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Genomics-assisted breeding - A revolutionary strategy for crop improvement

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Keywords
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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 throughout 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

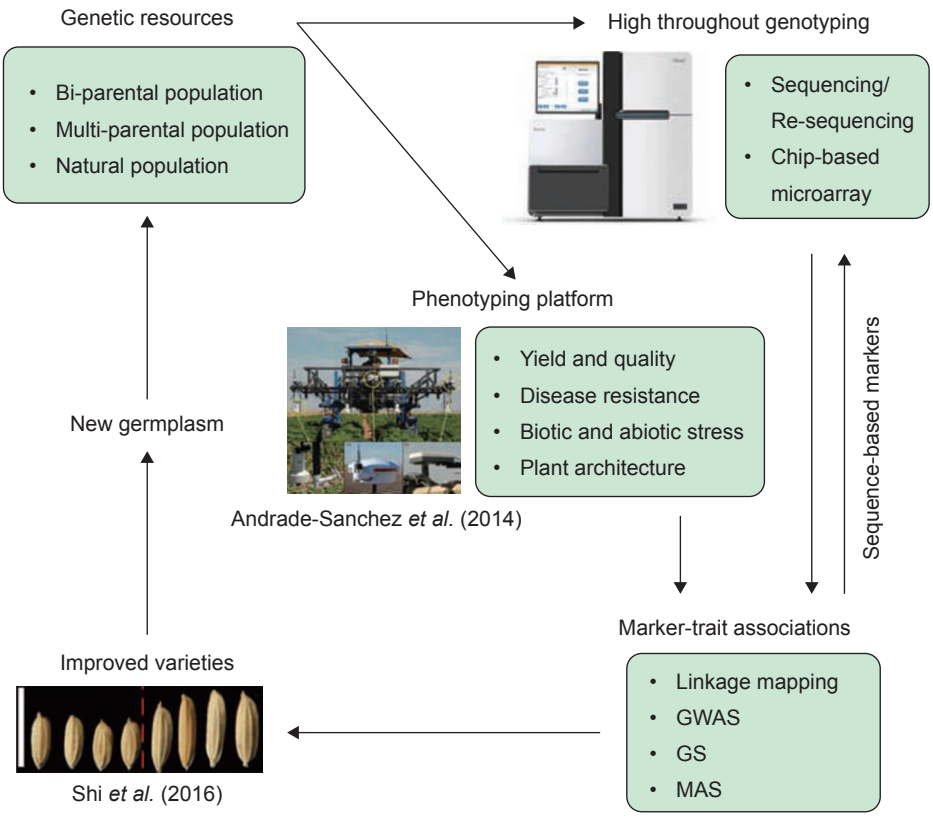

Fig. 1 A flowchart for genome-assisted breeding. GWAS, genome-wide association study; GS, genomic selection; MAS, marker-assisted selection.

utilized for crop improvement remains to be a big challenge. Besides, the use of artificial methods has become the main approach to create novel germplasm, such as recombinant inbred lines, near isogenic lines, and single segment substitution lines. These genetic resources have been widely used for gene isolation. Natural populations with higher genetic diversity usually consist of hundreds to thousands of lines. It is costly to evaluate each accession in term of genotyping and phenotyping. Core collection strategy defines a minimum set of germplasms to maintain the maximum genetic diversity of the full collection (Frankel 1984), which could greatly increase efficiency in utilization of genetic resources. Previously, core collection was constructed primarily based on geographical distribution and pedigrees, etc. Recently, application of plant genomics opens a new era for establishment and utilization of crop core collections (Jia *et al*. 2017). The core collections have been accomplished in wheat and rice (Kobayashi *et al*. 2016; Li *et al*. 2017). Genomic tools offer information at both DNA and transcriptome levels with reduced environmental effects. Meanwhile, to better manage genetic resources, the core collection needs to maintain its genetic diversity with updated genetic information.

3. Genome sequencing and sequence-based markers

In the last three decades, several DNA fingerprinting methodologies, such as restriction fragment length polymorphisms (Burr *et al*. 1988), random amplified polymorphic DNA (Williams *et al*. 1990), and simple sequence repeats (Sundaram *et al*. 2008), have been used for molecular plant breeding. These techniques are often labor-intensive and time-consuming, and it is impossible for them to be applied in large scale in modern plant breeding. To make things even worse, most markers are not localized in the target gene region, and thus failed to show any impact on plant breeding (Collard and Mackill 2008; Xu and Crouch 2008). By contrast, SNPs currently become the most popular markers in breeding programs because of their abundance and our ability to detect them with high throughput methods (Mammadov *et al*. 2012).

Next-generation sequencing has developed rapidly over the last decade, leading to an ever-increasing number of sequenced species. Because a single reference genome is not sufficient to represent the diversity within a species, re-sequencing of different cultivars, landraces, and wild accessions are critical to the identification of genetic variation. Progress in next-generation sequencing and whole-genome re-sequencing is valuable for discovery, validation, and assessment of diagnostic markers in plants (Lai *et al*. 2010) and therefore is beneficial for the development of informative genome-wide markers. Genome complexity reducing methods like genotype-by-sequencing helped to reduce the cost of genotyping large number of recombinant progenies (Elshire *et al*. 2011).

The sequences of crop genomes are useful for exploring genome organization and gaining insight into genetic variation *via* the re-sequencing of different accessions. A total of 278 maize lines, including public USA and elite Chinese lines, were re-sequenced and resulted in the identification of >27 million SNPs (Jiao *et al*. 2012). With the initiation of the "3 000 Rice Genomes Project", a large panel of rice accessions has been re-sequenced with an average of 14×sequencing depth, resulting in >18.9 million SNPs (Li 2014). In wheat, a combined strategy using methylation-sensitive digestion of genomic DNA and next-generation sequencing was carried out for high-throughput SNP discovery, resulting in ~23 500 SNPs (De Leeuw *et al*. 2009). In addition, whole-genome re-sequencing was also conducted for other crops, such as, barley (Takahagi *et al*. 2016), soybean (Valliyodan *et al*. 2016), and lupin (Yang *et al*. 2015), etc. Sequence-based markers associated with rare elite alleles will facilitate positional cloning and crop breeding.

The whole-genome re-sequencing data provide an unlimited resource for high-throughput SNP genotyping technologies, such as DNA chips, to detect genome-wide DNA polymorphisms. Rasheed *et al*. (2017) reviewed the progress, challenge and perspective of crop breeding chips and genotyping platforms, which provided great potential for crop breeding. Two chip-based technologies have been widely used, namely the GeneChip™ microarray technology from Affymetrix (Santa Clara, CA, USA; www.affimetrix.com) and the BeadArray™ technology from Illumina (San Diego, CA, USA; www.illumina.com). Some other newly developed commercial genotyping platforms including Eureka™ from Affymetrix® and Infinium from Illumina also depend on high-density SNP markers. Microarray-based characterization of plant genomes has revolutionized, to some extent, plant breeding and agricultural biotechnology. A standardized large-scale SNP genotyping array was established using more than 800 000 SNPs which were evenly distributed across the maize genome (Ganal *et al*. 2011). In addition, kompetitive allele-specific PCR (KASP), TaqMan real-time PCR, and semi-thermal asymmetric reverse PCR (STARP) assays utilize low-cost PCR to identify SNPs, thus providing flexibility with respect to the number of samples to be analyzed (He *et al*. 2014; Semagn *et al*. 2014; Long *et al*. 2017).

