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Crop Gene Chip and Its Applications

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Abstract Gene chip integrates multiple oligonucleotide sequences (probes) onto a solid-phase carrier or in a solution. Through the hybridization of probes with sample DNA and subsequent signal detection or sequence analysis, gene expression levels or genotypes can be detected. Single nucleotide polymorphisms (SNPs) are widely distributed across the genome and easily detectable, making them commonly used molecular markers for genotype detection and the development of gene chips. The development of SNP-based gene chips has gone through two stages: solid-phase and liquid-phase. Particularly since the application of high-throughput genome sequencing technology, a large number of SNPs have been identified in various crops, leading to the development of different SNP chips. These chips are widely used in variety identification, kinship analysis, genome-wide association analysis, genomic selection analysis, and other areas to assist breeding. This review introduces the detection principles related to gene chips, summarizes the SNP chips developed for different crops, and outlines the current application status of SNP chips, their existing defects and limitations, as well as future development trends. The aim is to provide a solid theoretical foundation for the optimization and innovation of gene chips in the future, promoting the continuous progress and refinement of related technologies.

Keywords Crop; Gene chip; Genotyping; Single nucleotide polymorphism

1 Introduction

Crop improvement is increasingly relying on the molecular biology analysis. Over the past two to three decades, reference genomes of various crops have been successively sequenced (Kawahara et al., 2013; IWGSC et al., 2018). Notably, the cost of high-throughput sequencing has exhibited an exponential decrease (Xu et al., 2020). Gene editing systems continue to improve (Pacesa et al., 2024), alongside the growing integration of artificial intelligence and multi-omics (Li et al., 2025b). In this context, crop improvement strategies have progressed to the precise manipulation of single genes, single regulatory elements, and even individual nucleotides. With the evolving needs in breeding, numerous deep-seated challenges remain to be overcome. These include the underutilization of existing genetic resources (Wang et al., 2020; Mark et al., 2022), the ineffective mining and utilization of functional genes (Jia et al., 2023). Moreover, the complex correspondence between genotype and phenotype prevents effective improvement of traits controlled by multiple functional genes (Wang et al., 2025).

After Sanger sequencing, gene chip emerged as a revolutionary tool in bioscience. It enables efficient genotyping and presents a solution to the aforementioned challenges. Gene chip has two developmental stages: solid-phase and liquid-phase. Solid-phase gene chip consist of thousands of individual DNA sequences arrayed at a high density on a single matrix, usually glass slides or quartz wafers, but sometimes on nylon substrates. Probes with known identity are used to determine complementary binding, thus allowing the analysis of gene expression, DNA sequence variation or protein levels in a parallel format (Zimdahl et al., 2005). With technological advances, the liquid-phase gene chip, also known as “Genotyping by Target Sequencing” (GBTS), has been successfully developed. This innovation overcomes limitations of traditional solid-phase gene chip, such as low flexibility, difficulty of updating. The liquid-phase gene chip not only efficiently captures target genomic regions by specific probes in solution environment, but also utilizes high-throughput sequencing to obtain genotype. As a result, this technology integrates the targeting ability and cost-effectiveness of chip-based methods with the high accuracy and rich information output of sequencing technologies.

Recent advances in association analysis enable the integration of genotyping data from gene chip with crop phenotypes. This integration marks a key shift from conventional to molecular assisted breeding, supporting the sustainable genetic improvement of crop varieties. However, current gene chip still face several limitations: (1) Restricted system-they can only detect known variants based on pre-designed probes, making it difficult to capture novel mutations or large-scale structural variants; (2) High customization thresholds and platform dependency-solid-phase gene chip entails high development costs. Liquid-phase gene chip, while offering greater flexibility, requires continuous optimization of probe pools, posing challenges for small and medium-sized breeding institutions; (3) Insufficient data standardization-batch effects (Luo et al., 2010) across different chips often hinder cross-project data integration. These effects can arise from factors such as different chips type/lot/platform or variations in sample preparation protocols. This study systematically reviews the fundamental principles, types, applications, and future prospects of crop gene chip. We aim to provide valuable insights for crop variety improvement and the refinement of gene chip.

