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Plant Breeding for Sustainable Agriculture and Global Food Security: The Era of Genomics-Assisted Breeding

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ABSTRACT

Genomics-assisted breeding is transforming plant breeding by accelerating the development of high-yielding, climate-resilient, nutrient-rich, and disease-resistant crop varieties essential for sustainable agriculture and global food security. Rapid advances in genomics, high-throughput phenotyping, molecular markers, genome-wide association studies, genomic selection, and gene-editing technologies have enabled breeders to identify and utilize valuable genetic variation with greater precision and efficiency. These approaches reduce breeding cycles while improving selection accuracy for complex traits such as drought tolerance, salinity resistance, heat adaptation, nutritional quality, and resource-use efficiency. Integration of genomic information with conventional breeding, bioinformatics, artificial intelligence, and speed breeding further strengthens crop improvement strategies. This chapter highlights recent advances, applications, opportunities, and challenges of genomics-assisted breeding and discusses its potential to develop resilient crop varieties capable of supporting sustainable production under changing climatic and environmental conditions.

Keywords: *Genomics-assisted breeding; Crop improvement; Genomic selection; Climate resilience; Food security.*

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INTRODUCTION

Agriculture is the base of human civilization and still the main source of subsistence for approximately two billion people around the world, especially in developing economies (Varshney et al., 2025; Varshney & Tuberosa, 2007). The 21st century faces plant breeders with a series of interlinked difficulties on a scale rarely seen in agricultural history. The current world population of more than eight billion is expected to reach 9.7-9.8 billion by 2050 and this will require double the food production compared to the early twenty-first century, yet agricultural area per capita is steadily decreasing (Varshney et al., 2025; Ray et al., 2013; & Prabhu L. Pingali, 2012). At the same time, the world is facing a chronic and in recent years, worsening crisis of hunger. The Food and Agriculture Organization and its partner UN agencies estimate that between 638 and 720 million people suffered hunger in 2024, with particularly severe and increasing food insecurity across sub-Saharan Africa and Western Asia (FAO, IFAD, UNICEF, WFP & WHO, 2023; 2025; 2026). Climate change exacerbates these pressures, altering the distribution, frequency and severity of abiotic stresses (drought, heat, salinity, flooding) and biotic stresses (emerging pest and pathogen races), while also reducing the predictability of growing seasons on which traditional agriculture relies (Ćeran et al., 2024; Kole et al., 2015; & Varshney et al., 2021).

Meeting these issues demands more than incremental gains in agronomic management; it requires a fundamental increase in the pace of genetic gain supplied by plant breeding programs (Varshney et al., 2021; & Ray et al., 2013). The mid-twentieth-century Green Revolution, based on conventional breeding, semi-dwarf genes and intensified agrochemical inputs, dramatically increased cereal productivity and averted famine across much of Asia and Latin America, but also narrowed the genetic base of major crops and in many contexts, reached a point of diminishing returns and yield plateaus (Prabhu L. Pingali, 2012). The apparent or quantifiable phenotype as a surrogate for the underlying genotype is the essential basis of conventional breeding methods (selection, hybridization, backcrossing, mutation breeding). However, phenotypic selection for many of the economically relevant traits, especially those controlled by several genes of minor effect, is slow, resource-intensive and imprecise due to the complex genotype-by-environment (G×E) interactions shaping the phenotypes Mangal et al., 2024; Leng et al., 2017; & Ghosh et al., 2024).

The merging of genomics and plant breeding, loosely termed genomics-assisted breeding (GAB), has revolutionized what is attainable in crop improvement. Instead of indirect selection on phenotype, GAB allows breeders to select directly on genotype, using information at the DNA level to anticipate the phenotypic performance of a plant before it flowers (Varshney et al. 2025; Leng et al., 2017; & Varshney et al., 2021). The phrase "genomics-assisted breeding" was coined in the mid-2000s to capture the gradual incorporation of genomics resources, functional molecular markers, rich genetic maps, sequenced genomes and bioinformatics tools, into applied breeding programs (Varshney et al., 2025). Since then, GAB has advanced rapidly due to the exponential decrease in the cost of DNA sequencing, the wide availability of high-density SNP genotyping arrays and genotyping-by-sequencing (GBS) platforms, the development of statistical and machine-learning methods for genomic prediction and the emergence of precise genome-editing tools such as CRISPR/Cas9 (Ćeran et al., 2024; Crossa et al., 2025; Alemu et al., 2024; & Daware et al., 2022).

