



Omics to Manage Abiotic Stresses

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Omics is a term used to describe high-throughput technologies that allow for the large-scale analysis of biological molecules, such as DNA, RNA, proteins, and metabolites. These technologies have revolutionized the field of agriculture, particularly in the area of crop improvement. Abiotic stresses, such as drought, salinity, and extreme temperatures, can have a significant impact on crop productivity and yield. The use of omics technologies can help identify the molecular mechanisms that plants use to cope with these stresses, which can be used to develop crops that are more resilient to environmental challenges. One example of the use of omics in abiotic resistance crops is in the study of drought tolerance in maize. Researchers have used transcriptomics, which involves the large-scale analysis of gene expression, to identify genes that are differentially expressed in response to drought stress. They have also used metabolomics, which involves the analysis of small molecules involved in metabolism, to identify metabolic pathways that are involved in drought tolerance. Another example is the use of genomics in the development of salt-tolerant crops.

Researchers have identified genes that are involved in salt tolerance and used genetic engineering techniques to introduce these genes into crops. These genetically modified crops have shown improved salt tolerance, which could help farmers grow crops in areas with high soil salinity. Overall, omics technologies have the potential to revolutionize crop improvement and help us develop crops that are more resilient to abiotic stresses. By understanding the molecular mechanisms that plants use to cope with these stresses, we can develop crops that are better able to withstand environmental challenges and provide food security for the growing global population.

Genomics for drought resistance crops

Genomics can be used in several ways to create drought-resistant crops. Here are some examples:

- **Genome sequencing:** The first step in creating drought-resistant crops is to understand the genetic makeup of the plant. Genome sequencing provides a comprehensive map of the plant's DNA, which can help identify genes that are involved in drought tolerance.
- **Transcriptomics:** Transcriptomics involves studying the expression of genes in response to drought stress. By comparing the gene expression profiles of drought-tolerant and susceptible plants, researchers can identify genes that are differentially expressed in response to drought stress.
- **Marker-assisted selection:** Marker-assisted selection (MAS) is a technique that uses DNA markers to identify plants that have desirable traits, such as drought tolerance. By selecting plants with the desired markers, breeders can speed up the process of developing drought-resistant crops.
- **Genetic engineering:** Genetic engineering involves introducing specific genes into plants to confer drought tolerance. For example, genes that are involved in the synthesis of

osmoprotectants, such as proline and trehalose, can be introduced into plants to help them cope with drought stress.

- **Genome editing:** Genome editing technologies, such as CRISPR-Cas9, can be used to make precise modifications to the plant's DNA. This allows researchers to edit specific genes that are involved in drought tolerance, without introducing foreign genes from other organisms.

Genomics involves the study of the structure, function, and evolution of the genome, which is the complete set of DNA sequences that make up an organism. The application of genomics to plant stress tolerance has led to the identification of key genes and pathways involved in stress response, which can be used to develop stress-tolerant crops. Genomics-assisted breeding (GAB) is a powerful approach for developing crops with improved abiotic stress resistance. GAB involves the identification of molecular markers associated with desirable traits using genomic technologies, which can then be used to select individuals with those traits more efficiently. For example, in wheat, the identification of quantitative trait loci (QTLs) associated with drought tolerance has led to the development of new varieties with improved drought resistance. Genome-wide association studies (GWAS) are another genomics approach that can be used to identify genes associated with abiotic stress resistance. GWAS involves the identification of genetic variants that are associated with a particular trait across a population of individuals. For example, a recent GWAS study in maize identified genetic variants associated with drought tolerance, which can be used to develop new varieties with improved drought resistance.

Overall, genomics provides a powerful set of tools for developing drought-resistant crops. By understanding the genetic basis of drought tolerance, we can develop crops that are better able to withstand water stress and provide food security for the growing global population.

