BOOK of ABSTRACTS

4th INTERNATIONAL CONFERENCE ON PLANT BIOLOGY 23rd SPPS Meeting







Serbian Plant Physiology Society

Institute for Biological Research "Siniša Stanković" National Institute of Republic of Serbia, University of Belgrade

Faculty of Biology, University of Belgrade

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SELECTED TALKS

Late embryogenesis abundant (LEA) proteins in *Ramonda serbica* Pancidentification, classification and structural characterization

ST3-1

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An ancient resurrection plant Ramonda serbica Panc. is able to survive a long desiccation period and reestablish metabolic activity upon watering. A hallmark of desiccation tolerance in the resurrection species is the accumulation of protective late embryogenesis abundant proteins (LEAPs). These intrinsically disordered proteins (IDPs) may stabilize the correct structure of proteins and membranes during cellular dehydration. The aim of our study was to assess LEA genes' expression levels in hydrated (HL) and desiccated leaves (DL) and to identify, characterise, and estimate the potential role of *R. serbica* LEAPs in desiccation tolerance. In total, 318 LEAPs from HL and DL were identified and classified into the seven LEA protein family groups ranging from LEA1-LEA5, seed maturation proteins (SMPs), and dehydrins (DEH). Analysis of the physicochemical properties, motif architecture, secondary structure, homology, and phylogenetic relationships demonstrated that R. serbica LEAPs greatly differed among the LEA family groups. The most abundant LEA2 proteins (mostly downregulated upon desiccation) exhibited lower hydrophilicity and propensity to fold into organised globular domains. Oppositely, hydrophilic LEA4 proteins tended to form amphipathic, A-type, α-helices. Most of desiccation-upregulated LEA genes encoded highly disordered DEH1, LEA1, LEA4.2, and LEA4.3 proteins. While dehydrins might chelate metals and bind DNA under water deficit, other ID LEAPs (e.g. LEA1, LEA3, LEA4) might participate in forming intracellular proteinaceous condensates or adopt amphipathic a-helical conformation, enabling them to stabilise desiccation-sensitive proteins and membranes. Taken together, possible functions of LEAPs are discussed with significant implications on drought tolerance improvement of crops grown in arid areas.

Keywords: 3D protein structure modelling, de novo transcriptome assembly, intrinsically disordered proteins, liquid-liquid phase separation, secondary structure prediction

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