2. Conventional Plant Breeding: Achievements and Limitations

Conventional plant breeding methods have been quite successful during the past century. These methods include mass selection, pure-line selection, pedigree breeding, backcross breeding, recurrent selection, hybridization and induced mutagenesis. They backed the semi-dwarf wheat and rice cultivars of the Green Revolution, generated hybrid maize

with drastically enhanced yield potential and delivered disease-resistant, climate-adapted and quality-improved cultivars in practically all major crop species (Mangal et al., 2024; & Prabhu L. Pingali, 2012). These advances helped more than double worldwide cereal production from 1960 to 2000, while the world population also roughly doubled and are credited with averting large-scale famines in South Asia and elsewhere (Prabhu L. Pingali, 2012).

Despite these improvements, conventional breeding has numerous inherent restrictions. First, it is very time consuming. The development of an inbred cultivar by pedigree selection usually takes eight to twelve years, and hybrid development can take even longer, as each cycle of intermating and selection requires an entire crop season (or more, for perennials) before phenotypic data can be collected (Mangal et al., 2024; & Ghosh et al., 2024). Second, conventional selection is strongly influenced by environment. Because phenotype is the product of both genotype and environment and because many economically important traits (yield, quality, stress tolerance) are quantitatively inherited and strongly influenced by G×E interactions, phenotypic selection has low precision, especially at early generations when plants are grown as single, unreplicated rows (Mangal et al., 2024; & Leng et al., 2017). Third, conventional breeding is ineffective for pyramiding many genes for the same characteristic (e.g., multiple disease resistance genes), because such genes cannot be easily discriminated phenotypically once at least one functional copy is present in a plant (Hasan et al., 2021; & Collard & Mackill, 2008). Fourth, for several crops, the realized genetic gain per breeding cycle has plateaued and the rate of yield improvement of some staple cereals is not sufficient to meet the expected demand expansion, as emphasized by worldwide yield-trend analyzes (Ray et al., 2013; & Fischer et al., 2014). Finally, rigorous selection for a small range of elite traits has destroyed genetic diversity in many crops, leaving breeding pools exposed to developing pests, diseases and climate extremes (Prabhu L. Pingali, 2012).

These restrictions, collectively, provided impetus for looking for breeding approaches that would improve both the precision and speed of selection. The answer to this search was found in the application of molecular genetics and subsequently, genomics to plant breeding.

3. The Genomics Revolution: Enabling Technologies

3.1 From Molecular Markers to Whole-Genome Sequencing

Genomics-assisted breeding relies on the use of DNA-based molecular markers, which are pieces of DNA linked to a specific region of the genome and can be detected and scored regardless of environmental effects. Early marker systems were restriction fragment length polymorphisms (RFLPs), random amplified polymorphic DNA (RAPD), amplified fragment length polymorphisms (AFLPs) and simple sequence repeats or microsatellites (SSRs) (Hasan et al., 2021; & Wanga et al., 2021). While valuable, these first-generation markers were hampered by low throughput, technical variability and relatively low genome coverage.

The mid-2000s brought the introduction of next-generation sequencing (NGS) technology, revolutionizing marker discovery and genotyping. NGS facilitated whole-genome and whole-transcriptome sequencing at a fraction of the cost and time of Sanger sequencing, resulting in the sequencing of reference genomes for virtually all major crop species and thousands of accessions within germplasm collections (Varshney et al., 2025; Ćeran et al., 2024; & Daware et al., 2022). This, in turn, has allowed the identification of millions of single nucleotide polymorphisms (SNPs), which have become the marker of choice for modern breeding due to their abundance, genome-wide distribution and suitability for high-throughput, low-cost genotyping through SNP arrays and genotyping-by-sequencing (GBS) (Hasan et al., 2021; Wanga et al., 2021; Daware et al.,

2022; & Thakur et al., 2025). The decreasing cost of sequencing and high-density SNP genotyping has enabled genotyping of thousands of breeding lines each season, providing the genomic backbone for GWAS, genomic selection and pangenome assembly (Ćeran et al., 2024; Crossa et al., 2025; & Daware et al., 2022).