Diagnostic markers, designed on target gene sequences, can be used to optimize the application of MAS in breeding without further validation. Genome sequencing/re-sequencing has been increasingly applied to the

development of diagnostic markers. Such kind of markers enables plant breeders to precisely engineer new cultivars with target traits to meet various food demands in future. So far, only limited diagnostic markers are applicable for MAS in yield and biotic/abiotic stress tolerance. Diagnostic markers were confirmed to be workable on a broad range of commercial lupin cultivars (Yang *et al*. 2015). Haplotype contigs (haplotigs) associated with soybean salinity were identified through whole-genome re-sequencing (Patil *et al*. 2016), which was applicated to the prediction of salt-tolerant/sensitive genotypes. Markers that define the haplotig could be assembled to form a genome-wide set of markers (Chin *et al*. 2016). RNA-seq technology enables the identification of haplotypes within a gene and allele specific gene expression simultaneously. Haplotype markers generated from transcriptome analysis will be extremely useful for uncovering genetic diversity and variation.

4. High-throughput phenotyping

Functional analysis of plant genomes has entered a high-throughput stage, whereas plant phenotyping remains a big challenge for modern plant breeding. Conventional phenotyping does not provide the large-scale, high-quality phenotypic data necessary for the accurate prediction of complex quantitative traits. Thus, high-throughput phenotyping platforms (HTPPs) need to be established for plant phenomics. HTPP is based on non-destructive phenotyping capability and high-capacity data recording and processing. Consequently, HTPP is particularly useful for detailed measurements of plant characteristics that collectively provide reliable estimates of phenotypic traits. In recent years, rapid progress has been made towards HTPPs due to the technological advances in computing and robotics, light detection and ranging (LiDAR), unmanned aerial vehicle remote sensing, etc. (Table 1). 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). Dynamic growth traits from the seedling to tasseling stage were quantified using a HTPP from a maize RIL population in the greenhouse (Zhang X *et al*. 2017).

Plant breeding has benefited from field phenotyping with the development of novel sensors, image analysis, robotics, etc. (Table 1). However, the capacity for rapidly and accurately phenotyping large numbers of field-grown plants remains unsatisfied. It is also deficiency of the precise estimation of association between genotype and phenotype under highly variable environments. A novel system for phenotyping dynamic traits has been developed that can rapidly and accurately measure multiple traits, including canopy height, under well-watered or water-limited field-growth conditions (Andrade-Sanchez *et al*. 2014). Undoubtedly, high-throughput phenotyping will contribute to our understanding of crop physiology by rapidly providing accurate information. 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 and Langridge 2016). The advent of additional HTPPs with increased reliability, accuracy, capacity, and affordability will assist the prediction of genotypic performance of different plant species under complex field conditions. However, for some complex traits, e.g., disease resistance, artificial inoculation is needed to assist disease development, and it cannot yet be replaced by robotization. Low cost and accessible data managements are urgently needed. Renovated technique will certainly assist further application of HTTP in GAB to benefit crop breeders.

5. Marker-trait association for genomics-assisted breeding

Most agronomically and economically important traits in crops are quantitative traits that are controlled by multiple

Table 1 Examples of high-throughput phenotyping platforms

Technology	Trait	Condition[1)]	Reference
Imaging	Plant growth and chlorophyll fluorescence	c	Jansen *et al*. (2009)
Camera	Leaf growth	c	Massonnet *et al*. (2010)
Spectroradiometer	Drought tolerance	c	Lu *et al*. (2011)
Imaging	Leaf area	f	Montes *et al*. (2011)
Visual	Root architectural traits	f	Trachsel *et al*. (2011)
Camera	Presence of rice bugs	f	Fukatsu *et al*. (2012)
Hydraulic push press	Root depth and distribution	f	Wasson *et al*. (2012)
Sensor	Canopy height	f	Andrade-Sanchez *et al*. (2014)

[1)] c, controlled conditions; f, field conditions.

QTL. Thus, discovery of QTL or even underlying causal genes/alleles is of great importance to marker-assisted breeding. Linkage mapping is a classical method towards the genetic dissection of the genetic basis of quantitative trait loci. So far, a huge number of QTL have been identified using this method (Emebiri *et al*. 2017; Liu *et al*. 2017; Zhang D *et al*. 2017). In addition, with the achievement of bioinformatics and massive genetic information, a meta-QTL analysis was developed by integrating published QTL to detect consistent QTL for crop improvement (Van and McHale 2017).

Genome-wide mapping in large populations facilitates the target gene mapping and cloning in crops. The availability of high-density SNP markers has opened a way for genome-wide association study (GWAS), an approach using natural populations. GWAS could overcome several constraints of conventional linkage mapping and provide a powerful complementary strategy for dissecting complex traits. By combining high-throughput phenotypic and genotypic data, GWAS provides insights into the genetic architecture of complex traits in maize, particularly given the rapid decay of linkage disequilibrium in maize (Yan *et al*. 2011). A total of 26 loci were identified to be associated with oil concentration in maize kernels through GWAS (Li *et al*. 2013), and this data set can now be directly used to facilitate marker-based breeding for oil quantity and quality. Numerous loci associated with maize traits have been detected through GWAS, such as flowering time (Buckler *et al*. 2009), leaf architecture (Tian *et al*. 2011), blight resistance (Kump *et al*. 2011), and male inflorescence (Wu *et al*. 2016), etc. GWAS for soybean domestication revealed relevance between selected regions and domestication as well as new loci for oil content and plant height (Zhou *et al*. 2015). QTLs associated with chilling tolerance during germination and young seedling stages were identified recently *via* GWAS (Schläppi *et al*. 2017), providing useful markers for chilling tolerance improvement in rice cultivars. GWAS has become a powerful tool for QTL mapping in plants because a broad range of genetic resources may be accessed for marker-trait association without any limitation on marker availability.

Genomic selection (GS) predicts genomic estimated breeding values (GEBVs) of lines by analyzing traits and high-density marker scores within an artificially created population at the whole-genome level (Meuwissen *et al*. 2001; Crossa *et al*. 2017). GS is another promising breeding strategy for rapid improvement of complex traits. Close correlations were found between genomic estimated and true breeding values, even for polygenic traits with low heritability (Jia and Jannink 2012). This level of accuracy was sufficient in approaches selected for agronomic performance using marker information alone. When using genome-wide markers to select plants for breeding, GS was proved to be advantageous for complex traits, e.g., grain yield (Saint Pierre *et al*. 2016). Moreover, GS can shorten the selection cycle and generate reliable phenotypes. In view of these advantages, GS has been applied to several traits in a variety of plant species including maize, barley, bread wheat, and rice. Data obtained from six maize segregating populations predicted higher levels of grain moisture and grain yield, at namely 0.90 and 0.58, respectively, and precise phenotyping led to accurate prediction across three to four locations (Zhao *et al*. 2012). Similar prediction accuracies were obtained for *Fusarium* head blight resistance in wheat through both independent validation and cross-validation (Jiang *et al*. 2017). Improved prediction accuracy towards rice heading dates was obtained with a novel genomic-prediction-and-crop modelling integrated phenological method, which can overcome influence of genotype-environment interaction in diverse environments (Onogi *et al*. 2016). This suggests great potential of the integrated approach compared with the two-step methods in all cross-validation schemes. With the achievement of crop genetic map coupled with the high-throughput marker detection technique, the application of GS is increasingly accepted by breeders. Although still costly, GS has been proved to be superior to marker-assisted recurrent selection for improving complex traits in crops, as it can effectively avoid issues associated with the number of QTL that control a trait.

