Proteomics refers to large scale comprehensive analysis of proteome that includes abundance level and modification of proteins, their interacting partners and networks. Proteome in general refers to the total set of proteins expressed by genome of a cell/ tissue/ organism whose dynamic nature upon exposure to environmental stimuli can be analyzed using technologies to decipher the underlying complex biological processes involved in turn leading to the discovery of potential biomarkers.

Pearl millet \([\textit{Cenchrus americanus} (\text{L.}) \text{ Morrone; synonym: } \textit{Pennisetum glaucum} (\text{L.}) \text{ R. Br.}]\) is a staple food crop among the poorer section of the global population, especially in the semi-arid tropical regions of Asia and Africa. Downy mildew disease caused by the obligate biotroph- \(\textit{Sclerospora graminicola}\) is a major biotic constraint that unfavorably affects the crop yield. In the current study, an attempt has been made to understand the interaction between pearl millet and downy mildew using proteomic approach.

Previous studies has shown that seed priming of a susceptible cultivar of pearl millet using \(\beta\)-aminobutyric acid (BABA) and \(\textit{Pseudomonas fluorescens}\) has reduced the downy mildew disease incidence level by more than 70\% under field studies. In the present study, 2DE-MS/MS based proteomic approach was used to reveal the poorly studied resistance mechanism in these elicitor primed pearl millet seedlings in response to \(\textit{Sclerospora graminicola}\) infection. The proteomic data revealed that majority of the 63 differentially accumulated (\(p < 0.05\)) proteins represented energy and metabolism followed by stress and defense category. Multivariate statistical analysis of the protein abundance profile unveiled that infection by the pathogen rather than elicitor treatment had a major impact on the dynamics of host proteome and the elicitors had different priming mechanism.

Among the differentially accumulated proteins, proteins pertaining to glucose metabolism were enriched, indicating that seed priming ensures plant protection against disease without affecting the balance in energy diversion towards normal growth and development. In addition, analysis of dynamics of proteome in resistant cultivar of pearl millet seedlings during early hours (i.e. 6 hours) of downy mildew infection revealed the timely events of early expressing genes such as those involved
Abstract

in hypersensitive mediated reaction were responsible for conferring the systemic immunity in the resistant cultivar of the plant.

To further characterize the genes encoding some of the differentially accumulated proteins, gene expression studies using quantitative real-time PCR (qPCR) approach was employed. Prior to the gene expression studies, detection of suitable reference genes (RGs) and optimal number of RGs as internal controls for normalization of gene expression data by qPCR was performed using geNorm, NormFinder, BestKeeper softwares. The study revealed that PP2A, TUB and UBQ were suitable and appropriate reference genes in normalizing the transcript abundance of proteomic dataset. Among the genes chosen for validating the proteomic data, correlation in the regulation of abundance at protein and transcript level of xylanase inhibitor-protein (XIP) and isocitrate lyase (ICL) were observed. This suggests their possible usage as bio-markers for screening resistant traits among the cultivars of pearl millet. The present study indicates that analysis of pearl millet-downy mildew interaction by proteomic and qPCR approach will provide a means to find suitable bio-markers useful in designing an effective strategy in crop protection and improvement.