3.2 Bioinformatics and Data Integration

Such creation of genetic data would be of little use without concomitant improvements in bioinformatics and data management. Modern breeding programs now rely on integrated databases that connect genotypic data (SNP calls, sequence variants, haplotypes), phenotypic data (from field trials and phenomics platforms) and increasingly envirotypic data (soil, weather and management records) within integrated analytical pipelines (Crossa et al., 2025; Bolger et al., 2019; & Alexandratos & Bruinsma, 2012). This genotype × phenotype × envirotype integration, schematically shown in Figure 1, is the heart of the operational basis of modern GAB and is the foundation of the analytical methodologies outlined in the following sections.

4. Marker-Assisted Selection and Its Applications

4.1 Principles of Marker-Assisted Selection

Marker-assisted selection (MAS) is the use of DNA markers that are intimately connected or associated with a gene or QTL controlling a trait of interest for selection based on the genetic profile rather than the phenotype of the individual (Hasan et al., 2021; Collard & Mackill, 2008; & Wanga et al., 2021). MAS requires (i) a marker closely associated to the target gene/QTL, (ii) adequate recombination between the marker and unwanted linked areas (to reduce "linkage drag") and (iii) a low-cost, high-throughput test for scoring large populations (Hasan et al., 2021; & Wanga et al., 2021). Since its inception in the 1990s, MAS has evolved into several related strategies, including marker-assisted backcrossing (MABC) for introgression of single genes into elite backgrounds while accelerating recovery of the recurrent parent genome, marker-assisted gene pyramiding (MAGP) for combining multiple resistance or quality genes that cannot be distinguished phenotypically and marker-assisted recurrent selection (MARS) for improving complex, polygenic traits over multiple breeding cycles (Guo-Liang Jiang, 2015; Hasan et al., 2021; & Wanga et al., 2021).

4.2 Applications and Case Studies

MAS has been widely used to traits regulated by one or a few main genes, especially for disease and pest resistance. Classic examples include pyramiding of Fusarium head blight resistance QTLs into wheat, conversion of normal maize lines to quality protein maize (QPM) by marker-assisted backcrossing of the opaque-2 locus and introgression of bacterial blight and blast resistance genes into elite rice cultivars (Guo-Liang Jiang, 2015; & Hasan et al., 2021). Also in fruit crops, MAS has proved to be useful, with markers for skin colour, flesh colour and other quality traits (e.g. MdCol markers for red skin colour in apple) allowing for early selection of seedlings before they fruit, thus significantly reducing breeding cycles in perennial species with long juvenile phases (De Mori & Cipriani, 2023). Despite these successes, the overall impact of MAS on plant breeding has been more limited than initially anticipated, partly because most economically important traits are quantitatively inherited by many genes of small effect, for which single-marker or few-marker selection strategies are ineffective, spurring the development of genome-wide approaches like GWAS and genomic selection (Collard & Mackill, 2008; & Wanga et al., 2021).

5. Genome-Wide Association Studies in Crop Plants

Genome-wide association studies (GWAS) detect statistical associations between genome-wide markers (most often single nucleotide polymorphisms (SNPs)) and phenotypic traits by leveraging historical recombination in diverse, largely unrelated germplasm panels, avoiding the need to produce a specific bi-parental mapping population (Alseekh et al., 2021; & Yang et al., 2020). GWAS panels

record recombination events accumulated over several generations; therefore, they usually have significantly higher mapping precision than traditional QTL mapping based on bi-parental populations, allowing the identification of candidate genes and in some cases, causative polymorphisms (Alseekh et al., 2021; Yang et al., 2020; & Bolger et al., 2019).

