simulation of natural desiccation, we observed a 60% lower fluorescence recovery rate. The extent of damage from desiccation depended on the stress conditions during the dry period. These results suggest that cyanobacteria activated protection mechanisms in response to desiccation stress but which were not activated in 5 min desiccation tests. Gene expression patterns during desiccation are being analyzed in order to provide a better understanding of desiccation stress protection mechanisms.