

# ***Proteomics for Crop Improvement under Abiotic Stresses***

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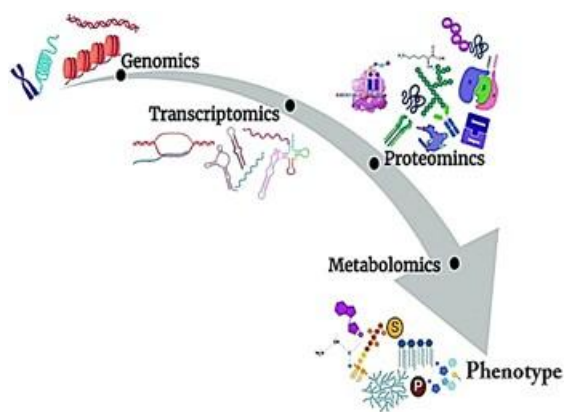
## **ABSTRACT**

The increasing global population and climate variability have intensified the demand for sustainable food production, necessitating innovative approaches for crop improvement. Among modern biotechnological tools, proteomics has emerged as a powerful platform to study the complete set of proteins expressed under specific physiological conditions. Unlike genomics and transcriptomics, proteomics provides direct insight into functional molecules that regulate plant responses to abiotic stresses such as drought, salinity, heat, cold, waterlogging and toxic metal exposure. These stresses drastically reduce crop productivity by disrupting cellular homeostasis, metabolic pathways and signaling networks. Through advanced analytical techniques like mass spectrometry, two-dimensional gel electrophoresis, and isotopic labeling, proteomics enables the identification, quantification and characterization of stress-responsive proteins. Such information facilitates the discovery of biomarkers, validation of stress-associated genes and understanding of tolerance mechanisms. The integration of proteomic data into breeding and genetic engineering programs offers promising avenues for developing resilient, high-yielding crop varieties adaptable to changing environmental conditions.

## INTRODUCTION

With the increase in global population there is a pressure on food production. Food security is a major challenge in present world due to erratic weather and climate change which leads to reduced crop yields so breeders need new and more precise tools to accelerate the breeding program. One such advantageous technology is multiomics which have made process of crop production more accurate and targeted so that future crops are depicted to have resistance to biotic and abiotic stresses, smart nutrient uptake, high yield and nutritional value if we employ omics method in crop production.

Abiotic stress encompasses various environmental factors such as drought, salt, temperature fluctuations, waterlogging and nutritional imbalances, all of which significantly impede plant growth and yield. These stresses create unfavourable conditions for plants. Predictions indicate that approximately half of all crop losses are attributed to abiotic stresses. Profound changes in the physiological, molecular and biochemical processes within plants limits their distribution, alter growth patterns and diminishes yield. (Ghosh and Xu, 2014)



The term “Proteomics” was first coined in 1994 by Marc Wilkins. Proteome refers to the total set of proteins expressed in a given cell at a given time. The study of proteome is termed

as proteomics. In contrast to the genome, a static structure inherited from parents that defines the plant genotype, alterations in the plant epigenome, transcriptome, proteome and metabolome collectively influence the plant phenotype (Suvarna *et al.*, 2024).

Proteins play a direct role in the plant stress response, serving as both structural components and regulators of the plant epigenome, transcriptome and metabolome. Additionally, the functionality of a protein is not solely determined by its molecular structure; it is also influenced by factors such as cellular localization, post-translational modifications and interactions with other proteins. These aspects collectively contribute to multifaceted role that proteins play in the intricate mechanisms of plant stress adaptation and response. Proteomics, a state-of-the-art molecular technique, provides distinct advantages over genome-based technologies by directly focusing on functional molecules rather than the genetic code or mRNA abundance (Kosová *et al.*, 2018).

## TYPES OF PROTEOMICS

- **Structural Proteomics:** The ultimate aim of this proteomics is to build a body of structural information that will help predict the probable structure and potential function for almost any protein from knowledge of its coding sequence. eg: X-ray crystallography and NMR spectroscopy.
- **Functional proteomics:** It refers to the use of proteomics techniques to analyze the characteristics of molecular protein-networks involved in a living cell.
- **Expression proteomics:** It refers to the quantitative study of protein expression between sample differing by some variable (Aslam *et al.*, 2016).

## STEPS IN PROTEOMICS

- **Protein Extraction**
- **Protein Separation**
- **Protein Identification**
- **Protein Characterization**

