



Review article

Triumphs of genomic-assisted breeding in crop improvement

Vikas Mangal^a, Lokesh Kumar Verma^b, Sandeep Kumar Singh^c, Kanak Saxena^d,
Anirban Roy^e, Anandi Karn^f, Rohit Rohit^g, Shruti Kashyap^g, Ashish Bhatt^{g,**},
Salej Sood^{a,*}

^a ICAR-Central Potato Research Institute (CPRI), Shimla, Himachal Pradesh, 171001, India

^b University of Agricultural Sciences (UAS), Dharwad, Karnataka, India

^c Department of Genetics and Plant Breeding, Faculty of Agricultural Sciences, Siksha 'O' Anusandhan University, Bhubaneswar, Odisha, 751030, India

^d Department of Genetics and Plant Breeding, Rabindranath Tagore University, Raisen, Madhya Pradesh, India

^e Division of Genetics and Plant Breeding, Ramakrishna Mission Vivekananda Educational and Research Institute (RKMVERI), Narendrapur, Kolkata, 700103, India

^f Plant Breeding & Graduate Program, IFAS - University of Florida, Gainesville, USA

^g Department of Genetics and Plant Breeding, GBPUA&T, Pantnagar, Uttarakhand, 263145, India



ARTICLE INFO

Keywords:

Genomic assisted breeding
Pan-genome
Allelic variants
Marker assisted selection
Climate-smart crops

ABSTRACT

Conventional breeding approaches have played a significant role in meeting the food demand remarkably well until now. However, the increasing population, yield plateaus in certain crops, and limited recombination necessitate using genomic resources for genomics-assisted crop improvement programs. As a result of advancements in the next-generation sequence technology, GABs have developed dramatically to characterize allelic variants and facilitate their rapid and efficient incorporation in crop improvement programs. Genomics-assisted breeding (GAB) has played an important role in harnessing the potential of modern genomic tools, exploiting allelic variation from genetic resources and developing cultivars over the past decade. The availability of pangenomes for major crops has been a significant development, albeit with varying degrees of completeness. Even though adopting these technologies is essentially determined on economic grounds and cost-effective assays, which create a wealth of information that can be successfully used to exploit the latent potential of crops. GAB has been instrumental in harnessing the potential of modern genomic resources and exploiting allelic variation for genetic enhancement and cultivar development. GAB strategies will be indispensable for designing future crops and are expected to play a crucial role in breeding climate-smart crop cultivars with higher nutritional value.

1. Introduction

Crop plants serve as a primary source of both sustenance and industrial resources. Despite advances in farming techniques/

Abbreviations: GAB, (Genomic assisted breeding); GWAS, (Genome wide association studies); MAS, (Marker assisted selection); MABC, (Marker assisted backcrossing); NGS, (Next-generation sequencing); SNP, (Single nucleotide polymorphism); QTLs, (Quantitative trait loci).

* Corresponding author.

** Corresponding author.

E-mail addresses: ashishbhattabc0312@gmail.com (A. Bhatt), salej1plp@gmail.com (S. Sood).

<https://doi.org/10.1016/j.heliyon.2024.e35513>

Received 3 March 2024; Received in revised form 23 July 2024; Accepted 30 July 2024

Available online 5 August 2024

2405-8440/© 2024 The Authors. Published by Elsevier Ltd. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

advanced breeding methods, there remains a considerable gap between crop yields and the demand for food. The impact of plant diseases, pests, and unfavourable environmental conditions regularly leads to significant losses in yield. These stresses coupled with a fast-growing global population could result in widespread food scarcity. To meet this challenge, crop breeders must keep producing new improved varieties with better yield potential, excellent quality, biotic or abiotic stresses tolerance, and efficient nutrient utilization. There is no doubt that the field of plant breeding has made remarkable strides in the previous century [1]. The conventional method of plant breeding involves the controlled cross-pollination of plants or selective mating to produce offspring with desired traits. By combining the best traits of two parents, conventional breeding has helped to create new varieties with adaptation to different growing conditions and resistance to diseases and pests. Conventional breeding approaches have achieved several notable outcomes over time, including improved yields and plant resilience, enhanced flavour, texture, nutritional content, development of disease and pest-resistant crops, climate resilience and better crop quality and appearance, leading to increased market value. These advances have helped attain food security, improved human nutrition, and reduced pesticide and herbicide use. Despite the remarkable success, the traditional breeding methods encounter various obstacles that impede the development of improved cultivars, like time-consuming, laborious, resource-intensive, and reliant on the environment. Moreover, the genetic gain over time is low in most of the crops. By 2050, the world’s population, which is currently 7.8 billion, is expected to reach 9.6 billion [2]. To adequately feed and sustain this rapidly growing population, global crop production must double over the next thirty years [3]. Genomics assisted breeding can play an important role in improving the genetic gain in crop breeding and can be instrumental in harnessing the potential of newly sequenced genomes.

In the last two decades, genotype rather than phenotype-based selection has become more prevalent in plant breeding due to recent developments in molecular biology and next-generation based high-throughput sequencing/genotyping technologies (NGS). MAS has been a prevailing technique in molecular breeding programs for several decades, enhancing breeding efficiency to some extent [4]. Various MAS approaches have been devised, including major genes/QTLs introgression or MABC, enrichment of positive alleles in early generations, and selection of quantitative traits using markers at multiple loci [5,6]. High-density SNP markers can now be used to evaluate the complete genome at a relatively low cost because of advancements in whole-genome sequencing (WGS) and marker technologies. Genomic-assisted breeding (GAB) can explore the genetic information of crop plants to speed up plant breeding and can develop climate-resilient, high-yielding crop varieties. The product resulting from GAB is non-genetically modified (non-GM) and, thus, enjoys wider acceptance among consumers and farmers. The Food and Agriculture Organization (FAO) has reported that GAB has immense potential to initiate a fresh “greener revolution” that can address the challenge of feeding the ever-growing population while conserving natural resources [7].

Genomics-assisted breeding is an innovative approach that utilizes modern molecular tools and genomic information to improve the accuracy and efficiency of conventional plant breeding (Fig. 1). It involves the use of molecular markers to identify desirable traits, genes and their functions, and genomic prediction models to predict the breeding value of individuals. GAB employs multiple

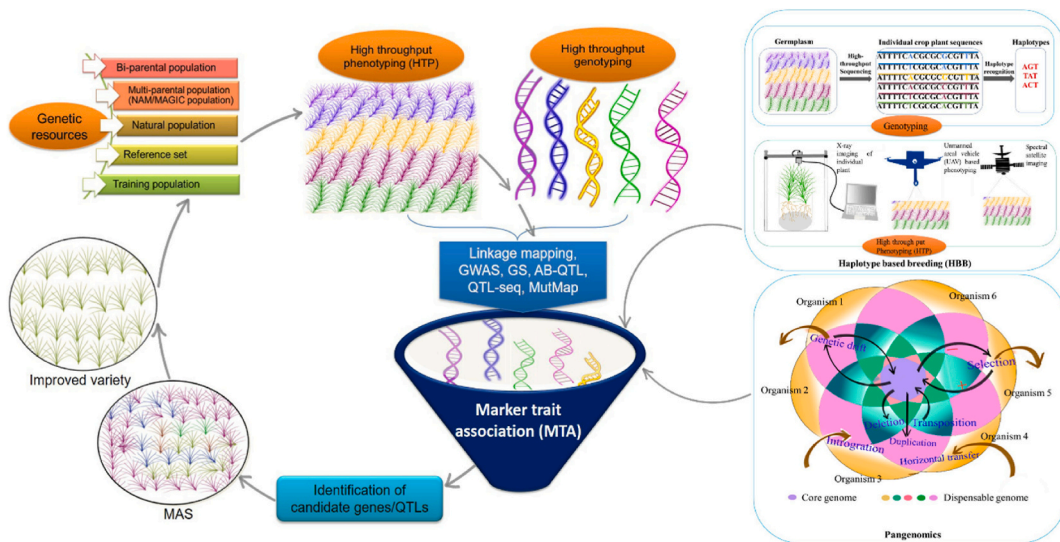


Fig. 1. A flow chart for genome-assisted breeding. MAS: Marker-assisted selection; GWAS: Genome-wide association studies; GS: Genomic selection; GEBV: Genomic estimated breeding value; AB-QTL: Advanced backcross QTL analysis; AM: Association mapping. The haplotype-based breeding approach: identification of haplotype (genotyping) along with high precision phenotyping (satellite-based phenotyping to phenotype a large area of cropping system, UAV-based phenotyping over a group of crop plant and individual plant-based X-ray imaging) helps to study the marker-trait association that ultimately identify the candidate gene for the trait of interest—the pangenomics approach: Dynamic analysis of the pangenome structure as a result of a variety of events and forces. Mutations, duplications, deletions, and transpositions add new sequences to the dispensable genome, while deletion and transposition reduce the core genome content. Introgression and horizontal transfer also have an impact on the dispensable genome compartment (sequence gain). Furthermore, both positive and purifying selections and genetic drift affect both the core and dispensable genomes (sequence gains and losses), as well as the pangenome (sequence losses).

techniques to improve crop yields and enhance desirable traits like MABC, Association Mapping, Genomic Selection (GS), Advanced Backcross QTLs (AB-QTLs), MARS (Marker Assisted Recurrent Selection), haplotype-based breeding (HBB) and other strategies. These approaches utilize the latest advancements in genomics to facilitate breeding programs and enhance the accuracy and efficiency of selecting desirable crop traits [8]. As a means of progressing plant breeding, these methods use DNA sequencing, gene expression analysis, high-throughput phenotyping, and genotyping. There is a great deal of genomic information available in databases that can be used to develop novel varieties with desired characteristics, including high yield, resistance to environmental stresses, nutritional value, improved quality and other essential agronomic characteristics.

Genetic gain, i.e. the improvement in the genetic potential of a population over time, usually achieved through selective breeding [9], has a close relationship with GAB. With genomic information, breeders can select individuals with desirable traits at an earlier

Table 1
Genome sequence information of major crops.

Crops	Variety	Estimated genome size (Mb)	Assembly size (Mb)	Number of gene predictions	Repeat (%)	Reference
Cereals						
<i>Oryza sativa</i> spp. <i>Indica</i> (Rice)	93–11	430.00	466.00	46,022–55,615	42.20	[14]
<i>Oryza sativa</i> spp. <i>japonica</i>	Nipponbare	420.00	389.80	37,544	35.00	[13]
<i>Triticum aestivum</i> (Bread wheat)	Chinese spring	17,000.00	3800.33	94,000–90,000	80.00	[119]
<i>Zea mays</i> (Maize)	B73	2300.00	2048.00	32,540	85.00	[120]
<i>Sorghum bicolor</i> (Sorghum)	BTx623	~730.00	698.00	27,640	62.00	[121]
Legumes						
<i>Cajanus cajan</i> (Pigeon pea)	Asha (ICPL 87119)	833.07	605.78	48,680	51.67	[122]
<i>Cicer arietinum</i> (Chickpea)	CDC Frontier	~738.00	532.29	28,269	49.41	[123]
<i>Glycine max</i> (Soybean)	Williams 82	1115.00	950.00	46,430	57.00	[124]
<i>Phaseolus vulgaris</i> (Common bean)	G19833	587.00	473.00	27,197	45.37	[125]
<i>Vigna radiata</i> (Mungbean)	VC1973A	579.00	431.00	22,427	43.00	[126]
<i>Vigna mungo</i> (Urd bean)	Pant U-31	574	475.91	42,115	49.6	[127]
<i>Arachis hypogaea</i> (Groundnut)	Tifrunner	2717.8	2540	66,469	64	[128]
Horticultural Crops						
<i>Solanum lycopersicum</i> (Tomato)	Heinz 1706	900.00	760.00	34,727	63.28	[129]
<i>Solanum tuberosum</i> (Potato)	DM1-3516 R44 and RH89-039-16	844.00	727.00	39,031	62.20	[130]
<i>Dioscorea rotundata</i> (Guinea yam)	TDr96_F1	570.00	594.00	26,198	–	[131]
<i>Musa acuminata</i> (Banana)	DH-Pahang	523.00	472.20	36,542	43.72	[132]
<i>Manihot esculenta</i> Krantz (Cassava)	AM560-2	770	532.5	30,666	37.5	[133]
<i>Beta vulgaris</i> (Sugar beet)	KWS2320	714.00–758.00	567.00	27,421	63.00	[134]
<i>Citrullus lanatus</i> (Watermelon)	97103	~425.00	353.50	23,440	45.20	[135]
<i>Allium cepa</i> L. (Onion)	DHCU066619	~16400	14940	540,925	72.4	[136]
<i>Citrus sinensis</i> (Sweet orange)	Valencia	367.00	320.50	29,445	20.50	[137]
<i>Cucumis sativus</i> (Cucumber)	Chinese long	367.00	243.50	26,682	24.00	[138]
<i>Malus domestica</i> (Apple)	Golden Delicious	742.3	603.9	57,386	67	[139]
<i>Vitis vinifera</i> (Grapevine)	ENTAV 115	504.6	477.1	29,585	27.4	[140]
<i>Capsicum annuum</i> (Hot pepper)	CM334	3480.00	3060.00	34,903	76.40	[141]
<i>Solanum melongena</i> (Eggplant)	Nakate-Shinkuro	1126.00	833.10	85,446	70.40	[142]
Industrial Crops						
<i>Elaeis guineensis</i> (Oil palm)	Deli dura	1800.00	1535.00	34,802	57.00	[143]
<i>Ricinus communis</i> (Castor bean)	Hale (NSL 4773)	320.00	350.00	31,237	50.33	[144]
<i>Gossypium arboreum</i> (Cotton)	Shixiya1 (SXY1)	1724	1694	41,330	68.5	[145]
<i>Nicotiana tabacum</i> (Tobacco)	TN90	4500.00	3700.00	90,000	72.00–78.00	[146]
<i>Brassica juncea</i> (Indian mustard)	Tumida	955	784	80,050	40.3	[147]
Beverages						
<i>Coffea canephora</i> (Robusta coffee)	–	710.00	568.60	25,574	50.00	[148]

breeding stage rather than wait until the traits are fully expressed. GAB allows breeders to identify individuals with the most desirable genetic traits and a deeper understanding of the genetic architecture of those traits for a given breeding program [10]. This information can help them identify the genes responsible for the desired traits, which can be effectively targeted in future breeding programs. By analysing the genetic makeup of potential parents, breeders can make more informed decisions about the individuals to be used in their breeding program, resulting in offspring with high genetic potential. This technique allows selection cycles to be completed much quicker, resulting in faster genetic gain [11,12].

2. Genome sequence information of major crops

The introduction of NGS technologies has facilitated the sequencing of more than 100 plant species. *The Arabidopsis thaliana genome was the first plant genome to be completely sequenced* (The Arabidopsis Genome Initiative, 2000), and it was subsequently followed by the sequencing of a draft genome of rice [13,14] and more recently, oat genome was sequenced in 2022 [15]. Plant genome sequencing plays a crucial role in assisting the development of elite varieties in various ways. It enables identifying, manipulating and analysing specific genes and molecular markers associated with desirable plant traits. Through MAS, plant breeders can make more informed selections at the early stages of plant development, reducing the time and resources required to develop elite varieties. Sequencing provides a comprehensive understanding of the genetic architecture of plants. This information enables the development of statistical models for genomic selection that can predict the performance of a plant based on its genetic makeup. Gene editing and other genetic

Table 2
Candidate gene/QTLs with successful trait introgression in various crops.