6. From genotype to phenotype

It is generally accepted that the phenotype corresponds to genotype in an approximately linear manner. Genomic research has unraveled various metabolic pathways and provided molecular markers for agronomic traits. To date, a large number of QTLs have been identified by linkage mapping and GWAS, and several genes with major effects have been functionally validated by both gain-of-function and loss-of-function approaches (Table 2). Genotype-phenotype databases record massive amounts of information about genetic variation, and thousands of genetic variants have been associated with important crop traits. Rapid genome-sequencing methods coupled with whole-genome transcription profiling suggest that it is possible to predict phenotypes from genotypes.

A number of genes or QTLs associated with yield-related traits and crop resistance/tolerance to abiotic and biotic stresses have been identified and proven to be valuable resources for crop improvement (Table 2). Our understanding towards the genetic architecture and molecular mechanisms for complex plant traits has been greatly improved with the identification of major QTLs/genes. Resistance to head smut was significantly enhanced

Table 2 Isolated genes associated with important plant traits

Cereal species	Trait	Gene	Reference
Maize	Zein storage protein	*Opaque-2*	Schmidt *et al.* (1992)
	Resistance to the fungus	*HM1*	Johal and Briggs (1992)
	Domestication	*tb1*	Doebley *et al.* (1995)
	Flowering time	*id1*	Colasanti *et al*. (1998)
		dlf1	Muszynski *et al*. (2006)
		zfl1	Bomblies and Doebley (2006)
		Vgt1	Salvi *et al*. (2007)
		conz1	Miller *et al*. (2008)
		ZCN8	Meng *et al*. (2011)
	Photoperiod sensitivity	*CCT*	Yang *et al.* (2013)
	Resistance to head smut	*WAK*	Zuo *et al*. (2015)
	Drought tolerance	*VPP1*	Wang X *et al*. (2016)
	Male sterility	*Ms7*	Zhang D *et al*. (2017)
	Resistance to southern leaf blight, gray leaf spot and northern leaf blight	*caffeoyl-CoA O-methyltransferase*	Yang *et al*. (2017)
Rice	Resistance to *Xanthomonas oryzae* pv. *oryzae*	*Xa21*	Song *et al*. (1995)
	Grain size	*GS3*	Fan *et al*. (2006)
		GW2	Song *et al*. (2007)
		GW5	Shomura *et al*. (2008)
		GS5	Li *et al*. (2011)
		GW8	Wang *et al*. (2012)
		GS2	Hu *et al*. (2015)
		GL7	Wang *et al*. (2015)
	Bacterial streak disease	*Rxo1*	Zhao *et al*. (2005)
	Blast resistance	*Pi9*	Zhou *et al*. (2006)
		Pi2	Qu *et al*. (2006)
		Piz, *Pigm*	Deng *et al*. (2017)
		bsr-d1	Li *et al*. (2017)
	Grain chalkiness	*Chalk5*	Li *et al*. (2014)
	Resistance to rice stripe virus	*STV11*	Wang *et al*. (2014)
	Chilling tolerance	*COLD1*	Ma *et al*. (2015)
	Thermo tolerance	*ERECTA*	Shen *et al*. (2015)
		TOGR1	Wang D *et al*. (2016)
Wheat	Leaf rust disease resistance	*Lr10*	Feuillet *et al*. (2003)
	Grain protein, zinc, and iron content	*NAM-B1*	Uauy *et al*. (2006)
	Stripe rust resistance	*Yr36*	Fu *et al*. (2009)
		WKS1	Gou *et al*. (2015)
	Grain width, thousand-kernel weight, polyploidization and evolution	*TaGW2*	Qin *et al*. (2014)
	Wheat rust, powdery mildew	*Lr67*	Moore *et al*. (2015)
	Leaf width, flowering time and chlorophyll	*STENOFOLIA*	Liu *et al*. (2017)
Barley	Freezing tolerance	*Dhn1*, *Dhn2*	Pan *et al*. (1994)
	Water deficit and salt stress	*HVA1*	Xu *et al*. (1996)
	Resistance to powdery mildew	*Rar1*	Shirasu *et al*. (1999)
		Sgt1	Azevedo *et al*. (2002)
	Stem rust-resistance	*Rpg1*	Brueggeman *et al*. (2002)
	Stem rust resistance	*Sr50*	Mago *et al*. (2015)

by introducing the gene *ZmWAK* into the susceptible line HZ4 (Zuo *et al*. 2015), and disease incidence was greatly reduced *via* MAS (Zhao *et al*. 2012). This demonstrates the great potential of *ZmWAK* in the genetic control of head smut disease in maize. Subsequent research showed that, apart from inducing enhanced maize resistance to head smut, *ZmWAK* has multiple effects on other traits including yield components (Konlasuk *et al*. 2015). A natural variant of *ZmVPP1*, caused by a transposon insertion in the *ZmVPP1* promoter, was found to be associated with maize drought tolerance at the seedling stage, a result that provided genetic insights into the natural variation of maize drought tolerance (Wang X *et al*. 2016). The QTL *COLD1* confers chilling tolerance to *japonica* rice and was identified *via* map-based gene cloning (Ma *et al*. 2015). Thus, *ZmVPP1* and *COLD1* represent promising targets for improving maize-drought and rice-cold tolerance. With the continuous saturation of crop genetic maps, more QTLs will be mapped, enabling

the pyramiding of multiple genes/QTLs. Several grain yield-related QTLs have been identified in rice: *GW2* (Song *et al*. 2007), *GW5* (Shomura *et al*. 2008), *GW8* (Wang *et al*. 2012), *GS2* (Hu *et al*. 2015), *GS3* (Fan *et al*. 2006), and *GS5* (Li *et al*. 2011). These loci that control grain width, filling, weight, and size provide growers with great opportunity to breed super high-yielding elite rice varieties.

Natural variants are a valuable resource for GAB, and even though they do not necessarily induce pleiotropic effects, they may lead to different phenotypes. Most of the genetic variation present in wild species and unadapted germplasm usually has a negative effect on the adaptation of plants to agroecological environments. Domestication has generated remarkable variation in plant architecture and appearance (Chen *et al*. 2014). Analysis of genetic variation in modern maize cultivars, early-domesticated maize, and wild teosinte identified almost 1 200 genes that were affected during domestication and accompanied by reduced genetic diversity (Bevan *et al*. 2017). Different rice subspecies exhibit substantial heterogeneity in the natural variations of metabolites and their underlying genetic architectures. The challenge now is how to validate and make use of the alleles identified as being superior in breeding programs.

Discovery of new haplotypes and the selection of superior haplotypes can advance plant breeding. Gore *et al*. (2009) constructed the first plant haplotype map that identified and genotyped millions of sequence polymorphisms among 27 diverse maize inbred lines. Their findings revealed that the genome was characterized by highly divergent haplotypes and showed 10- to 30-fold variation in recombination rate. In rice *GS5* gene, three haplotypes of its promoter region were identified from a wide geographic range of rice accessions, suggesting that natural variation in *GS5* might contribute to grain size diversity, which would benefit rice yield improvement. Recently, an analytical framework for haplotype-based *de novo* assembly of the low-coverage sequencing data for rice was implemented using 950 worldwide rice varieties. In wheat, a favorable haplotype *Hap-6B-1* was found to have an even stronger influence on increasing grain yield that had undergone strong positive selection in global wheat breeding (Qin *et al*. 2014). Superior varieties with attributes of abiotic and biotic stress tolerance, and high yield, either alone or in combination, may ultimately result from new genetic variants, rare alleles, and new haplotypes. The coupling of genome-wide haplotypes with GS has been shown to be feasible and may greatly accelerate plant breeding by offering greater specificity and predictability (Spindel *et al*. 2016). Haplotigs may also be used to track their own incorporation into breeding pedigrees.

