Sub-cellular proteomics for deep understanding.

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Introduction

Protein functions have acquired more importance since the completion of the first genome studies in 2000's. We have learned that we have more proteins than genome size while the introduction of omics technologies and their development in the course of time have shown that the protein profiles of the organisms are changeable under different stimuli. Since the first introduction of the term "proteome", a number of studies on proteomics have been carried out especially in animal samples due to the less complex sample preparation methods. However, plant and plant-microbe interaction in proteomics studies was delayed due to their calcitrant nature. Proteomics studies involve several applications such as descriptive proteomics, differential proteomics, determination of Post Translational Modifications of proteins, secretomics and interaction proteomics. The knowledge obtained from these approaches is invaluable while highly abundant and generally cytosolic proteins can be identified with these approaches. Maximum 10-12000 proteins have been identified with gel free techniques and this number is lower with the gel-based techniques. Levels of some effector/elicitor proteins, disease markers, and emerged membrane receptors under different stress circumstances such as PAMPs/MAMPs are below the detection limit in total cell lysates. Enrichment of organelles and identification of proteins belonging to organelles and mining of yielded protein data by bioinformatics tools will provide opportunity to decrease the complexity and increase the elucidated proteins and underlying mechanisms of the stress conditions. Sub-cellular proteomics studies are very limited among animals, plants and fungi. Although proteome of subcellular organelles of A. thaliana such as mitochondria, peroxisomes, and nuclei is studied [1] but this kind of research for phytofungus is thin on the ground. These are haustoria-formed by *Blumeria graminis f. sp. hordei*, and *Puccinia triticina*- proteomics studies [2,3] for biotrophic pathogens, and cell wall proteome of both necrotrophic and biotrophic fungi [4] whereas organelles, Endoplasmic Reticulum (ER) and golgi with complex and heterogeneous nature belong to animal and human samples especially in some cancers [5]. These organelles have been attractive in recent years especially for diseases caused misfolded proteins. As expected, researches involving the proteome of these organelles for plant-fungus interaction and fungus lonely have not been revealed yet. If researchers will focus on these organelles reserving crucial clues underlying different secretion pathways, several small but important elucidations will be obtained. We know that today ER-Golgi system is not unique secretion pathway for living organisms, besides this secretion system non-canonical secretion pathway is crucial especially during plant-pathogen interaction. These are vacuolar secretion and endocytic secretion via extracellular vesicles. This non-canonical secretion is important in view of PRR protein secretion and also ability of pathogen to change the host membrane trafficking to its favour. In recent study performed by [6] has shown that extrahaustorial membrane of *Blumeria graminis* f. sp. *Hordei* has plant ER like structure, but this membrane is not dependent conventional secretion. Although secreted proteins in plants do not have signal peptide, mechanisms underlying remains unknown so we need deep sub-cellular proteome analysis either for plant-pathogen interaction or pathogen alone.

References

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