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# Frontier Technologies for Crop Improvement



# **Chapter 1 Introduction: Frontier Technologies for Crop Improvement**



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**Abstract** The last two decades have witnessed the rapid development and application of several frontier technologies for crop improvement, which have brought speed, precision and cost-effectiveness in making selection decisions for improved breeding lines with better genetics. A few such technologies to be mentioned are accurate and efficient germplasm characterization of diverse genebank accessions, high-throughput sequencing and genotyping, rapid generation advancement, modern sequencing-based trait mapping and gene discovery followed by identification of superior haplotypes, genomic selection, gene editing, forward breeding and multiomics approaches including better bioinformatics tools/software. While there is still scope for improving phenotyping protocols for various traits, especially the complex ones, the above-mentioned frontier technologies provide huge opportunities in improving the precision and speed in developing new cultivars with future traits to ensure the sustainability of different crop plants. The integration and use of these technologies on a large scale using a common platform to provide flawless support to

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crop improvement programs is still a challenge for many crop species, but will be accomplished sooner or later.

**Keywords** Frontier technologies · Speed breeding · Genetic gain · Productivity · Genomics-assisted breeding

### 1.1 Introduction

The importance of agriculture to global economic growth and the livelihood of households makes it one of the most important sectors in the world. It serves as the primary source of human food, animal feed, and raw materials for industry. Agricultural products are traded worldwide and generate substantial income. In sub-Saharan Africa, for example, agriculture employs more than 50% of the labour force and contributes about 15% of the GDP (OECD/FAO 2016). Governments and donors have, therefore, prioritized expenditures in agricultural research for development in order to increase the sector's productivity. A significant area of impact has been crop improvement. Breeders have historically relied heavily on the conventional breeding (crop improvement) approach to develop improved varieties with high yields. The approach is based on the art and science of creating variations to select improved varieties based on phenotypic diversity. The efforts have led to the release and adoption of several improved varieties for various crops, which have considerably improved the standard of living for smallholder households in developing countries and the profitability of farming/agribusinesses in developed countries. Albeit considerable disparity between countries, as an illustration, we know how improved varieties, in combination with fertilizer and pesticides, almost doubled the productivity of crops like wheat, rice, and others during the green revolution, which helped many farmers overcome poverty (Pingali 2012). In general, about 50% of the increase in crop productivity over the past century can be attributed to plant breeding, with the other 50% coming from improved crop management, such as fertilizers, irrigation, and weeding (Evenson and Gollin 2003).

Improved varieties remain the cheapest and the main inputs to improve agricultural productivity to feed and meet the nutritional needs of the growing population, which is expected to hit about 10 billion by 2050 (UN 2017). Hence, the development of improved varieties for food security and sustainable agriculture is considered a major element in tackling poverty and rural displacement. Crop improvement has a high return on investment value (Renkow and Byerlee 2010). The development of varieties with improved productivity and yield stability contributes to food security; drought-resistant varieties that lower production costs and increase the viability of marginal agribusinesses enhance economic benefits; varieties with high-nutrient contents improve nutrition; and varieties that are less reliant on pesticides or more efficient in their use of water and nutrients benefit the environment.

Conventional breeding, although still commonly used today, may not meet the ever-increasing food demand in the face of climate change and variability. This is due to practical limitations including the slow process of taking more than 10 years

to develop and commercialize a variety and heavy reliance on natural variability which may not be available for some important traits. In recent years, massive efforts were invested in developing technologies and innovations for improving the accuracy and efficiency of the breeding process. Consequently, the last two decades have witnessed the rapid development and use of several frontier technologies for crop improvement, which have brought speed, precision and cost-effectiveness in making selection decisions for improved breeding lines with better genetics. Hence, aided by such progress, the conventional breeding approach has evolved to integrated (modern) breeding, which has provided ample opportunities for developing high-yielding improved varieties that meet farmer preferences and consumer/market needs.

This book, divided into ten chapters, presents a review and vision on use of the frontier technologies covering important crop improvement areas including exploiting genebanks, modern bioinformatics tools, contemporary genotyping platforms, rapid generation advancement (speed breeding) approach, multi-omics, sequence-based breeding, forward breeding, genomic selection and gene editing. Each chapter, authorship led by subject matter experts, discusses the technologies and their practical applications in plant breeding and presents future strategies. However, the authors have emphasized that the combined use of these frontier technologies has enormous potential to positively impact crop plant genetic improvement to develop improved varieties in a faster and more precise way. A common platform coupled with open breeding informatics involving different stakeholders and active support from donors is expected to realize the impacts on the improvement of various crop species. A brief overview of chapters 2–10 is provided below.