Recently, genome-editing technologies emerged as powerful tools for creating new allelic variants in the genomes of cultivated varieties. Genome editing represents an alternative to standard breeding processes based on recombination and, to some extent, to genetic transformation. Several years ago, sequence-specific nucleases, including zinc-finger nucleases and transcription activator-like effector nucleases (TALEN), were proposed for use in targeted genome editing. The haploid induction in maize is triggered by a mutation in a pollen-specific phospholipase, novel edits generated by TALEN lead to a 6.7% haploid induction rate (Kelliher *et al*. 2017). More recently, the clustered regularly interspaced short palindromic repeats/associated Protein-9 Nuclease (CRISPR/Cas9) System has been widely used for precise genomic editing. With the CRISPR/Cas9 System, the homozygous transgene-free wheat mutants were produced, offering the potential to accelerate plant genome editing process (Zhang *et al*. 2016). Genome editing on the gene promoter region could give rise to differential *cis*-transcription alleles, providing beneficial quantitative variation for plant breeding. This was confirmed by evaluating numerous promoter variants for genes regulating tomato yield traits (Rodríguez-Leal *et al*. 2017). It could be used for the quick isolation of new alleles and finely the control of yield traits. Meanwhile, it is also significant in uncovering the relationship between the gene regulation and complex quantitative traits. Genome-editing technology has already been a useful tool for the improvement of crop breeding including yield and durable resistance. However, study on the CRISPR/Cas9 System, such as the induction efficiency of mutations, specificity, and heredity in different crops, are still not clear.

7. Perspectives

Despite the great potential of GAB, several bottlenecks still challenge its immediate application. The first is the establishment of high-throughput phenotyping platforms in the field. None of the current pioneering phenome projects comes close to realizing the full potential of GAB, mainly because of costs and limited phenotyping capabilities. As a huge amount of information would be generated from high-throughput phenotyping, two main limiting factors to mine the huge volume of accumulated phenotypic data are data management and bioinformatics usage. Inheritance mechanisms related to agronomically important traits are also extensively concerned, for example, epigenetic phenomena such as DNA methylation, genomic imprinting, maternal effects, RNA editing, etc. Although epigenetics research has advanced considerably in recent years, the mechanisms of epigenetic phenomena are only beginning to be understood, and their potential role in crop improvement is unknown. The eventual elucidation of epigenetic mechanisms may provide input for molecular

genetic innovation in crop improvement.

The availability of plant genome information has generated many next-generation sequencing-based approaches for allele mining and candidate genes identification. At present, high-throughput trait-associated markers, cost-effective genotyping approaches, and precise phenotyping platforms will facilitate the rapid deployment of GAB. Newly developed genetic and genomics tools will enhance, but not replace, conventional breeding and evaluation processes. In the coming years, we believe that extensive implementation of MAS and GS either alone or in combination will help improve plant breeding at genomic level.

References

Andrade-Sanchez P, Gore M A, Heun J T, Thorp K R, Carmo-Silva A E, French A N, Salvucci M E, White J W. 2014. Development and evaluation of a field-based high-throughput phenotyping platform. *Functional Plant Biology*, **41**, 68–79.

Azevedo C, Sadanandom A, Kitagawa K, Freialdenhoven A, Shirasu K, Schulze-Lefert P. 2002. The RAR1 interactor SGT1, an essential component of *R* gene-triggered disease resistance. *Science*, **295**, 2073–2076.

Bergelson J, Roux F. 2010. Towards identifying genes underlying ecologically relevant traits in *Arabidopsis thaliana*. *Nature Reviews Genetics*, **11**, 867–879.

Bevan M W, Uauy C, Wulff B B H, Zhou J, Krasileva K, Clark M D. 2017. Genomic innovation for crop improvement. *Nature*, **543**, 346–354.

Bomblies K, Doebley J F. 2006. Pleiotropic effects of the duplicate maize FLORICAULA/LEAFY genes *zfl1* and *zfl2* on traits under selection during maize domestication. *Genetics*, **172**, 519–531.

Brueggeman R, Rostoks N, Kudrna D, Kilian A, Han F, Chen J, Druka A, Steffenson B, Kleinhofs A. 2002. The barley stem rust-resistance gene *Rpg1* is a novel disease-resistance gene with homology to receptor kinases. *Proceedings of the National Academy of the United States of America*, **99**, 9328–9333.

Buckler E S, Holland J B, Bradbury P J, Acharya C B, Brown P J, Browne C, Ersoz E, Flint-Garcia S, Garcia A, Goodman M M, Harjes C, Guill K, Kroon D E, Larsson S, Lepak N K, Li H, Mitchell S E, Pressoir G, Peiffer J A, Rosas M O, *et al*. 2009. The genetic architecture of maize flowering time. *Science*, **325**, 714–718.

Burr B, Burr F A, Thompson K H, Albertson M C, Stuber C W. 1988. Gene mapping with recombinant inbreds in maize. *Genetics*, **118**, 519–526.

Chen W, Gao Y, Xie W, Gong L, Lu K, Wang W, Li Y, Liu X, Zhang H, Dong H, Zhang W, Zhang L, Yu S, Wang G, Lian X, Luo J. 2014. Genome-wide association analyses provide genetic and biochemical insights into natural variation in rice metabolism. *Nature Genetics*, **46**, 714–721.

Chin C S, Peluso P, Sedlazeck F J, Nattestad M, Concepcion G T, Clum A, Dunn C, O'Malley R, Figueroa-Balderas R, Morales-Cruz A, Cramer G R, Delledonne M, Luo C, Ecker J R, Cantu D, Rank D R, Schatz M C. 2016. Phased diploid genome assembly with single-molecule real-time sequencing. *Nature Methods*, **13**, 1050–1054.

Colasanti J, Yuan Z, Sundaresan V. 1998. The indeterminate gene encodes a zinc finger protein and regulates a leaf-generated signal required for the transition to flowering in maize. *Cell*, **93**, 593–603.

Collard B C Y, Mackill D J. 2008. Marker-assisted selection: an approach for precision plant breeding in the twenty-first century. *Philosophical Transactions of the Royal Society* (B: Biological Sciences), **363**, 557–572.

Cooper M, Messina C D, Podlich D, Totir L R, Baumgarten A, Hausmann N J, Wright D, Graham G. 2014. Predicting the future of plant breeding: complementing empirical evaluation with genetic prediction. *Crop and Pasture Science*, **65**, 311–336.

Crossa J, Pérez-Rodríguez P, Cuevas J, Montesinos-López O, Jarquín D, de Los Campos G, Burgueño J, González-Camacho J M, Pérez-Elizalde S, Beyene Y, Dreisigacker S, Singh R, Zhang X, Gowda M, Roorkiwal M, Rutkoski J, Varshney R K. 2017. Genomic selection in plant breeding: Methods, models, and perspectives. *Trends in Plant Science*, **22**, 961–975.

Deng Y, Zhai K, Xie Z, Yang D, Zhu X, Liu J, Wang X, Qin P, Yang Y, Zhang G, Li Q, Zhang J, Wu S, Milazzo J, Mao B, Wang E, Xie H, Tharreau D, He Z. 2017. Epigenetic regulation of antagonistic receptors confers rice blast resistance with yield balance. *Science*, **355**, 962–965.

Doebley J, Stec A, Gustus C. 1995. *Teosinte branched1* and the origin of maize: Evidence for epistasis and the evolution of dominance. *Genetics*, **141**, 333–346.