Crop	Trait	Genes/QTLs	References	
Rice	Bacterial Leaf Blight	<i>xa5, xa13, Xa4, Xa21, Xa33, Xa38</i>	[68–70]	
	Blast	<i>Pi1, Pi2, Pi5, Pi9, Pi33, Pi54, Pi25, Pita, Pi1</i>	[69,73,149]	
	Gall midge	<i>Gm1, Gm4</i>	[71]	
	Salt tolerance	<i>SALTOL, qSSISFH8.1, OsSAP16</i>	[150,151]	
	Submergence	<i>Sub1</i>	[90]	
	Drought	<i>DTY1.1, 2.1, 2.2, 3.1, 4.1</i>	[92]	
	Sheath Blight	<i>qSBR11-1</i>	[152]	
	Semi dwarf	<i>Sd1</i>	[153]	
	Herbicide tolerance	<i>AHAS</i>	[99]	
	Phosphorous tolerance	<i>Pup1</i>	[99]	
	Nitrogen Use Efficiency	<i>qNUE6</i>	[154]	
	Low temperature Germination	<i>LOC_Os01g23580, LOC_Os01g23620 (OsSar1a)</i>	[155]	
	Heat tolerance	<i>LOC_Os08g07010, LOC_Os08g07440</i>	[156]	
	Spikelet number	<i>SPIKE</i>	[117]	
	Fusarium Head Blight	<i>Fhb1 and Fhb2</i>	[157]	
	Wheat	Stripe/yellow Rust	<i>Yr10, Yr15, Yr17, Yr26, Yr40</i>	[158]
Leaf rust		<i>Lr19, Lr34, Lr37, Lr57</i>	[159]	
Stem rust		<i>Sr2, Sr36, Sr24, Sr25, Sr26</i>	[160]	
Dwarfing gene		<i>Rht1</i>	[24]	
Photoperiod		<i>Ppd-D1</i>	[24]	
Powdery mildew		<i>Dx5, Dx10</i>	[77]	
Yield		<i>Qyld.csdh.7AL</i>	[118]	
Maize		Quality Protein	<i>opaque-2, o-16</i>	[161,162]
		Provitamin and vitamin E	<i>LcyE and VTE4</i>	[163]
		Beta carotene	<i>CrtRB1</i>	[111]
	Maize rough dwarf disease	<i>qMrdd8</i>	[81]	
	Head smut	<i>qHSR1</i>	[82]	
Brassica	<i>Leptosphaeria maculans</i> resistance	<i>Rlm1, Rlm2, Rlm3, Rlm4, LepR1, LepR2 & LepR3</i>	[164]	
	Flowering time	<i>FTA09, FTA10, and FTC05</i>	[165]	
Sorghum	Shoot fly resistance	<i>SBI-01/LG A + SBI-07/LG E + SBI-10/LGG</i>	[80]	
Pearlmillet	Downy mildew resistance	<i>qRSg1, qRSg4, qRSg3.1, qRSg4.2, qRSg6.1</i>	[78]	
Chickpea	Fusarium wilt resistance	<i>foc1, foc2, foc3, foc4, foc5</i>	[88,89]	
	Ascochyta blight	<i>ABQTL-I, ABQTL-II</i>	[87]	
	Drought	QTL hotspot	[103]	
Groundnut	Oleic acid	<i>FAD2a, FAD2b</i>	[108]	
Soybean	YMV resistance	<i>Rymv</i>		
	Asian soybean rust	<i>Rpp1-b, Rpp4, Rpp5</i>	[166]	
	Phytophthora	<i>Rps2</i>	[84]	
	Powdery mildew	<i>Rmd-c</i>	[84]	
	Drought	<i>AREB1</i>	[104]	
	Kunitz trypsin inhibitor	Null allele of KTi	[113]	
	Lipoxygenase-2 free	<i>lox1, lox2, lox3</i>	[114]	
	Early maturity	Null allele of E1	–	
	Pod shattering	<i>Pdh1</i>	[116]	
	Plant Height	<i>Glyma.02G133000, Glyma.05G240600</i>	[167]	
	Nodulation	<i>rj2</i>	[84]	
	Buckwheat	Yield & Grain weight	<i>FtBRI1, FtAGB1, FtTGW6, FtMADS1, FtMKK4</i>	[168]

engineering techniques can be used to introduce or modify genes responsible for desirable traits [16]. The evolution of sequencing platforms has made sequencing more affordable, although certain challenges still exist. Long-read sequencing technologies (PacBio and Oxford Nanopore), combined with chromosome conformation capture techniques such as HiC, have significantly improved genome assembly quality by providing longer contiguous sequences and higher resolution of genome structures [17,18]. Likewise, pangenome sequencing and whole genome resequencing have proven instrumental in identifying novel genes and QTLs within wild relatives of various plant species [19]. However, the affordability of these technologies remains a concern. While costs have decreased, they can still be prohibitive for large-scale projects or resource-limited research programs. Additionally, the complexity of data analysis and interpretation from these advanced sequencing methods requires significant bioinformatics expertise and resources. Despite these challenges, the benefits of integrating long-read sequencing and Hi-C technologies are substantial, as they provide deeper insights into the genetic basis of important agricultural traits [20].

These approaches have been particularly valuable for incorporating these genes into elite varietal backgrounds through MAS and MABC. These advancements significantly contribute to developing elite varieties with improved traits, including higher yields, increased nutritional value, and resistance to environmental stresses. However, re-sequencing and gene expression studies are still being conducted to learn how genes work behind each trait and to pinpoint any hidden allelic variations. Many genome projects are currently underway or in the planning stages, adding to the crop genomes that have already been sequenced. The key features of the sequenced genomes of the 31 important crop species are illustrated in Table 1.

3. Genetic resources as a source of valuable genes

Plant genetic resources are considered valuable for present and future generations of humans because they contain novel genes for climate resilience, adaptability and nutritional quality. Landraces carry different important alleles that may be utilized for gene introgression, like in rice Gobindobhog, Bhutmuri, and Radhunipagal have been used as donors of *PUP1* QTL for phosphate tolerance in breeding programme [21]. Rice fragrance gene *BADH2* and Basmati's intermediate amylose trait were introduced into 'Manawthukha from Basmati 370 in Myanmar through MAS [22]. Low-grain arsenic accumulating allele 'ABCCI' has been identified in Gobindobhog, small-grain Bengal aromatic rice [23]. Likewise, in wheat AP-1 line of *Aegilops ventricosa* contributed eyespot resistance gene *Ach1* for developing an improved version of Almatense H-10-15 [24]. Another novel fertility restoration *Rf9* gene in Gerek and 71R1203 [25], increased spikelet number per spike along with stability QTL conferring higher yield in PI272527 [26], stem/leaf rust and powdery mildew gene in *Triticum timopheevii* [27], and high protein content in Farnum, Westmore, Lillian, Somerset, and Burnside wheat variety have been identified or developed which can be used for further wheat improvement [28]. Haplotype mining of genes responsible for drought tolerance in pigeon pea has been exploited from different accessions like *C. cajan* 23080-H2, 26230-H5 and 30211-H6 [29]. Two important genes *RING-H2* finger protein and zeaxanthin epoxidase, have been identified from two contrasting groundnut genotypes, ICGV 97045 and ICGV 00350, for dormancy which controls abscisic acid accumulation during germination [30]. Photoperiod-responsive gene *ELF3* in lentil can be used for breeding thermotolerance under delayed sown conditions [31]. Candidate genes viz. *TB1*, *LAX1/BA1*, *GRAS8*, *ERF*, and *MAX2* were identified for complex branch number traits in Chickpea [32]. Higher plant biomass, leaf area, plant height, and canopy area have been linked with 'QTL hot spot' found in chickpea genotype ICC4958 [33]. All these studies demonstrate the potential and benefits of genome sequencing and genomic resources in crop breeding programs. Table 2 shows the list of successfully introgressed candidate genes/QTLs in crop plants.

4. Molecular markers and their role in the post-genomic era

Molecular markers are DNA fragments that indicate the presence or absence of specific alleles associated with specific traits in a plant genome. SSR markers have been widely used in the past few decades in diversity analysis, genetic mapping, and improving crop improvement programs' efficiency [34]. Before the discovery of SNPs, SSR markers, also known as microsatellites, were widely used in GAB. SSRs had co-dominant inheritance, high abundance, and polymorphism, making them useful for genetic mapping, population genetics, and breeding experiments. However, with the introduction of high-throughput sequencing technologies, SNPs, which are single nucleotide polymorphisms caused by base substitutions, insertions, or deletions, became a more potent alternative. SNPs are abundant across the genome and can be easily genotyped utilizing automated approaches, allowing for precise genetic mapping and analysis. SNPs have transformed molecular markers, allowing for large-scale genomic investigations, association studies, and population genomics. Because of their ubiquitous nature, the availability of cost-effective genotyping platforms and bioinformatics tools, they are currently the favoured markers in many genetic research domains. While SSR markers are still used in certain circumstances, the arrival of SNPs has substantially widened the boundaries of genetic studies, providing researchers with greater insights into genetic diversity and evolutionary links [35]. SNP genotyping panels have been developed and used recently, like an Amplified-fragment single nucleotide polymorphism and methylation (AFSM), another sequencing method that facilitates the simultaneous detection of methylation sites by identifying variant sites in the genome. Restriction-site Associated DNA sequencing (RADseq) has gained popularity in various species, as it does not require reference genome information and has made the resequencing procedure easier [35].

KASP markers have considerably aided plant breeding by allowing for more efficient and precise genotyping, allowing breeders to make more informed decisions, accelerate breeding processes, and generate improved crop varieties with improved attributes (Sood et al., 2022). They are utilized in MAS, genetic mapping, QTL analysis, hybrid purity testing, germplasm characterization, diversity studies, etc. For instance, the development of the KASP functional marker *TaTAP46-5A* is associated with Kernal weight in wheat [36]. The DaRT SNP platform continues to be a popular tool in plant breeding and genetic research. Its capacity to efficiently capture genetic

variation and provide useful insights into genome structure and diversity has aided developments in breeding programmes and crop variety production. For different crop species, the mid-density DArT SNP platform have been developed for genotyping and genomic selection. The mid density DArT platform for wheat has 3900 SNPs, Maize has 3305 SNPs, cowpea has 2602 SNPs, groundnut has 2500 SNPs, potato has 2147 SNPs, pigeon pea has 2000, and common bean has 1861 SNPs [37].

Rapid advances in genotyping platforms have resulted in the development of more than 50 SNP arrays and 15 GBS platforms for about 25 crop species and perennial trees [38]. SNP Affymetrix arrays have been widely used for SNP discovery and genotyping in food, horticultural, and woody crops [39]. Compared to GBS and PCR-based methods, microarray technology, particularly SNP microarrays, provides faster, more efficient, and customizable genotyping, with liquid-phase chips more commonly used than solid-phase chips, allowing flexibility in marker selection and sample size. Liquid-phase chips for soybean and barley have been developed, and SNP arrays are being used to analyse haplotypes in polyploid plants, assisting in understanding their evolutionary history. The KPS wheat 90K chip with 85K loci and the rice 60K whole-genome chip with high distribution density are two notable examples. The rice 56K high-density SNP chip has been used to build prediction models for yield and quality in hybrid rice [35].

Further progress in the fine mapping of the QTLs and designing of functional SNP chips will improve the efficiency of crop biotic and abiotic stress breeding [40]. GBS and chip-based SNPs are frequently used to identify genetic loci associated with specific traits. Drought stress GWAS studies have used SNP microarray chips such as the 90K Illumina Infinium SNP array in wheat, SNP50 Bead Chip in maize, SoySNP6k iSelect BeadChip in soybean, and 9K Illumina iSELECT genotyping BeadChip in barley [41]. Due to their genome-specificity, high density, and efficacy, various SNP solid chips (15K, 35K, 90K, 55K, 660K, and 820K) are now available for genome analysis in wheat [42]. The Illumina Infinium 40K SNP array version 1.0 was created to capture haplotypic diversity in barley and wheat germplasm [43]. For sugarcane genotyping, a 345K Sugarcane SNP Chip has been developed [44]. High-density 62K genic-SNP array allow for discovering novel QTLs associated with yield, nutrition quality, and stress resistance in *Cajanus* spp. [45]. These advancements in SNP arrays and GBS facilitate comprehending and improving various crops.

5. QTLs mapping in the post-genomic era

QTL mapping is a molecular technique used in crop improvement to identify genetic regions, known as Quantitative Trait Loci (QTLs), linked with desirable attributes. This method analyses genetic markers and phenotypic data from a plant population to precisely locate these QTLs. For example, an SSR-based QTL study of the $F_{2:3}$ population (C-214 \times WR-315) revealed two QTLs for fusarium wilt (*FOCI*) resistance on linkage group 6 (LG6) [46]. The generated data is a vital tool for breeders, aiding the selection and production of plants with enhanced features through marker-assisted selection procedures. Linkage mapping is a bi-parental mapping strategy using genetic and molecular markers to detect links between markers and QTLs. Linkage analysis has limitations in mapping resolution and allele richness. The Nested association mapping (NAM) population, combining association and linkage mapping, has been employed to study agronomic traits in crops [47]. Complex traits, such as crop yield, are frequently influenced by multiple genes or QTLs or haplotypes, each with minor effects that interact with the environment. Due to the minimal individual effects of these components, capturing their contributions in isolation becomes difficult.

On the other hand, association mapping uses historical recombination events in natural populations to locate QTLs. GWAS provides improved resolution, lower costs, and the flexibility to test multiple alleles for their interactions. For example, 25 DEGs were discovered to be linked with flowering time in maize by combining GWAS, QTL, and transcriptome analysis. Three specific candidates (Zm00001d011673, Zm00001d011668 and Zm00001d011666) among these genes were identified as putative regulators of the trait associated with flowering time in maize [48]. Association studies, such as GWAS, use statistical approaches to identify connections between genetic markers and phenotypic characteristics, allowing potential relationships between specific genomic regions and observable phenotypes to be identified. Several crop attributes, including yield, quality, and stress tolerance, have been effectively found using haplotype-based GWAS in various plant species, including wheat, rice, barley, maize, and soybean [49]. Recent GWAS research based on empirical and simulated data has shown that haplotype blocks, compared to individual SNPs, offer increased mapping accuracy and power for discovering QTLs/genes [50]. Haplotype-based mapping has proven to be more effective than SNP-based mapping at identifying genetic loci associated with maize biomass and plant height, as well as with drought tolerance in maize with higher phenotypic variation explained (PVE) values [51]. Since the haplotype blocks can explain typical patterns of genetic variation, haplotyping the complete genome also enables the identification of tag-SNPs that represent the haplotype blocks employed in genetic studies. As a result, there is no longer a need to examine each SNP individually, saving money and time on GWAS. Evolutionary biologists employ QTL mapping techniques to explore the genetic underpinnings of adaptation in plants such as Arabidopsis and wheat by utilization of the MAGIC population. Recent advances in genetic profiling and QTL mapping have significantly enhanced the precision and efficiency of identifying QTLs associated with desirable crop traits. High-throughput sequencing technologies have revolutionized next-generation mapping, generating high-resolution genetic maps. Innovations such as MutMap and its variants (e.g., QTL-seq and MutMap+) have streamlined the rapid identification of QTLs, which showed their effectiveness in rice [52]. The integration of CRISPR/Cas9 genome editing with QTL mapping has opened new avenues for functional genomics in rice [53]. Additionally, multi-omics integration has enhanced the understanding of complex traits, e.g. Li et al. [54] identified candidate genes for heat tolerance in rice through combined GWAS and transcriptome analysis. This approach helps elucidate the specific genomic regions associated with adaptive traits in these plant species [55].

