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Insights into Multi-Omics Approach

Chandana H. S.[1] and Prajwal S. K.[2]
[1]Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi
[2]Division of Microbiology, ICAR-Indian Agricultural Research Institute, New Delhi

SUMMARY

A multi-omics approach integrates genomics, transcriptomics, proteomics, and metabolomics to enhance crop improvement. By combining these disciplines, researchers gain a comprehensive understanding of the genetic, molecular, and biochemical networks that underpin crop traits. Genomics provides insights into genetic variations, while transcriptomics reveals gene expression patterns. Proteomics identifies and quantifies proteins, and metabolomics profiles metabolites to understand biochemical processes. This holistic view helps in identifying key traits related to stress resistance, yield, and quality. For instance, integrating these omics data can pinpoint specific genes, proteins, and metabolites involved in drought tolerance or disease resistance. This multi-omics strategy accelerates crop breeding by enabling more precise selection and genetic modifications, ultimately improving crop resilience and productivity.

INTRODUCTION

Over the past few decades, various omics technologies have revolutionized the exploration of the genetic and molecular basis of crop development. These approaches, including genomics, transcriptomics, proteomics, metabolomics, phenomics, and ionomics, have enabled detailed insights into DNA modifications, transcript levels, proteins, metabolites, and mineral nutrients under environmental and physiological stress conditions (Muthamilarasan *et al*., 2019). The advent of next-generation sequencing (NGS) has facilitated high-throughput data generation across these domains, enhancing our understanding of gene functions and networks during stress responses and crop yields (Grobkinsky *et al*., 2018). Traditional crop breeding methods, including phenotype-based selection, hybrid breeding, and molecular breeding, have evolved with the integration of advanced technologies like multi-omics, artificial intelligence (AI), and genome editing, ushering in a new era known as breeding 4.0 . The integration of multiple omics approaches, particularly with NGS technologies, has proven invaluable in overcoming the limitations of single-omics methods. By combining comprehensive data analysis with genome editing tools, multi-omics not only reveals the molecular mechanisms of plant development and stress responses but also offers novel strategies for crop improvement.