Eathington S R, Crosbie T M, Edwards M D, Reiter R S, Bull J K. 2007. Molecular markers in a commercial breeding program. *Crop Science*, **47**, S154–S163.

Elshire R J, Glaubitz J C, Sun Q, Poland J A, Kawamoto K, Buckler E S, Mitchell S E. 2011. A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species. *PLoS One*, **6**, e19379.

Emebiri L C, Tan M K, El-Bouhssini M, Wildman O, Jighly A, Tadesse W, Ogbonnaya F C. 2017. QTL mapping identifies a major locus for resistance in wheat to Sunn pest (*Eurygaster integriceps*) feeding at the vegetative growth stage. *Theoretical and Applied Genetics*, **130**, 309–318.

Fan C, Xing Y, Mao H, Lu T, Han B, Xu C, Li X, Zhang Q. 2006. *GS3*, a major QTL for grain length and weight and minor QTL for grain width and thickness in rice, encodes a putative transmembrane protein. *Theoretical and Applied Genetics*, **112**, 1164–1171.

Feuillet C, Travella S, Stein N, Albar L, Nublat A, Keller B. 2003. Map-based isolation of the leaf rust disease resistance gene *Lr10* from the hexaploid wheat (*Triticum aestivum* L.) genome. *Proceedings of the National Academy of the United States of America*, **100**, 15253–15258.

Frankel O H. 1984. Genetic perspectives of germplasm conservation. In: Arber W, Illmensee K, Peacock W J,

Starlinger P, eds., *Genetic Manipulation*: *Impact on Man and Society*. Cambridge University Press, Cambridge, UK. pp. 161–170.

Fu D, Uauy C, Distelfeld A, Blechl A, Epstein L, Chen X, Sela H, Fahima T, Dubcovsky J. 2009. A kinase-START gene confers temperature-dependent resistance to wheat stripe rust. *Science*, **323**, 1357–1360.

Fukatsu T, Watanabe T, Hu H, Yoichi H, Hirafuji M. 2012. Field monitoring support system for the occurrence of *Leptocorisa chinensis* Dallas (Hemiptera: Alydidae) using synthetic attractants, Field Servers, and image analysis. *Computers and Electronics in Agriculture*, **80**, 8–16.

Ganal M W, Durstewitz G, Polley A, Bérard A, Buckler E S, Charcosset A, Clarke J D, Graner E M, Hansen M, Joets J, Le Paslier M C, McMullen M D, Montalent P, Rose M, Schön C C, Sun Q, Walter H, Martin O C, Falque M. 2011. A large maize (*Zea mays* L.) SNP genotyping array: Development and germplasm genotyping, and genetic mapping to compare with the B73 reference genome. *PLoS One*, **6**, e28334.

Gore M A, Chia J M, Elshire R J, Sun Q, Ersoz E S, Hurwitz B L, Peiffer J A, McMullen M D, Grills G S, Ross-Ibarra J, Ware D H, Buckler E S. 2009. A first-generation haplotype map of maize. *Science*, **326**, 1115–1117.

Gou J Y, Li K, Wu K, Wang X, Lin H, Cantu D, Uauy C, Dobon-Alonso A, Midorikawa T, Inoue K, Sánchez J, Fu D, Blechl A, Wallington E, Fahima T, Meeta M, Epstein L, Dubcovsky J. 2015. Wheat stripe rust resistance protein WKS1 reduces the ability of the thylakoid-associated ascorbate peroxidase to detoxify reactive oxygen species. *The Plant Cell*, **27**, 1755–1770.

Guo Q, Wu F, Pang S, Zhao X, Chen L, Liu J, Xue B, Xu G, Li L, Jing H, Chu C. 2017. Crop 3D — A LiDAR based platform for 3D high-throughput crop phenotyping. *Science China* (Life Sciences), doi: 10.1007/s11427-017-9056-0

Gupta P K, Langridge P, Mir R R. 2010. Marker-assisted wheat breeding: Present status and future possibilities. *Molecular Breeding*, **26**, 145–161.

He C, Holme J, Anthony J. 2014. SNP genotyping: The KASP assay. *Crop Breeding*: *Methods and Protocols*, **1145**, 75–86.

Holbrook C C, Anderson W F. 1995. Evaluation of a core collection to identify resistance to late leafspot in peanut. *Crop Science*, **35**, 1700–1702.

Hospital F, Chevalet C, Mulsant P. 1992. Using markers in gene introgression breeding programs. *Genetics*, **231**, 1199–1210.

Hu J, Wang Y, Fang Y, Zeng L, Xu J, Yu H, Shi Z, Pan J, Zhang D, Kang S, Zhu L, Dong G, Guo L, Zeng D, Zhang G, Xie L, Xiong G, Li J, Qian Q. 2015. A rare allele of *GS2* enhances grain size and grain yield in rice. *Molecular Plant*, **8**, 1455–1465.

Jansen M, Gilmer F, Biskup B, Nagel K A, Rascher U, Fischbach A, Briem S, Dreissen G, Tittmann S, Braun S, Jaeger I D, Metzlaff M, Schurr U, Scharr H, Walter A. 2009. Simultaneous phenotyping of leaf growth and chlorophyll fluorescence *via* GROWSCREEN FLUORO allows detection of stress tolerance in *Arabidopsis thaliana* and other rosette plants. *Functional Plant Biology*, **36**, 902–914.

Jia J, Li H, Zhang X, Li Z, Qiu L. 2017. Genomics-based plant germplasm research (GPGR). *The Crop Journal*, **5**, 166–174.

Jia Y, Jannink J L. 2012. Multiple-trait genomic selection methods increase genetic value prediction accuracy. *Genetics*, **192**,1513–1522.

Jiang Y, Schulthess A W, Rodemann B, Ling J, Plieske J, Kollers S, Ebmeyer E, Korzun V, Argillier O, Stiewe G, Ganal M W, Röder M S, Reif J C. 2017. Validating the prediction accuracies of marker-assisted and genomic selection of Fusarium head blight resistance in wheat using an independent sample. *Theoretical and Applied Genetics*, **130**, 471–482.

Jiao Y, Zhao H, Ren L, Song W, Zeng B, Guo J, Wang B, Liu Z, Chen J, Li W, Zhang M, Xie S, Lai J. 2012. Genome-wide genetic changes during modern breeding of maize. *Nature Genetics*, **44**, 812–815.

Johal G S, Briggs S P. 1992. Reductase activity encoded by the *HM1* disease resistance gene in maize. *Science*, **258**, 985–987.

Kelliher T, Starr D, Richbourg L, Chintamanani S, Delzer B, Nuccio M L, Green J, Chen Z, McCuiston J, Wang W, Liebler T, Bullock P, Martin B. 2017. MATRILINEAL, a sperm-specific phospholipase, triggers maize haploid induction. *Nature*, **542**, 105–109.

Kobayashi F, Tanaka T, Kanamori H, Wu J Z, Katayose Y, Handa H. 2016. Characterization of a mini core collection of Japanese wheat varieties using single-nucleotide polymorphisms generated by genotyping-by-sequencing. *Breeding Science*, **66**, 213–225.

Konlasuk S, Xing Y, Zhang N, Zuo W, Zhang B, Tan G, Xu M. 2015. *ZmWAK*, a quantitative resistance gene to head smut in maize, improves yield performance by reducing the endophytic pathogen *Sporisorium reiliana*. *Molecular Breeding*, **35**, 1–10.

