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Plant Genetics and Molecular Biology: An Introduction

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Abstract The rapidly evolving technologies can serve as a potential growth engine in agriculture as many of these technologies have revolutionized several industries in the recent past. The tremendous advancements in biotechnology methods, cost-effective sequencing technology, refinement of genomic tools, and standardization of modern genomics-assisted breeding methods hold great promise in taking the global agriculture to the next level through development of improved climate-smart seeds. These technologies can dramatically increase our capacity to understand the molecular basis of traits and utilize the available resources for accelerated development of stable high-yielding, nutritious, input-use efficient, and climate-smart crop varieties. This book aimed to document the monumental advances witnessed during the last decade in multiple fields of plant biotechnology such as genetics, structural and functional genomics, trait and gene discovery, transcriptomics, proteomics, metabolomics, epigenomics, nanotechnology, and analytical tools. This book will serve to update the scientific community, academicians, and other stakeholders in global agriculture on the rapid progress in various areas of agricultural biotechnology. This chapter provides a summary of the book, "Plant Genetics and Molecular Biology."

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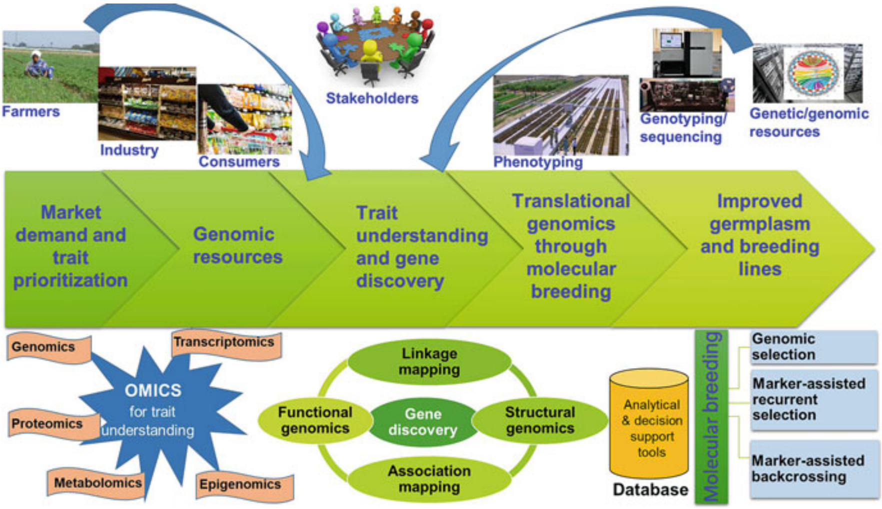
Graphical Abstract



Keywords Decision support tools, Epigenomics, Genomics, Metabolomics, Nanotechnology, Plant biotechnology, Proteomics, Transcriptomics

Contents

1 Introduction

Making society hunger-free and malnutrition-free is the main goal for the stakeholders in world agriculture. Feeding the global population has never been so challenging, especially in the context of diminishing land and water resources together with an ever-increasing global population and climate changes. One of the possible solutions is to develop climate-smart varieties of plants complimented with appropriate agricultural management practices. Today world agriculture is facing an acute shortage in developing improved germplasm to replace the old varieties existing in farmers' fields. The global agriculture needs a "game-changer" strategy to be implemented with high priority in order to develop improved germplasm and cultivation practices rapidly and with high precision to tackle the current and future adverse environmental conditions. Improved crop varieties together with improved agricultural practices will be able to address the global food security issue in an equitable and sustainable manner.

A recent survey on hunger and malnutrition has identified 52 of 119 countries as having a serious, alarming, or extremely alarming situation. Even today, 13% of the global population is undernourished and 27.8% of children under 5 years of age are stunted (http://www.globalhungerindex.org/pdf/en/2017.pdf). Despite the availability of sufficient food production, these problems still exist as a large number of people do not have access to nutritious food. The quality and nutrition of food products define the physical and mental health of the global population, not the quantity. In this context, agricultural research on developing nutrition-rich crops should be given equal importance to the major objective of increasing productivity. The genetic gains achieved over the decades in several crop species have been able to feed starving populations and have saved the lives of millions of people. Food and nutritional security in the coming years can only be made possible by achieving rapid and higher genetic gains in food crops with enhanced quality, nutrition, and adaptation to adverse climatic conditions. This goal can be achieved by integrating available biotechnological interventions with ongoing efforts. Not only agriculture but also biotechnology has been a great support in boosting several sectors such as the pharmaceutical, medical, and food processing sectors. In fact, the biotechnology interventions have already produced game-changing contributions in agriculture and the future contributions from biotechnology for society depend on strong policy, commitment, and the investment made in biotechnology research in coming years.

