

Construction and analysis of protein-protein interaction networks based on nuclear proteomics data of the desiccation-tolerant *Xerophyta schlechteri* leaves subjected to dehydration stress

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Abstract

In order to understand the mechanism of desiccation tolerance in *Xerophyta schlechteri*, we carried out an in silico study to identify hub proteins and functional modules in the nuclear proteome of the leaves. Protein-protein interaction networks were constructed and analyzed from proteome data obtained from Abdalla and Rafudeen. We constructed networks in Cytoscape using the GeneMania software and analyzed them using a Network Analyzer. Functional enrichment analysis of key proteins in the respective networks was done using GeneMania network enrichment analysis, and GO (Gene Ontology) terms were summarized using REViGO. Also, community analysis of differentially expressed proteins was conducted using the Cytoscape Apps, GeneMania and ClusterMaker. Functional modules associated with the communities were identified using an online tool, ShinyGO. We identified HSP 70-2 as the super-hub protein among the up-regulated proteins. On the other hand, 40S ribosomal protein S2-3 (a protein added by GeneMANIA) was identified as a super-hub protein associated with the down-regulated proteins. For up-regulated proteins, the enriched biological process terms were those associated with chromatin organization and negative regulation of transcription. In the down-regulated protein-set, terms associated with protein synthesis were significantly enriched. Community analysis identified three functional modules that can be categorized as chromatin organization, anti-oxidant activity and metabolic processes.