



Genomics - Assisted Breeding – A Significant Breakthrough for Crop Improvement

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ABSTRACT

Conventional breeding methods mainly depends on breeders skills to develop new plant varieties. These methods are laborious and take several years to develop a new variety. Molecular markers, next generation sequencing, association mapping are genomics tool, developed in recent past which has increased the efficiency of conventional breeding to great extent. The combination of conventional breeding techniques with genomic tools has been used in several crops for their genetic improvement with reference to yield, fertility, stress tolerance and climatic resilience etc.

Keywords: Genomics-assisted breeding, QTL, NGS, High throughput phenotyping

INTRODUCTION

Rapidly increasing global population has increased the global demand for food and industrial raw supply worldwide. Climate changes, continuously reducing area under farming and stresses *i.e.* abiotic and biotic to crops are serious causes to yield losses. Plant breeding is the only way to develop new varieties with increased productivity, nutrition, quality parameters and resistance to abiotic and biotic stress. Conventional breeding methods are mainly depends on breeders skills to identify superior phenotypes. Conventional breeding techniques for cross and self pollinated crop has very low efficiency, laborious and take several years to develop a

new variety. Several molecular markers are developed in recent past which has increased the efficiency of conventional breeding to great extent. The combination of conventional breeding techniques with genomic tools and approaches is leading to a new genomics-based plant breeding techniques like association mapping, marker assisted selection, gene pyramiding and genome selection (GS), which greatly accelerates the breeding. Cheaper sequencing has opened many possibilities to apply genomics tools to advance crop-breeding programs for complex traits, such as climate resilience (Kole et al. 2015) and quality traits (Migicovsky et al., 2017).

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GAB enables the integration of genomic tools with high throughput phenotyping to assist breeding practices through molecular markers to facilitate the prediction of phenotype from genotype. Use of advanced DNA technologies, high throughput phenotyping protocols, knowledge from other approaches as gene expression via transcriptomics, protein function via proteomics, and metabolic pathways via metabolomics, allows the identification of molecular markers linked to complex traits, the dissection of genetic variability, identification of potential candidate genes, and their alleles for gene expression or gene function (Friedmann et al., 2018).

Molecular marker assisted selection: For a quantitatively-inherited characters, numerous QTLs or genes are usually involved. Thus, discovery of QTL or even underlying causal genes/alleles is of great importance to marker-assisted breeding. Genetic mapping via QTL analysis have accelerated identification of QTL controlling the desired traits of agronomic, quality or nutritional importance in created populations. GAB allows breeders to rapid screening of large population and select subset for more expensive phenotypic evaluation. After identifying the molecular markers associated with gene(s)/QTLs for traits of interest, the next step is to use molecular markers in back-crossing programmes to improve selection efficiency and to implement gene pyramiding especially for disease resistances.

Plant germplasm resources worldwide, comprising of wild plant species, modern cultivars, and their crop wild relatives, are the important reservoirs of natural genetic variations, originated from a number of historical genetic events as a respond to environmental stresses and selection through crop domestication (Abdurakhmonov & Abdurakhmonov (2008). The availability of high-density SNP markers has opened a way for genome wide association study (GWAS), an approach using natural populations. Association mapping could overcome several limitations of conventional linkage mapping and provide a powerful strategy for dissecting complex traits.

Next generation sequencing: Next generation sequencing (NGS) describe a DNA sequencing technology which has revolutionised genomic research. The vast amounts of data generated by NGS have broadened our understanding of structural and functional genomics. The NGS technologies are different from the classical methods of sequencing as they provide massively parallel analysis, extremely high-throughput from multiple samples at much reduced cost. Conventional phenotyping has limited ability of phenotyping of traits related to yield and stress tolerance (e.g., yield potential as well as increased drought, heat tolerance, and nutrient efficiency, etc.). NGS generates huge amounts of sequenced data in a cost-effective manner and allows profiling for nucleotide variation and large-scale discovery of functional markers. These markers will help in selection of economically-important traits in plant breeding.