Kump K L, Bradbury P J, Wisser R J, Buckler E S, Belcher A R, Oropeza-Rosas M A, Zwonitzer J C, Kresovich S, McMullen M D, Ware D, Balint-Kurti P J, Holland J B. 2011. Genome-wide association study of quantitative resistance to southern leaf blight in the maize nested association mapping population. *Nature Genetics*, **43**, 163–168.

Lai J, Li R, Xu X, Jin W, Xu M, Zhao H, Xiang Z, Song W, Ying K, Zhang M, Jiao Y, Ni P, Zhang J, Li D, Guo X, Ye K, Jian M, Wang B, Zheng H, Liang H, *et al*. 2010. Genome-wide patterns of genetic variation among elite maize inbred lines. *Nature Genetics*, **42**, 1027–1030.

Lee M. 1995. DNA markers and plant breeding programs. *Advances in Agronomy*, **55**, 265–344.

De Leeuw M, Martinant J P, Duborjal H, Laffaire J B, Beugnot R. 2009. High throughput SNP discovery in wheat using methylation-sensitive digestion and next-generation sequencing. In: INRA (Institut National de la Recherche Agronomique), ed., *19th International Triticeae Mapping Initiative Meeting*. Clermont-Ferrand, France.

Li H, Peng Z, Yang X, Wang W, Fu J, Wang J, Han Y, Chai

Y, Guo T, Yang N, Liu J, Warburton M L, Cheng Y, Hao X, Zhang P, Zhao J, Liu Y, Wang G, Li J, Yan J. 2013. Genome-wide association study dissects the genetic architecture of oil biosynthesis in maize kernels. *Nature Genetics*, **45**, 43–50.

Li J Y, Wang J, Zeigler R S. 2014. The 3,000 rice genomes project: Nw opportunities and challenges for future rice research. *Giga Science*, **3**, 7.

Li K, Bao J, Corke H, Sun M. 2017. Association analysis of markers derived from starch biosynthesis related genes with starch physicochemical properties in the USDA rice mini-core collection. *Frontiers in Plant Science*, **8**, 424.

Li W, Zhu Z, Chern M, Yin J, Yang C, Ran L, Cheng M, He M, Wang K, Wang J, Zhou X, Zhu X, Chen Z, Wang J, Zhao W, Ma B, Qin P, Chen W, Wang Y, Liu J, *et al*. 2017. A natural allele of a transcription factor in rice confers broad-spectrum blast resistance. *Cell*, **170**, 114–126.

Li Y, Fan C, Xing Y, Jiang Y, Luo L, Sun L, Shao D, Xu C, Li X, Xiao J, He Y, Zhang Q. 2011. Natural variation in *GS5* plays an important role in regulating grain size and yield in rice. *Nature Genetics*, **43**, 1266–1269.

Li Y, Fan C, Xing Y, Yun P, Luo L, Yan B, Peng B, Xie W, Wang G, Li X, Xiao J, Xu C, He Y. 2014. *Chalk5* encodes a vacuolar H^+-translocating pyrophosphatase influencing grain chalkiness in rice. *Nature Genetics*, **46**, 398–404.

Liu M, Lei L, Miao F, Powers C, Zhang X, Deng J, Tadege M, Carver B F, Yan L. 2017. The *STENOFOLIA* gene from Medicago alters leaf width, flowering time and chlorophyll content in transgenic wheat. *Plant Biotechnology Journal*, doi: 10.1111/pbi.12759

Liu Q, Yang T, Yu T, Zhang S, Mao X, Zhao J, Wang X, Dong J, Liu B. 2017. Integrating small RNA sequencing with QTL mapping for identification of mirnas and their target genes associated with heat tolerance at the flowering stage in rice. *Frontiers in Plant Science*, **8**, 43.

Long Y M, Chao W S, Ma G J, Xu S S, Qi L L. 2017. An innovative SNP genotyping method adapting to multiple platforms and throughputs. *Theoretical and Applied Genetics*, **130**, 597–607.

de Los Campos G, Naya H, Gianola D, Crossa J, Legarra A, Manfredi E, Weigel K, Cotes J M. 2009. Predicting quantitative traits with regression models for dense molecular markers and pedigree. *Genetics*, **182**, 375–385.

Lu Y, Hao Z, Xie C, Crossa J, Arausa J L, Gao S, Vivek B S, Magorokosho C, Mugo S, Makumbi D, Taba S, Pan G, Li X, Rong T, Zhang S, Xu Y. 2011. Large-scale screening for maize drought resistance using multiple selection criteria evaluated under water-stressed and well-watered environments. *Field Crops Research*, **124**, 37–45.

Ma Y, Dai X, Xu Y, Luo W, Zheng X, Zeng D, Pan Y, Lin X, Liu H, Zhang D, Xiao J, Guo X, Xu S, Niu Y, Jin J, Zhang H, Xu X, Li L, Wang W, Qian Q, *et al*. 2015. *COLD1* confers chilling tolerance in rice. *Cell*, **160**, 1209–1221.

Mago R, Zhang P, Vautrin S, Šimková H, Bansal U, Luo M C, Rouse M, Karaoglu H, Periyannan S, Kolmer J, Jin Y, Ayliffe M A, Bariana H, Park R F, McIntosh R, Doležel J, Bergès H, Spielmeyer W, Lagudah E S, Ellis J G, *et al*. 2015. The wheat *Sr50* gene reveals rich diversity at a cereal disease resistance locus. *Nature Plants*, **1**, 15186.

Mammadov J, Aggarwal R, Buyyarapu R, Kumpatla S. 2012. SNP markers and their impact on plant breeding. *International Journal of Plant Genomics*, **2012**, 728398.

Massonnet C, Vile D, Fabre J, Hannah M A, Caldana C, Lisec J, Beemster G T, Meyer R C, Messerli G, Gronlund J T, Perkovic J, Wigmore E, May S, Bevan M W, Meyer C, Rubio-Díaz S, Weigel D, Micol J L, Buchanan-Wollaston V, Fiorani F, *et al*. 2010. Probing the reproducibility of leaf growth and molecular phenotypes: A comparison of three *Arabidopsis* accessions cultivated in ten laboratories. *Plant Physiology*, **152**, 2142–2157.

Meng X, Muszynski M G, Danilevskaya O N. 2011. The FT-like *ZCN8* gene functions as a floral activator and is involved in photoperiod sensitivity in maize. *The Plant Cell*, **23**, 942–960.

Meuwissen T H E, Hayes B J, Goddard M E. 2001. Prediction of total genetic value using genome-wide dense marker maps. *Genetics*, **157**, 1819–1829.

Miller T A, Muslin E H, Dorweiler J E. 2008. A maize CONSTANS-like gene, *conz1*, exhibits distinct diurnal expression patterns in varied photoperiods. *Planta*, **227**, 1377–1388.

Montes J M, Technow F, Dhillon B S, Mauch F, Melchinger A E. 2011. High-throughput non-destructive biomass determination during early plant development in maize under field conditions. *Field Crops Research*, **121**, 268–273.

Muraya M M, Chu J, Zhao Y, Junker A, Klukas C, Reif J C, Altmann T. 2016. Genetic variation of growth dynamics in maize (*Zea mays* L.) revealed through automated non-invasive phenotyping. *The Plant Journal*, **89**, 366–380.

Muszynski M G, Dam T, Li B, Shirbroun D M, Hou Z, Bruggemann E, Archibald R, Ananiev E V, Danilevskaya O N. 2006. *Delayed flowering1* encodes a basic leucine zipper protein that mediates floral inductive signals at the shoot apex in maize. *Plant Physiology*, **142**, 1523–1536.