6. Pangénomics

In the next few years, the world's population is expected to reach 840 million undernourished people by 2030. Therefore, crop

improvement is more important than ever to fulfil the demand of this increasing population. The advancement in sequencing technologies, computing power and sequencing of complete, or even gap-free high-quality genome have led to the insight that a single genome of a species may not be adequate to manifest the landscape of that species. This is due to the greater number of variations present among accessions, which could lead to biased genetic analyses. The “pan-genome” idea was developed to characterize all the genetic information regarding a species, which includes core genes that are present in all strains as well as dispensable genes that are present in only a subset of strains. In the first generation of pan-genome studies, the aim is usually to identify as many structural variants using a diverse but limited sample of genotypes. With this breakthrough, crop genomics shifted from a single reference genome to tens or more of reference-quality genome assemblies within a species.

Single reference genome based QTL mapping and GWAS studies provide an incomplete relationship between structural variants and phenotypes. Therefore, many SNP trait associations could not be validated based on single genome information. However, with a pan-genome approach, this picture could become clearer. Recently in rice, a high-quality pangenome using an international rice panel (413 diverse accessions) and 12 representative rice genomes successfully identified causal structural variations for plant height and grain weight and characterized a new locus (*qPH8-1*) on chromosome 8 for plant height, which was undetected by the SNP-based GWAS [19]. Similarly, the genomic prediction for complex traits based on pan-genome could help improve genomic prediction accuracy due to bias reduction. According to Lyra [56], adding a few hundred copy number variations to an analysis of around 20k SNPs improved the prediction accuracy of plant height in maize under low nitrogen conditions.

The pan-genome studies have been carried out in model plants, *Arabidopsis* and crop plants like rice [57,58], wheat [59], tomato [60], brassica [61], apple [62], maize [63], sunflower [64] and pepper [65]. The structural variants discovered by the pangenome studies provide genomic information to identify genes/alleles related to various environmental stresses and other desirable traits. In addition, they can improve the efficiency of genome editing approaches such as CRISPR-Cas by providing useful information on new target genes. The availability of pangenomes for major crops has been a significant development, albeit with varying degrees of completeness. However, the expansion of pan-genomic studies beyond individual species holds great potential for harnessing the genetic diversity found in wild relatives of crops. This expansion would facilitate the incorporation of novel gene sequences into crop improvement efforts, enabling the development of customized or “designer” crops.

Furthermore, with the establishment of pangenomes for numerous diverse species, we can understand how species and higher taxonomic groups are defined at the genomic level. This deeper insight into plant evolution and diversification will contribute to our overall knowledge of plant biology and inform future breeding strategies [66]. Pangenomics has shed light on the evolutionary genomics of numerous species. Core genes, for example, have been found to have much greater expression levels in maize than dispensable genes [63]. Furthermore, compared to core regions, dispensable areas of the genome have a larger content of transposable elements (TEs) [60].

7. Success stories of GABs

In most food crops, genomic-assisted breeding has produced numerous varieties resistant to biotic stress, abiotic stress, improved quality and agronomic related traits. Some notable examples have been discussed in the following paragraphs.

7.1. Biotic stress

Either candidate genes or significant effect QTLs are most favoured for introducing disease resistance using GAB. GAB has resulted in the development of many disease-resistant varieties or improved advanced breeding lines in many crops. For instance, the rice variety ‘Improved Pusa Basmati 1’ was engineered with two stacked genes (*xa13+Xa21*) to confer resistance against bacterial blight disease [67]. Likewise, ‘Improved Samba Mahsuri’ originally containing three resistance genes (*xa5+xa13+Xa21*), was further stacked by two additional major blast resistance genes (*Pi-2*, *Pi-54*) and one blight resistance gene (*Xa38*) [68–70]. Variety, ‘Improved Tapswini’ [71] and ‘Improved Lalat’ [72] were developed by pyramiding gene combinations (*Xa4+xa5+xa13+Xa21*). Additionally, six tolerance/resistance genes/QTLs (*Pi2*, *Pi9*, *Gm1*, *Gm4*, *Saltol* and *Sub1*) were added to the ‘Improved Tapswini’ to supplement the blast resistance genes [71], acquiring long-lasting resistance to several diseases. Resistance genes were pyramided in the rice cultivars Pusa Basmati 1609 (*Piz5+Pi54*), Pusa Samba 1850 (*Pi1+Pi54+Pita*) and an improved version of ‘Pusa Basmati 1’ (*Pi54+ Pi1+ Pita + Pi2+ Pib + Pi5+ Pi9*) to achieve a high level of resistance to blast disease [73]. In wheat, several varieties/cultivars were improved for rust resistance by gene introgression, like ‘Jagger’ and ‘Overley’ having the genes *Lr57/Yr40* [74] and *Lr58*, HUW510 (*Lr34*) [75], Unnat PBW 343 (*Yr17+Yr40+Lr37+Lr57*), HD 2733 (*Lr19/Sr25+Sr26+Yr10*), HD 2932 (*Lr19/Sr25+Lr24/Sr24+Yr10*) [76] and Xiaoyan 22 [77].

The transfer of the eyespot resistance gene *Pch1*, barley yellow mosaic virus resistance genes *rym4/rym5*, and barley powdery mildew resistance gene *mlo* were other examples highlighting the potential of GAB in cereal breeding. Downy mildew resistance genes were stacked in the pearl millet original cultivar HHB 67 and HHB 67 improved’ (*qRSg1 + qRSg4*) and ‘HHB 67 improved 2’ cultivars were released, which demonstrated increased resistance to downy mildew [78]. Three QTLs for striga resistance in sorghum were transferred in the background of ‘Tabet’ and ‘Wad Ahmed’, a well-known cultivar in Sudan [79]. By pyramiding three QTLs from the donors J2658, J2614, and J2714, the popular Indian varieties Parbhani Moti and ICSB 29004 were improved for shoot fly [80]. Seven elite lines of maize were improved for rough dwarf disease in China using a QTL (*qMrdd8*) [81], and another ten advanced lines were similarly made resistant to head smut by introducing a head smut resistant QTL (*qHSR1*) [82].

Compared to cereals, grain legume crops have lagged behind in terms of GAB product delivery; nonetheless, genotyping-based choices are currently being used in breeding programs more and more. For instance, at USDA-ARS, pyramiding against different

Table 3
Improved varieties/lines introgressed with various biotic stresses using Genomic assisted breeding.

Crop	Improved varieties/advanced breeding lines/recurrent parent	Gene combination	Trait(s) target	References
Rice	Improved Pusa Basmati I, Pusa 6A, Pusa 6B of Pusa RH 10 rice hybrid, Punjab Basmati-3, Punjab Basmati-4, Pusa Basmati 1728, Pusa Basmati 1718, Pusa1592, PRR78 of Pusa RH 10 rice hybrid, Improved Pusa Basmati 1121, Pusa Basmati 6	<i>xa13 + Xa21</i>	Bacterial blight	[67,149, 153,169]
	Improved Samba Mahsuri, CR Dhan 800 (Swama MAS), Triguna	<i>xa5 + xa13 + Xa21</i>		[68,99,170]
	KMR3 Restorer, Improved Tapaswini, Improved Lalat, CRMS 32B and CRMS 32A	<i>Xa4+ xa5 + xa13 + Xa21</i>		[71,72,171, 172]
	Improved Mangeumbye	<i>Xa4+ xa5 + Xa21</i>		[173]
	DRR Dhan 53	<i>Xa21+ xa13+ xa5 + Xa38</i>		[99]
	DRR Dhan 59	<i>Xa33</i>		[99]
	Pusa Basmati 1609, Pusa 1612 (Pusa 6), PRR78 of Pusa RH10 rice hybrid, Improved Pusa Basmati 1121, Pusa Basmati 6	<i>Pi2 + Pi54</i>	Rice blast	[149,174]
	Pusa Basmati 1	<i>Pi9 + Pita</i>		[73]
	Samba Mahsuri (BPT 5204)	<i>Pil</i>		[175]
	Pusa Basmati 1637	<i>Pi9</i>		[99]
	DRR Dhan 51	<i>Pi2</i>		[99]
	Pusa Samba 1850	<i>Pi1 + Pi54 + Pita</i>		[176]
	ADT 43	<i>Pi54+Pi33+Pi1</i>		[177]
	MushkBudj	<i>Pi54+ Pil + Pita</i>		[178]
	Pusa 1604	<i>qSBR11-1</i>	Sheath blight	[152]
	Pusa Basmati 1847, 1885, 1886	<i>Xa21+ xa13+ Pi2 + Pi54</i>	Bacterial blight & blast	[99]
	DRR Dhan 62	<i>Xa21+ xa13+ xa5+ Pi2 + Pi54</i>		
	Swama	<i>Xa4+xa5+xa13+Xa21+Sub1</i>	Bacterial blight & Submergence	[179]
	Ranbir Basmati	<i>xa13 + Xa21 + sd1</i>	Bacterial blight and semi dwarf	[153]
	DRR Dhan 58	<i>Xa21+ xa13+ xa5 + qSaltol</i>	Bacterial blight resistance & seedling stage salinity tolerance	[99]
DRR Dhan 60	<i>Xa21+ xa13+ xa5 + qPup1</i>	Bacterial blight resistance & low soil phosphorous tolerance	[99]	
Wheat	PBW 761 (Unnat PBW 550), PBW 757	<i>Yr15</i>	Stripe rust resistance	[76,158]
	PBW 752	<i>Yr10</i>		
	HI8498	<i>Sr2 and Sr36</i>	Stem rust	[160]
	HUW510	<i>Lr34</i>	Spot blotch	[75]
	PBW 723 (Unnat PBW 343)	<i>Yr17+Yr40+ Lr37 + Lr57</i>	Stripe & leaf rust resistance	[76,180]
	PBW 771	<i>Yr40 + Lr57</i>		
	HD2967	<i>Lr19 + Yr10+Lr34</i>		
	HD2733	<i>Lr19/Sr25+ Lr24/Sr24+ Yr10</i>		
	HD2932	<i>g Lr19/Sr25, Sr26 and Yr10</i>	three rust together	[76]
	Xiaoyan22	<i>Dx5+ Dy10+Yr26+ML91260</i>	Stripe rust + powdery mildew and glutenin	[77]
RIL-169, RIL -151, SDAU1881, SDAU1886	<i>Fhb1 and Fhb2</i>	Fusarium Head Blight	[157,181, 182]	
Sorghum	Tabet, Wad Ahmed	two or more qtls	Striga resistance	[79]
	Parbhani Moti, ICSB 29004	<i>SBI-01/LG A + SBI-07/LG E + SBI-10/LG G</i>	Shoot fly resistance	[80]
Pearlmillet	HBB 67 Improved	<i>qRSg1 + qRSg4</i>	Downy mildew resistance	[78]
	HBB 67 Improved 2	<i>qRSg3.1+ qRSg4.2 + qRSg6.1</i>		[99]
Chickpea	IPCMB 19-3 (Samridhhi), Pusa 256	<i>foc2</i>	Fusarium wilt resistance	[88,89,183]
	Super Annigeri-1, JG 74315-14	<i>foc4</i>		
	Pusa Chickpea 20211	<i>foc1+ foc3+ foc4 + foc5</i>		
C 214	<i>foc1+ABQTL-I + ABQTL-II</i>	Fusarium wilt (FW) and Ascochyta blight (AB)	[87]	
Soybean	NRCSL 1	<i>Rymv</i>	YMV resistance	
	SJ10-122-040, SJ10-173-072 and SJ10-158-039	<i>Rpp1-b + Rpp5 and Rpp4 + Rpp5</i>	Asian soybean rust	[166]
	CO 3, JS 335	<i>Rps2+Rmd-c + rj2</i>	Phytophthora rot and powdery mildew resistance and effective nodulating gene	[84]
Ground nut	ICGV 13192, 13193, 13200, 13206, 13228 and ICGV 13229	Major QTL for	rust and late leaf spot resistance	[86]
Maize	Huangzao4, Ye478, Chang7-2, Zheng58, Zhonghuang68, B73, and Ji846	<i>qMrdd8</i>	Maize rough dwarf disease	[81]
	Ji853, 444, 98107, 99094, Chang7-2, V4, V022, 982, 8903, and 8902	<i>qHSR1</i>	Head smut	[82]
Brassica	Improved Topas DH16516	<i>Rlm1, 2, 3, 4, LepR1, LepR2 & LepR3</i>	<i>Leptosphaeria maculans</i> resistance	[164]

rices of the soybean cyst nematode has created the disease-resistant and high-yielding genotype ‘JTN 5503’ [83]. Two rust resistance gene combinations (*Rpp4+Rpp5* and *Rpp1-b + Rpp5*) were integrated into three elite lines, SJ10-173-072, SJ10-122-040 and SJ10-158-039 to introgress Asian soybean rust resistance. The powdery mildew resistance and efficient nodulating gene combinations (*Rps2+Rmd-c + rj2*) were stacked into the soybean cultivars JS335 and CO3 for multiple disease resistance [84]. [85] developed many introgression lines in groundnut by introducing a major QTL for rust resistance into the three susceptible cultivars JL 24, ICGV 91114, and TAG 24, which showed higher yield and increased rust resistance. Similar to this, a significant QTL that conferred multiple disease resistance, including rust and late leaf spot, was inserted into the same above three groundnut cultivars from which six lines (ICGV 13192, 13193, 13200, 13206, 13228, and ICGV 13229) were derived [86].

Popular chickpea cultivar C 214 was improved parallel to fusarium wilt (*foc1*) and ascochyta blight (*ABQTL-I* and *II*) by MABC [87]. In order to achieve long-lasting resistance against fusarium wilt, Pusa Chickpea 20211 was developed by transferring the four different race combinations (*foc1 + foc3 + foc4 + foc5*) in the background of ‘Pusa 391’ [88]. By introducing genomic region (*foc4*) resistant to fusarium wilt (race 4), the elite desi cultivars JG 74 and Annigeri 1 were improved and made available as super JG 74315-14 and Annigeri 1 [89]. Table 3 illustrates the development of several improved varieties and lines with enhanced resistance to various biotic stresses through the application of genomic-assisted breeding techniques.

7.2. Abiotic stress

The recent introgression of salt tolerance (*Saltol*), submergence tolerance (*sub1*), and drought tolerance QTL in rice cultivars for increasing abiotic stress tolerance indicates the great potential of GAB (Table 2). *Sub1* QTL was introduced into several high-yielding varieties in India, including Swarna [90], Samba, Pusa Basmati [91], Bahadur and Ranjit [92]. Following the QTL-introgression for submergence, higher survival rates of Samba Mahsuri (BPT 5204), Thadokkham 1 (TDK1), CR 1009 and BR 11 were observed [93]. The potential rice varieties that were used for introgressing *Saltol* QTL were Pusa Basmati 1 [91], Pusa Basmati 1121 [94], AS 996, BT 7, Q5DB, and BRRI-Dhan 49 [95]. A pyramiding of two major QTLs of drought tolerance into Sabitri (drought-susceptible variety of Nepal) is similar to the breeding for salinity and submergence tolerance instances stated above [96]. Other established varieties with drought and submergence tolerance are CR Dhan 801 [97], Subhash [98], Samba Mahsuri-Sub 1, and IR64-Sub1 [92]. Herbicide-tolerant QTL (*AHAS*) was incorporated in the development of Pusa Basmati 1979 and Pusa Basmati 1985 [99].

