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Comparative proteomics of dehydration-responsive changes in the nucleus reveals genotype-specific adaptation

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Water-deficit or dehydration is the most crucial factor that is detrimental to plant growth, development, and productivity. With progressive global climate change, shortage of water resources and worsening eco-environment, the situation is likely to turn more serious. The nucleus not only hosts the genome but also administers its transcription and the regulated expression of proteins, thereby playing vital role as modulator of cellular phenotype. A nucleus-specific proteome was developed in IR-64, a dehydration-susceptible cultivar of rice and critically compared with that of dehydration-tolerant Rasi. 2-DE coupled with MS/MS led to the identification of around hundred dehydration-responsive proteins (DRPs), presumably involved in signaling and gene regulation, cell defense and rescue, transcriptional regulation and chromatin remodeling, among others. More than three-fourth of the dataset are predicted as nuclear-localized. The cohorts of identified proteins, interacting in a concerted manner have been mapped into a functional association network. The relatively low overlap of the DRPs between the two cultivars suggest that their differential response may be due to the qualitative and quantitative differences of DRPs involved in common regulatory pathways, though there might be alternative pathways involved in dehydration response that make a plant susceptible or tolerant. The findings indicate that well-orchestrated reactive oxygen species management and protein quality control mechanism may render better dehydration adaptation. To assess the stress-responsive mechanisms operative in the nucleus of different plants, a comparative analysis of various proteome datasets was performed. It revealed limited conservation of regulatory proteins but conserved induction of proteins involved in stress response.

Biography

Doel Ray is working as Project Investigator under Bio-CARe (Biotechnology Career Advancement and Re-orientation) Programme of Department of Biotechnology (DBT), Govt. of India at NIPGR, New Delhi since 2012. In 2009, she was selected in ‘DBT-Postdoctoral Program in Biotechnology & Life Sciences’. Exploring the fascinating field of signal transduction has been her humble endeavor during research spanning the last decade, ranging from stress-related signaling in parasitic protist (Ph.D. from Saha Institute of Nuclear Physics, Kolkata) to the application of cutting-edge technologies like proteomics to dissect stress-tolerance in plants. She has publications in journals of repute.