

Transcriptomic analysis of the lichen photobiont *Trebouxia gelatinosa* subjected to dehydration and rehydration processes

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All *Trebouxia* species, the most common lichen-forming genus of aero-terrestrial green algae, are desiccation tolerant. This remarkable adaptation is, however, poorly known on its molecular bases. We applied a transcriptomic approach to investigate changes in the gene expression of *T. gelatinosa* induced by changes in the cell water status. The mRNA of three sample groups (control, dehydrated, rehydrated) was subjected to Illumina massive sequencing (2×100 bp), that produced a total of 243×10⁶ fragments. From this pool 13,648 protein-coding transcripts could be annotated and used for the subsequent gene expression analysis. During the dehydration/rehydration cycle c. 92% of the total protein-coding transcripts displayed a stable expression, suggesting that the desiccation tolerance of *T. gelatinosa* mostly relies on constitutive mechanisms. Components of the photosynthetic apparatus, the ROS-scavenging system, expansins, and Desiccation Related Proteins (DRP) were those most affected by changes in the cell water status. The assembled *T. gelatinosa* transcriptome here presented is a valuable standard reference for future RNA-seq based gene expression studies and represents a new tool to investigate the mechanisms of desiccation tolerance in aero-terrestrial green algae and lichen photobionts.