Since the technique was adopted from human genetics to plant genomics, GWAS has been successfully used to virtually all major and many minor crops. GWAS panels for rice, wheat and maize with hundreds to thousands of accessions have discovered marker-trait relationships for yield components, grain quality and stress tolerance in cereals (Daware et al., 2022; Thakur et al., 2025; & Yang et al., 2020). GWAS has been applied in legumes and pulses to understand the genetic architecture of agronomic and quality parameters in soybean, cowpea and field pea, such as seed weight, seed yield, plant height, pod length and photosynthetic traits (Sansa et al., 2024; Contreras-Soto et al., 2017; Gali et al., 2019; & Abebe et al., 2023). GWAS has also been extended to neglected and orphan crops such as foxtail millet and kenaf, where genotyping-by-sequencing techniques have created the SNP resources needed for association mapping in the absence of a large prior genomic infrastructure (Kim et al., 2024; & Jaiswal et al., 2019). Recent methodological advances such as haplotype-based GWAS (which combines multiple SNPs into haplotype blocks to enhance statistical power and better capture epistatic and rare-variant effects) and web-based platforms that democratize access to curated genomic-variation datasets for under-resourced research groups further extend the reach and utility of GWAS in crop improvement (Bhat et al., 2021; & Daware et al., 2022).

However, GWAS in crop plants has some well-established challenges: population structure and cryptic relatedness can lead to spurious associations if not controlled appropriately by statistical methods; linkage disequilibrium decay varies tremendously across species (and even across genomic regions within species), impacting mapping resolution and many agronomically relevant traits have small-effect, highly polygenic architectures that demand very large panels and dense marker sets to detect (Alseekh et al., 2021; Kim et al., 2021; & Yang et al., 2020). These issues have led to a shift, outlined in the next section, to genomic selection procedures that do not require identifying individually significant markers.

6. Genomic Selection and Genomic Prediction

6.1 Principles

Genomic selection (GS), initially proposed conceptually in animal breeding and adapted for plants, uses genome-wide dense marker data to estimate an individual's breeding value, the genomic estimated breeding value (GEBV), without requiring prior identification of significant marker-trait associations (Alemu et al., 2024; & Crossa et al., 2025). Initially, a statistical model is trained on a "training population" that has been genotyped and phenotyped, and then applied to a much larger "breeding" or "candidate" population, which has been genotyped but not yet phenotyped, allowing breeders to predict performance and make selection decisions before plants reach maturity (Alemu et al., 2024; Crossa et al., 2025; & Piepho et al., 2022).

6.2 Statistical and Machine-Learning Models

A plethora of statistical models have been proposed for genomic prediction, including linear mixed models (e.g., genomic best linear unbiased prediction (GBLUP) and ridge-regression BLUP), Bayesian variable-selection methods (BayesA, BayesB, BayesCπ) and non-parametric and semi-parametric methods such as reproducing kernel Hilbert space (RKHS) regression (Alemu et al., 2024; & Crossa et al., 2025; 20). More recently, machine-learning and deep-learning methods, such as random forests, support vector machines, convolutional neural networks and multimodal deep-learning architectures that integrate genomic, phenomic and environmental data streams, have been applied

to genomic prediction, often improving predictive accuracy for complex traits with non-additive genetic architecture (Crossa et al., 2025; Montesinos-López et al., 2024; & Kumawat et al., 2021). Prediction accuracy is also highly influenced by the choice of model, the composition and size of the training population, marker density and genetic relatedness between the training and breeding populations; optimizing these factors remains an active area of methodological research (Belamkar et al., 2018; Alemu et al., 2024; & Crossa et al., 2025).

6.3 Applications and Impact

Empirical studies in cereals, legumes and even perennial species like rubber tree have shown that GS can substantially increase the rate of genetic gain per unit time over pedigree- or phenotype-based selection, primarily because it shortens the breeding cycle (candidates can be selected as seedlings rather than after full field evaluation), increases selection intensity and - for low-heritability traits - can even improve selection accuracy compared to a single season of phenotyping (Alemu et al., 2024; Crossa et al., 2025; Souza et al., 2019; & Piepho et al., 2022). In maize breeding, GS has been incorporated into commercial breeding pipelines to speed up the development and testing of inbred lines and hybrids. In wheat, GS models have been assessed for their ability to predict the performance of preliminary yield-trial lines under actual breeding-programme conditions. GS is also being expanded to genomic-enabled germplasm enhancement or 'genomic pre-breeding', where GEBVs are utilized to discover valuable, but previously unexploited genetic diversity in gene bank accessions for introgression into elite breeding pools (Crossa et al., 2025).

