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# Characterization of the late embryogenesis abundant (LEA) proteins family in hydrated and desiccated *Ramonda serbica* Panc. leaves

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Endemic plant species, *Ramonda serbica* is a resurrection plant that can tolerate extreme dehydration (desiccation, loss of 95% of cellular water) even over months. The accumulation of late embryogenesis abundant proteins (LEAPs) is a crucial step in the mechanism of desiccation tolerance. The role of LEAPs is not completely resolved, but they are accepted as intrinsically disordered proteins (IDPs). Based on previously established *de novo* transcriptome database of *R. serbica* leaves we identify around 160 members of LEA gene family. Identified LEAPs were classified into six groups: LEA 1-5 and seed maturation proteins (SMPs) according to protein family (Pfam) database. Based on multiple sequence alignment, secondary structure prediction and 3D structure modeling, we conducted LEA protein structure analysis. We showed that more than 50% of identified LEAPs exhibited a high propensity to form  $\alpha$ -helices. As predicted by several bioinformatic tools, more than 70% of identified LEAPs were found to be highly disordered. Thus, these proteins are predicted to be disordered in solution, but they acquire a secondary, predominantly  $\alpha$ -helical structure during drying, in contrast to globular proteins, which most often causes the loss of structure upon dehydration. By using molecular dynamic simulations, we identified the most favorable conformations of representative LEAPs and we have studied conformational transitions driven by the water scarcity. Structural characterization of LEAPs is a key to understand their function and regulation of their intrinsic structural disorder-to-order transition during desiccation as a requirement for biological function, in order to promote development of new therapeutic strategies in neurodegenerative disorders, cell preservation technology and the improvement of crop drought tolerance.

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