2 Classification and Principles of Gene Chip

Gene chips are categorized into two types according to their reaction environment: Solid-phase and liquid-phase (Li et al., 2024). Since advent, chips have been developed using SNPs as markers. Hence they are also referred to SNP arrays. The solid-phase gene chip emerged in the late 1980s to early 1990s. A key commercial milestone was the GeneChip® microarrays based on photolithographic synthesis, developed by company Affymetrix in the early 1990s. And in 1994, it produced the first commercial solid-phase gene chip for HIV genotyping (John et al., 2000; Cook et al., 2002). Subsequently, Illumina introduced its GoldenGate and Infinium assays based on its BeadArray/BeadChip technology, thereby becoming a popular provider of cost-effective genomic platforms. Meanwhile, Beckman Coulter focused on developing chips with lower SNP throughput but ultra-high sample capacity, carving out a unique market niche with its SNPstream platform (Gupta et al., 2008). With the maturation of solid-phase gene chip applications in the medical field, Akhunov et al. (2009) employed the Illumina GoldenGate assay to genotype 96 SNP loci across 53 homozygous tetraploid and 38 homozygous hexaploid wheat lines. They obtained high-quality genotyping data and thereby marking the beginning of solid-phase gene chip application in crops.

Today, both Affymetrix and Illumina have established mature solid-phase gene chip platforms, offering distinct array fabrication assay and software analysis packages for genotyping. Despite these differences, their hybridization and signal detection principles remain similar: Following nucleic acid extraction, the target is amplified and labeled with biotin. After hybridization, the array undergoes automated washing and staining with a fluorescent streptavidin-phycoerythrin conjugate (SAPE) that binds to the biotin, enabling the detection of hybridized targets by scanning the array for fluorescence intensity (Dalma-Weiszhausz et al., 2006). Crop ploidy significantly influences the effect of solid-phase gene chips application. In diploid crops, each SNP loci typically generates three fluorescence signal types-two homozygous (AA and BB) and one heterozygous (AB)-each clustering distinctly to enable accurate genotyping. However, in auto- or allopolyploid species, each SNP loci may produce more than three signal types, substantially complicating the analysis of genotyping results. You et al. (2018) systematically reviewed the limitations of solid-phase gene chips in polyploid crops by comparing the principles of various platforms and analytical software, offering valuable strategies for genotyping polyploid species. As solid-phase gene chips are custom-designed for specific known SNPs with fixed marker loci, they lack flexibility for study-specific adjustments. Coupled with their high cost, these limitations restrict their widespread adoption in breeding programs (Guo et al., 2019).

The liquid-phase gene chip was developed based on high-throughput genome sequencing technology. It is also known as Genotyping-by-Target-Sequence (GBTS). Unlike whole-genome sequencing, this approach first captures targeted genomic regions before sequencing them. Two primary methods are used for targets capture: The first is solution-phase probes hybridization, where custom-designed probes hybridize with target DNA fragments in a liquid environment through base complementarity, thereby enriching the target regions. Subsequent steps include sequencing library construction and sequencing. Representative products employing this method include NimbleGen, SureSelect, and GenoBaits (Guo et al., 2019). The second method relies on multiplex PCR, which

uses biotin-labeled specific primers to amplify target genomic regions. The amplified fragments are then captured via biotin binding, eluted, and sequenced. Notable examples of this approach include AmpliSeq and GenoPlexs. The GBTS technology enables the capture of multiple SNPs (mSNPs) within a single amplicon. This mSNPs strategy allows simultaneous acquisition of multiple SNPs information in a single sequencing run, thereby yielding richer data that facilitates haplotype analysis. Xu et al. (2020) reviewed the principles and applications of two GBTS technologies-GenoBaits (Figure 1) and GenoPlexs-outlined (Figure 2) the workflow of the mSNPs strategy, provided a comparative analysis with genotyping by sequencing technology, and offered valuable references for the broader adoption of GBTS.

It is noteworthy that SNP data acquisition is a prerequisite for gene chip development. In the development of the rice C6AIR array (Thomson et al., 2017) and soybean NJAU 355K SoySNP array (Wang et al., 2016), selected varieties were resequenced to obtain SNP information. The Rice3K56 SNP array (Zhang et al., 2023) and Wheat Breeders' Array (Allen et al., 2017) screened candidate SNPs based on previous studies according to research objectives. The rice 580K_KNU chip (Kim et al., 2022) integrated existing SNP databases and filtered key SNP loci for development.