In the case of wheat, the variety ‘HD 2733’ was improved for drought tolerance by transferring three significant QTLs, and five prospective varieties were identified, including HD2733-208-96-204-36-42, HD2733-297-235-609-70-35, HD2733-217-8-22-9, HD2733-208- 23-6-18, and HD2733-208-18-4-25 [100]. For instance, the first pulse molecular breeding product in India, Pusa 10216, was created as a result of the introgression of the “QTL hotspot” region governing drought tolerance traits into the Pusa 372 [101]. Additional drought-tolerant cultivars created by adding QTL hotspot include Improved JG 11 [102], KAK2, Chefe [103], and Pusa Chickpea 4005 [101]. The elite soybean germplasm lines LS93-0375 and BMX Desafio RR introgressed with drought-tolerant gene *AtAREB1* [104].

7.3. Quality traits

One of the advances in quality improvement using genomic assisted breeding has been the introgression of the high protein content gene *GPC-B1* into wheat (Table 5). As a result of this, high GPC cultivars have been developed in the USA (Westmore, Desert King-High Protein and Lassik), Australia (Gladius, VR1128) and Canada (Burnside, Lillian) [28]. A gene *PsyE1* encoding for Phytoene Synthase

Table 4
Improved mega varieties/lines introgressed with various abiotic stress resistance genes using Genomic assisted breeding.

Crop	Name of the lines/variety	Gene combination	Trait(s) target	References
Rice	Swarna (CR 2539-1), Samba, CRI009, CO 43, ADT 46, HUR 105, Bahadur, MTU 1075, Pratikshya, Pooja, Rajendra Mahsuri, Ranjit, CR Dhan 803 (Trilochan)	<i>Sub1</i>	Submergence	[90,92,184, 185]
	Pusa Basmati 1, Pusa Basmati 1121, Pusa Basmati 1509, Improved Sarjoo and Improved Pusa 44	<i>Saltol</i>	Salinity	[91,94,150]
	ADT 45, Gayatri, MTU 1010, PR 114, Pusa 44, Sarjoo 52	<i>qSALTOL + qSSISFH8. 1</i>	Salinity	[92]
	IR 64 Drt1 (DRR Dhan 42)	<i>qDTY2.2 + qDTY4.1</i>	Drought tolerance	[99]
	Aiswarya	<i>Saltol + Sub1</i>	Salinity & submergence	[186]
	Pusa Basmati 1979, Pusa Basmati 1985	<i>AHAS</i>	Herbicide tolerance	[99]
	CR Dhan 801	<i>qDTY1. 1+qDTY2.1+qDTY3.1 + Sub1</i>	Drought and submergence	[97]
CR Dhan 802 (Subhash), DRR Dhan 50	<i>qDTY2.1+qDTY3.1+Sub1</i>		[98]	
Samba Mahsuri-Sub 1	<i>Sub1+DTY1. 1+DTY2. 1+DTY2. 2 +DTY3.1</i>		[92]	
IR64-Sub1	<i>Sub1+qDTY1.1+qDTY2.2+qDTY3.1</i>		[92]	
Wheat	HD2733	Three QTLs for drought	Drought tolerance	[100]
Soybean	LS93-0375, BMX Desafio RR	<i>AtAREB1</i>		[104]
Chick pea	JG 11, KAK2, Chefe, Pusa Chickpea 10216, Pusa Chickpea 4005, IPCL4-14	QTL hotspot		[101–103]

encoding Y gene was recently identified in wheat [105], which can increase the carotenoid content and have tremendous scope for developing biofortified wheat varieties. Improved lines of rice for intermediate amylose and fragrance content were produced by transferring *Wx* and *badh2* (mutant alleles) from basmati into Manawthukha cultivar [22]. [106] developed groundnut lines ‘Tifguard High O/L’ with high oleic acid content (*AhFAD2B*) and nematode resistance (*Rma*). The peanut variety, ‘TifNV-High O/L’, was made to be resistant to nematodes, tomato spotted wilt, and to have a high oleic acid content [107]. Three peanut lines (ICGV 06110, 06142, 06420) with altered mutant alleles (*ahFAD2A* and *ahFAD2B*) were developed for the control of the composition of the three major fatty acids (oleic, palmitic acids and linoleic) which together determine the quality of peanut oil [108].

In three well-known Indian groundnut varieties (GJG9, GJGHPS1 and GG20) [109], coupled the resistance to foliar diseases (rust and late leaf spot) with high oleic acid. A QPM variant of the elite line BML-7 in maize was created by transferring the *opaque-2* with the help of linked marker *umc1066* [110]. The β -carotene hydroxylase (*crtRB1*) gene was introduced into seven parental lines (V335, V345, VQL1, VQL2, HKI1105, HKI323, and HKI161) of the elite maize hybrids and CO6 (UMI1200 \times UMI 1230) to increase β -carotene content [111,112]. To increase the quality of the protein the Kunitz trypsin inhibitor (*KTI*) was removed from two superior soybean genotypes, ‘DS9712’ and ‘DS9814’, and six KTI free lines were developed [113]. To increase the nutritional value of the soybean, tetra recessive alleles (*lox1lox2lox3/lox1lox2lox3-ti/ti-le/le-cgy1/cgy1*) for the anti-nutritional factors were incorporated in the genetic background of ‘Daewonkong’ and the first soybean strain with absence of lipoxygenase, lectin, KTI, and 7S α' subunit proteins was developed [114].

7.4. GAB for yield and agronomic traits

The immediate improvement of yield and agronomic traits through GAB has been subject to limited studies. However, notable impacts have been observed in a few instances, as summarized in Table 4. For example, incorporating yield QTL into the soybean varieties ‘AG4501’ and ‘AG2401’ using GAB resulted in significant improvements in their yield [115]. Similarly, introducing the null allele of E1 into the variety ‘NRC 138’ enhanced its earliness [99]. Genome-based breeding utilizing the pod-shattering-resistant gene (*pdh1* mutant) from ‘Hayahikari’ has led to the development of four soybean cultivars resistant to pod dehiscence, namely ‘Sachiyutaka A1 gou’, ‘Fukuyutaka A1 gou’, ‘Enreinosora’, and ‘Kotoyutaka A1 gou’ [116]. Introducing the SPIKE gene into the variety ‘NSIC Rc 158’ in rice resulted in increased grain yield and spikelet number [117]. Furthermore, the transplantation of a QTL (Qyld.csdh.7AL) improved grain yield in four wheat cultivars, namely HUW468, HUW234, DBW17 and K307 [118]. These studies demonstrate the potential of GAB in directly enhancing yield and agronomic traits in various crop species. Table 6 presents the improved varieties and lines that have been developed by introgressing genes related to yield and agronomic traits using genomic-assisted breeding techniques.

8. Conclusions

Conventional plant breeding has made tremendous progress in ensuring food as well as nutritional security. However, the increasing population and varied food and lifestyle demands have made it hard for conventional breeding to keep up. Genomics-assisted breeding promises high precision and efficiency compared to traditional plant breeding. The new approaches of GAB, like genomic selection (GS), have shown promise in designing new breeding programs and in developing new genetic evaluation models based on molecular genetic markers. The successful and efficient utilization of GAB methodologies in crop species heavily relies on the accessibility of genome-wide, cost-effective, high-throughput and flexible markers that exhibit minimal bias and can be applied to both model and non-model crop species, regardless of the availability of a reference genome sequence. These factors were significant

Table 5
Improved varieties/lines introgressed with quality traits related genes using Genomic assisted breeding.

Crop	Name of the lines/variety	Gene combination	Trait(s) target	References
Soybean	NRC 127, MACSNRC 1667, DS9712, DS9814, JS97-52	Null allele of <i>KTi</i>	KTI free	[99,113, 187]
	NRC 109 Daewonkong	Null allele of <i>lox2</i> <i>lox1lox2lox3/lox1lox2lox3-ti/ti-le/le-cgy1/cgy1</i>	lipoxygenase-2 free lipoxygenase, Kunitz trypsin inhibitor (KTI), lectin, and 7S α' subunit proteins	- [114]
Ground nut	Girnar 4, Girnar 5, ICGV 06110, 06142 and 06420 TifNV-High O/L	<i>ahFAD2a</i> + <i>ahFAD2b</i> <i>Rma</i> + <i>AhFAD2</i>	Oleic acid Nematode resistance + Tomato spotted wilt + oleic acid	[99,108] [107]
Maize	Vivek QPM9, Pusa HM4/HM8/HM9 Improved, BML-7	<i>opaque2</i>	Lysine & tryptophan	[99,110, 161]
	Pusa Vivek QPM9 Improved, VQL1, VQL2, V335, V345, Pusa Vivek Hybrid-27 Improved, HKI1105, HKI323, and HKI161, CO6	<i>crtRB1</i>	Provitamin-A	[99,112, 188]
	Pusa HQPM-1, 5, 7 Improved, Pusa Biofortified Maize Hybrid-1	<i>crtRB1</i> + <i>lcyE</i>	Provitamin-A	[99]
	QCL5008, HQPM-1, 4, 5, 7 HQPM-1- PV, HQPM- 5- PV, HQPM- 4- PV, and HQPM- 7- PV o16 o16w x w x	<i>o-16</i> <i>CrtRB1</i> , <i>LcyE</i> and <i>VTE4</i> <i>o-2</i> and <i>o-16</i>	Quality Protein QPM, Provitamin and vitamin E QPM and Waxy corn	[162,189] [163] [190]

Table 6
Improved varieties/lines introgressed with yield and agronomic traits related genes using Genomic assisted breeding.

Crop	Name of the lines/variety	Gene combination	Trait(s) target	References
Rice	NSIC Rc 158	<i>SPIKE</i>	Spikelet number	[117]
Soybean	NRC 138	Null allele of <i>E1</i>	Early maturity	–
	AG4501, AG2401	Yield QTL	Yield	[115]
Wheat	Sachiyutaka A1 gou, Fukuyutaka A1 gou, Enreinosora and Kotoyutaka A1 gou	<i>Pdh1</i>	Pod shattering	[116]
	HUW234, HUW468, K307 and DBW17	<i>Qyld.csdh.7AL</i>	yield	[118]
	Mentana, Ardito, Villa Glori, and Damiano	<i>Rht1</i> and <i>Ppd-D1</i>	Dwarfing gene and Photoperiod	[24]

limitations in earlier marker systems, such as SSR and array-based approaches, which were inconceivable before the advent of NGS technologies. NGS has revolutionized genotyping by providing novel platforms for SNP genotyping, particularly through genotyping by sequencing. Third-generation sequencing technologies (PacBio SMRT and Oxford Nanopore sequencing) offer long-read capabilities that accurately resolve complex genomic regions and structural variants. These advancements enable complete genome assemblies and a comprehensive pan-genome representation, which is crucial for capturing genetic diversity. Consequently, these technologies enhance the precision of genomics-assisted breeding, supporting the development of resilient, high-yield, and nutritionally superior crops.

CRedit authorship contribution statement

Vikas Mangal: Writing – review & editing. **Lokesh Kumar Verma:** Writing – original draft. **Sandeep Kumar Singh:** Writing – original draft. **Kanak Saxena:** Conceptualization. **Anirban Roy:** Writing – original draft. **Anandi Karn:** Supervision. **Rohit Rohit:** Writing – review & editing. **Shruti Kashyap:** Conceptualization. **Ashish Bhatt:** Writing – review & editing, Writing – original draft. **Salej Sood:** Writing – review & editing, Conceptualization.

Declaration of competing interest

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests:

I am working as associate editor in the Journal.

References

- [1] D. Zamir, Improving plant breeding with exotic genetic libraries, *Nat. Rev. Genet.* 2 (2001) 983–989.
- [2] J. Skurie, On world population day, unpacking 9.6 billion by 2050, *Natl. Geogr. Natl. Geogr. Soc.* 11 (2013).
- [3] J.M. Ribaut, M.C. De Vicente, X. Delannay, Molecular breeding in developing countries: challenges and perspectives, *Curr. Opin. Plant Biol.* 13 (2010) 213–218.
- [4] Y. Xu, J.H. Crouch, Marker-assisted selection in plant breeding: from publications to practice, *Crop Sci.* 48 (2008) 391–407.
- [5] S.R. Eathington, T.M. Crosbie, M.D. Edwards, R.S. Reiter, J.K. Bull, Molecular markers in a commercial breeding program, *Crop Sci.* 47 (2007) S–154, <https://doi.org/10.2135/cropsci2007.04.00151PBS>.
- [6] P.K. Gupta, P. Langridge, R.R. Mir, Marker-assisted wheat breeding: present status and future possibilities, *Mol. Breed.* 26 (2010) 145–161, <https://doi.org/10.1007/s11032-009-9359-7>.
- [7] A.M. Perez-de-Castro, S. Vilanova, J. Cañizares, L. Pascual, J. M Blanca, M. J Diez, J. Prohens, B. Picó, Application of genomic tools in plant breeding, *Curr. Genom.* 13 (2012) 179–195.
- [8] P. Leng, T. Lübberstedt, M. Xu, Genomics-assisted breeding—a revolutionary strategy for crop improvement, *J. Integr. Agric.* 16 (2017) 2674–2685.
- [9] M. Goddard, Genomic selection: prediction of accuracy and maximisation of long term response, *Genetica* 136 (2009) 245–257, <https://doi.org/10.1007/s10709-008-9308-0>.
- [10] J. Crossa, P. Pérez-Rodríguez, J. Cuevas, et al., Genomic selection in plant breeding: methods, models, and perspectives, *Trends Plant Sci.* 22 (2017) 961–975, <https://doi.org/10.1016/j.tplants.2017.08.011>.
- [11] J.L. Jannink, A.J. Lorenz, H. Iwata, Genomic selection in plant breeding: from theory to practice, *Briefings Funct. Genom. Proteomics* 9 (2010) 166–177, <https://doi.org/10.1093/bfpg/elq001>.
- [12] R. Bernardo, Molecular markers and selection for complex traits in plants: learning from the last 20 years, *Crop Sci.* 48 (2008) 1649–1664.
- [13] S.A. Goff, D. Ricke, T.H. Lan, et al., A draft sequence of the rice genome (*Oryza sativa* L. ssp. japonica), *Science* (80-) 296 (2002) 92–100, <https://doi.org/10.1126/science.1068275>.
- [14] J. Yu, S. Hu, J. Wang, et al., A draft sequence of the rice genome (*Oryza sativa* L. ssp. indica), *Science* (80-) 296 (2002) 79–92, <https://doi.org/10.1126/science.1068037>.
- [15] S.G. Krattinger, B. Keller, Oat genome — sequence of a superfood, *Nat. Plants* 8 (2022) 602–603, <https://doi.org/10.1038/s41477-022-01169-z>.
- [16] R.K. Varshney, P. Sinha, V.K. Singh, A. Kumar, Q. Zhang, J.L. Bennetzen, 5Gs for crop genetic improvement, *Curr. Opin. Plant Biol.* 56 (2020) 190–196, <https://doi.org/10.1016/j.pbi.2019.12.004>.
- [17] Y. Jiao, P. Peluso, J. Shi, et al., Improved maize reference genome with single-molecule technologies, *Nature* 546 (2017) 524–527, <https://doi.org/10.1038/nature22971>.
- [18] M.H.W. Schmidt, A. Vogel, A.K. Denton, et al., De novo assembly of a new *Solanum pennellii* accession using nanopore sequencing, *Plant Cell* 29 (2017) 2336–2348, <https://doi.org/10.1105/tpc.17.00521>.
- [19] R. Della Coletta, Y. Qiu, S. Otu, M.B. Hufford, C.N. Hirsch, How the pan-genome is changing crop genomics and improvement, *Genome Biol.* 22 (2021) 1–19, <https://doi.org/10.1186/s13059-020-02224-8>.
- [20] E. Espinosa, R. Bautista, R. Larrosa, O. Plata, Advancements in long-read genome sequencing technologies and algorithms, *Genomics* 116 (2024) 110842, <https://doi.org/10.1016/j.ygeno.2024.110842>.
- [21] S. Sarkar, R. Yelne, M. Chatterjee, P. Das, S. Debnath, A. Chakraborty, N. Mandal, K. Bhattacharya, S. Bhattacharyya, Screening for phosphorus(P) tolerance and validation of Pup-1 linked markers in indica rice, *Indian J. Genet. Plant Breed.* 71 (2011) 209–213.