High throughput phenotyping: Modern phenomics tools aim to record data on such traits on hundreds to thousands of plants in a single day, as a phenomics revolution. An International Plant Phenomics Network was set up for high throughput phenotyping via robotic, non-invasive imaging across the life cycle of small, short-lived model plants and crops (Muraya et al., 2016). Plant height, leaf length, width, and angle were measured on a phenotyping platform in the greenhouse, which was developed by the integration of LiDAR, high-resolution camera, and hyperspectral imager (Guo et al., 2017). Physiological breeding based on HTPPs and probably together with genomic selection is beneficial for the improvement of breeding methodologies, and brings out more precise breeding strategies for stress tolerance and yield (Reynolds & Langridge 2016). Laser scanning technologies (Dornbusch et al., 2012) and digital stereocameras allowing one to obtain a 3D model of a plant (Chéné *et al.* 2012) are used for determination of the leaf location and orientation on the stem, determination of the traits changing in the process of diurnal rhythm, and study of the plant circadian rhythms.

Use of genomics assisted breeding in crops

improvement: A number of genes or QTLs associated with yield related traits and crop resistance/tolerance to abiotic and biotic stresses have been identified for crop improvement. In last few years, species-specific genomic resources are being generated and genomic resources from related cereal species are being transferred through comparative genomics studies. Several grain yield-related QTLs in rice: GW2 (Song et al., 2007), GW5 (Shomura et al., 2008) have been identified, In pearl millet during moisture stress three major QTL for grain yield (Bidinger et al., 2007) were reported. A numbers of polymorphic markers were identified associated with resistance to biotic stresses (Bohra et al., 2011; Saxena et al., 2010), fertility restoration (Bohra et al., 2011), earliness, plant height (Kumawat et al., 2012) and determinacy (Mir et al., 2013, 2014) in pigeon pea reported. Other than cereal crops genome sequencing in perennial fruit crops such as apple (Velasco et al., 2010), grape (Velasco et al., 2007), banana (D'Hont et al., 2012), cocoa (Argout et al., 2011), peach (Ahmad *et al.*, 2011), and sweet orange (Xu et al., 2013) were also performed. Genetic region associated with abiotic stress resistance were also reported as winter hardiness (Thomas & James, 1993), vernalization response and frost tolerance (Galiba et al., 1995; Hayes et al., 1998), cold and drought-induced ABA production (Laurie et al., 1995), and osmotic stress-tolerance (Galiba et al., 1993), his includes drought-adaptive traits (Serraj et al., 2009; Tuberosa, 2012), root architecture (Wasson et al., 2012; Uga et al., 2013; Lynch et al., 2014), accumulation of water-soluble carbohydrates and their partitioning to storage organs (Salem et al., 2007; Snape et al., 2007; Rebetzke et al., 2008), abscisic acid concentration (Rebetzke et al., 2008; Rehman et al., 2011), stay-green (Yang et al., 2007; Borrell et al., 2014) also reported.

Advantages of Genomics assisted breeding:

(i) Most agronomical and economically important traits in crops are quantitative traits that are controlled by multiple QTL. Thus,

discovery of QTL or even underlying causal genes/alleles is of great importance to marker-assisted breeding. So far, a huge number of QTL have been identified using this method.

(ii) Use of genomic tools also modify the selection criteria to focus on resistance gene rather than total yield

(ii) Use of GAB increase the efficiency to identify stress-tolerance genes in several crop and their exploitability in elite material and wider breeding germplasm, selection of lines with improved drought adaptation has also been successful.

(iii). Genomic assisted breeding also expand the use of minor crops, which may possess better nutritional qualities, environmental sustainability or resilience and require lower inputs than major crops.

(iv). Genomics possesses the potential to increase the diversity of alleles available to breeders through mining the gene pools of crop wild relatives (CWRs).

FUTURE THRUST: Conventional plant breeding has limited efficiency to develop new plant varieties with enhanced yield, and inbuilt stress resistance to biotic and abiotic stress. Newly developed genetic and genomics tools will enhance the efficiency of conventional breeding and evaluation processes. At present, high-throughput trait-associated markers, cost-effective genotyping approaches, and precise phenotyping platforms will help the rapid deployment of GAB and identification of candidate gene. Genomics-assisted breeding in particular is predicted to playing a significant role in the development of new and advanced varieties. Advances in DNA sequencing technologies along with advanced genomics tools will expedite the identification of novel genes and key regulatory regions of yield and stress tolerance toward the development of new cultivars.

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