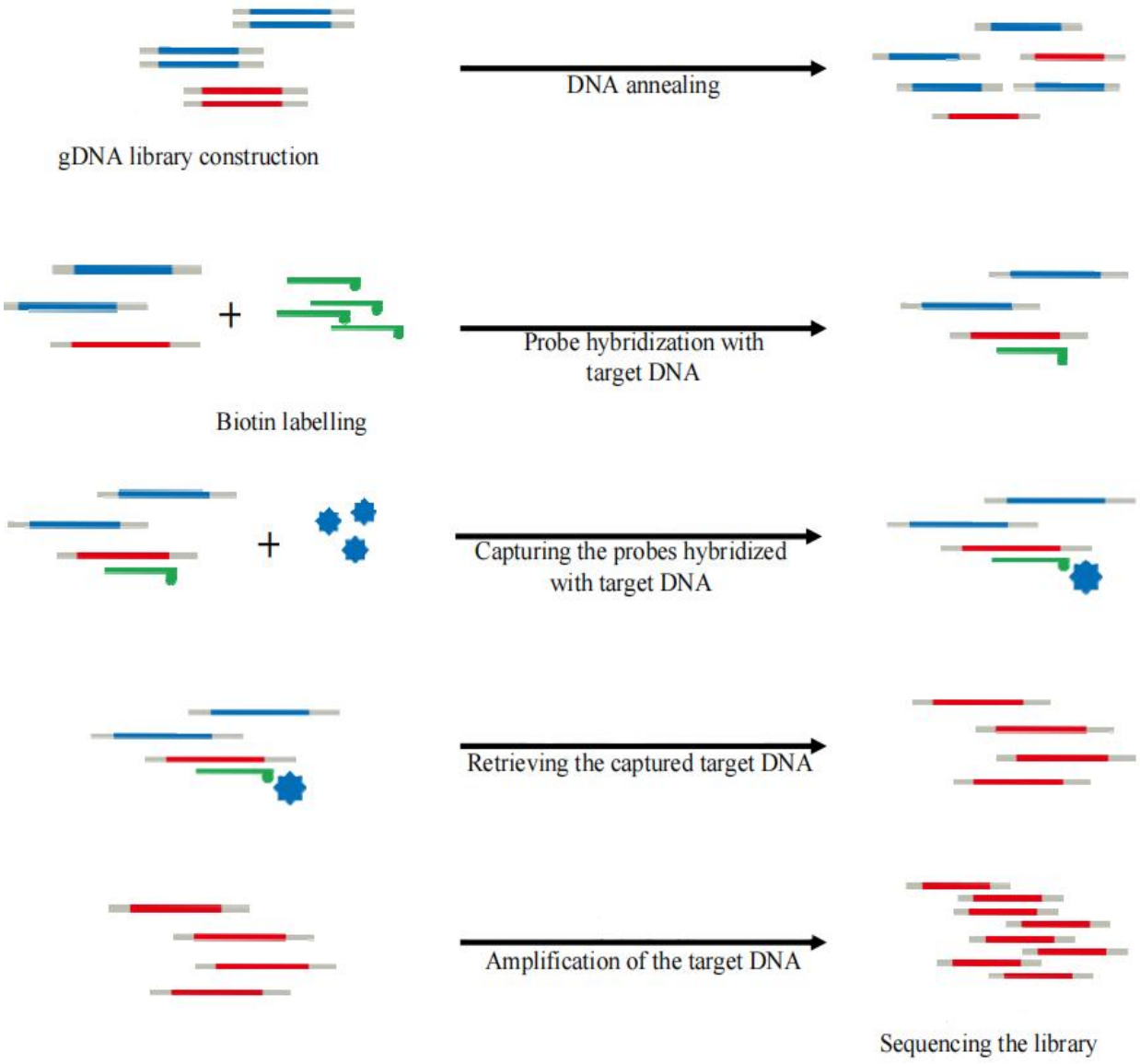

Figure 1 Flowchart for genotyping by target sequencing with GenoBaits (Adopted from Xu et al., 2020)