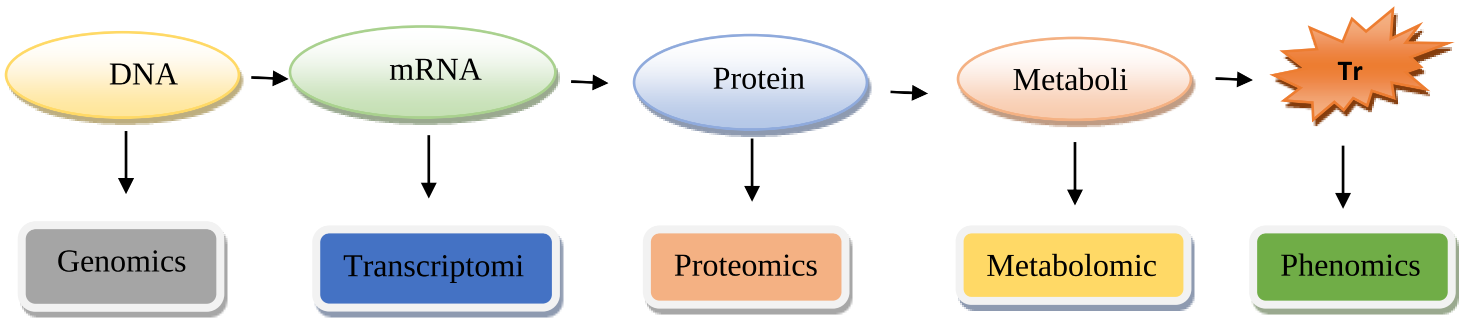

Fig. Multi omics approach

Components of Multi-omics approach

1.Genomics

Genomics is the study of genes and genomes, focusing on their structure, function, evolution, mapping, and modifications, including epigenomic and mutagenomic aspects (Muthamilarasan *et al*., 2019). This field plays a crucial role in uncovering genetic variations, which can enhance crop breeding efficiency and contribute to the genetic improvement of crop species. Genomics is divided into several subfields, each with a specific focus. Structural Genomics deals with sequence polymorphism and chromosomal organization, enabling the construction of physical and genetic maps that identify traits of interest for plant biologists. Functional Genomics provides insights into the roles of genes in regulating traits of interest. This subfield includes the study of Epigenomics, which focuses on epigenetic changes at the genomic level, such as histone modifications, DNA, or small RNA methylations. Mutagenomics and Pangenomics are more recent approaches. Mutagenomics focuses on the genetic modifications resulting from mutational events, while Pangenomics examines the sum of a core genome shared by all individuals and a dispensable genome that is partially shared or individual-specific, providing a broader view of genome variation within species .

2. Transcriptomics

Transcriptomics refers to the study of the complete set of RNA transcripts produced by the genome of an organism in a specific cell or tissue. This field has emerged as a powerful tool for analyzing gene expression dynamics in response to various stimuli over time (Duque *et al*., 2013). Initially, traditional techniques like cDNA-AFLP, differential display-PCR (DD-PCR), and suppression subtractive hybridization (SSH) were used for transcriptome profiling, though they provided limited resolution (Nataraja *et al*., 2017). The advent of more advanced techniques, such as microarrays, digital gene expression profiling, RNA sequencing (RNA-seq), and Serial Analysis of Gene Expression (SAGE), has significantly improved the accuracy and depth of transcriptome analysis (Kawahara *et al*., 2012).

3. Proteomics

Proteomics involves the comprehensive analysis of the entire set of proteins expressed by an organism, encompassing sequence, structural, functional, and expression proteomics. Sequence proteomics focuses on identifying amino acid sequences using techniques like high-performance liquid chromatography (HPLC). Structural proteomics aims to determine protein structures to infer their functions, employing methods such as nuclear magnetic resonance (NMR), X-ray crystallography, electron microscopy, and computer-based modeling (Sali *et al*., 2003). Functional proteomics explores protein functions through methods like yeast two-hybrid assays and protein microarrays.

4. Metabolomics

Metabolomics involves the comprehensive study of metabolites in a biological system, encompassing the full array of compounds produced through metabolic pathways in plants. Next-generation sequencing (NGS) technologies have emerged as valuable tools for understanding gene expression regulation and cellular responses to biotic and abiotic stresses in crops. When combined with metabolomics, NGS helps predict metabolic networks from genomic sequences, providing insights for crop improvement . Metabolites, as end products of gene expression, reflect the biochemical state of cells. Unlike proteomics, which focuses on gene products, metabolomics reveals the metabolic expression of proteins and the biochemical processes crucial for gene function (Lindon and Nicholson, 2008).

5. Phenomics

Phenomics is the field focused on characterizing phenotypes through the acquisition of extensive phenotypic data on an organism-wide scale.The term "phenome" refers to the complete set of phenotypic traits, which are influenced by interactions between genotype (G), environment (E), and management (M). This interaction is also known as genotype–phenotype–envirotype (G–P–E) interactions. Accurate phenotyping is crucial for mapping genes and quantitative trait loci (QTL) related to specific traits, aiding genetic improvement in crops. Automated high-throughput imaging technologies enhance this process by providing non-invasive and rapid assessment of traits. These technologies include color imaging for biomass, far infrared imaging for canopy analysis, lidar for growth measurement, and magnetic resonance imaging for root systems (Furbank and Tester, 2011). Additionally, root imaging techniques such as electrical resistance tomography, electrical capacitance, X-ray computed tomography, and positron emission tomography enable detailed root system analysis without damaging plant samples

CONCLUSION

The integration of multi-omics approaches in crop improvement offers a robust framework for understanding and enhancing complex traits such as stress resistance and yield. By combining genomics, transcriptomics, proteomics, and metabolomics, researchers can unravel the intricate biological networks that govern crop performance. Future prospects include refining these techniques for more precise and faster data analysis, leveraging advancements in artificial intelligence and machine learning to interpret multi-omics data, and developing targeted breeding strategies. Continued innovation in this field promises to revolutionize crop improvement, addressing global challenges like food security and climate change.

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