

## Unraveling of integrated mechanisms in Omics technology for crop improvement

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In present-day the comprehensive analysis of biological information can be understood by applying the 'OMICS' technologies (i.e. genomics, transcriptomics, proteomics and metabolomics). The system biologists need tools not only to analyze the massive experimental data but also their accurate annotation. We aim to extract biological knowledge from publically available large-scale experimental data sets using comparative sequence as well as expression analysis, and network exploration. Identification of key enzymes and their encoding genes for the enrichment of important metabolites using computational analysis, RNAi based gene silencing, and their validation using analytical approaches are another vital aspect for metabolomic study. Identification of the less informative Transcription Factor Genes in gene expression databases, their expression analysis for constructing the gene network and in silico analysis of differentially co-expressed Transcription Factor Genes during abiotic stresses conferring the stress tolerance by regulating the downstream genes will be presented.

### Biography

Dev Mani Pandey has completed his Ph. D. in 2000 from CCS Haryana Agricultural University, Hisar, India. He worked as Post-Doctoral Fellow in Plant Molecular Biology and Functional Genomics Laboratories in South Korea and has presented his research findings in various international symposia. He was invited to work as a Consultant at IRRI, Los Banos, Philippines. Currently he is an Associate Professor in the Department of Biotechnology, BIT, Mesra, Ranchi, India. His primary areas of scientific interest and expertise include rice functional genomics, stress physiology, bioinformatics, molecular biology approaches on medicinal and aromatic plants.

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