- [22] M. Yi, K.T. Nwe, A. Vanavichit, W. Chai-arree, T. Toojinda, Marker assisted backcross breeding to improve cooking quality traits in Myanmar rice cultivar Manawthukha, *F. Crop. Res.* 113 (2009) 178–186, <https://doi.org/10.1016/j.fcr.2009.05.006>.
- [23] D. Das, P. Sen, S. Purkayastha, A.K. Saha, A. Roy, P. Rai, S. Sen, S. Saha, B.K. Senapati, T. Biswas, S. Bhattacharyya, A perfect PCR based co-dominant marker for low grain-arsenic accumulation genotyping in rice, *Ecotoxicol. Environ. Saf.* 212 (2021), <https://doi.org/10.1016/j.ecoenv.2021.111960>.
- [24] S. Salvi, O. Porfiri, S. Ceccarelli, Nazareno strampelli, the ‘prophet’ of the green revolution, *J. Agric. Sci.* 151 (2013) 1–5, <https://doi.org/10.1017/S0021859612000214>.
- [25] F. Shahinnia, M. Geyer, A. Block, V. Mohler, L. Hartl, Identification of Rf9, a gene contributing to the genetic complexity of fertility restoration in hybrid wheat, *Front. Plant Sci.* 11 (2020) 1720, <https://doi.org/10.3389/fpls.2020.577475>.
- [26] A.R. Peters Haugrud, Q. Zhang, A.J. Green, S.S. Xu, J.D. Faris, Identification of stable QTL controlling multiple yield components in a durum 3 cultivated emmer wheat population under field and greenhouse conditions, *G3 Genes, Genomes, Genet.* 13 (2023) jkac281, <https://doi.org/10.1093/g3journal/jkac281>.
- [27] G. Doussinault, A. Delibes, R. Sanchez-Monge, F. Garcia-Olmedo, Transfer of a dominant gene for resistance to eyespot disease from a wild grass to hexaploid wheat, *Nature* 303 (1983) 698–700, <https://doi.org/10.1038/303698a0>.
- [28] O.P. Mitrofanova, A.G. Khakimova, New genetic resources in wheat breeding for increased grain protein content, *Russ. J. Genet. Appl. Res.* 7 (2017) 477–487, <https://doi.org/10.1134/S2079059717040062>.
- [29] P. Sinha, V.K. Singh, R.K. Saxena, A.W. Khan, R. Abbai, A. Chitikineni, A. Desai, J. Molla, H.D. Upadhyaya, A. Kumar, R.K. Varshney, Superior haplotypes for haplotype-based breeding for drought tolerance in pigeonpea (*Cajanus cajan* L.), *Plant Biotechnol. J.* 18 (2020) 2482–2490, <https://doi.org/10.1111/pbi.13422>.
- [30] R. Kumar, P. Janila, M.K. Vishwakarma, A.W. Khan, S.S. Manohar, S.S. Gangurde, M.T. Variath, Y. Shasidhar, M.K. Pandey, R.K. Varshney, Whole-genome resequencing-based QTL-seq identified candidate genes and molecular markers for fresh seed dormancy in groundnut, *Plant Biotechnol. J.* 18 (2020) 992–1003, <https://doi.org/10.1111/pbi.13266>.
- [31] A. Roy, M.H. Reddy, M. Sarkar, D. Sagolsem, S.K. Murmu, C. Das, D. Roy, S. Ganguly, R. Nath, P.K. Bhattacharyya, A. Sarker, S. Bhattacharyya, A mis-splicing early flowering 3 (elf3) allele of lentil is associated with yield enhancement under terminal heat stress, *J. Appl. Genet.* 64 (2023) 265–273, <https://doi.org/10.1007/s13353-023-00753-z>.
- [32] D. Bajaj, H.D. Upadhyaya, S. Das, V. Kumar, C.L.L. Gowda, S. Sharma, A.K. Tyagi, S.K. Parida, Identification of candidate genes for dissecting complex branch number trait in chickpea, *Plant Sci.* 245 (2016) 61–70, <https://doi.org/10.1016/j.plantsci.2016.01.004>.
- [33] R. Barmukh, M. Rookiwal, G.P. Dixit, et al., Characterization of ‘QTL-hotspot’ introgression lines reveals physiological mechanisms and candidate genes associated with drought adaptation in chickpea, *J. Exp. Bot.* 73 (2022) 7255–7272, <https://doi.org/10.1093/jxb/erac348>.
- [34] D. Deres, T. Feyissa, Concepts and applications of diversity array technology (DART) markers for crop improvement, *J. Crop Improv.* (2022), <https://doi.org/10.1080/15427528.2022.2159908>.
- [35] C. Zhang, S. Jiang, Y. Tian, X. Dong, J. Xiao, Y. Lu, T. Liang, H. Zhou, D. Xu, H. Zhang, M. Luo, Z. Xia, Smart breeding driven by advances in sequencing technology, *Mod. Agric. For.* 1 (2023) 43–56, <https://doi.org/10.1002/MODA.8>.
- [36] Y. Zhang, T. Li, Y. Geng, Y. Wang, Y. Liu, H. Li, C. Hao, H. Wang, X. Shang, X. Zhang, Identification and development of a KASP functional marker of TaTAP46-5A associated with kernel weight in wheat (*Triticum aestivum*), *Plant Breed.* 140 (2021) 585–594, <https://doi.org/10.1111/pbr.12922>.
- [37] J. Semalappan, S. Selvanayagam, A. Rathore, et al., Development of a new AgriSeq 4K mid-density SNP genotyping panel and its utility in pearl millet breeding, *Front. Plant Sci.* 13 (2023) 1068883, <https://doi.org/10.3389/fpls.2022.1068883>.
- [38] A. Rasheed, Y. Hao, X. Xia, A. Khan, Y. Xu, R.K. Varshney, Z. He, Crop breeding chips and genotyping platforms: progress, challenges, and perspectives, *Mol. Plant* 10 (2017) 1047–1064, <https://doi.org/10.1016/j.molp.2017.06.008>.
- [39] I. Medina-Lozano, A. Díaz, Applications of genomic tools in plant breeding: crop biofortification, *Int. J. Mol. Sci.* 23 (2022) 3086, <https://doi.org/10.3390/ijms23063086>.
- [40] H. Liu, B. Zeng, J. Zhao, S. Yan, J. Wan, Z. Cao, Genetic research progress: heat tolerance in rice, *Int. J. Mol. Sci.* 24 (2023) 7140, <https://doi.org/10.3390/ijms24087140>.
- [41] A. Raza, M.S. Mubarak, R. Sharif, M. Habib, W. Jabeen, C. Zhang, H. Chen, Z.H. Chen, K.H.M. Siddique, W. Zhuang, R.K. Varshney, Developing drought-smart, ready-to-grow future crops, *Plant Genome* 16 (2023) e20279, <https://doi.org/10.1002/tpg2.20279>.
- [42] L. Song, R. Wang, X. Yang, A. Zhang, D. Liu, Molecular markers and their applications in marker-assisted selection (MAS) in bread wheat (*Triticum aestivum* L.), *Agriculture* 13 (2023) 642, <https://doi.org/10.3390/agriculture13030642>.
- [43] G. Keeble-Gagnère, R. Pasam, K.L. Forrest, D. Wong, H. Robinson, J. Godoy, A. Rattey, D. Moody, D. Mullan, T. Walmsley, H.D. Daetwyler, J. Tibbits, M. J. Hayden, Novel design of imputation-enabled SNP arrays for breeding and research applications supporting multi-species hybridization, *Front. Plant Sci.* 12 (2021) 2659, <https://doi.org/10.3389/fpls.2021.756877>.
- [44] K.S. Aitken, A. Farmer, P. Berkman, C. Muller, X. Wei, E. Demano, P.A. Jackson, M. Magwire, B. Dietrich, R. Kota, Generation of a 345K sugarcane SNP chip, *Int. Sugar J.* 119 (2017) 1165–1172.
- [45] S. Singh, A.K. Mahato, P.K. Jayaswal, N. Singh, M. Dheer, P. Goel, R.S. Raju, J.K. Yasin, R. Sreevathsa, V. Rai, K. Gaikwad, N.K. Singh, A 62K genic-SNP chip array for genetic studies and breeding applications in pigeonpea (*Cajanus cajan* L. Millsp.), *Sci. Rep.* 10 (2020) 1–14, <https://doi.org/10.1038/s41598-020-61889-0>.
- [46] M.M. Sabbavarapu, M. Sharma, S.K. Chamrathi, N. Swapna, A. Rathore, M. Thudi, P.M. Gaur, S. Pande, S. Singh, L. Kaur, R.K. Varshney, Molecular mapping of QTLs for resistance to Fusarium wilt (race 1) and Ascochyta blight in chickpea (*Cicer arietinum* L.), *Euphytica* 193 (2013) 121–133, <https://doi.org/10.1007/s10681-013-0959-2>.
- [47] J.K. Kitony, H. Sunohara, M. Tasaki, J.I. Mori, A. Shimazu, V.P. Reyes, H. Yasui, Y. Yamagata, A. Yoshimura, M. Yamasaki, S. Nishiuchi, K. Doi, Development of an aus-derived nested association mapping (Aus-nam) population in rice, *Plants* 10 (2021) 1255, <https://doi.org/10.3390/plants10061255>.
- [48] X. Wu, Y. Liu, X. Lu, L. Tu, Y. Gao, D. Wang, S. Guo, Y. Xiao, P. Xiao, X. Guo, A. Wang, P. Liu, Y. Zhu, L. Chen, Z. Chen, Integration of GWAS, linkage analysis and transcriptome analysis to reveal the genetic basis of flowering time-related traits in maize, *Front. Plant Sci.* 14 (2023), <https://doi.org/10.3389/fpls.2023.1145327>.
- [49] J.A. Bhat, D. Yu, A. Bohra, S.A. Ganie, R.K. Varshney, Features and applications of haplotypes in crop breeding, *Commun. Biol.* 4 (2021) 1–12, <https://doi.org/10.1038/s42003-021-02782-y>.
- [50] R.K. Srivastava, R.B. Singh, V.L. Pujarula, S. Bollam, M. Pusuluri, T.S. Chellapilla, R.S. Yadav, R. Gupta, Genome-wide association studies and genomic selection in pearl millet: advances and prospects, *Front. Genet.* 10 (2020) 1389, <https://doi.org/10.3389/fgene.2019.01389>.
- [51] Y. Yuan, J.E. Cairns, R. Babu, et al., Genome-wide association mapping and genomic prediction analyses reveal the genetic architecture of grain yield and flowering time under drought and heat stress conditions in maize, *Front. Plant Sci.* 9 (2019) 1919, <https://doi.org/10.3389/fpls.2018.01919>.
- [52] H. Takagi, A. Abe, K. Yoshida, S. Kosugi, S. Natsume, C. Mitsuoka, A. Uemura, H. Utsushi, M. Tamiru, S. Takuno, H. Innan, L.M. Cano, S. Kamoun, R. Terauchi, QTL-seq: rapid mapping of quantitative trait loci in rice by whole genome resequencing of DNA from two bulked populations, *Plant J.* 74 (2013) 174–183, <https://doi.org/10.1111/TPJ.12105>.
- [53] A.N. Chan, L.L. Wang, Y.J. Zhu, Y.Y. Fan, J.Y. Zhuang, Z.H. Zhang, Identification through fine mapping and verification using CRISPR/Cas9-targeted mutagenesis for a minor QTL controlling grain weight in rice, *Theor. Appl. Genet.* 134 (2021) 327–337, <https://doi.org/10.1007/s00122-020-03699-6>.
- [54] P. Li, J. Jiang, G. Zhang, S. Miao, J. Lu, Y. Qian, X. Zhao, W. Wang, X. Qiu, F. Zhang, J. Xu, Integrating GWAS and transcriptomics to identify candidate genes conferring heat tolerance in rice, *Front. Plant Sci.* 13 (2023) 1102938, <https://doi.org/10.3389/fpls.2022.1102938>.
- [55] M.F. Scott, O. Ladejebi, S. Amer, et al., Multi-parent populations in crops: a toolbox integrating genomics and genetic mapping with breeding, *Heredity* 125 (2020) 396–416, <https://doi.org/10.1038/s41437-020-0336-6>.
- [56] D.H. Lyra, G. Galli, F.C. Alves, Í.S.C. Granato, M.S. Vidotti, M. Bandeira e Sousa, J.S. Morosini, J. Crossa, R. Fritsche-Neto, Modeling copy number variation in the genomic prediction of maize hybrids, *Theor. Appl. Genet.* 132 (2019) 273–288, <https://doi.org/10.1007/s00122-018-3215-2>.