The rapid advances in biotechnological processes, approaches, and technologies have revolutionized agricultural research by developing a better understanding of plant genomes, gene discovery, genomic variations, and manipulation of desired traits in plant species. Additionally, these approaches also help researchers in developing a better understanding beyond genomes such as plant-pathogen and plant-environment interactions. The advanced technology support has helped to track the entire journey from genomes to phenotype using different "omics" approaches such as genomics (DNA/genome/genes), epigenomics (epigenetic modifications on the genetic material), transcriptomics (transcripts/RNA), proteiomics (proteins), metabolomics (metabolites), interactomics (protein interactions), and phenomics (phenotype) (Fig. 1). The other important intervention is nanobiotechnoloy (a combination of nanotechnology and biology), which provides very sophisticated technical approach/devices for tracking, understanding, and solving biological problems. This book aimed to document current updates and advances in these frontier areas of biotechnology research. This chapter provides an overview of the different chapters included in the book.

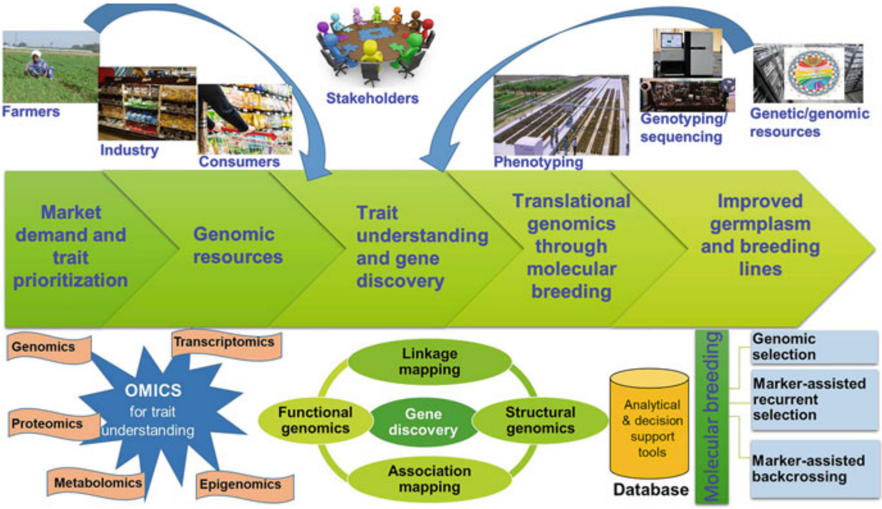


Fig. 1 Plant genetics and molecular biology for trait dissection and crop improvement

2 High-Throughput Genotyping Platforms

The tremendous advances in sequencing technologies have made it possible to sequence complete genomes of plant species for better understanding of the genome architecture evolution including whole genome duplications, dynamics of transposable elements, and several other components of the genome that define and control genome function leading to a particular phenotype [1]. Chapter 2 on "*Advances in Sequencing and Resequencing in Crop Plants,*" authored by SD Rounsley and other colleagues from Dow Agrosciences, USA and Genus plc, UK, provides updates on advancements in different sequencing technologies over the last two decades and their impact on plant genomics research. Cost-effective sequencing technologies have facilitated sequencing of a large number of plant genomes, which have impacted greatly on developing better understanding of plant genomes and their evolution [1, 2]. These advances have further helped in faster gene discovery, characterization, and deployment in plant improvement [3]. In addition to this, this chapter discusses the current challenges and future opportunities in further exploiting genomics information for plant improvement.

The reference genome of any plant species provides the foundation for genomics research, but mere sequencing of only one genome is not enough for harnessing the wealth of genetic diversity available within and across plant species. Therefore, sooner or later genome sequences will eventually be available for all the germplasm and exist in different genebanks for capturing the sequence variations followed by their manipulations using appropriate genetic improvement approaches such as molecular breeding, genetic engineering (transgenics), genome editing, and any other such technology developed in future. Sequence variations in different genomes of the same species have been exploited as genetic markers for conducting different genetics and breeding studies.

Chapter 3 on "*Revolution in Genotyping Platforms for Crop Improvement,*" authored by David Edwards and his colleagues from the University of Western Australia (UWA), Australia, describes how different types of genetic variations can be used in genetics research and breeding applications through different genotyping platforms. Similar to sequencing, genotyping platforms have also gone through a rapid evolution and played an important role in advancing crop genetics and breeding. These genotyping platforms have been deployed in a range of genetic and breeding applications in most of the plant species. This chapter not only provides details on the evolution of different genotyping platforms over the decades, but also compares different genotyping platforms and predicts the future of genotyping in plants. This chapter clearly advocates the sequencing of entire genetic and breeding populations in future crop improvement programs for more precise and efficient plant selection in field.