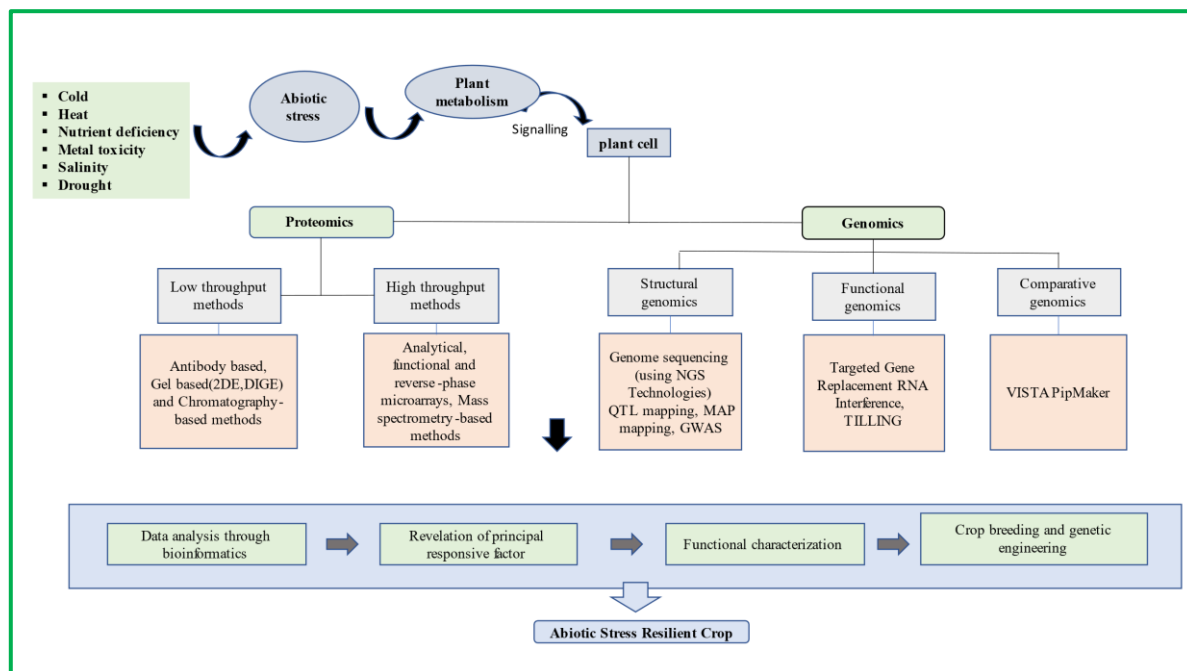
Proteomics in abiotic resistance in crop

Proteomics is the large-scale study of proteins, including their structures, functions, and interactions. Proteomics technologies have been increasingly used in agriculture to study the molecular mechanisms that underlie abiotic stress responses in crops. Here are some examples of how proteomics can be used in abiotic resistance in crops:

- **Protein profiling:** Proteomics can be used to identify proteins that are differentially expressed in response to abiotic stress. By comparing the protein profiles of stress-tolerant and stress-susceptible plants, researchers can identify proteins that are involved in stress tolerance.
- **Post-translational modifications:** Proteomics can also be used to study post-translational modifications (PTMs) of proteins in response to abiotic stress. PTMs, such as phosphorylation, acetylation, and glycosylation, can modulate protein activity and stability in response to stress.
- **Protein-protein interactions:** Proteomics can be used to study protein-protein interactions in response to abiotic stress. By identifying proteins that interact with each other under stress conditions, researchers can gain insight into the molecular pathways that are involved in stress responses.
- **Targeted proteomics:** Targeted proteomics involves the selective analysis of specific proteins or PTMs. By targeting proteins that are involved in stress responses, researchers can gain a deeper understanding of the molecular mechanisms that underlie stress tolerance.
- **Biomarker discovery:** Proteomics can be used to identify biomarkers, such as proteins or peptides, that are associated with stress tolerance. These biomarkers can be used to develop diagnostic tests for stress tolerance, which can help farmers select stress-tolerant varieties of crops.

Two-dimensional gel electrophoresis (2D-GE) and liquid chromatography-mass spectrometry (LC-MS) are the two main proteomics approaches used for abiotic stress research. 2D-GE involves the separation of proteins based on their isoelectric point and molecular weight using two-dimensional gel electrophoresis. LC-MS involves the separation of proteins using liquid chromatography, followed by the identification of proteins using mass spectrometry.

Overall, proteomics provides a powerful set of tools for studying the molecular mechanisms that underlie abiotic stress responses in crops. By understanding the proteomic changes that occur in response to stress, we can develop crops that are more resilient to environmental challenges and provide food security for the growing global population.



(Proteomics and Genomics for abiotic stress resilient crop production)

Transcriptomics in abiotic resistance on Crop

Transcriptomics is the study of the transcriptome, which includes all the RNA molecules in a cell or organism. Transcriptomics technologies have been widely used in agriculture to study the molecular mechanisms that underlie abiotic stress responses in crops. Transcriptomics can be used to identify genes that are differentially expressed in response to abiotic stress. By comparing the gene expression profiles of stress-tolerant and stress-susceptible plants, researchers can identify genes that are involved in stress tolerance. Transcriptomics can also be used to study alternative splicing (AS) events in response to abiotic stress. AS can generate multiple mRNA isoforms from a single gene, which can lead to functional diversity in stress responses. Transcriptomics can be used to study non-coding RNAs (ncRNAs), such as microRNAs and long non-coding RNAs, in response to abiotic stress. ncRNAs can regulate gene expression at the post-transcriptional level and play important roles in stress responses. Transcriptomics can be used to construct co-expression networks, which identify groups of genes that are co-regulated under stress conditions. By analyzing these networks, researchers can identify functional modules that are involved in stress responses.

Transcriptomics can be used to identify candidate genes for gene editing using technologies such as CRISPR-Cas9. By targeting genes that are involved in stress tolerance, researchers can develop crops that are more resilient to environmental challenges. Transcriptomics involves the study of the complete set of RNA transcripts that are produced by a cell or tissue under a particular set of conditions. Transcriptomics can be used to identify

genes that are differentially expressed in response to abiotic stress, providing insights into the molecular mechanisms underlying stress response. Microarray technology and RNA sequencing (RNA-seq) are the two main transcriptomics approaches used for abiotic stress research. Microarray technology involves the hybridization of labelled cDNA or RNA to a microarray chip containing thousands of probes that correspond to different genes. RNA-seq involves the sequencing of RNA transcripts using next-generation sequencing technology.