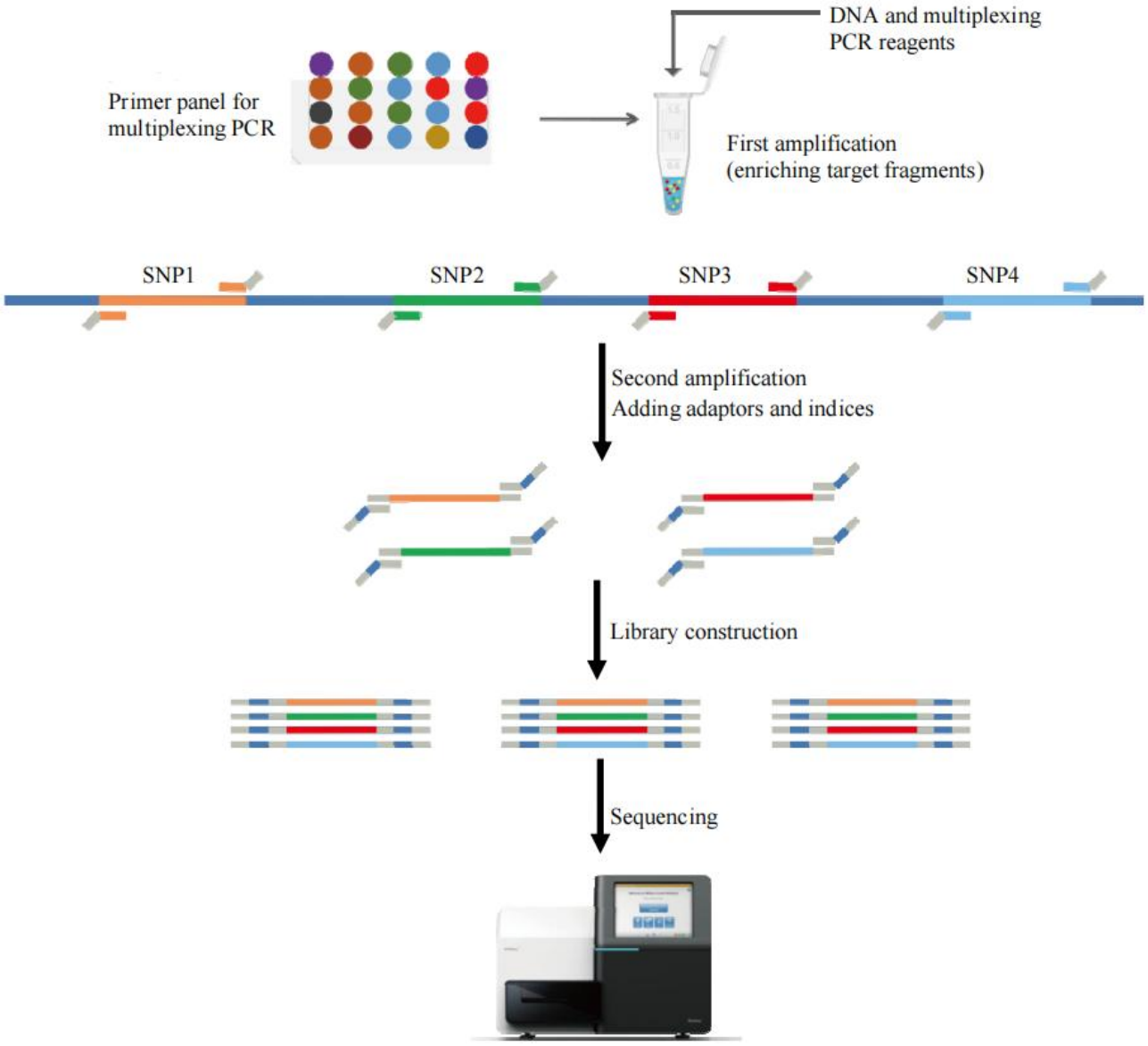

Figure 2 Flowchart for genotyping by target sequencing with GenoPlexs (Adopted from Xu et al., 2020)

3 Applications of Gene Chips

3.1 Genetic research

Cultivar identification is the process of analyzing the genotypic or phenotypic characteristics of plant varieties to confirm their genetic background, and varietal purity. It is also an important aspect of crop breeding, germplasm management, and intellectual property protection (Korir et al., 2012; Samarina et al., 2025). Misidentification of crop varieties is relatively common: crops with the same genotype may be assigned different names, while those with different genotypes may be incorrectly classified as the same variety. This situation seriously infringes upon the rights of breeders. To avoid this problem, scientific identification of crop varieties is particularly important. Gene chips have thus become a key tool in addressing this issue. Liu et al. (2025a) developed the TEA5K mSNP array based on GBTS, stably identifying 5 781 (5K) mSNP markers and 36 357 (36 K) SNP markers in a diverse set of tea germplasm. Among the 36K markers, 5K markers (core SNP) exhibited higher polymorphism, with high PIC and GD values. The study calculated genetic similarity for all possible variety combinations (different individuals of the same variety, homologous but artificially mutagenized varieties, and bud mutant varieties) using three marker sets (5K core SNP, 36K SNP, and 5K mSNP). Theoretically, the genetic similarity between different individuals of the same variety should be 100%. Through comparison, it was found that the 5K core SNP panel