- [57] J. Wang, W. Yang, S. Zhang, H. Hu, Y. Yuan, J. Dong, L. Chen, Y. Ma, T. Yang, L. Zhou, J. Chen, B. Liu, C. Li, D. Edwards, J. Zhao, A pangenome analysis pipeline provides insights into functional gene identification in rice, *Genome Biol.* 24 (2023) 1–22, <https://doi.org/10.1186/s13059-023-02861-9>.
- [58] Y. Zhou, D. Chebotarov, D. Kudrna, et al., A platinum standard pan-genome resource that represents the population structure of Asian rice, *Sci. Data* 7 (2020) 1–11, <https://doi.org/10.1038/s41597-020-0438-2>.
- [59] J.D. Montenegro, A.A. Goliz, P.E. Bayer, B. Hurgobin, H.T. Lee, C.K.K. Chan, P. Visendi, K. Lai, J. Dolezel, J. Batley, D. Edwards, The pangenome of hexaploid bread wheat, *Plant J.* 90 (2017) 1007–1013, <https://doi.org/10.1111/tpj.13515>.
- [60] L. Gao, I. Gonda, H. Sun, et al., The tomato pan-genome uncovers new genes and a rare allele regulating fruit flavor, *Nat. Genet.* 51 (2019) 1044–1051, <https://doi.org/10.1038/s41588-019-0410-2>.
- [61] A.A. Goliz, P.E. Bayer, G.C. Barker, et al., The pangenome of an agronomically important crop plant Brassica oleracea, *Nat. Commun.* 7 (2016) 1–8, <https://doi.org/10.1038/ncomms13390>.
- [62] X. Sun, C. Jiao, H. Schwaninger, C.T. Chao, Y. Ma, N. Duan, A. Khan, S. Ban, K. Xu, L. Cheng, G.Y. Zhong, Z. Fei, Phased diploid genome assemblies and pangenomes provide insights into the genetic history of apple domestication, *Nat. Genet.* 52 (2020) 1423–1432, <https://doi.org/10.1038/s41588-020-00723-9>.
- [63] G. Haberer, N. Kamal, E. Bauer, et al., European maize genomes highlight intraspecies variation in repeat and gene content, *Nat. Genet.* 52 (2020) 950–957, <https://doi.org/10.1038/s41588-020-0671-9>.
- [64] S. Hübner, N. Bercovich, M. Todesco, et al., Sunflower pan-genome analysis shows that hybridization altered gene content and disease resistance, *Nat. Plants* 5 (2019) 54–62, <https://doi.org/10.1038/s41477-018-0329-0>.
- [65] L. Ou, D. Li, J. Lv, W. Chen, Z. Zhang, X. Li, B. Yang, S. Zhou, S. Yang, W. Li, H. Gao, Q. Zeng, H. Yu, B. Ouyang, F. Li, F. Liu, J. Zheng, Y. Liu, J. Wang, B. Wang, X. Dai, Y. Ma, X. Zou, Pan-genome of cultivated pepper (*Capsicum*) and its use in gene presence–absence variation analyses, *New Phytol.* 220 (2018) 360–363, <https://doi.org/10.1111/nph.15413>.
- [66] J. Shi, Z. Tian, J. Lai, X. Huang, Plant pan-genomics and its applications, *Mol. Plant* 16 (2023) 168–186, <https://doi.org/10.1016/j.molp.2022.12.009>.
- [67] M. Joseph, S. Gopalakrishnan, R.K. Sharma, V.P. Singh, A.K. Singh, N.K. Singh, T. Mohapatra, Combining bacterial blight resistance and Basmati quality characteristics by phenotypic and molecular marker-assisted selection in rice, *Mol. Breed.* 13 (2004) 377–387, <https://doi.org/10.1023/B:MOLB.0000034093.63593.4c>.
- [68] R.M. Sundaram, M.R. Vishnupriya, S.K. Biradar, G.S. Laha, G.A. Reddy, N.S. Rani, N.P. Sarma, R.V. Sonti, Marker assisted introgression of bacterial blight resistance in Samba Mahsuri, an elite indica rice variety, *Euphytica* 160 (2008) 411–422, <https://doi.org/10.1007/s10681-007-9564-6>.
- [69] K. Ratna Madhavi, R. Rambabu, V. Abhilash Kumar, S. Vijay Kumar, J. Aruna, S. Ramesh, R.M. Sundaram, G.S. Laha, M. Sheshu Madhav, V. Ravindra babu, M. S. Prasad, Marker assisted introgression of blast (Pi-2 and Pi-54) genes in rice to the genetic background of elite, bacterial blight resistant indica rice variety, Improved Samba Mahsuri, *Euphytica* 212 (2016) 331–342, <https://doi.org/10.1007/s10681-016-1784-1>.
- [70] A. Yugander, R.M. Sundaram, K. Singh, D. Ladhakshmi, L.V. Subba Rao, M.S. Madhav, J. Badri, M.S. Prasad, G.S. Laha, Incorporation of the novel bacterial blight resistance gene Xa38 into the genetic background of elite rice variety Improved Samba Mahsuri, *PLoS One* 13 (2018) e0198260, <https://doi.org/10.1371/journal.pone.0198260>.
- [71] G. Das, G.J.N. Rao, M. Varier, A. Prakash, D. Prasad, Improved Tapaswini having four BB resistance genes pyramided with six genes/QTLs, resistance/tolerance to biotic and abiotic stresses in rice, *Sci. Rep.* 8 (2018) 1–16, <https://doi.org/10.1038/s41598-018-20495-x>.
- [72] P. Dokku, K.M. Das, G.J.N. Rao, Genetic enhancement of host plant-resistance of the Lalat cultivar of rice against bacterial blight employing marker-assisted selection, *Biotechnol. Lett.* 35 (2013) 1339–1348, <https://doi.org/10.1007/s10529-013-1212-8>.
- [73] A. Khanna, V. Sharma, R.K. Ellur, et al., Development and evaluation of near-isogenic lines for major blast resistance gene(s) in Basmati rice, *Theor. Appl. Genet.* 128 (2015) 1243–1259, <https://doi.org/10.1007/s00122-015-2502-4>.
- [74] V. Kuraparthi, S. Sood, D.R. See, B.S. Gill, Development of a PCR assay and marker-assisted transfer of leaf rust and stripe rust resistance genes Lr57 and Yr40 into hard red winter wheats, *Crop Sci.* 49 (2009) 120–126, <https://doi.org/10.2135/cropsci2008.03.0143>.
- [75] N.K. Vasistha, A. Balasubramanian, V.K. Mishra, J. Srinivasa, R. Chand, A.K. Joshi, Molecular introgression of leaf rust resistance gene Lr34 validates enhanced effect on resistance to spot blotch in spring wheat, *Euphytica* 213 (2017) 1–10, <https://doi.org/10.1007/s10681-017-2051-9>.
- [76] N. Mallick, Vinod, J.B. Sharma, R.S. Tomar, M. Sivasamy, K.V. Prabhu, Marker-assisted backcross breeding to combine multiple rust resistance in wheat, *Plant Breed.* 134 (2015) 172–177, <https://doi.org/10.1111/pbr.12242>.
- [77] W. Zheng, S. Li, Z. Liu, Q. Zhou, Y. Feng, S. Chai, Molecular marker assisted gene stacking for disease resistance and quality genes in the dwarf mutant of an elite common wheat cultivar Xiaoyan22, *BMC Genet.* 21 (2020) 1–8, <https://doi.org/10.1186/s12863-020-00854-2>.
- [78] C.T. Hash, A. Sharma, M.A. Kolesnikova-Allen, S.D. Singh, R.P. Thakur, A.B. Raj, M.R. Rao, D.C. Nijhawan, C.R. Beniwal, P. Sagar, Teamwork delivers biotechnology products to Indian small-holder crop-livestock producers: pearl millet hybrid “HHB 67 Improved” enters seed delivery pipeline, *J. SAT Agric. Res.* 2 (2006) 1–3, <http://ejournal.icrisat.org/bioinformatics/v2i1/v2i1teamwork.pdf>. (Accessed 20 May 2023).
- [79] R. Ali, C.T. Hash, O. Damaris, A. Elhoussein, A.H. Mohamed, Introgression of striga resistance into popular Sudanese sorghum varieties using marker assisted selection, *World J. Biol. Biotechnol.* 1 (2016) 49, <https://doi.org/10.33865/wjb.001.01.0006>.
- [80] S. Gorthy, L. Narasu, A. Gaddameedi, H.C. Sharma, A. Kotla, S.P. Deshpande, A.K. Are, Introgression of shoot fly (*Atherigona soccata* L. Moench) resistance QTLs into elite post-rainy season sorghum varieties using marker assisted backcrossing (MABC), *Front. Plant Sci.* 8 (2017) 1494, <https://doi.org/10.3389/fpls.2017.01494>.
- [81] Z. Xu, J. Hua, F. Wang, Z. Cheng, Q. Meng, Y. Chen, X. Han, S. Tie, C. Liu, X. Li, Z. Wang, J. Weng, Marker-assisted selection of qmrd8 to improve maize resistance to rough dwarf disease, *Breed. Sci.* 70 (2020) 183–192, <https://doi.org/10.1270/jsbbs.19110>.
- [82] X. Zhao, G. Tan, Y. Xing, L. Wei, Q. Chao, W. Zuo, T. Lübberstedt, M. Xu, Marker-assisted introgression of qHSR1 to improve maize resistance to head smut, *Mol. Breed.* 30 (2012) 1077–1088, <https://doi.org/10.1007/s11032-011-9694-3>.
- [83] P.R. Arelli, L.D. Young, A. Mengistu, Registration of high yielding and multiple disease-resistant soybean germplasm JTN-5503, *Crop Sci.* 46 (2006) 2723–2724, <https://doi.org/10.2135/cropsci2005.12.0471crg>.
- [84] J. Ramalingam, G. Alagarasan, P. Savitha, K. Lydia, G. Pothiraj, E. Vijayakumar, R. Sudhagar, A. Singh, K. Vedna, C. Vanniarajan, Improved host-plant resistance to Phytophthora rot and powdery mildew in soybean (*Glycine max* (L.) Merr.), *Sci. Rep.* 10 (2020) 1–11, <https://doi.org/10.1038/s41598-020-70702-x>.
- [85] R.K. Varshney, M.K. Pandey, P. Janila, S.N. Nigam, H. Sudini, M.V.C. Gowda, M. Sriswathi, T. Radhakrishnan, S.S. Manohar, P. Nagesh, Marker-assisted introgression of a QTL region to improve rust resistance in three elite and popular varieties of peanut (*Arachis hypogaea* L.), *Theor. Appl. Genet.* 127 (2014) 1771–1781, <https://doi.org/10.1007/s00122-013-338-3>.
- [86] J. Pasupuleti, M.K. Pandey, S.S. Manohar, M.T. Variath, P. Nallathambi, H.L. Nadaf, H. Sudini, R.K. Varshney, Foliar fungal disease-resistant introgression lines of groundnut (*Arachis hypogaea* L.) record higher pod and haulm yield in multilocation testing, *Plant Breed.* 135 (2016) 355–366, <https://doi.org/10.1111/pbr.12358>.
- [87] R.K. Varshney, S.M. Mohan, P.M. Gaur, S.K. Chamarthi, V.K. Singh, S. Srinivasan, N. Swapna, M. Sharma, S. Pande, S. Singh, L. Kaur, Marker-assisted backcrossing to introgress resistance to Fusarium wilt race 1 and ascochyta blight in C 214, an elite cultivar of chickpea, *Plant Genome* 7 (2014), <https://doi.org/10.3835/plantgenome2013.10.0035>.
- [88] C. Bharadwaj, J. Jorben, A. Rao, et al., Development of high yielding Fusarium wilt resistant cultivar by pyramiding of “genes” through marker-assisted backcrossing in chickpea (*cicer arietinum* L.), *Front. Genet.* 13 (2022) 1747, <https://doi.org/10.3389/fgene.2022.924287>.
- [89] D.M. Mannur, A. Babbar, M. Thudi, et al., Super Annigeri 1 and improved JG 74: two Fusarium wilt-resistant introgression lines developed using marker-assisted backcrossing approach in chickpea (*Cicer arietinum* L.), *Mol. Breed.* 39 (2019) 1–13, <https://doi.org/10.1007/s11032-018-0908-9>.
- [90] C.N. Neeraja, R. Maghirang-Rodriguez, A. Pamplona, S. Heuer, B.C.Y. Collard, E.M. Septiningsih, G. Vergara, D. Sanchez, K. Xu, A.M. Ismail, D.J. Mackill, A marker-assisted backcross approach for developing submergence-tolerant rice cultivars, *Theor. Appl. Genet.* 115 (2007) 767–776, <https://doi.org/10.1007/s00122-007-0607-0>.