#### 1.2 Linking of Genebank to Breeding and Food Security

This chapter authored by Singh et al. discusses the role of genebank in conserving and contributing to making available trait diversity for breeding future-ready crops. It provides detailed information on efforts towards germplasm collection, conservation, and characterization as well as making these available to breeders for use in breeding new varieties. This chapter also discusses the impact of genebank's diverse germplasm in achieving higher yield and genetic gain, adaptation to climate challenges and stresses, increasing nutritional compounds and consumer/industrypreferred traits in several crops. A high-throughput large-scale phenotypic assessment for key traits as well as the use of multi-omic tools, including high-throughput genotyping, are suggested as new frontier technologies to improve our understanding of genetic diversity in germplasm collection in genebank and their use in diversifying the primary and more specifically cultivated gene pool. The chapter also discusses access to germplasm and the impact of genebank by contributing to the sustainability of world agriculture.

# **1.3** Bioinformatics for Plant Genetics and Breeding Research

The volume and frequency of data generation have increased multiple folds which need to be well documented and analysed using efficient software to get an insight to a specific biological question. This chapter authored by Naik et al. discusses the use of bioinformatics and computational tools to make good sense of the tremendous wealth of data generated each day as part of plant genetics, genomics, and breeding research. The field of bioinformatics and computational biology have witnessed huge advancements in developing and deploying the most advanced software or tools in the last two decades as the field needed to match the speedy developments in sequencing and genotyping data generation platforms. The different bioinformatics and computational tools are providing great support to molecular genetics and genomics research, right from developing reference genomes to molecular breeding product in farmers' fields.

# **1.4 Evolution in the Genotyping Platforms for Plant** Breeding

Genotyping of diverse germplasm and breeding materials is required for performing genetic diversity analysis, genome-wide association study, hybridity confirmation, genetic mapping, foreground selection using Kompetitive Allele Specific PCR (KASP) markers for selected traits, background selection for genome recovery, genomic selection and genetic purity. There is no 'one-size-fits-all' solution, and this chapter led by Rasheed et al. provides detailed information on the efforts around developing cost-effective, high-throughput and breeding-oriented crop genotyping platforms.

## **1.5 Rapid Generation Advancement for Accelerated Plant** Improvement

Faster varietal replacement using new varieties with improved genetics is key to achieving higher genetic gains in farmers' fields (Varshney et al. 2019; Pandey et al. 2020). This milestone can only be achieved if the breeding cycle of the new varieties can be shortened using modern technologies such as rapid generation advancement (RGA) to support speed breeding. This chapter led by Hamwieh et al. explores different such technologies which can help in breeding new varieties faster. Some of these technologies include shuttle breeding, double haploidy, speed breeding, genome editing, marker-assisted selection and genomic selection.

#### **1.6 Multi-Omics for Crop Improvement**

The last couple of decades have witnessed sharply increased adoption of different new technologies in the area of different omics sciences such as genomics, transcriptomics, proteomics, metabolomics and phenomics. Most of such studies are done using a single approach or sometimes using two approaches, however, it's very rare to see research wherein all the omics platforms are used for trait understanding and gene discovery. The results are going to be more reliable upon integrating these omics platforms together, which will also ensure faster deployment in crop breeding. This chapter led by Chaturvedi et al. provides the current progress, opportunities and challenges in this direction. These authors also termed this as PANOMICS approach which is very much essential in moving forward while deploying more data-driven and science-based crop breeding to develop futureready crops.

#### 1.7 Sequence-Based Breeding for Crop Improvement

Sequencing technologies have enabled high-quality genome sequence assemblies, pangenomes, high-density genetic maps, various marker genotyping platforms, and trait discovery in most of the crop plants. This chapter led by Sinha et al. discusses the significant improvement in breeding programs utilizing modern genomic tools and technologies. The scientific community is continuously witnessing the success stories of new improved varieties being successfully bred utilizing genomicsassisted backcrossing and, more recently, genomic selection. It is necessary to continuously work on population improvement after every breeding cycle in order to obtain long-term genetic gains and hasten the genetic gains in crops. In this context, the chapter proposes a sequencing-based breeding approach involving parental selection, enhancement of genetic diversity of breeding materials, forward breeding for early generation selection, and genomic selection using sequencing/ genotyping technologies. This chapter also emphasizes the integration of other modern technologies such as speed breeding technology which allows for four to six generations per year and has great potential to further accelerate the pace of delivering genetic gain in farmers' fields.

