

Role of Genomics in Crop Improvement

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Abstract

Agriculture in India is one of the most prominent sectors in the economy and about 43% of the country's land is used for agriculture related activities. The agricultural condition of our country today is very different from what it was in the last century. Small land holding size, inadequate water resources, increased demand for food grains due the rapid population explosion, widespread land and water degradation, climate change, are some of the unprecedented challenges our agriculture faces today. In order to achieve sustainable agriculture in such adverse conditions, it is imperative that we adopt new and innovative ways to enhance our agricultural productivity. The science of genomics has opened up a whole new surfeit of opportunities and avenues, which can help us achieve enhanced productivity under the present day challenges. The recent advances in the field of genomics offer great potential in hastening our various crop improvement programmes. Efforts must be undertaken to integrate this genomics knowledge and expertise that we have acquired over the last few decades, into our conventional crop improvement programmes.

Keywords: Genomics, Crop Improvement, Gene sequencing, Genome Mapping

Introduction

Recent developments in genomics in combination with high-throughput and precision phenotyping facilitate the identification of genes controlling critical agronomic traits. The discovery of these genes can now be paired with genome editing techniques to rapidly develop climate change resilient crops, including plants with better biotic and abiotic stress tolerance and enhanced nutritional value. Utilizing the genetic potential of crop wild relatives enables the domestication of new species and the generation of synthetic polyploids. The high-quality crop plant genome assemblies and annotations provide new, exciting research targets, including long non-coding RNAs and cis-regulatory regions. Metagenomic studies give insights into plant-microbiome interactions and guide selection of optimal soils

for plant cultivation. Together, all these advances will allow breeders to produce improved, resilient crops in relatively short timeframes meeting the demands of the growing population and changing climate

Using Genomics to Improve Crop Plant Diversity and Resilience

- **Accessing genetic diversity of crop wild relatives** -In Brassica, a comparison of crop wild relatives *Brassica macrocarpa*, with nine cultivated lines of *Brassica oleracea* showed that the former harbored unique disease resistance genes most likely lost during the domestication and improvement of elite *B. oleracea* germplasm (Goliczct.al. 2016). The increasing abundance of genomic resources for CWRs will significantly aid future breeding efforts, helping identify the optimal crosses and genome editing targets.
- **New crop domestication** - Another strategy for utilization of the wild plant resources new crop domestication. The domestication syndrome refers to unique collection of phenotypic traits associated with the genetic change of an organism from a wild progenitor to domesticated one. most of the changes linked to the domestication syndrome, such as grain dispersal in wheat, barley, and rice; apical dominance in maize; fruit size in tomato; and grain quality in wheat, result from modification of single or few genes. It is important to note that the ease of genome editing and therefore its use for crop de novo domestication and other applications is related to plant ploidy. Gene Knockout efficiency is lower in polyploids compared to diploids, as multiple alleles must be edited simultaneously to achieve a similar effect (Zhang *et al.*, 2019b).
- **Engineering Polyploidy**-The engineering of polyploid plants has been proposed as one of the routes for the generation of improved crop varieties (Katche *et al.*, 2019). Recent modeling work linked the occurrence of polyploidy to domestication (Salman-Minkos *et.al.*, 2016). Higher genome copy number masks deleterious mutations, increases the adaptive potential, and provides the opportunity for genes to gain new function. Thus, polyploidy is considered •a major driver of evolution (Sattler *et al.*, 2016).
- **Harnessing Plant-Microbe Interactions to Boost Agricultural Output** - Combined analysis of microbiome genomic and metabolomic data provides an accurate tool



necessary to understand plant-microbe interactions and predict the most favorable crop plant—soil microbiome combinations, allowing for mapping or suitable crops to specific locations.

- **The Challenge of Climate Change and Plant Diseases** - Climate change affects the epidemiology of pathogens at specific locations and the geographic distribution of plant diseases. The life extension of genetic resistance could be an effective and ecologically sustainable way to control diseases. Climate change affects not only the crop but also the pathogen survival and reproduction. The discovery of the genes underlying resistance has led to an improved understanding of their molecular function and established an entry point for studies of the defense pathways. Genome sequencing provides a rapid method of pathogen identification (Boykin *et.al.*, 2019). outbreak progression, and tracking of its spread to new locations.
- **Genome Editing for Nutritionally Enhanced Crop Production** - Breeding of crops for enhanced nutrient content has been a long standing goal of plant research. Nutrient profile can be altered by manipulation of biochemical pathways involved in macro- and micro-nutrient biosynthesis. Advances in genome sequencing and annotation provided the necessary resource to identify the candidate genes involved in plant metabolism. As a result, genome editing technologies could be used to modify nutritional profiles of crops. In addition, genome editing facilitated new crop domestication of new nutrient rich crops could lead to a more diversified and healthier diet.

Accessing New Breeding Targets Using Genomic Technologies

- **Third-generation sequencing for improved reference genomes** - The introduction of third-generation sequencing and long reads produced by PacBio and Oxford Nanopore now allows for chromosomal level assemblies of plant genomes. The long-read sequencing technologies are often combined with optical mapping and conformation capture, achieving draft genomes of unprecedented contiguity (Belser *et.al.*, 2018). The availability of high-quality, chromosome scale genome assemblies substantially improves the accuracy of the downstream genomic analysis, including gene and regulatory region annotation, GWAS, gene expression quantification, and homologue detection.