3 Trait Dissection and Gene Discovery

The availability of genetic diversity is crucial for further improving the existing cultivars, which can sustain higher productivity under ever-challenging environments by acting as a buffer for adaptation and fighting climate change [4]. The development of improved cultivars using the diverse germplasm has helped farmers to replace these cultivars with older released or local varieties. The faster replacement of improved cultivars in the farmer's field will help in achieving higher productivity under changing environments. Genomics-assisted breeding (GAB) holds great promise for accelerated development of improved cultivars; however, information on genes and diagnostic markers is required for deployment in any plant species. There are three major approaches of trait mapping, namely linkage mapping, linkage disequilibrium mapping/genome-wide association study (GWAS), and joint-linkage association mapping (JLAM).

Linkage mapping uses bi-parental genetic populations for traits with high variability between the parental genotypes. Chapter 4 on "*Trait Mapping Approaches through Linkage Mapping in Plants,*" authored by Pawan Kulwal from Mahatma Phule Agricultural University (MPAU), India, discusses different types of bi-parental populations and software for genetic mapping and quantitative trait locus (QTL) analysis in several plant species. Detailed information on key factors affecting the precision and accuracy of QTL discovery is presented. This mapping approach has been the most successful as diagnostic markers could be developed and deployed in breeding in several crop plants and many of these improved cultivars are grown in farmers' fields.

In contrast to linkage mapping, the second trait mapping approach, genome-wide association study/linkage disequilibrium mapping, uses the diverse set of germplasm (natural population) and, therefore, no time is spent on development of genetic populations. The other advantage is that the association mapping panel can be used for mapping for several traits, while linkage mapping is possible for a couple of traits in a single bi-parental population. Furthermore, in many of the plant species, the development of bi-parental populations is not feasible or possible.

Chapter 5 on "*Trait Mapping Approaches through Association Analysis in Plants,*" authored by Joy Roy and his colleagues from the National Agri-Food Biotechnology Institute (NABI), India, provides greater insights different technical and applied aspects of GWAS analysis, advantages, and disadvantages of different software, and key factors affecting the precision and accuracy of results. This mapping approach has been deployed in many plant species.

The above two trait-mapping approaches have certain limitations and, therefore, the joint linkage association mapping approach came into existence; this approach can harness the advantages of both trait-mapping approaches. In this context, the shift now has moved from bi-parental to multi-parental populations, which allow high recombination leading to greater resolution for trait dissection. James Cockram and Ian Mackay from the National Institute of Agricultural Botany (NIAB), UK, in chapter 6 on "*Genetic Mapping Populations for Conducting High Resolution Trait Mapping in Plants*" summarize in-depth information on development and deployment of multi-parent populations such as multi-parent advanced generation intercross (MAGIC) and nested association mapping (NAM). This chapter also provides examples that showed better results in trait mapping in larger population size than in smaller ones.

All three above trait-mapping methods for trait mapping are forward genetics approaches, while Targeting Induced Local Lesions IN Genomes (TILLING) is a reverse genetics approach [5]. The TILLING approach involves creation of genetic variation through mutagenesis and then identification of genomic variation causing a change in phenotype. Chapter 7 on "*TILLING: The Next Generation,*" authored by Bradley Till and his colleagues from International Atomic Energy Agency (IAEA), Austria, describes the entire process of developing and deploying TILLING population for trait dissection and gene discovery. The chapter also discusses how integration of NGS technologies with TILLING have greatly accelerated the process of gene discovery. These populations also serve as a very good source for breeding and functional genomics studies.

4 Beyond Genomics

Genome sequencing greatly helped in understanding of genome organization and gene(s) structure that determines the basic features of each species. Nevertheless, just having genes in its genome does not provide certainty about the expected phenotype, which depends hugely upon other aspects of gene regulation. The journey of a gene to a particular phenotype is very complicated, depending on as and when the DNA passes through different levels of regulation following the central dogma. It is, therefore, very essential to see beyond genomics for better clarity on gene function, networks, and interactions. In this context, the other "omics" approaches such as transcriptomics, proteomics, metabolomics, and interactomics play important roles in gene function and phenotype development. The phenotype is also affected by non-genomic elements, which bring epigenetic modifications to the genetic material, called as epigenomics. The epigenomic compounds modify the function of DNA without changing the sequence, thereby deviating from following the instruction of the genome. The interesting part is that these epigenetic features are being passed down over generations.