Genomic prediction models must additionally consider genotype-by-environment (G×E) interaction, because the breeding value of a genotype may differ across the target settings. More and more sophisticated approaches use environmental covariates directly in genomic prediction models, called environmental-to-phenotype association or genomic × environment (G×E) kernel modeling, to improve the transferability of genomic predictions across sites and years and to leverage historical multi-environment trial data and machine learning (Crossa et al., 2025) to predict genotype performance in new or future environments.

7. Pangenomes, Super-Pangenomes and Haplotype-Based Breeding

However, a single reference genome only captures part of the genetic diversity of a crop species, because structural variants such as presence/absence variation, copy-number variation, inversions and translocations are often not detected when sequence reads from various accessions are aligned to one reference (Raza et al., 2026; FAO, IFAD, UNICEF, WFP & WHO, 2025). The pangenome concept overcomes this limitation by combining sequence data from multiple individuals of a species (or in the case of "super-pangenomes" a species and its wild relatives) into a single framework that includes both core genes shared by all individuals and dispensable or variable genes present in only subsets of the population (Raza et al., 2026).

Pangenome and super-pangenome resources are particularly beneficial for two goals important to genomics-assisted breeding. First, they reduce reference bias in GWAS and genomic-selection analyzes, boosting the discovery of structural variations and uncommon alleles that influence stress adaptation and trait evolution, but that would be invisible to single-reference-genome techniques (Raza et al., 2026). Second, they facilitate systematic haplotype mining, i.e., identification and cataloging of favorable allelic combinations (haplotypes) across germplasm collections, which can then be used through haplotype-based GWAS, haplotype-based breeding and haplotype-assisted genomic selection to more efficiently capture complex, multi-gene trait architectures (Bhat et al., 2021). Haplotype-based breeding strategies are viewed as particularly promising for the protection of food security under climate change, because they allow breeders to follow and recombine whole blocks of

favorable genes (including linked co-adapted alleles) rather than only individual markers and because wild relatives and landraces, often underexploited in elite breeding pools, can be systematically screened for novel, climate-adaptive haplotypes (Bhat et al., 2021; & Raza et al., 2026).

8. Genome Editing: CRISPR/Cas and Beyond

8.1 From Nucleases to Precision Editing

Targeted genome-editing tools, including meganucleases, zinc-finger nucleases (ZFNs), transcription activator-like effector nucleases (TALENs) and most transformatively the clustered regularly interspaced short palindromic repeats (CRISPR)-CRISPR-associated protein (Cas) system, allow breeders to make precise, targeted changes in a plant genome, instead of using the essentially random mutations generated by classical mutagenesis or the multigenerational recombination needed by conventional and even marker-assisted breeding (Rasheed et al., 2021; Haider et al., 2026; & Atia et al., 2024). Since its development for plant genome engineering, CRISPR/Cas9 has rapidly become the dominant platform for genome editing because of its relatively simple design, low cost, high efficiency and short experimental cycle compared to older nuclease systems (Kumar et al., 2022; Muha-Ud-Din et al., 2024; & Alemu et al., 2024). Recent advances such as base editing (precise single nucleotide conversions without creating double stranded breaks) and prime editing (targeted insertions, deletions and all possible base substitutions with high precision) have further expanded the arsenal and safety profile of genome editing applications in crops (Muha-Ud-Din et al., 2024).

8.2 Applications in Crop Improvement

CRISPR/Cas-mediated genome editing has been employed to modify a broad spectrum of characteristics and crops. In staple cereals (rice, wheat, barley and maize) and vegetable crops (potato and tomato), CRISPR editing has been used to improve nutritional and quality traits such as starch, protein, gamma-aminobutyric acid (GABA), oleic acid, anthocyanin and phytic acid content, aroma, shelf life and sweetness, providing a route to crop biofortification that complements conventional and marker-assisted breeding approaches (Kumar et al., 2022; & Rasheed et al., 2021). Genome editing has also been used to engineer resistance to fungal, bacterial and viral diseases by either introducing resistance alleles or by disruption of susceptibility (S) genes exploited by pathogens to establish infection and to improve tolerance to drought, salinity and heat stress by modifying genes involved in stress-signalling pathways (Rasheed et al., 2021; Muha-Ud-Din et al., 2024; & Atia et al., 2024). In many cases, CRISPR/Cas editing can be achieved without stable integration of foreign DNA (particularly if delivered as ribonucleoproteins or if the Cas9/guide-RNA transgene can be segregated out), which may exempt edited plants from the regulatory framework applied to conventional transgenic (GMO) crops in some jurisdictions, a significant practical and political consideration for adoption of the technology (Haider et al., 2026; & Atia et al., 2024).