was most suitable for cultivar identification, and a genetic similarity value of at least 90% was established as the criterion for consistency in tea. This study provides a clear and operable industry standard for tea cultivar identification. DNA fingerprint is an extended application of cultivar identification. It involves analyzing specific DNA sequences or polymorphic sites in the plant genome to generate unique genetic characteristics that serve as a "genetic ID" for the variety. Li et al. (2025a) collected SNPs from 377 cassava samples. After screening and optimization, they selected 35 369 SNP loci to design the Cassava 35K chip based on GenoBaits technology. Among these, 203 loci with the highest polymorphism (i.e., showing the greatest variation among different varieties) were selected to construct cassava DNA fingerprint. This dataset can clearly distinguish representative cassava germplasms, providing a powerful tool for cassava variety identification and varietal rights protection.

Genetic relatedness analysis involves comparing genotypes across multiple germplasms to assess the similarity of their genetic backgrounds, thereby inferring the degree of kinship between samples. This analysis reveals the population structure and genetic diversity of crops, assisting breeders in germplasm selection. Gene chips can capture SNP information from numerous samples and loci, facilitating genetic relationship analysis (Anglin et al., 2024; Liu et al., 2024). Leber et al. (2024) used the TaBW 35K SNP array to genotype 755 bread wheat germplasm resources from different regions, conducting principal component analysis (PCA), hierarchical clustering analysis, and admixture kinship analysis to rapidly assess the genetic background of breeding materials and guide cross-breeding combinations. They found that the genetic diversity of these germplasm resources was higher than that of 632 previously studied landraces and 17 high-quality sequenced wheat germplasms, with the additional genetic diversity mainly originating from landraces in Turkey, Iran, and Pakistan. Guo et al. (2019) developed a GBTS platform in maize.

Specifically, a 20 K SNP panel, with markers evenly distributed across maize genome, was developed from a 55 K SNP array (Xu et al., 2017) with improved genome coverage. From this single marker panel, 20 K, 10 K, 5 K, and 1 K SNP markers can be generated by sequencing the samples at the average sequencing depths of 50×, 20×, 7.5×, and 2.5×, respectively. All panels clearly delineated the eight major maize heterotic groups in a phylogenetic tree of 96 lines. The average nucleotide differences between groups aligned with established heterotic patterns, validating the platform's utility for genetic relationship analysis. They also confirmed that selecting the most cost-effective 1K panel could reduce genotyping costs. This research served as a foundation for the development of an mSNP strategy. Later, Guo et al. (2021) developed and validated the mSNP strategy, successfully creating three different types of markers (40K mSNPs, 251K SNPs, and 690K haplotypes) based on a 40K maize mSNP panel. By adjusting sequencing depth, they generated multiple marker panels ranging from 1K to 40K in density, successfully classifying 867 maize inbred lines into the known eight heterotic groups and identifying a new sweet corn population. This strategy meets the demand for obtaining rich, multidimensional genetic information at low cost.

3.2 Crop breeding

Marker-assisted selection (MAS) is a technique that utilizes molecular markers (e.g., DNA sequences, proteins) to identify functional genes associated with desirable crop traits. Its principle relies on the genetic linkage between a target gene and its neighbouring molecular markers, enabling gene localization through marker detection (Asif et al., 2024). The widespread application of MAS helps shorten the breeding cycle. For instance, at early developmental stages (such as the seedling or even seed stage), materials carrying target beneficial genes (e.g., dwarfing genes, optimal disease resistance gene combinations) can be screened via gene chip. Xiang et al. (2023) developed a 0.1K liquid-phase gene chip based on 101 functional or closely linked wheat markers. They used it to genotype 174 wheat germplasm resources and, through genotype-phenotype association analysis, confirmed that the chip could accurately select for dwarfing genes and stripe rust resistance genes. This facilitates the avoidance of inbreeding, management of germplasm with unclear origins, and tracing of breeding lineages.

