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REVIEW

Genomics-assisted breeding — A revolutionary strategy for crop improvement



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Abstract

Food shortages arise more frequently owing to unpredictable crop yield losses caused by biotic and abiotic stresses. With advances in molecular biology and marker technology, a new era of molecular breeding has emerged that has greatly accelerated the pace of plant breeding. High-throughput genotyping technology and phenotyping platforms have enabled large-scale marker-trait association analysis, such as genome-wide association studies, to precisely dissect the genetic architecture of plant traits. Large-scale mapping of agronomically important quantitative trait loci, gene cloning and characterization, mining of elite alleles/haplotypes, exploitation of natural variations, and genomic selection have paved the way towards genomics-assisted breeding (GAB). With the availability of more and more informative genomic datasets, GAB would become a promising technique to expedite the breeding cycle for crop improvement.

Keywords: germplasm, genotyping technology, phenotyping platform, genomics-assisted breeding

1. Introduction

Crops are the major source of food supply and industrial raw materials. Significant gaps still exist between crop yields and global food consumption. Plant diseases, insects, and adverse environmental conditions frequently cause serious yield losses, which, together with a rapidly increasing global population, can result in severe food shortages worldwide.

Thus, sustainable crop productivity requires crop breeders to continuously release new varieties with high yield potential, high quality, resistance/tolerance to biotic/abiotic stresses, high nutrition-use efficiency, etc.

Plant breeding has made great progress in the last century (Zamir 2001). Conventional breeding mostly depends on phenotypic selection based on breeders' experiences, which resulted in the release of large numbers of high-yielding varieties. Nevertheless, labor intensity, time consumption, low efficiency, and environment dependence, etc., are major barriers that nowadays impede conventional plant breeding. With advances in molecular biology and high-throughput genotyping technology, the focus of plant breeding has gradually switched from phenotype-based to genotype-based selection. Marker-assisted selection (MAS) has improved breeding efficiency to some extent and prevailed in breeding programs for decades (Xu and Crouch 2008). Numerous MAS strategies have been developed: marker-assisted backcrossing or introgression of major

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genes or quantitative trait loci (QTL), enrichment of favorable alleles in early generations, and selection for quantitative traits using markers at multiple loci (Hospital *et al.* 1992; Lee 1995; Eathington *et al.* 2007; Gupta *et al.* 2010). Over the last two decades, the rapid development of whole-genome sequencing and marker development technologies enabled the use of high-density single nucleotide polymorphism (SNP) markers to analyze the whole genome at very low cost.

Whole genome and transcriptome sequencing bridges between the genotype and phenotype, and leads to a new revolution in plant breeding, especially for complex traits. Integration of genomics tools and conventional breeding triggers new breeding strategies, like gene pyramiding and genome selection (GS), which greatly accelerates the breeding. In recent years, genomics-assisted breeding (GAB) has become a powerful strategy for plant breeding (Fig. 1). 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 (Fig. 1). GAB allows breeders to start out with a large population of only genotypically characterized offspring, and then only use a selected subset for more expensive phenotypic evaluation (Cooper *et al.*

2014). In addition, genotypic evaluation can be done off-season, e.g., in winter nurseries, where yield trials are usually not conducted, which also helps to speed up breeding. GAB is especially useful for the improvement of complex traits due to its advantages of high accuracy, direct improvement, short breeding cycle, and high selection efficiency. The ultimate goal of GAB is to find the best combinations of alleles (or haplotypes), optimal gene networks, and specific genomic regions to facilitate crop improvement (Xu *et al.* 2012). As such, GAB is promising to accelerate the generation of new plant varieties and promote the development of modern agriculture. Here, we summarize the recent progress in germplasm enhancement, high throughput genotyping and phenotyping technologies, marker-trait associations, and exploration of natural variations, which altogether make it available for GAB in crop improvement.

2. Germplasm collection and enhancement

Crop germplasm resources, also known as genetic resources, have great impacts on crop genetic improvement. Large amounts of natural germplasm resources have been collected and preserved. However, how they can be

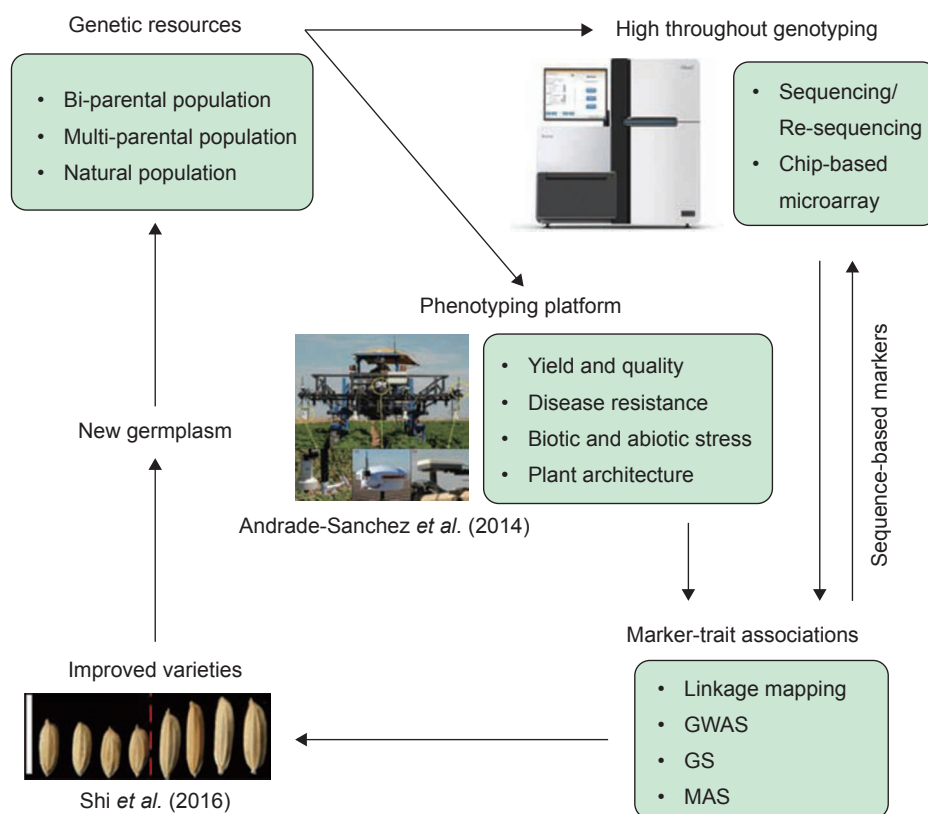


Fig. 1 A flowchart for genome-assisted breeding. GWAS, genome-wide association study; GS, genomic selection; MAS, marker-assisted selection.

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