Onogi A, Watanabe M, Mochizuki T, Hayashi T, Nakagawa H, Hasegawa T, Iwata H. 2016. Toward integration of genomic selection with crop modelling: The development of an integrated approach to predicting rice heading dates. *Theoretical and Applied Genetics*, **129**, 805–817.

Pan A, Hayes P M, Chen F, Chen T, Blake T, Wright S, Karsai I, Bedo Z. 1994. Genetic analysis of the components of winter hardiness in barley (*Hordeum vulgare* L.). *Theoretical and Applied Genetics*, **89**, 900–910.

Patil G, Do T, Vuong T D, Valliyodan B, Lee J D, Chaudhary J, Shannon J G, Nguyen H T. 2016. Genomic-assisted haplotype analysis and the development of high-throughput SNP markers for salinity tolerance in soybean. *Scientific Reports*, **6**, 19199.

Qin L, Hao C, Hou J, Wang Y, Li T, Wang L, Ma Z, Zhang X. 2014. Homologous haplotypes, expression, genetic effects and geographic distribution of the wheat yield gene *TaGW2*. *BMC Plant Biology*, **14**, 107.

Qu S, Liu G, Zhou B, Bellizzi M, Zeng L, Dai L, Han B, Wang G L. 2006. The broad-spectrum blast resistance gene

Pi9 encodes a nucleotide-binding site-leucine-rich repeat protein and is a member of a multigene family in rice. *Genetics*, **172**, 1901–1914.

Rasheed A, Hao Y, Xia X, Khan A, Xu Y, Varshney R K, and He Z. 2017. Crop breeding chips and genotyping platforms: Progress, challenges and perspectives. *Molecular Plant*, **10**, 1047–1064.

Reynolds M, Langridge P. 2016. Physiological breeding. *Current Opinion in Plant Biology*, **31**, 162–171.

Rodríguez-Leal D, Lemmon Z H, Man J, Bartlett M, Lippman Z. 2017. Engineering quantitative trait variation for crop improvement by genome editing. *Cell*, **171**, 470–480.

Saint Pierre C, Burgueño J, Crossa J, Fuentes Dávila G, Figueroa López P, Solís Moya E, Ireta Moreno J, Hernández Muela V M, Zamora Villa V M, Vikram P, Mathews K, Sansaloni C, Sehgal D, Jarquin D, Wenzl P, Singh S. 2016. Genomic prediction models for grain yield of spring bread wheat in diverse agro-ecological zones. *Scientific Reports*, **6**, 27312.

Salvi S, Sponza G, Morgante M, Tomes D, Niu X, Fengler K A, Meeley R, Ananiev E V, Svitashev S, Bruggemann E, Li B, Hainey C F, Radovic S, Zaina G, Rafalski J A, Tingey S V, Miao G H, Phillips R L, Tuberosa R. 2007. Conserved noncoding genomic sequences associated with a flowering-time quantitative trait locus in maize. *Proceedings of the National Academy of Sciences of the United States of America*, **104**, 11376–11381.

Schläppi M R, Jackson A K, Eizenga G C, Wang A, Chu C, Shi Y, Shimoyama N, Boykin D L. 2017. Assessment of five chilling tolerance traits and gwas mapping in rice using the USDA mini-core collection. *Frontiers in Plant Science*, **8**, 957.

Schmidt R J, Ketudat M, Aukerman M J, Hoschek G. 1992. Opaque-2 is a transcriptional activator that recognizes a specific target site in 22-kD zein genes. *The Plant Cell*, **4**, 689–700.

Semagn K, Babu R, Hearne S, Olsen M. 2014. Single nucleotide polymorphism genotyping using Kompetitive Allele Specific PCR (KASP): Overview of the technology and its application in crop improvement. *Molecular Breeding*, **33**, 1–14.

Shen H, Zhong X, Zhao F, Wang Y, Yan B, Li Q, Chen G, Mao B, Wang J, Li Y, Xiao G, He Y, Xiao H, Li J, He Z. 2015. Overexpression of receptor-like kinase ERECTA improves thermotolerance in rice and tomato. *Nature Biotechnology*, **33**, 996–1003.

Shirasu K, Lahaye T, Tan M W, Zhou F, Azevedo C, Schulze-Lefert P. 1999. A novel class of eukaryotic zinc-binding proteins is required for disease resistance signaling in barley and development in *C. elegans*. *Cell*, **99**, 355–366.

Shomura A, Izawa T, Ebana K, Ebitani T, Kanegae H, Konishi S, Yano M. 2008. Deletion in a gene associated with grain size increased yields during rice domestication. *Nature Genetics*, **40**, 1023–1028.

Song W Y, Wang G L, Chen L L, Kim H S, Pi L Y, Holsten T, Gardner J, Wang B, Zhai W X, Zhu L H, Fauquet C, Ronald P. 1995. A receptor kinase-like protein encoded by the rice disease resistance gene, *Xa21*. *Science*, **270**, 1804–1806.

Song X J, Huang W, Shi M, Zhu M Z, Lin H X. 2007. A QTL for rice grain width and weight encodes a previously unknown RING-type E3 ubiquitin ligase. *Nature Genetics*, **39**, 623–630.

Spindel J E, Begum H, Akdemir D, Collard B, Redoña E, Jannink J L, McCouch S. 2016. Genome-wide prediction models that incorporate *de novo* GWAS are a powerful new tool for tropical rice improvement. *Heredity*, **116**, 395–408.

Sundaram R M, Naveenkumar B, Biradar S K, Balachandran S M, Mishra B, IlyasAhmed M, Viraktamath B C, Ramesha M S, Sarma N P. 2008. Identification of informative SSR markers capable of distinguishing hybrid rice parental lines and their utilization in seed purity assessment. *Euphytica*, **163**, 215–224.

Takahagi K, Uehara-Yamaguchi Y, Yoshida T, Sakurai T, Shinozaki K, Mochida K, Saisho D. 2016. Analysis of single nucleotide polymorphisms based on RNA sequencing data of diverse bio-geographical accessions in barley. *Scientific Reports*, **6**, 33199.

Tian F, Bradbury P J, Brown P J, Hung H, Sun Q, Flint-Garcia S, Rocheford T R, McMullen M D, Holland J B, Buckler E S. 2011. Genome-wide association study of leaf architecture in the maize nested association mapping population. *Nature Genetics*, **43**, 159–162.

Trachsel S, Kaeppler S M, Brown K M, Lynch J P. 2011. Shovelomics: High throughput phenotyping of maize (*Zea mays* L.) root architecture in the field. *Plant and Soil*, **341**, 75–87.

Uauy C, Distelfeld A, Fahima T, Blechl A, Dubcovsky J. 2006. A *NAC* gene regulating senescence improves grain protein, zinc, and iron content in wheat. *Science*, **314**, 1298–1301.

Valliyodan B, Ye H, Song L, Murphy M, Shannon J G, Nguyen H T. 2016. Genetic diversity and genomic strategies for improving drought and waterlogging tolerance in soybeans. *Journal of Experimental Botany*, **68**, 1835–1849.

Van K, McHale L K. 2017. Meta-analyses of QTLs associated with protein and oil contents and compositions in soybean [*Glycine max* (L.) Merr.] seed. *International Journal of Molecular Sciences*, **18**, 1180.