Beyond genotyping, many studies utilized gene chips to map quantitative trait loci (QTL) associated with important agronomic traits. Xu et al. (2023) genotyped the wheat varieties JS16 and BN64, along with a population of 171 recombinant inbred lines (RILs) derived from their cross, using a 15K SNP chip. Further genotyping of

JS16 and BN64 with a 660K SNP chip, combined with field resistance data and composite interval mapping (CIM), led to the identification of four QTLs related to powdery mildew resistance. These QTLs exhibited additive effects, specific resistance, and no linkage to other traits, effectively utilizing the important cultivar BN64 to uncover novel QTLs. Zhou et al. (2022) genotyped an RIL population from a cross between wheat cultivars Pindong 34 and Mingxian 169 using a 90K SNP chip. By integrating phenotypic data and CIM analysis, they mapped 15 QTLs associated with stripe rust resistance. This work provided the first comprehensive dissection of the genetic basis of resistance in the excellent source 'Pindong 34', revealing that its resistance is controlled by multiple QTLs and thereby enriching the gene resource pool for MAS. Gene chip technology is also widely used for mining QTLs governing other crucial agronomic traits, such as wheat culm morphology (tiller number (Ren et al., 2018), flag leaf morphology (Cheng et al., 2023)), yield (Shi et al., 2017; Cao et al., 2019; Liu et al., 2023) and starch content (Fu et al., 2019), barley disease resistance (Choudhury et al., 2019), cotton fiber quality (Ramesh et al., 2019), and sugarcane tiller number (Fang et al., 2025).

Gene chips not only facilitate QTL discovery but are also integrated with genome-wide association studies (GWAS). By associating genotype with phenotype data, GWAS serves as a powerful tool for mapping qualitative trait genes, achieving significant success in crops like rice, wheat, and cotton. Zhang et al. (2023) developed a high-quality custom chip Rice3K56 using resequencing data from 3 024 rice accessions worldwide. By testing extensively in 192 representative rice samples, this chip contains 56,606 SNP markers with a high genotyping reliability of 99.6%. Based on genotype and phenotype data from 84 rice accessions, GWAS identified 108 loci controlling 13 agronomic traits. While the functions of some loci have been reported, the genetic mechanisms underlying many novel loci remain to be explored. In association analysis, factors like population structure and kinship among samples can lead to false positives, where non-functional loci are identified as significantly associated (Vos et al., 2022).

In wheat research, Tian et al. (2025) genotyped 341 wheat accessions using a 40K SNP chip and conducted GWAS combined with phenotype data to identify functional genes controlling protein quality traits. PCA divided the 341 accessions into two distinct subpopulations, indicating significant population structure. Consequently, the study employed a linear mixed model to reduce false positives. Sun et al. (2018) genotyped 713 upland cotton accessions at the seedling stage using the CottonSNP63K chip and performed GWAS combined with their salt tolerance phenotypes to dissect the genetic basis of cotton salt tolerance. The analysis identified 280 potential candidate genes. Subsequent validation confirmed differential expression of six candidate genes between salt-tolerant and salt-sensitive cotton varieties, further supporting their important roles in cotton salt tolerance.

Currently, researchers using GWAS have successfully identified functional loci related to crop physiology and environmental adaptability, including key agronomic traits such as plant height, flowering time, stress tolerance, and yield (Cai et al., 2017; Tu et al., 2021; Li et al., 2023; Sahito et al., 2024). These findings lay a crucial foundation for crop genetic improvement, enabling breeders to move beyond traditional phenotype selection and achieve precise design and regulation of crop quality at the genetic level (Yasir et al., 2022).

3.3 Genomic selection

After identifying QTLs or major genes controlling important agronomic traits, researchers have raised an intriguing question: Can we accurately predict the post-cultivation phenotype of a crop using only its genotype information obtained before cultivation or at the seedling stage? Consequently, genomic selection (GS) emerged. All statistical and machine learning models that use genome wide genetic markers to calculate genomic estimated breeding values (GEBV) fall under GS tools. These models are highly significant for selecting superior parents, increasing genetic diversity, and shortening breeding cycles, and are widely applied in crops such as wheat, rice, and maize (Kumar et al., 2020; Gebremedhin et al., 2024; Lee et al., 2024).

Kang et al. (2023) genotyped diverse 567 Korean (K)-wheat core collection using the Axiom® 35K wheat DNA chip and identified multiple SNPs associated with target agronomic traits through GWAS. They evaluated GS prediction accuracy using six predictive models (G-BLUP, LASSO, BayseA, RKHS, SVM, and random forest) and various training populations, while also conducting a "blind test" on a variety of Korean wheat cultivars with

known phenotypes. Among the 10 cultivars, the RKHS model correctly predicted the phenotypes for 7 cultivars, demonstrating its strong predictive capability. Based on genotyping results from the Rice3K56 chip for hundreds of multi-parent advanced generation inter-cross and RIL populations, Zhang et al. (2023) conducted genomic selection analysis on plant height and heading date using nine prediction models, including GBLUP and EGBLUP. The results demonstrated that prediction accuracy is co-influenced by three key factors: population structure, trait heritability, and statistical model, with the optimal model varying depending on the target trait.