#### **1.8 Forward Breeding for Efficient Selection**

Crop improvement coupled with the modern plant breeding approaches such as genomic-assisted breeding is a proven solution to meet the food security of a rapidly growing global population. This chapter led by Bohar et al. emphasizes combining the power of genomic selection and foreground selection for key traits into the breeding pipeline by employing low-cost genotyping solutions. Currently, multiple SNPs marker-based genotyping platforms are available for deployment in an array of applications in crop improvement. A shared genotyping platform coupled with open breeding informatics involving different stakeholders and active support from donors will make genotyping cost-effective with a quicker turnaround. This will address several constraints faced by public breeding programs to employ forward breeding. Currently available forward-breeding genomic resources in the low-mid density genotyping platform space are also covered in detail in this chapter, with special emphasis on shared services.

#### **1.9 Genomic Selection in Crop Improvement**

Genomic Selection (GS) is the most promising approach for improving multiple traits including those with complex genetic control in addition to accommodating the benefits of marker-assisted selection. This breeding approach is still going through the maturity phase and may become one of the futuristic breeding methods not just for breeding varieties but also for population improvement. This chapter led by Veerendrakumar et al. provides information on such progress made during the last decade in multiple crops. This chapter also briefly discusses the methodology, current progress, its advantages, different genomic prediction models as well as factors affecting prediction accuracy. Suggestions are also made to integrate other frontier technologies together such as genomic selection with rapid generation advancements and single-seed chipping-based genotyping for achieving greater benefits.

# **1.10** Genetic Engineering: A Powerful Tool for Crop Improvement

The applications of genetic engineering including genome editing are important as they can complement modern breeding activities to mitigate the effects of changing environments and boost crop production. This chapter led by Bhattacharjee et al. emphasizes on the importance of genetically modified (GM) technology which delivered multiple plant attributes such as herbicide resistance, tolerance against pests and pathogens, and nutritional enhancement. The chapter also briefly discusses technologies, namely, Zinc Finger Nucleases (ZFNs), Transcription Activator-Like Effector Nucleases (TALENs), and Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)/Cas. The chapter also provides information on success stories in many plant species already commercialized, namely, soybean, papaya, maize, cotton, common bean, sweet potato, cowpea, etc. Furthermore, the technology holds immense promise to achieve the UN's sustainable development goals (SDGs) to fight hunger, attain food security, enhance nutrition, and promote sustainable agriculture.

#### 1.11 Summary and Outlook

In summary, this book presents articles in leading frontier technologies for crop improvement. As mentioned above, some of above technologies are already under use for crop improvement in some crop species. It is anticipated that with costs going down on several of these technologies, their adoption will be enhanced. Furthermore, some new areas such as single cell genomics, systems biology and synthetic biology are emerging for crop improvement. However, optimisation of these approaches is still in infancy for majority of crops. We envisage the successful utilization of some of these approaches for crop improvement in coming years.

#### References

- Evenson RE, Gollin D (2003) Assessing the impact of the green revolution, 1960-2000. Science 300:758–762
- OECD/FAO (2016) Agriculture in sub-Saharan Africa: prospects and challenges for the next decade. In: OECD-FAO Agricultural Outlook. OECD Publishing, Paris. 2016–2025. https:// doi.org/10.1787/agr\_outlook-2016-5-en
- Pandey MK, Pandey AK, Kumar R, Nwosu V, Guo B, Wright G, Bhat RS, Chen X, Bera SK, Yuan M, Jiang H, Faye I, Radhakrishnan T, Wang X, Liang X, Liao B, Zhang X, Varshney RK, Zhuang W (2020) Translational genomics for achieving higher genetic gains in groundnut. Theor Appl Genet 133:1679–1702
- Pingali PL (2012) Green revolution: impacts, limits, and the path ahead. PNAS 109(31): 12302–12308. https://doi.org/10.1073/pnas.0912953109
- Renkow M, Byerlee D (2010) The impacts of CGIAR research: a review of recent evidence. Food Policy 35:391–402
- UN (2017) The World Population Prospects: The 2017 Revision, UN Department of Economic and Social Affairs. https://www.un.org/en/desa/world-population-projected-reach-98-billion-2050and-112-billion-2100
- Varshney RK, Pandey MK, Bohra A, Singh VK, Thudi M, Saxena RK (2019) Toward sequencebased breeding in legumes in the post-genome sequencing era. Theor Appl Genet 132(3): 797–816