Wang C, Ren H, Shen J, Zhao X, Cao S, Wang Z. 2016. Molecular evaluation of Guizhou local maize genetic diversity and construction of Core Collection. *Southwest China Journal of Agricultural Sciences*, **29**, 1018–1022. (in Chinese)

Wang D, Qin B, Li X, Tang D, Zhang Y, Cheng Z, Xue Y. 2016. Nucleolar DEAD-Box RNA helicase TOGR1 regulates thermotolerant growth as a pre-rRNA chaperone in rice. *PLoS Genetics*, **12**, e1005844.

Wang Q, Liu Y, He J, Zheng X, Hu J, Liu Y, Dai H, Zhang Y, Wang B, Wu W, Gao H, Zhang Y, Tao X, Deng H, Yuan D, Jiang L, Zhang X, Guo X, Cheng X, Wu C, *et al*. 2014. *STV11* encodes a sulphotransferase and confers durable resistance to rice stripe virus. *Nature Communications*, **5**, 4768.

Wang S, Wu K, Yuan Q, Liu X, Liu Z, Lin X, Zeng R, Zhu H, Dong G, Qian Q, Zhang G, Fu X. 2012. Control of grain size, shape and quality by *OsSPL16* in rice. *Nature Genetics*,

44, 950–954.

Wang X, Wang H, Liu S, Ferjani A, Li J, Yan J, Yang X, Qin F. 2016. Genetic variation in *ZmVPP1* contributes to drought tolerance in maize seedlings. *Nature Genetics*, **48**, 1233–1241.

Wang Y, Xiong G, Hu J, Jiang L, Yu H, Xu J, Fang Y, Zeng L, Xu E, Xu J, Ye W. 2015. Copy number variation at the *GL7* locus contributes to grain size diversity in rice. *Nature Genetics*, **47**, 944–948.

Wasson A P, Richards R A, Chatrath R, Misra S C, Prasad S V, Rebetzke G J, Kirkegaard J A, Christopher J, Watt M. 2012. Traits and selection strategies to improve root systems and water uptake in water-limited wheat crops. *Journal of Experimental Botany*, **63**, 3485–3498.

Williams J G K, Kubelik A R, Livak K J, Rafalski J A, Tingey S V. 1990. DNA polymorphisms amplified by arbitrary primers are useful as genetic markers. *Nucleic Acids Research*, **18**, 6531–6535.

Wu X, Li Y, Shi Y, Song Y, Zhang D, Li C, Buckler E S, Li Y, Zhang Z, Wang T. 2016. Joint-linkage mapping and GWAS reveal extensive genetic loci that regulate male inflorescence size in maize. *Plant Biotechnology Journal*, **14**, 1551–1562.

Xu D, Duan X, Wang B, Hong B, Ho T H D, Wu R. 1996. Expression of a late embryogenesis abundant protein gene, HVA1, from barley confers tolerance to water deficit and salt stress in transgenic rice. *Plant Physiology*, **110**, 249–257.

Xu Y, Crouch J H. 2008. Marker-assisted selection in plant breeding: From publications to practice. *Crop Science*, **48**, 391–407.

Xu Y, Lu Y, Xie C, Gao S, Wan J, Prasanna B M. 2012. Whole-genome strategies for marker-assisted plant breeding. *Molecular Breeding*, **29**, 833–854.

Yan J, Warburton M, Crouch J. 2011. Association mapping for enhancing maize (*Zea mays* L.) genetic improvement. *Crop Science*, **51**, 433–449.

Yang H, Jian J, Li X, Renshaw D, Clements J, Sweetingham M W, Li C. 2015. Application of whole genome re-sequencing data in the development of diagnostic DNA markers tightly linked to a disease-resistance locus for marker-assisted selection in lupin (*Lupinus angustifolius*). *BMC Genomics*, **16**, 1.

Yang Q, He Y, Kabahuma M, Chaya T, Kelly A, Borrego E, Bian Y, El Kasmi F, Yang L, Teixeira P, Kolkman J, Nelson R, Kolomiets M, L Dangl J, Wisser R, Caplan J, Li X, Lauter N, Balint-Kurti P. 2017. A gene encoding maize caffeoyl-CoA O-methyltransferase confers quantitative resistance to multiple pathogens. *Nature Genetics*, **49**, 1364–1372.

Yang Q, Li Z, Li W, Ku L, Wang C, Ye J, Li K, Yang N, Li Y, Zhong T, Li J, Chen Y, Yan J, Yang X, Xu M. 2013. CACTA-like transposable element in *ZmCCT* attenuated photoperiod sensitivity and accelerated the postdomestication spread of maize. *Proceedings of the National Academy of Sciences of the United States of America*, **110**, 16969–16974.

Zamir D. 2001. OPINION: Improving plant breeding with exotic genetic libraries. *Nature Reviews Genetics*, **2**, 983.

Zhang D, Wu S, An X, Xie K, Zhou Y, Xu L, Fang W, Liu S, Liu S, Zhu T, Li J, Rao L, Zhao J, Wan X. 2017. Construction of a multi-control sterility system for a maize male-sterile line and hybrid seed production based on the *ZmMs7* gene encoding a PHD-finger transcription factor. *Plant Biotechnology Journal*, doi: 10.1111/pbi.12786

Zhang X, Huang C, Wu D, Qiao F, Li W, Duan L, Wang K, Xiao Y, Chen G, Liu Q, Xiong L, Yang W, Yan J. 2017. High-throughput phenotyping and QTL mapping reveals the genetic architecture of maize plant growth. *Plant Physiology*, **173**, 1554–1564.

Zhang Y, Liang Z, Zong Y, Wang Y, Liu J, Chen K, Qiu J L, Gao CX. 2016. Efficient and transgene-free genome editing in wheat through transient expression of CRISPR/Cas9 DNA or RNA. *Nature Communications*, **7**, 12617.

Zhao B, Lin X, Poland J, Trick H, Leach J, Hulbert S. 2005. A maize resistance gene functions against bacterial streak disease in rice. *Proceedings of the National Academy of Sciences of the United States of America*, **102**, 15383–15388.

Zhao X, Tan G, Xing Y, Wei L, Chao Q, Zuo W, Lübberstedt T, Xu M. 2012. Marker-assisted introgression of *qHSR1* to improve maize resistance to head smut. *Molecular Breeding*, **30**, 1077–1088.

Zhao Y, Gowda M, Liu W, Würschum T, Maurer H P, Longin F H, Ranc N, Reif J C. 2012. Accuracy of genomic selection in European maize elite breeding populations. *Theoretical and Applied Genetics*, **124**, 769–776.

Zhou B, Qu S, Liu G, Dolan M, Sakai H, Lu G, Bellizzi M, Wang G L. 2006. The eight amino-acid differences within three leucine-rich repeats between *Pi2* and *Piz-t* resistance proteins determine the resistance specificity to Magnaporthe grisea. *Molecular Plant-Microbe Interactions*, **19**, 1216–1228.

Zhou Z, Jiang Y, Wang Z, Gou Z, Lyu J, Li W, Yu Y, Shu L, Zhao Y, Ma Y, Fang C, Shen Y, Liu T, Li C, Li Q, Wu M, Wang M, Wu Y, Dong Y, Wan W, *et al*. 2015. Resequencing 302 wild and cultivated accessions identifies genes related to domestication and improvement in soybean. *Nature Biotechnology*, **33**, 408–414.

Zuo W, Chao Q, Zhang N, Ye J, Tan G, Li B, Xing Y, Zhang B, Liu H, Fengler K A, Zhao J, Zhao X, Chen Y, Lai J, Yan J, Xu M. 2015. A maize wall-associated kinase confers quantitative resistance to head smut. *Nature Genetics*, **47**, 151–157.

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