This study further validates the application potential of genomic selection in breeding programs. Guan et al. (2024) tested the performance of the MaizeGerm50K array in genomic selection analysis by applying RKHS and RR-BLUP models to predict five maize traits (days to anthesis, plant height, ear height, ear weight, and grain yield per plant). The results showed that both models achieved relatively high prediction accuracy (>0.59), with the highest accuracy observed for days to anthesis (0.76 ± 0.03 for RKHS and 0.71 ± 0.029 for RR-BLUP). Furthermore, the RKHS model outperformed RR-BLUP in predicting the four traits above, demonstrating the particular suitability of the MaizeGerm50K array for genomic selection.

The integration of GS with gene chip provides an efficient and precise predictive tool for modern crop breeding. GS harnesses genome-wide, high-density SNP markers to predict breeding values through statistical and machine learning models. This approach is successfully improving traits such as yield (Kim et al., 2022), advancing the transition to digital breeding.

4 Conclusion

As a vital tool in crop improvement, nearly 100 gene chips have been developed for plant research, covering over 25 crop species and perennial trees. These chips have facilitated the identification of QTLs and major genes closely linked to crop traits, significantly advancing breeding improvement in wheat, rice, maize, soybean, cotton, and other crops (Rasheed et al., 2017). Although solid-phase and liquid-phase gene chips differ in their technical principles, they offer analogous solutions for genotyping. While the former is less flexible, the SNP marker sets accumulated during their development continue to provide valuable resources, informing the design and optimization of liquid-phase gene chips. For instance, Liu et al. (2025b) referenced SNP datasets from the solid-phase gene chip Wheat 660K during the development of the WheatSNP16K chip, while Guo et al. (2019) optimized the existing SNP set from a 55K solid-phase gene chip (Xu et al., 2017) to develop 20K GBTS probes, and conducted a comparative analysis between the new and old chips based on genotyping data from diverse maize germplasms.

Among the various applications of gene chips, kinship analysis and GWAS are the most frequently applied (Table 1), primarily because the genotype information obtained can be directly correlated with phenotype, converting sequence variation into actionable insights for breeders' selection decisions. Research on gene chips has slowed in recent years, mainly due to the increasingly comprehensive mining of SNPs across crop genomes. However, for polyploid crops like wheat, whose chromosome complexity makes whole-genome sequencing costly, there remains considerable scope for developing more cost-effective gene chips.

Furthermore, novel genotyping technologies such as Hyper-seq (Zou et al., 2022) have emerged, which combine PCR with high-throughput sequencing. This method offers advantages such as low cost, high efficiency, a high degree of automation, and good flexibility. It has been successfully applied to library construction, sequencing, and genotyping of 2 094 samples from six crops.

Despite continuous innovation in genotyping technologies, methods such as KASP, solid-phase gene chips, GBS, GBTS, and Hyper-seq do not simply replace one another. Instead, each demonstrates unique strengths and applicability within specific domains. This diversity enriches the toolbox for genotyping, enabling researchers to select the most appropriate method based on their specific objectives and conditions to unravel genetic information.

Table 1 Gene chips developed for major crops

Crop	Chip Name (Abbreviation)	Number of Markers	Application (s)	Year
Rice	44 K chip (Affymetrix)	44,100 SNPs	Population structure and genetic diversity analysis; GWAS	2011 (Zhao et al., 2011)
Rice	OsSNPnks (Affymetrix)	50,051 SNPs	Kinship analysis; Background recovery analysis of backcross-bred lines	2015 (Singh et al., 2015)
Rice	High-density rice array, HDRA (Illumina)	700,000 SNPs	Kinship analysis; GWAS	2016 (McCouch et al., 2016)
Rice	5K SNP Array (Illumina)	5,246 SNPs	Identified two major QTLs for heat tolerance in rice	2017 (Shanmugavadivel et al., 2017)
Rice	Cornell_6K_Array_Infinium_Rice, C6AIR (Illumina)	6,000 SNPs	Genetic diversity analysis; QTL mapping; Introgression identification	2017 (Thomson et al., 2017)
Rice	Cornell-IR LD Rice Array, C7AIR (Illumina)	7,098 SNPs	Kinship analysis; GWAS; Identified twenty QTLs associated with plant height in rice	2020 (Sundaram et al., 2020)
Rice	580 K Axiom Rice Genotyping Chip, 580 K_KNU chip (Affymetrix)	581,006 SNPs	GWAS; GS	2022 (Kim et al., 2022)
Rice	Rice3K56 SNP array (Affymetrix)	56,606 SNPs	Kinship analysis; Cultivar identification; GWAS; GS	2023 (Zhang et al., 2023)
Wheat	Wheat NimbleGen array (NimbleGen)	132,605 features	Identified 511,439 SNPs	2012 (Winfield et al., 2012)
Wheat	Wheat 90K array (Illumina)	91,829 SNPs	Genetic mapping	2014 (Wang et al., 2014)
Wheat	Axiom® HD Wheat Genotyping array (Affymetrix)	819,571 SNPs	Kinship analysis	2016 (Winfield et al., 2015)
Wheat	Wheat Breeders' Array (Affymetrix)	35,143 SNPs	Genetic mapping; Kinship analysis; Identified novel genetic variants (including deletions, introgressions, and rearrangements)	2017 (Allen et al., 2017)
Wheat	Affymetrix ® Axiom ® Wheat660,	660K SNPs	Genetic mapping;	2017