- [91] V.K. Singh, B.D. Singh, A. Kumar, S. Maurya, S.G. Krishnan, K.K. Vinod, M.P. Singh, R.K. Ellur, P.K. Bhowmick, A.K. Singh, Marker-assisted introgression of saltol QTL enhances seedling stage salt tolerance in the rice variety "pusa basmati 1," *Int. J. Genomics*. 2018 (2018) <https://doi.org/10.1155/2018/8319879>.
- [92] A. Bhandari, P. Jayaswal, N. Yadav, et al., Genomics-assisted backcross breeding for infusing climate resilience in high-yielding green revolution varieties of rice, *Indian J. Genet. Plant Breed.* 79 (2019) 160–170, <https://doi.org/10.31742/ijgpb.79s.1.5>.
- [93] M.M. Hasan, M.Y. Rafii, M.R. Ismail, M. Mahmood, H.A. Rahim, M.A. Alam, S. Ashkani, M.A. Malek, M.A. Latif, Marker-assisted backcrossing: a useful method for rice improvement, *Biotechnol. Equip.* 29 (2015) 237–254, <https://doi.org/10.1080/13102818.2014.995920>.
- [94] N.N. Babu, S.G. Krishnan, K.K. Vinod, S.L. Krishnamurthy, V.K. Singh, M.P. Singh, R.K. Ellur, V. Rai, H. Bollinedi, P.K. Bhowmick, A.K. Yadav, M. Nagarajan, N.K. Singh, K.V. Prabhu, A.K. Singh, Marker aided incorporation of saltol, a major QTL associated with seedling stage salt tolerance, into oryza sativa 'pusa basmati 1121, *Front. Plant Sci.* 8 (2017) 41, <https://doi.org/10.3389/fpls.2017.00041>.
- [95] A. Waziri, Kumar, R. Purty, Saltol QTL and their role in salinity tolerance in rice, *Austin J Biotechnol Bioeng. Austin J Biotechnol Bioeng.* 3 (2016), 1067–3, www.austinpublishinggroup.com. (Accessed 21 May 2023).
- [96] S. Dixit, R.B. Yadav, K.K. Mishra, A. Kumar, Marker-assisted breeding to develop the drought-tolerant version of Sabitri, a popular variety from Nepal, *Euphytica* 213 (2017) 1–16, <https://doi.org/10.1007/s10681-017-1976-3>.
- [97] A. Kumar, N. Sandhu, C. Venkateshwarlu, R. Priyadarshi, S. Yadav, R.R. Majumder, V.K. Singh, Development of introgression lines in high yielding, semi-dwarf genetic backgrounds to enable improvement of modern rice varieties for tolerance to multiple abiotic stresses free from undesirable linkage drag, *Sci. Rep.* 10 (2020) 1, <https://doi.org/10.1038/s41598-020-70132-9>.
- [98] R. Singh, Y. Singh, S. Xalaxo, et al., From QTL to variety-harnessing the benefits of QTLs for drought, flood and salt tolerance in mega rice varieties of India through a multi-institutional network, *Plant Sci.* 242 (2015) 278–287, <https://doi.org/10.1016/j.plantsci.2015.08.008>.
- [99] D.K. Yadava, P.R. Choudhury, F. Hossain, D. Kumar, Biofortified varieties: sustainable way to alleviate malnutrition, *Indian counc, Agric. Res.* (2022). <https://icar.org.in/files/BiofortifiedEnglish.pdf>. (Accessed 21 May 2023).
- [100] N. Rai, A. Bellundagi, P.K.C. Kumar, R. Kalasapura Thimmappa, S. Rani, N. Sinha, H. krishna, N. Jain, G.P. Singh, P.K. Singh, S. Chand, K.V. Prabhu, Marker-assisted backcross breeding for improvement of drought tolerance in bread wheat (*Triticum aestivum* L. em Thell), *Plant Breed.* 137 (2018) 514–526, <https://doi.org/10.1111/pbr.12605>.
- [101] C. Bharadwaj, S. Tripathi, K.R. Soren, et al., Introgression of "QTL-hotspot" region enhances drought tolerance and grain yield in three elite chickpea cultivars, *Plant Genome* 14 (2021) e20076, <https://doi.org/10.1002/tpg2.20076>.
- [102] R.K. Varshney, P.M. Gaur, S.K. Chamarthi, L. Krishnamurthy, S. Tripathi, J. Kashiwagi, S. Samineni, V.K. Singh, M. Thudi, D. Jaganathan, Fast-track introgression of "QTL-hotspot" for root traits and other drought tolerance traits in JG 11, an elite and leading variety of chickpea, *Plant Genome* 6 (2013), <https://doi.org/10.3835/plantgenome2013.07.0022> plantgenome2013.07.0022.
- [103] M. Thudi, P.M. Gaur, L. Krishnamurthy, R.R. Mir, H. Kudapa, A. Fikre, P. Kimurto, S. Tripathi, K.R. Soren, R. Mulwa, C. Bharadwaj, S. Datta, S.K. Chaturvedi, R.K. Varshney, Genomics-assisted breeding for drought tolerance in chickpea, *Funct. Plant Biol.* 41 (2014) 1178–1190, <https://doi.org/10.1071/FP13818>.
- [104] A.L.H. Caranhato, J. Angelotti-Mendonça, L.M. Mertz-Henning, S.R.R. Marin, C.L.P. de Melo, J.S.S. FOLONI, N. Neumaier, J.R.B. Farias, A.L. Nepomuceno, Drought tolerance of elite soybean cultivars with the introgression of transgene AtAREB1, *Pesqui. Agropecu. Bras.* 57 (2022) e02656, <https://doi.org/10.1590/S1678-3921.PAB2022.V57.02656>.
- [105] A.K. Padhy, A. Sharma, H. Sharma, R. Rajput, A. Pandey, P. Srivastava, S. Kaur, H. Kaur, S. Singh, L. Kashyap, G.S. Mavi, J. Kaur, V.S. Sohu, P. Chhuneja, N. S. Bains, Bread wheat with enhanced grain carotenoid content: a novel option for wheat biofortification, *Mol. Breed.* 42 (2022) 1–16, <https://doi.org/10.1007/s11032-022-01338-0>.
- [106] Y. Chu, C.L. Wu, C.C. Holbrook, B.L. Tillman, G. Person, P. Ozias-Akins, Marker-assisted selection to pyramid nematode resistance and the high oleic trait in peanut, *Plant Genome* 4 (2011) 110–117, <https://doi.org/10.3835/plantgenome2011.01.0001>.
- [107] C.C. Holbrook, P. Ozias-Akins, Y. Chu, A.K. Culbreath, C.K. Kvien, T.B. Brenneman, Registration of 'TiNV-high O/L' peanut, *J. Plant Registrations* 11 (2017) 228–230, <https://doi.org/10.3198/jpr2016.10.0059rc>.
- [108] P. Janila, M.K. Pandey, Y. Shasidhar, M.T. Variath, M. Sriswathi, P. Khera, S.S. Manohar, P. Nagesh, M.K. Vishwakarma, G.P. Mishra, T. Radhakrishnan, N. Manivannan, K.L. Dobariya, R.P. Vasanthi, R.K. Varshney, Molecular breeding for introgression of fatty acid desaturase mutant alleles (ahFAD2A and ahFAD2B) enhances oil quality in high and low oil containing peanut biotypes, *Plant Sci.* 242 (2016) 203–213, <https://doi.org/10.1016/j.plantsci.2015.08.013>.
- [109] Y. Shasidhar, M.T. Variath, M.K. Vishwakarma, S.S. Manohar, S.S. Gangurde, M. Sriswathi, H.K. Sudini, K.L. Dobariya, S.K. Bera, T. Radhakrishnan, M. K. Pandey, P. Janila, R.K. Varshney, Improvement of three popular Indian groundnut varieties for foliar disease resistance and high oleic acid using SSR markers and SNP array in marker-assisted backcrossing, *Crop J* 8 (2020) 1–15, <https://doi.org/10.1016/j.cj.2019.07.001>.
- [110] M.S.R. Krishna, M. Surender, S. Sokka Reddy, Marker assisted breeding for introgression of opaque-2 allele into elite maize inbred line BML-6, *Acta Ecol. Sin.* 37 (2017) 340–345, <https://doi.org/10.1016/j.chnaes.2017.04.002>.
- [111] V. Muthusamy, F. Hossain, N. Thirunavukkarasu, M. Choudhary, S. Saha, J.S. Bhat, B.M. Prasanna, H.S. Gupta, Development of β -carotene rich maize hybrids through marker-assisted introgression of β -carotene hydroxylase allele, *PLoS One* 9 (2014) e113583, <https://doi.org/10.1371/journal.pone.0113583>.
- [112] S. Natesan, T. Duraisamy, B. Pukalenty, S. Chandran, J. Nallathambi, K. Adhimoolum, D. Manickam, V. Sampathrajan, S.J. Muniyandi, L.J. Meitel, N. Thirunavukkarasu, G. Kalipatty Nalliappan, R. Rajasekaran, Enhancing β -carotene concentration in parental lines of CO6 maize hybrid through marker-assisted backcross breeding (MABB), *Front. Nutr.* 7 (2020) 134, <https://doi.org/10.3389/fnut.2020.00134>.
- [113] S. Maranna, K. Verma, A. Talukdar, S.K. Lal, A. Kumar, K. Mukherjee, Introgression of null allele of Kunitz trypsin inhibitor through marker-assisted backcross breeding in soybean (*Glycine max* L. Merr.), *BMC Genet.* 17 (2016) 1–9, <https://doi.org/10.1186/s12863-016-0413-2>.
- [114] S.W. Choi, W.G. Chae, G.Y. Kang, J. Il Chung, Breeding of tetra null soybean (*Glycine max*) for lipoxygenase, kunitz trypsin inhibitor, lectin, and 7S α ' subunit proteins, *Plant Breed.* 140 (2021) 123–129, <https://doi.org/10.1111/pbr.12870>.
- [115] V.C. Concibido, B. La Vallee, P. Mcclaird, N. Pineda, J. Meyer, L. Hummel, J. Yang, K. Wu, X. Delannay, Introgression of a quantitative trait locus for yield from *Glycine soja* into commercial soybean cultivars, *Theor. Appl. Genet.* 106 (2003) 575–582, <https://doi.org/10.1007/s00122-002-1071-5>.
- [116] T. Yamada, M. Hajika, H. Funatsuki, K. Takahashi, K. Hirata, A. Hishinuma, J. Tanaka, Causal analysis of yield-increase by introgression of shattering resistance gene *pdh1* in Soybean, *Japanese J. Crop Sci.* 86 (2017) 251–257, <https://doi.org/10.1626/jcs.86.251>.
- [117] D. Fujita, K.R. Trijatmiko, A.G. Tagle, M.V. Sapasap, Y. Koide, K. Sasaki, N. Tsakirpaloglou, R.B. Gannaban, T. Nishimura, S. Yanagihara, Y. Fukuta, T. Koshiba, I.H. Slamet-Loedin, T. Ishimaru, N. Kobayashi, NAL1 allele from a rice landrace greatly increases yield in modern indica cultivars, *Proc. Natl. Acad. Sci. U. S. A.* 110 (2013) 20431–20436, <https://doi.org/10.1073/pnas.1310790110>.
- [118] T. Gautam, Amardeep, G. Saripalli, Rakhi, A. Kumar, V. Gahlaut, D.A. Gadekar, M. Oak, P.K. Sharma, H.S. Balyan, P.K. Gupta, Introgression of a drought insensitive grain yield QTL for improvement of four Indian bread wheat cultivars using marker assisted breeding without background selection, *J. Plant Biochem. Biotechnol.* 30 (2021) 172–183, <https://doi.org/10.1007/s13562-020-00553-0>.
- [119] R. Brenchley, M. Spannagl, M. Pfeifer, et al., Analysis of the bread wheat genome using whole-genome shotgun sequencing, *Nature* 491 (2012) 705–710, <https://doi.org/10.1038/nature11650>.
- [120] P.S. Schnable, D. Ware, R.S. Fulton, et al., The B73 maize genome: complexity, diversity, and dynamics, *Science* 326 (2009) 1112–1115, <https://doi.org/10.1126/science.1178534>.
- [121] A.H. Paterson, J.E. Bowers, R. Bruggmann, et al., The Sorghum bicolor genome and the diversification of grasses, *Nature* 457 (2009) 551–556, <https://doi.org/10.1038/nature07723>.
- [122] R.K. Varshney, W. Chen, Y. Li, et al., Draft genome sequence of pigeonpea (*Cajanus cajan*), an orphan legume crop of resource-poor farmers, *Nat. Biotechnol.* 30 (2012) 83–89, <https://doi.org/10.1038/nbt.2022>.
- [123] R.K. Varshney, C. Song, R.K. Saxena, et al., Draft genome sequence of chickpea (*Cicer arietinum*) provides a resource for trait improvement, *Nat. Biotechnol.* 31 (2013) 240–246, <https://doi.org/10.1038/nbt.2491>.

- [124] J. Schmutz, S.B. Cannon, J. Schlueter, et al., Erratum: genome sequence of the palaeopolyploid soybean (Nature (2010) 463 (178-183)), Nature 465 (2010) 120, <https://doi.org/10.1038/nature08957>.
- [125] J. Schmutz, P.E. McClean, S. Mamidi, et al., A reference genome for common bean and genome-wide analysis of dual domestications, Nat. Genet. 46 (2014) 707–713, <https://doi.org/10.1038/ng.3008>.
- [126] Y.J. Kang, S.K. Kim, M.Y. Kim, et al., Genome sequence of mungbean and insights into evolution within Vigna species, Nat. Commun. 5 (2014) 1–9, <https://doi.org/10.1038/ncomms6443>.
- [127] S. Jegadeesan, A. Raizada, P. Dhanasekar, P. Suprasanna, Draft genome sequence of the pulse crop blackgram [Vigna mungo (L.) Hepper] reveals potential R-genes, Sci. Rep. 11 (2021) 1–10, <https://doi.org/10.1038/s41598-021-90683-9>.
- [128] D.J. Bertioli, J. Jenkins, J. Cleverger, et al., The genome sequence of segmental allotetraploid peanut Arachis hypogaea, Nat. Genet. 51 (2019) 877–884, <https://doi.org/10.1038/s41588-019-0405-z>.
- [129] S. Sato, S. Tabata, H. Hirakawa, et al., The tomato genome sequence provides insights into fleshy fruit evolution, Nature 485 (2012) 635–641, <https://doi.org/10.1038/nature11119>.
- [130] X. Xu, S. Pan, S. Cheng, et al., Genome sequence and analysis of the tuber crop potato, Nature 475 (2011) 189–195, <https://doi.org/10.1038/nature10158>.
- [131] M. Tamiru, S. Natsume, H. Takagi, et al., Genome sequencing of the staple food crop white Guinea yam enables the development of a molecular marker for sex determination, BMC Biol. 15 (2017) 1–20, <https://doi.org/10.1186/s12915-017-0419-x>.
- [132] A. D'hont, F. Denoeud, J.M. Aury, et al., The banana (Musa acuminata) genome and the evolution of monocotyledonous plants, Nature 488 (2012) 213–217, <https://doi.org/10.1038/nature11241>.
- [133] S. Prochnik, P.R. Marri, B. Desany, P.D. Rabinowicz, C. Kodira, M. Mohiuddin, F. Rodriguez, C. Fauquet, J. Tohme, T. Harkins, D.S. Rokhsar, S. Rounsley, The cassava genome: current progress, future directions, Trop. Plant Biol. 5 (2012) 88–94, <https://doi.org/10.1007/s12042-011-9088-z>.
- [134] J.C. Dohm, A.E. Minoche, D. Holtgräwe, et al., The genome of the recently domesticated crop plant sugar beet (Beta vulgaris), Nature 505 (2014) 546–549, <https://doi.org/10.1038/nature12817>.
- [135] Y. Xu, J. Wang, S. Guo, et al., The draft genome of watermelon (Citrullus lanatus) and resequencing of 20 diverse accessions, Nat. Genet. 45 (2013) 51–58, <https://doi.org/10.1038/ng.2470>.
- [136] R. Finkers, M. van Kaauwen, K. Ament, K. Burger-Meijer, R. Egging, H. Huits, L. Kodde, L. Kroon, M. Shigyo, S. Sato, B. Vosman, W. van Workum, O. Scholten, Insights from the first genome assembly of Onion (Allium cepa), G3 Genes, Genomes, Genet. 11 (2021), <https://doi.org/10.1093/g3journal/jkab243>.
- [137] Q. Xu, L.L. Chen, X. Ruan, et al., The draft genome of sweet orange (Citrus sinensis), Nat. Genet. 45 (2013) 59–66, <https://doi.org/10.1038/ng.2472>.
- [138] S. Huang, R. Li, Z. Zhang, et al., The genome of the cucumber, Cucumis sativus L, Nat. Genet. 41 (2009) 1275–1281, <https://doi.org/10.1038/ng.475>.
- [139] R. Velasco, A. Zharkikh, J. Affourtit, et al., The genome of the domesticated apple (Malus × domestica Borkh.), Nat. Genet. 42 (2010) 833–839, <https://doi.org/10.1038/ng.654>.
- [140] R. Velasco, A. Zharkikh, M. Troglio, et al., A high quality draft consensus sequence of the genome of a heterozygous grapevine variety, PLoS One 2 (2007) e1326, <https://doi.org/10.1371/journal.pone.0001326>.
- [141] S. Kim, M. Park, S.I. Yeom, et al., Genome sequence of the hot pepper provides insights into the evolution of pungency in Capsicum species, Nat. Genet. 46 (2014) 270–278, <https://doi.org/10.1038/ng.2877>.
- [142] H. Hirakawa, K. Shirasawa, K. Miyatake, T. Nunome, S. Negoro, A. Ohyama, H. Yamaguchi, S. Sato, S. Isobe, S. Tabata, H. Fukuoka, Draft genome sequence of eggplant (solanum melongena L.): the representative solanum species indigenous to the old world, DNA Res. 21 (2014) 649–660, <https://doi.org/10.1093/dnares/dsu027>.
- [143] R. Singh, M. Ong-Abdullah, E.T.L. Low, et al., Oil palm genome sequence reveals divergence of interfertile species in Old and New worlds, Nature 500 (2013) 335–339, <https://doi.org/10.1038/nature12309>.
- [144] A.P. Chan, J. Crabtree, Q. Zhao, H. Lorenzi, J. Orvis, D. Puiu, A. Melake-Berhan, K.M. Jones, J. Redman, G. Chen, E.B. Cahoon, M. Gedil, M. Stanke, B.J. Haas, J.R. Wortman, C.M. Fraser-Liggett, J. Ravel, P.D. Rabinowicz, Draft genome sequence of the oilseed species Ricinus communis, Nat. Biotechnol. 28 (2010) 951–956, <https://doi.org/10.1038/nbt.1674>.
- [145] F. Li, G. Fan, K. Wang, et al., Genome sequence of the cultivated cotton gossypium arboreum, Nat. Genet. 46 (2014) 567–572, <https://doi.org/10.1038/ng.2987>.
- [146] N. Sierro, J.N.D. Battey, S. Ouadi, N. Bakaher, L. Bovet, A. Willig, S. Goepfert, M.C. Peitsch, N.V. Ivanov, The tobacco genome sequence and its comparison with those of tomato and potato, Nat. Commun. 5 (2014) 1–9, <https://doi.org/10.1038/ncomms4833>.
- [147] J. Yang, D. Liu, X. Wang, C. Ji, F. Cheng, B. Liu, Z. Hu, S. Chen, D. Pental, Y. Ju, P. Yao, X. Li, K. Xie, J. Zhang, J. Wang, F. Liu, W. Ma, J. Shopan, H. Zheng, S. A. Mackenzie, M. Zhang, The genome sequence of allopolyploid Brassica juncea and analysis of differential homoeolog gene expression influencing selection, Nat. Genet. 48 (2016) 1225–1232, <https://doi.org/10.1038/ng.3657>.
- [148] F. Denoeud, L. Carretero-Paulet, A. Dereeper, et al., The coffee genome provides insight into the convergent evolution of caffeine biosynthesis, Science 345 (2014) 1181–1184, <https://doi.org/10.1126/science.1255274>.
- [149] R.K. Ellur, A. Khanna, A. Yadav, S. Pathania, H. Rajashekara, V.K. Singh, S. Gopala Krishnan, P.K. Bhowmick, M. Nagarajan, K.K. Vinod, G. Prakash, K. K. Mondal, N.K. Singh, K. Vinod Prabhu, A.K. Singh, Improvement of Basmati rice varieties for resistance to blast and bacterial blight diseases using marker assisted backcross breeding, Plant Sci. 242 (2016) 330–341, <https://doi.org/10.1016/j.plantsci.2015.08.020>.
- [150] S.L. Krishnamurthy, P. Pundir, A.S. Warrach, S. Rathor, B.M. Lokeshkumar, N.K. Singh, P.C. Sharma, Introgressed saltol QTL lines improves the salinity tolerance in rice at seedling stage, Front. Plant Sci. 11 (2020) 833, <https://doi.org/10.3389/fpls.2020.00833>.
- [151] L. Lei, H. Zheng, Y. Bi, L. Yang, H. Liu, J. Wang, J. Sun, H. Zhao, X. Li, J. Li, Y. Lai, D. Zou, Identification of a major QTL and candidate gene analysis of salt tolerance at the bud break stage in rice (oryza sativa L.) using QTL-seq and RNA-seq, Rice 13 (2020) 1–14, <https://doi.org/10.1186/s12284-020-00416-1>.
- [152] R.T.P. Pandian, P. Sharma, V.K. Singh, A. Singh, R.K. Ellur, A.K. Singh, U.D. Singh, Validation of sheath blight resistance derived from Tetep in a Basmati variety and parental lines of rice hybrid, Indian Phytopathol. 65 (2012) 233–237.
- [153] R.K. Salgotra, M. Raina, R. Rathore, J.A. Bhat, Marker-assisted gene pyramiding (MAGP) for semi dwarfed bacterial blight resistance genes into traditional basmati variety “Ranbir Basmati,” Plant Gene 26 (2021) 100276 <https://doi.org/10.1016/j.plgene.2021.100276>.
- [154] X. Yang, X. Xia, Z. Zhang, B. Nong, Y. Zeng, F. Xiong, Y. Wu, J. Gao, G. Deng, D. Li, QTL mapping by whole genome re-sequencing and analysis of candidate genes for Nitrogen use efficiency in rice, Front. Plant Sci. 8 (2017) 1634, <https://doi.org/10.3389/fpls.2017.01634>.
- [155] F. Mao, D. Wu, F. Lu, X. Yi, Y. Gu, B. Liu, F. Liu, T. Tang, J. Shi, X. Zhao, L. Liu, L. Ji, QTL mapping and candidate gene analysis of low temperature germination in rice (Oryza sativa L.) using a genome wide association study, PeerJ 10 (2022) e13407, <https://doi.org/10.7717/peerj.13407>.
- [156] L. Chen, Q. Wang, M. Tang, X. Zhang, Y. Pan, X. Yang, G. Gao, R. Lv, W. Tao, L. Jiang, T. Liang, QTL mapping and identification of candidate genes for heat tolerance at the flowering stage in rice, Front. Genet. 11 (2021) 1840, <https://doi.org/10.3389/fgene.2020.621871>.
- [157] C. Lv, Y. Song, L. Gao, Q. Yao, R. Zhou, R. Xu, J. Jia, Integration of QTL detection and marker assisted selection for improving resistance to Fusarium head blight and important agronomic traits in wheat, Crop J. 2 (2014) 70–78, <https://doi.org/10.1016/j.cj.2013.10.004>.
- [158] N. Mallick, P. Agarwal, S.K. Jha, M. Niranjana, Vinod, Marker-assisted breeding for rust management in wheat, Indian Phytopathol. 74 (2021) 365–370, <https://doi.org/10.1007/s42360-020-00317-9>.
- [159] M. Aoun, J.A. Kolmer, M.N. Rouse, E.M. Elias, M. Breiland, W.D. Bulbula, S. Chao, M. Acevedo, Mapping of novel leaf rust and stem rust resistance genes in the Portuguese durum wheat landrace PI 192051, G3 Genes, Genomes, Genet. 9 (2019) 2535–2547, <https://doi.org/10.1534/g3.119.400292>.
- [160] S. Venkata Sai Prasad, S. Kumar Singh, V. Kumar, S. Lal Kantwa, V. Gajanan Dubey, D. Ambati, T. Linganna Prakasha, A. Nandan Mishra, Pyramiding of resistance genes Sr36 and Sr2 in durum wheat background (HI 8498) through marker assisted selection for resistance to stem rust race 117-group pathotypes, Proc. Int. Symp. Genet. Breed. Durum Wheat. Bari CIHEAM (2014) 419–429. (Accessed 21 May 2023). <http://om.ciheam.org/article.php?IDPDF=00007098> <http://www.ciheam.org/http://om.ciheam.org/>.
- [161] H.S. Gupta, B. Raman, P.K. Agrawal, V. Mahajan, F. Hossain, M. Thirunavukkarasu, Accelerated development of quality protein maize hybrid through marker-assisted introgression of opaque-2 allele, Plant Breed. 132 (2013) 77–82, <https://doi.org/10.1111/pbr.12009>.