### List of different proteomic approaches

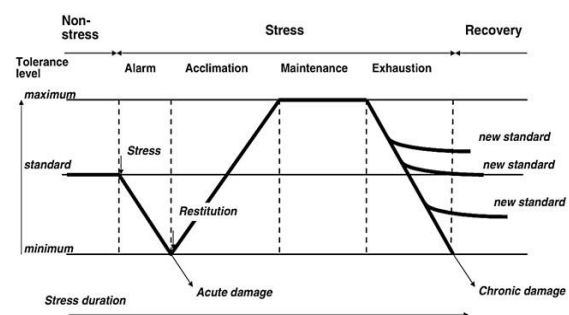
Conventional Approaches	
<b>A</b>	<b>Chromatography-based approaches</b>
1	Ion-exchange chromatography (IEC)
2	Size-exclusion chromatography (SEC)
3	Affinity chromatography
<b>B</b>	<b>Enzyme-linked immunosorbent assay (ELISA)</b>
<b>C</b>	<b>Western blotting</b>
<b>D</b>	<b>Edman sequencing</b>
Advanced Techniques	
<b>A</b>	<b>Protein microarrays</b>
1	Analytical protein microarray
2	Functional protein microarray
3	Reverse-phase protein microarray
<b>B</b>	<b>Gel-based approaches</b>
1	Sodium Dodecyl Sulphate-Polyacrylamide Gel Electrophoresis (SDS-PAGE)
2	Two-dimensional Polyacrylamide gel electrophoresis (2D PAGE)
3	Two-dimensional differential gel electrophoresis (2D-DIGE)
<b>C</b>	<b>Quantitative techniques</b>
1	ICAT labelling (isotope-coded affinity tags)
2	Stable isotopic labelling with amino acids in cell culture (SILAC)
3	Isobaric tag for relative and absolute quantitation (iTRAQ)
<b>D</b>	<b>X-ray crystallography</b>
High-Throughput Techniques	
<b>A</b>	<b>Mass spectrometry</b>
<b>B</b>	<b>NMR spectroscopy</b>

### Bioinformatic tools:

- SWISS- 2D PAGE for protein identification.
- NCBI/ BLAST – sequence database.
- SWISS-PORT – sequence database.
- SWISS- MODEL – 3D structure.
- PROSITE – for domain structure.
- Gene Bank and EMBL – DNA data banks (Bagga, 2004).

## ABIOTIC STRESS

Abiotic stresses, including drought, heat, salinity, waterlogging and toxic metal stress, can negatively impact plant growth, leading to reduced crop yield and quality. Plants employ two key strategies, avoidance and tolerance, to adapt to such stress, making cellular and metabolic adjustments to withstand adverse conditions. Acclimatization results in significant changes in a plant's proteome, crucial for its stress response. Proteins encoded by a plant's genome play a vital role in environmental adaptation, supporting biotechnological advancements in plant breeding, utilizing data from proteomic investigations. Proteomics provides unique insights into post-translational modifications and their impact on crop yield. Subcellular proteomics aids in understanding cellular responses and interactions during growth and responses to biotic and abiotic stresses. Proteomic tools, like mass spectrometry, liquid chromatography, protein microarrays and antibody-based assays, are integral to proteomic studies, contributing to our understanding of protein functions and interactions. Developing stress-tolerant crops is crucial for enhancing crop productivity and growth (Khalid *et al.*, 2019).



### Five phases characterizing plant responses to abiotic stress

1. **Initial Alarm Phase:** When plants first encounter stress, they activate immediate defense mechanisms. This includes the synthesis of stress-protective proteins like



chaperones, COR/LEA proteins, phytochelatins (PCs), and reactive oxygen species (ROS) scavenging enzymes. These proteins help protect cellular structures and maintain function under stress.

2. **Acclimation Phase:** During this phase, plants adapt to the stress by adjusting their physiological and biochemical processes. This leads to increased tolerance and helps the plant survive the adverse conditions.
3. **Maintenance Phase:** In this phase, plants sustain their tolerance levels. They continue to produce stress-protective proteins and other molecules to maintain homeostasis and ensure survival under prolonged stress conditions.
4. **Exhaustion Phase:** If the stress persists for too long, plants may enter the exhaustion phase. During this phase, their tolerance declines due to the inability to maintain homeostasis. This can lead to cellular damage and reduced growth or productivity.
5. **Recovery Phase:** Upon the removal of stress, plants enter the recovery phase. They gradually regain normal homeostasis and resume regular growth and development.

#### APPLICATIONS OF PROTEOMICS IN CROP IMPROVEMENT UNDER ABIOTIC STRESS:

1. **Identification of Stress-Responsive Proteins:** Proteomics helps detect specific proteins involved in drought, salinity, heat, cold and metal stress responses, aiding in understanding plant tolerance mechanisms.
2. **Elucidation of Stress Pathways:** It reveals molecular pathways such as oxidative stress regulation, osmotic adjustment, and energy metabolism activated during abiotic stresses.

#### 3. Discovery of Stress Biomarkers:

Proteomic profiling identifies potential protein biomarkers that can be used for screening and developing stress-tolerant crop varieties.

4. **Gene Function Validation:** By linking proteins to their genes, proteomics supports validation of stress-related genes identified through genomics or transcriptomics.

5. **Targeted Breeding and Genetic Engineering:** Information from proteomic studies guides breeders and biotechnologists in selecting or manipulating key proteins and genes to enhance stress tolerance.

6. **Comparative Stress Analysis Across Species:** Comparative proteomics enables cross-species analysis, helping to transfer knowledge from model plants to major crops for improving resilience under multiple stress conditions.

#### CONCLUSION

Proteomics has proven to be an indispensable component of plant stress biology, offering a detailed understanding of the molecular mechanisms underlying abiotic stress tolerance. By focusing on proteins, the functional executors of the genome, proteomics bridges the gap between genetic information and phenotypic expression. It enables the identification of key stress-related proteins, elucidation of complex signalling pathways, and discovery of biomarkers for stress tolerance. The combination of proteomics with other omics platforms, bioinformatics, and high-throughput technologies enhances the precision of crop improvement strategies. Future advances in quantitative and subcellular proteomics, coupled with integrative systems biology, will accelerate the development of stress-resilient crops capable of sustaining productivity under

diverse and changing environmental conditions.

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