Crop	Chip Name (Abbreviation)	Number of Markers	Application (s)	Year
Wheat	Wheat660K (Affymetrix)		Identified a major QTL controlling grains per panicle	(Cui et al., 2017)
Wheat	0.1K chip (GenoBaits)	101 SNPs	Kinship analysis	2023 (Xiang et al., 2023)
Wheat	'*Triticum aestivum* Next Generation' array ,TaNG (Affymetrix)	43,372 SNPs	Genetic mapping; GWAS; Copy number variation (CNV) analysis	2024 (Burridge et al., 2024)
Wheat	GenoBaits WheatSNP16K,GBW16K (GenoBaits)	37,669 SNPs	Genetic mapping; Kinship analysis; Identified a novel QTL for stripe rust resistance	2025 (Liu et al., 2025b)
Soybean	SoySNP50K (Illumina)	52,041 SNPs	Kinship analysis	2013 (Zhang et al., 2013)
Soybean	NJAU 355K SoySNP array (Affymetrix)	355,595 SNPs	Kinship analysis; GWAS	2016 (Wang et al., 2016)
Soybean	Illumina SoySNP8k iSelect BeadChip (Illumina)	7,189 SNPs	Population structure analysis; GWAS	2018 (Akond et al., 2013; Wang et al., 2018)
Soybean	SoySNP618K array (Affymetrix)	618,888 SNPs	Kinship analysis; GWAS; Fine-mapped two genes associated with flowering time; Identified a novel candidate gene for flowering time	2022 (Li et al., 2022)
Soybean	GenoBaits Soy40K array (GenoBaits)	40,019 SNPs 315 InDels	Kinship analysis; GWAS; Linked phenotypes to functional genes, and confirmed the additive effects of five flowering-related genes	2022 (Liu et al., 2022)
Maize	MaizeSNP50 array (Illumina)	49,585 SNPs	Kinship analysis	2011 (Ganal et al., 2011)
Maize	Maize 55 K SNP array (Affymetrix)	55,229 SNPs	DNA fingerprinting; Kinship analysis	2017 (Xu et al., 2017)
Maize	MaizeGerm50K array	50,852 SNPs	Kinship analysis; GWAS; Identified a gene regulating flowering time; GS	2024 (Guan et al., 2024)
Rapeseed	*Brassica napus* Illumina array	52,157 SNPs	Genetic mapping	2016

Crop	Chip Name (Abbreviation)	Number of Markers	Application (s)	Year
	(Illumina)			(Clarke et al., 2016)
Rapeseed	Bnapus50K (Illumina)	42,090 SNPs	Genetic mapping; Cultivar identification; Introgression identification; Transgenic element detection	2021 (Xiao et al., 2021)
Cotton	CottonSNP63K array (Illumina)	63,058 SNPs	Genetic mapping	2015 (Hulse-Kemp et al., 2015)
Cotton	CottonSNP80K array (Illumina)	82,259 SNPs	Kinship analysis; GWAS	2017 (Cai et al., 2017)
Cotton	ZJU CottonSNP40K (GenoBaits)	40,071 SNPs	Genetic mapping	2022 (Si et al., 2022)
Cassava	GenoBaits Cassava35K (GenoBaits)	35,955 SNPs	DNA fingerprinting; Kinship analysis; GWAS	2025 (Li et al., 2025a)

Conflict of interest

The authors declare no conflict of interest.

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