Transcriptomics studies have identified numerous genes and pathways involved in abiotic stress response in plants. For example, in rice, transcriptomics studies have identified genes involved in the synthesis of osmoprotectants, such as proline and glycine betaine, which help plants cope with drought and salinity stress.

Overall, transcriptomics provides a powerful set of tools for studying the molecular mechanisms that underlie abiotic stress responses in crops. By understanding the transcriptomic changes that occur in response to stress, we can develop crops that are more resilient to environmental challenges and provide food security for the growing global population.

Metabolomics in abiotic resistance on Crop

Metabolomics is the study of the complete set of small molecule metabolites present in a biological sample. It is a powerful tool for understanding the metabolic changes that occur in response to abiotic stress in crops. Metabolomics can identify specific metabolites that are involved in stress resistance and can provide insights into the underlying biochemical pathways.

Metabolomics studies have shown that crops respond to abiotic stress by altering their primary metabolism, including the synthesis of amino acids, sugars, and organic acids. For example, drought stress can lead to the accumulation of proline, which acts as an osmoprotectant and helps maintain cell turgor. Similarly, salinity stress can result in the accumulation of organic acids such as citrate and malate, which can help maintain pH homeostasis and ion balance. Metabolomics studies have also revealed changes in the secondary metabolism of crops in response to abiotic stress. Plants can synthesize a diverse array of secondary metabolites, including flavonoids, phenolics, and terpenoids, which have roles in plant defence, UV protection, and antioxidant activity. For example, the synthesis of flavonoids has been shown to increase in response to UV radiation and can protect plants from damage to DNA and photosynthetic pigments. Metabolomics can also be used to identify biomarkers of stress resistance in crops. By comparing the metabolite profiles of stress-tolerant and stress-sensitive varieties of crops, researchers can identify specific metabolites that are associated with stress resistance. These biomarkers can then be used to screen large populations of crops to identify stress-tolerant varieties.

In conclusion, metabolomics is a powerful tool for understanding the metabolic changes that occur in response to abiotic stress in crops. By identifying specific metabolites and biochemical pathways that are involved in stress resistance, researchers can develop strategies to enhance stress tolerance in crops and improve agricultural productivity and sustainability.

Future of omics in stress tolerance breeding

Omics technologies have already made significant contributions to stress tolerance breeding in crops, and their potential for further advances is enormous. Here are some of the potential future developments of omics in stress tolerance breeding:

- **Multi-omics integration:** The integration of multiple omics data sets, including genomics, proteomics, and metabolomics, will provide a more comprehensive understanding of stress tolerance mechanisms in crops. This approach can help identify

key pathways and targets for genetic manipulation and accelerate the development of stress-tolerant crops.

- **High-throughput phenotyping:** Advances in high-throughput phenotyping technologies, such as remote sensing and imaging, can provide large-scale and accurate measurements of stress-related traits. Coupled with omics technologies, high-throughput phenotyping can provide insights into the complex relationships between genotype, phenotype, and environment.
- **Synthetic biology:** Advances in synthetic biology can provide new tools for engineering crops with enhanced stress tolerance. Synthetic biology approaches involve the construction of novel genetic circuits and regulatory systems that can optimize plant growth and stress response.
- **Genome editing:** Genome editing technologies, such as CRISPR-Cas9, provide precise and targeted modifications to the plant genome. These technologies can be used to introduce novel alleles or modify existing genes to enhance stress tolerance in crops.
- **Big data and machine learning:** The integration of omics data sets with big data and machine learning can help identify patterns and relationships that are difficult to discern manually. This approach can lead to the discovery of new genes and pathways involved in stress tolerance and facilitate the development of stress-tolerant crops.

Overall, omics technologies are likely to play an increasingly important role in stress tolerance breeding in crops. The integration of different omics data sets, together with advances in high-throughput phenotyping, synthetic biology, genome editing, and machine learning, can accelerate the development of crops with enhanced stress tolerance, ensuring food security for the growing global population.

Conclusion

Abiotic stresses like drought, cold, salinity and heavy metal stress adversely affect the productivity. To overcome the negative effect of these adverse effects, two major strategies are adopted: crop management strategies and crop breeding. Crop breeding technologies have now been supported by multi-omics approaches like genomics, transcriptomics, proteomics and metabolomics. These help in the functional analysis and identification of new genes and protein regulatory networks. Among these omics' approaches, genomics and transcriptomics help majorly by identification of abiotic stress-responsive genes, genome-wide analysis of various rice accession for development of various markers and QTLs for marker-assisted breeding. Transcriptome analysis combined with NGS helps in the identification of novel genes, transcription factors and non-coding RNAs involved in abiotic stress response. By using this technology its possible to fight against the abiotic factors and help in the crop improvement.