

Proteomics and metabolomics approaches to understand plant-pathogen interactions

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Nucleic acid-based technologies have been widely used in studies of comparative gene expression profiling in plant-pathogen interactions. However, it is essential that these studies also be carried out at protein and metabolite levels as they are the functional readouts of the genetic information. Further, usually there is a substantial discordance between transcript abundance and functional output that causes phenotypic plasticity. Two leading technological platforms for quantitative protein profiling are two-dimensional gel electrophoresis (2DE) followed by MS and a liquid chromatography (LC)/MS/MS analysis called shotgun proteomics. We

have used the label-free shotgun proteomics (LC-MS^E) approach to identify and quantify the proteome of chickpea plants inoculated with *Fusarium oxysporum* f.sp. *ciceri*. Compared to 2DE, the LC-MS^E has a wide dynamic range and less bias against protein classes. As a result, a large number of proteins have been identified using this approach. To complement the proteomics data, we have used NMR to understand changes in metabolites during plant-pathogen interactions that could open up new vistas to understand the dynamic biochemical networks of plant defense against the fungal pathogen.

Biography

I have completed Post-graduation in Biotechnology from University of Pune and presently doing Ph.D. at National Chemical Laboratory under the supervision of Dr. Vidya Gupta and Dr. Ashok Giri.