- **Accurate Gene Prediction and Functional Annotation for Precise Candidate Gene Identification-**
- Currently, addition of long reads generated by PacBio or Oxford Nanopore sequencing technologies allows for recovery of full-length transcripts, providing new insights into the extent of alternative splicing and transcriptome diversity (Cook *et.al.*, 2019). Annotation of loci harboring non-coding transcripts is also becoming routine, further improving our understanding of the complexity of plant transcriptomes (Van Bel *et.al.*, 2019). Rapid progress in application of CRISPR/Cas9 genome editing will soon allow construction of genome-wide mutant libraries for key crops, significantly contributing to the functional annotation efforts.
- **Non-coding Part of Genome as a Reservoir of New Breeding Targets -** Recent technological and conceptual developments revealed that plant genomes encode thousands of potentially functional ncRNAs as well as prevalence of distant regulatory elements including enhancers (Weber *et.al.* 2016). Improved understanding of the function of the non-coding elements of the genome will provide a new, yet untapped pool of breeding targets.

Beyond Single Reference Genomics — The Pan-Genome Approach

Pangenome represents the entirety of the genomic sequence and gene content found within a species rather than a single individual. Pangenomes have been constructed for key crop species, such as rice, soybean, bread wheat, and oilseed rape (Gao *et al.*, 2019). In addition, the pangenome offers a natural replacement for the current paradigm of using a single reference genome, as the choice of the reference affects downstream genomic analyses, including G WAS and gene expression quantification (Gage *et.al.*, 2019). Using pangenome as a reference improves read mapping and variant calling accuracy (Tian *et.al.*, 2019). The adoption of the pangenome reference will also allow the inclusion of variants beyond SNPs in GWAS.

Pairing Genomics with other Emerging Technologies to Maximize their Potential

- **Machine learning and crop plant genomics -** Almost all aspects of genomic analyses can now be supported by the development and implementation of machine learning algorithms. Machine learning algorithms find new patterns and "learn" the necessary predictive features from the data, rather than rely on pre-existing criteria.

This property makes them suitable for analysis of complex, multilayer datasets, where expert knowledge is incomplete or inaccurate, and when the amount of data is too large to be handled manually (Yip *et.al.*,2013). Machine learning methods have the potential to add significant value to the existing genomic resources and methodologies.

- **Speed breeding to accelerate the development of new crops** - Advances in molecular and genomic technologies resulted in isolation and characterization of many ergonomically important genes. Improved understanding of the molecular function of these genes makes the new crop domestication and improvement of orphan crops feasible. Speed breeding is a procedure, which accelerates crop generation time by changing growth conditions, such as day length and temperature. Growing long-day species under extended photoperiod (22 h light/2 h dark) and controlled temperature stimulates rapid flowering and maturation. The technology successfully shortened the plant generation time of some of the world's major agri-food crops, such as bread wheat, pasta wheat, barley, and canola (Watson *et.al.*, 2018). Production of up to six generations for wheat and barley is documented using speed breeding, which is much more efficient compared to two generations per year in traditional methods.
- **High-Throughput Phenotyping**- There is a great need to study plant stresses in dynamic environmental conditions to thoroughly understand the complete picture of plant-stress responses. The introduction of hyperspectral imaging technology combined with drones and manned aircrafts provides an opportunity for high throughput in-field phenotyping of traits, such as canopy temperature, chlorophyll fluorescence, as well as other biochemical plant characteristics (Camino *et.al.*, 2019). This technology increases the resolution and accuracy of measurements and is becoming cost-effective. Machine learning based methods have shown promise in high-throughput phenotyping data processing. In-field high throughput phenotyping is perfectly suited for evaluation of the complex physiological traits such as abiotic stresses tolerance.

Conclusion



Recent advances in genome sequencing, assembly, and annotation allowed unprecedented access to crop plant genomic information. High-throughput phenotyping techniques have been significantly advanced through the introduction of hyperspectral cameras and specialized processing software. Integration of genomic and phenomic data provides an opportunity to identify new agronomically relevant genes and characterize their functions. This knowledge has direct practical implications and can be translated to crop plant improvement using genome editing. While genome editing is currently applied in major crops and model plants, the technique has the potential to accelerate the domestication and allow rapid improvement of underutilized crop plants, targeting the current and future climate challenges. The success of genomics in crop improvement is also influenced by the type of trait under investigation. For example, traits strongly affected by the environment and the interaction between genotype and the environment are more challenging to study and modify. Disease resistance and dwarfing genes were introduced into crops such as wheat and rice during the green revolution. Breeders developed the high yielding varieties using the extra supply of nitrogen fertilizers in the presence of sufficient water under the climate conditions of the 1950—1960. The equation is different today as climate change causes water shortages and temperature increases. However, the information gained from genomics and phenomics will drive candidate gene identification and enable genome editing, initiating the new crop plant breeding revolution.

References

- Singh BD and Singh AK (2017). Marker Assisted Plant Breeding: Principles and Practices, 1st edn. Springer, New Delhi. pp 295-311.
- Singh Phundan (2009). Plant Breeding: Molecular and New Approaches 2nd edn. Kalyani Publishers, New Delhi, pp 247-255.