Transcriptomics plays an important role in gene discovery and functional characterization of the gene and its network. Chapter 8, authored by Nitin Mantri and his colleagues from RMIT University, Australia, on "*Advances in Transcriptomics of Plants*" discusses in detail discovery of transcriptional regulatory elements and deciphering mechanisms underlying transcriptional regulation. This chapter also covers related important aspects of gene regulation such as RNA splicing, microRNAs, small interfering RNAs (siRNAs), and long non-coding RNAs in plant development and response to biotic and abiotic stresses.

Metabolomics is very complex to understand due to development and interaction of the large number of metabolites produced during attaining metabolic homeostasis and biological balance in response to multiple cellular and extra-cellular factors. Wolfram Weckwerth and his colleagues from the University of Vienna, Austria, in chapter 9 on "*Metabolomics in Plant Stress Physiology,*" describe the importance of the study of metabolomics for functional genomics and system biology research leading to functional annotation of genes and better understanding of cellular responses for different biotic and abiotic stresses in plants. This chapter also provides details on different modern techniques that play a key role in developing more precise and high throughput data for comprehensive analysis. In addition to the above, this chapter also describes the complete processes involved in metabolomics study and lists the limitations faced by this scientific stream.

The epigenetic marks modifying the function of the gene can pass on over generations, making epigenomics an important component in better understanding the phenotype development. In other words, mere genome sequence is not responsible for phenotype development, and the epigenetic modifications play a key role by altering the chromatin structure and forcing deviation from the instructions contained in the genome. Detailed information on the types of epigenetic changes and their impact on phenotype development in plants is provided in chapter 10, entitled "*Epigenetics and Epigenomics of Plants,*" authored by Manoj Prasad and his colleagues from the National Institute of Plant Genome Research (NIPGR), India. This chapter also discusses the key role of NGS technologies and improved analytical software in better understanding the role of epigenomics in plant development and defense. Further information is also provided on different types of studies conducted in plants for identifying epigenetic factors and their potential role in plant improvement.

Nanotechnology has emerged recently as a very useful approach for plants and has already demonstrated its potential in the development of several nanomaterials in the pharmaceutical industry and in improving human health. Plants are the best source for developing such nanomaterials due to their large-scale availability and ease of production. Chapter 11 on "*Nanotechnology in Plants,*" authored by Ismail Ocsoy and Weihong Tan and their colleagues from Erciyes University, Turkey and University of Florida, USA, explains the importance of nanotechnology in plants by citing several successful examples in medicine and industrial applications. The chapter mentions several advantages of plant extract over other biomolecules such as protein, enzyme, peptide, and DNA followed by their use in food, medicine, nanomaterial synthesis, and biosensing. This chapter also provides information on different extract preparation techniques, their use in the synthesis of nanoparticles, and demonstration of their antimicrobial properties against pathogenic and plant-based bacteria.

5 Data Management and Analytical Decision Supporting Tools

Large-scale data are generated at each step of the plant experiment related to understanding of the genome, gene discovery, functional characterization of gene, marker discovery, and deployment of diagnostic markers in the breeding program in addition to phenotyping data. All these data sets require efficient and effective database management systems, and analytical and decision support tools for storing and retrieving useful information that impacts the genetic improvement efforts. Chapter 12 on "*Current Status and Future Prospects of Next-generation Data Management and Analytical Decision Support Tools for Enhancing Genetic Gains in Crops,*" authored by Abhishek Rathore and his colleagues from ICRISAT, India, provides details on data management and analysis and decision support tools (DMAST) for plant improvement. The chapter also provides examples of how DMAST has simplified and empowered researchers in data storage, data retrieval, data analytics, data visualization, and sharing.

6 Summary

Ensuring food and nutritional security for an ever-increasing global population under the changing global climate is a top priority for policy makers across the globe. The existing conventional research efforts and traditional technologies will not be able to provide adequately nutritious food for the global population, necessitating the incorporation of modern science into the current genetic improvement programs. Biotechnology has great potential in bridging the supply-demand gap in food through developing improved agricultural technologies. All the scientific streams are witnessing a rapid pace of development due to integration of new technologies such as robotics, automation, etc. Theses advancements have improved our understanding of genome architecture and its complexity: gene structure, function, and interactions, and improved methodologies for modification of the genome/ gene to achieve a desired phenotype. The plant-pathogen and plant-environment interactions complicate the expression of scripts in the plant genome. This book covers these important research areas pertaining to plant biotechnology, which are key for achieving higher genetic gains. This wealth of information will be a great value for students, researchers, academicians, and policymakers.

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