- [162] K. Sarika, F. Hossain, V. Muthusamy, R.U. Zunjare, A. Baveja, R. Goswami, J.S. Bhat, S. Saha, H.S. Gupta, Marker-assisted pyramiding of opaque2 and novel opaque16 genes for further enrichment of lysine and tryptophan in sub-tropical maize, *Plant Sci.* 272 (2018) 142–152, <https://doi.org/10.1016/j.plantsci.2018.04.014>.
- [163] F. Hossain, V. Muthusamy, N. Pandey, A.K. Vishwakarma, A. Baveja, R.U. Zunjare, N. Thirunavukkarasu, S. Saha, K.M. Manjaiah, B.M. Prasanna, H.S. Gupta, Marker-assisted introgression of opaque2 allele for rapid conversion of elite hybrids into quality protein maize, *J. Genet.* 97 (2018) 287–298, <https://doi.org/10.1007/s12041-018-0914-z>.
- [164] N.J. Larkan, F. Yu, D.J. Lydiate, S.R. Rimmer, M.H. Borhan, Single R gene introgression lines for accurate dissection of the Brassica - leptosphaeria pathosystem, *Front. Plant Sci.* 7 (2016) 1771, <https://doi.org/10.3389/fpls.2016.01771>.
- [165] Q. Meng, Z. Liu, C. Feng, H. Zhang, Z. Xu, X. Wang, J. Wu, H. She, W. Qian, Quantitative trait locus mapping and identification of candidate genes controlling bolting in spinach (*spinacia oleracea* L.), *Front. Plant Sci.* 13 (2022) 2321, <https://doi.org/10.3389/fpls.2022.850810>.
- [166] J. Larzábal, N. Yamanaka, S. Ceretta, M. Rodríguez, S. Stewart, Introgression of Asian soybean rust resistant genes into elite soybean lines from Uruguay, *Int. J. Pest Manag.* 68 (2022) 319–327, <https://doi.org/10.1080/09670874.2022.2118894>.
- [167] J. Wang, B. Hu, Y. Jing, X. Hu, Y. Guo, J. Chen, Y. Liu, J. Hao, W.X. Li, H. Ning, Detecting QTL and candidate genes for plant height in soybean via linkage analysis and GWAS, *Front. Plant Sci.* 12 (2022) 3322, <https://doi.org/10.3389/fpls.2021.803820>.
- [168] R. Li, Z. Chen, R. Zheng, Q. Chen, J. Deng, H. Li, J. Huang, C. Liang, T. Shi, QTL mapping and candidate gene analysis for yield and grain weight/size in Tartary buckwheat, *BMC Plant Biol.* 23 (2023) 1–16, <https://doi.org/10.1186/s12870-022-04004-x>.
- [169] A.K. Singh, S. Gopalakrishnan, V.P. Singh, et al., Marker assisted selection: a paradigm shift in Basmati breeding, *Indian J. Genet. Plant Breed.* 71 (2011) 120–128. www.apeda.gov. (Accessed 25 May 2023).
- [170] R.M. Sundaram, M.R. Vishnupriya, G.S. Laha, N.S. Rani, P.S. Rao, S.M. Balachandran, G.A. Reddy, N.P. Sarma, R.V. Sonti, Introduction of bacterial blight resistance into *Triguna*, a high yielding, mid-early duration rice variety, *Biotechnol. J.* 4 (2009) 400–407, <https://doi.org/10.1002/biot.200800310>.
- [171] M.L. Shanti, G.L. Devi, G.N. Kumar, H.E. Shashidhar, Molecular marker-assisted selection: a tool for insulating parental lines of hybrid rice against bacterial leaf blight, *Int. J. Plant Pathol.* 1 (2010) 114–123, <https://doi.org/10.3923/ijpp.2010.114.123>.
- [172] A.K. Dash, R.N. Rao, G.J.N. Rao, R.L. Verma, J.L. Katara, A.K. Mukherjee, O.N. Singh, T.B. Bagchi, Phenotypic and marker-assisted genetic enhancement of parental lines of Rajalaxmi, an elite rice hybrid, *Front. Plant Sci.* 7 (2016) 1005, <https://doi.org/10.3389/fpls.2016.01005>.
- [173] J.P. Suh, J.U. Jeung, T.H. Noh, Y.C. Cho, S.H. Park, H.S. Park, M.S. Shin, C.K. Kim, K.K. Jena, Development of breeding lines with three pyramided resistance genes that confer broad-spectrum bacterial blight resistance and their molecular analysis in rice, *Rice* 6 (2013) 1–11, <https://doi.org/10.1186/1939-8433-6-5>.
- [174] V.K. Singh, A. Singh, S.P. Singh, R.K. Ellur, D. Singh, S. Gopala Krishnan, P.K. Bhowmick, M. Nagarajan, K.K. Vinod, U.D. Singh, T. Mohapatra, K.V. Prabhu, A. K. Singh, Marker-assisted simultaneous but stepwise backcross breeding for pyramiding blast resistance genes *Piz5* and *Pi54* into an elite Basmati rice restorer line “PRR78”, *Plant Breed.* 132 (2013) 486–495, <https://doi.org/10.1111/pbr.12077>.
- [175] S.V. Kumar, M.S. Prasad, R. Rambabu, K.R. Madhavi, B. Bhaskar, V. Abhilash Kumar, R.M. Sundaram, A.K. Satya, M.S. Madhav, V. Prakasam, Marker-assisted introgression of *pi-1* gene conferring resistance to rice blast pathogen *pyricularia oryzae* in the background of samba mahsuri, *Int. J. Curr. Microbiol. Appl. Sci.* 8 (2019) 2133–2146, <https://doi.org/10.20546/ijcmas.2019.801.223>.
- [176] S. Vijay Kumar, R. Rambabu, B. Bhaskar, K.R. Madhavi, S. Srikanth, V. Prakasam, R.M. Sundaram, M. Sheshu Madhav, L.V. Subba Rao, M.S. Prasad, Introgression of durable blast resistance gene *Pi-54* into indica rice cv. samba mahsuri, through Marker Assisted Backcross Breeding, *Electron. J. Plant Breed.* 9 (2018) 705–715, <https://doi.org/10.5958/0975-928X.2018.00084.4>.
- [177] B.A. Pandian, J. Joel, V.V. Nachimuthu, M. Swaminathan, P. Govinatharaj, S. Tannidi, R. Sabariappan, Marker-aided selection and validation of various *Pi* gene combinations for rice blast resistance in elite rice variety ADT 43, *J. Genet.* 97 (2018) 945–952, <https://doi.org/10.1007/s12041-018-0988-7>.
- [178] G.H. Khan, A.B. Shikari, R. Vaishnavi, S. Najeeb, B.A. Padder, Z.A. Bhat, G.A. Parray, M.A. Bhat, R. Kumar, N.K. Singh, Marker-assisted introgression of three dominant blast resistance genes into an aromatic rice cultivar Mushk Budji, *Sci. Rep.* 8 (2018) 1–13, <https://doi.org/10.1038/s41598-018-22246-4>.
- [179] S.K. Pradhan, E. Pandit, S. Pawar, S.Y. Baksh, A.K. Mukherjee, S.P. Mohanty, Development of flash-flood tolerant and durable bacterial blight resistant versions of mega rice variety ‘Swarna’ through marker-assisted backcross breeding, *Sci. Rep.* 9 (2019) 1–15, <https://doi.org/10.1038/s41598-019-49176-z>.
- [180] P. Suryavanshi, Assessment of Unnat PBW 343 (rust resistant wheat variety) in mohali, Punjab, *Indian J. Pure Appl. Biosci.* 8 (2020) 64–69, <https://doi.org/10.18782/2582-2845.8102>.
- [181] J. Guo, X. Zhang, Y. Hou, J. Cai, X. Shen, T. Zhou, H. Xu, H.W. Ohm, H. Wang, A. Li, F. Han, H. Wang, L. Kong, High-density mapping of the major FHB resistance gene *Fhb7* derived from *Thinopyrum ponticum* and its pyramiding with *Fhb1* by marker-assisted selection, *Theor. Appl. Genet.* 128 (2015) 2301–2316, <https://doi.org/10.1007/s00122-015-2586-x>.
- [182] H. Wang, S. Sun, W. Ge, et al., Horizontal gene transfer of *Fhb7* from fungus underlies *Fusarium* head blight resistance in wheat, *Science* (2020) 368, <https://doi.org/10.1126/science.aba5435>.
- [183] A. Pratap, S.K. Chaturvedi, R. Tomar, N. Rajan, N. Malviya, M. Thudi, P.R. Saabale, U. Prajapati, R.K. Varshney, N.P. Singh, Marker-assisted introgression of resistance to fusarium wilt race 2 in Pusa 256, an elite cultivar of desi chickpea, *Mol. Genet. Genomics.* 292 (2017) 1237–1245, <https://doi.org/10.1007/s00438-017-1343-z>.
- [184] S. Robin, P. Jayaprakash, K. Amudha, R. Pushpam, S. Rajeswari, S. Manonmani, V. Ravichandran, R.P. Soundararajan, A. Ramanathan, K. Ganesamurthy, Rice CR1009 Sub 1 (IET 22187)-A new flood tolerant rice variety, *Electron. J. Plant Breed.* 10 (2019) 995–1004, <https://doi.org/10.5958/0975-928X.2019.00128.5>.
- [185] H. Rahman, V. Dakshinamurthi, S. Ramasamy, S. Manickam, A.K. Kaliyaperumal, S. Raha, N. Panneerselvam, V. Ramanathan, J. Nallathambi, R. Sabariappan, M. Raveendran, Introgression of submergence tolerance into co 43, a popular rice variety of India, through marker-assisted backcross breeding, *Czech J. Genet. Plant Breed.* 54 (2018) 101–108, <https://doi.org/10.17221/149/2017-CJGPB>.
- [186] M.M. Nair, K.S. Shylaraj, Introgression of dual abiotic stress tolerance QTLs (*Saltol* QTL and *Sub1* gene) into Rice (*Oryza sativa* L.) variety Aiswarya through marker assisted backcross breeding, *Physiol. Mol. Biol. Plants* 27 (2021) 497–514, <https://doi.org/10.1007/s12298-020-00893-0>.
- [187] V. Kumar, A. Rani, R. Rawal, V. Mourya, Marker assisted accelerated introgression of null allele of kunitz trypsin inhibitor in soybean, *Breed Sci.* 65 (2015) 447–452, <https://doi.org/10.1270/jsbbs.65.447>.
- [188] V. Muthusamy, F. Hossain, N. Thirunavukkarasu, M. Choudhary, S. Saha, J.S. Bhat, B.M. Prasanna, H.S. Gupta, Development of β -carotene rich maize hybrids through marker-assisted introgression of β -carotene hydroxylase allele, *PLoS One* 9 (2014) e113583, <https://doi.org/10.1371/JOURNAL.PONE.0113583>.
- [189] L. Yang, W. Wang, W. Yang, M. Wang, Marker-assisted selection for pyramiding the waxy and opaque-16 genes in maize using cross and backcross schemes, *Mol. Breed.* 31 (2013) 767–775, <https://doi.org/10.1007/s11032-012-9830-8>.
- [190] W. Zhang, W. Yang, M. Wang, W. Wang, G. Zeng, Z. Chen, Y. Cai, Increasing lysine content of waxy maize through introgression of opaque-2 and opaque-16 genes using molecular assisted and biochemical development, *PLoS One* 8 (2013) e56227, <https://doi.org/10.1371/journal.pone.0056227>.