

Integrative transcriptomic and TMT-based proteomic analysis reveals the desiccation tolerance in *Ramonda serbica* Panc.

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Ramonda serbica Panc. is a resurrection plant that can survive long periods of desiccation and fully restores its metabolic functions just one day after watering. The aim of this study was to identify key candidates and metabolic pathways involved in *R. serbica* desiccation tolerance. We combined differential transcriptomics and proteomics with the analysis of phenolics, sugars, cell wall polymers and photosynthetic electron transport (PET) chain. TMT-based proteomic analysis allowed the relative quantification of 1192 different protein groups, 408 of which were differentially abundant between hydrated (HL) and desiccated leaves (DL). Almost all differentially abundant proteins and transcripts related to photosynthetic processes were downregulated in DL. Chlorophyll fluorescence measurements showed a shift from linear PET to cyclic electron transport (CET). The levels of H₂O₂-scavenging enzymes, ascorbate-glutathione cycle components, catalases, peroxiredoxins, Fe-, and Mn superoxide dismutase (SOD) were reduced in DL. However, six germin-like proteins (GLPs), four Cu/ZnSOD isoforms, three polyphenol oxidases, and 22 late embryogenesis abundant proteins (LEAPs; mainly LEA4 and dehydrins), were desiccation-inducible. Desiccation led to cell wall remodelling related to GLP-derived H₂O₂/HO[•] activity and pectin demethylesterification. This comprehensive study contributes to understanding the role and regulation of important metabolic pathways during desiccation with the final aim to help improving the drought tolerance in crops.

Keywords: cell wall remodelling, drought, germin-like proteins, late embryogenesis abundant proteins, resurrection plant.

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