

Multi-Omics: A New Approach for Breeding Crop Varieties

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SUMMARY

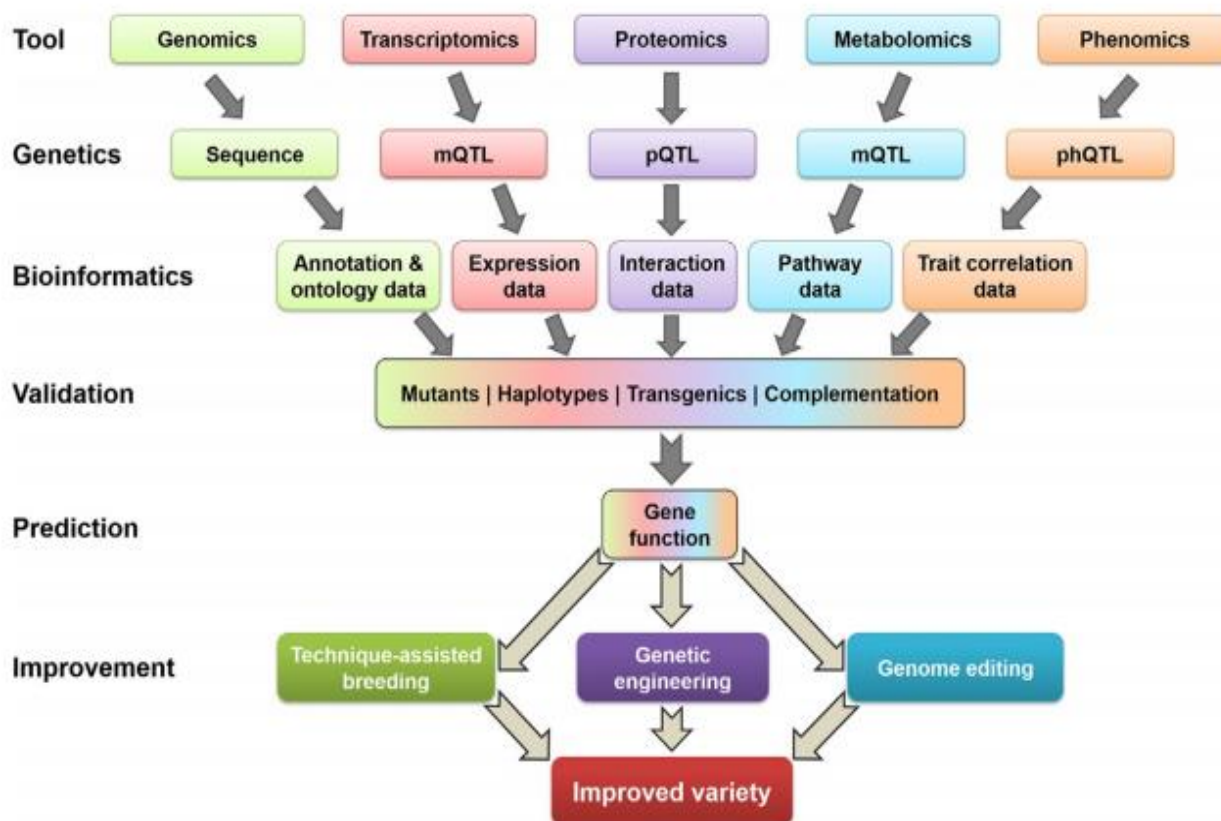
Genomics has been widely used in developing improved plant varieties. Also, due to advancements in molecular plant biology and due to availability of next generation sequencing facilities, other omics tools such as phenomics, transcriptomics, proteomics are also used in deciphering the plant biology. But, when these tools are used in an integrated manner, they will certainly help us to get an insight into the cellular and molecular networks within the plant systems. The multi-omics approach will also help in understanding the mechanism underlying a complex trait and will help to solve multiple problems in a very short time. Hence multi-omics approach will hasten the overall breeding process which will help to obtain sustainable crop production.

INTRODUCTION

Omics' refers to the collective technologies used for a comprehensive assessment of biological molecules i.e. to explore the structure, function, role and actions of the various types of molecules that make up the cells of an organism. It includes Genomics, "It is the branch of molecular biology dealing with the study of genes and genomes, their functions and interaction. It includes structural genomics (It deals with the study of the structure of all the genes, the organization of these different genes within the genomes. It includes DNA sequencing and genome annotation), functional genomics (It deals with decoding of the function of individual genes and their roles in a particular metabolic pathway), Comparative genomics (Study of the relationship of genome structure and function across different biological species or strains) and epigenomics (Study of different epigenetic changes that leads to the regulation of genes in the genome is called epigenomics). Proteomics, the study of the complete protein structure of a cell, tissue, or organism under a specific, defined set of conditions. Metabonomics, the study of molecules involved in cellular metabolism Transcriptomics, the study of all the different RNA molecules that are produced by the genome, their structures and functions. Transcriptomics particularly deals with mRNA transcripts because they are the expressed coding sequences. Phenomics is a new branch of science involving the use of modern noninvasive imaging technologies for the precise and accurate phenotyping of our genotypes for accurate mapping of genes, QTLs responsible for the trait-of-interest.

Need for Integration of Different Omics Technologies

- These omics technologies are providing independent information about the genes, genomes, RNAomes, proteomes and metabolomes; however, integrating this information will allow us to discover the gene networks that would improve the current understanding of various vital characters, and develop new strategies for plant improvement.
- Although there are many computational tools and databases available to analyze biological network models, but they do not solely provide complete information of cellular and molecular networks within the plant systems. Thus, integration of different omics approaches is important to understand the physiological, biochemical, and molecular levels in plants in order to develop high yielding climate resilient varieties.
- The multi-omics approach will help to expand our knowledge to the genotype-phenotype relationship and genotype-phenotype- environment relationship.
- This interactome network studies will help to accelerate conventional breeding programs by systematically integrating multi-omics data and will provide and deeper insight into the different genes and the effect of their interaction on various plant processes.
- Single omics approach such as genomics or transcriptomics do not alone provide all the information of a complex plant system hence combining 2 or more omics tools will help to get detailed knowledge about complex plant systems.



(Mehanathan Muthamilarasan *et al.*, 2019)

Figure: Flowchart showing the methodology for integrating the different omics approaches to identify target gene(s) for crop improvement.

Challenges:

- A large amount of data will be generated by using multi-omics approach. Hence efficient data management tools and systems should be developed in order to properly interpret the big volume data.
- Cost-effective and precise phenomics platforms should be developed in order to precisely map genes or QTLs responsible for the trait-of-interest and to correlate the information between genomic and phenotypic data.
- Development of more efficient algorithms and bioinformatic tools for high-throughput data analysis and processing standards will be required to further advance the multi-omics approach for more comprehensive understanding.

Conclusions:

In spite of these challenges, multi-omics approach provides a great opportunity to reliably predict plant responses to given genomic information and environmental situations and to bred varieties that are climate resilient.

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