8.3 Limitations and Governance

Genome editing in crops holds great promise, but technical and societal challenges remain, including off-target effects, genotype-dependent transformation and regeneration efficiencies, polyploid genomes of many major crops (making it difficult to edit multiple gene copies simultaneously) and perhaps most importantly, divergent regulations in different countries, ranging from treating edited crops the same as conventional cultivars to regulating them as stringently as transgenic GMOs (Rasheed et al., 2021; Muha-Ud-Din et al., 2024; & Atia et al., 2024). Responsible, coordinated and science-based control of genome-editing technology will be key to realizing its potential contributions to global food security equitably (Muha-Ud-Din et al., 2024).

9. High-Throughput Phenotyping and Plant Phenomics

The rapid growth of genomic data has ironically identified phenotyping as the primary bottleneck in the rate of genetic gain

in modern breeding programs. Whereas genotyping thousands of samples is now fast and cheap, accurately and precisely measuring plant phenotypes across large populations and multiple environments is still relatively slow, labour-intensive and often subjective when done through conventional visual assessment (Yang et al., 2020; Li et al., 2021; & Foley et al., 2011). HTP provides a solution to this bottleneck by combining optical sensors (RGB, multispectral, hyperspectral, thermal and fluorescence imaging), unmanned aerial vehicles (UAVs) and other robotic platforms and computational image-analysis and machine-learning algorithms to enable non-destructive, rapid and objective measurement of morphological, physiological and biochemical traits on hundreds or thousands of plots (Kim et al., 2021; Abebe et al., 2023; Nguyen et al., 2025; & Gill et al., 2022).

HTP platforms have been developed for controlled environments (glasshouses and growth chambers, useful for early-stage screening) and for open-field conditions (ground-based proximal sensing and aerial remote sensing, essential for assessing traits under realistic agronomic conditions and for very large breeding populations) (Li et al., 2021; & Ray et al., 2013). Applications include phenotyping of drought and other abiotic-stress responses, disease and insect damage assessment and complex architectural features like canopy structure and lodging susceptibility, the last of which has been demonstrated at scale using UAV-based imaging in wheat (Kim et al., 2021; Singh et al., 2019; & Ray et al., 2013). In addition to data acquisition, HTP research is placing increasing emphasis on integrating phenomic and genomic data to accelerate gene and QTL discovery, as well as on the use of data standards such as Minimum Information About a Plant Phenotyping Experiment (MIAPPE) to enable the reuse and cross-study integration of phenotypic datasets (Bolger et al., 2019; & Ray et al., 2013). This combination immediately enables the QTL mapping, MAS, GWAS and genomic-selection processes outlined in the previous sections when genomic and high-throughput phenotypic data are strongly associated, thus providing the missing connection between genotype and phenotype that constitutes modern GAB (Li et al., 202).

10. Speed Breeding and Rapid Generation Advance

There is a basic biological limitation that even the most accurate genomic selection technology can't get beyond: the time it takes for a plant to complete a full life cycle from seed to seed. The limitation is overcome by SB and associated rapid generation advance (RGA) methods by manipulating environmental conditions (e.g., extended photoperiod, optimized light quality and intensity and controlled temperature) to accelerate flowering and seed set, thus compressing the time needed to advance breeding populations through successive generations (Wanga et al., 2021; Chaudhary and Sandhu, 2024; Williams et al., 2024; Watson et al., 2018; & Ghosh et al., 2018).

Protocols for speed breeding have been established and verified in many crops. In long-day cereals and legumes such as spring wheat, durum wheat, barley, chickpea and pea, SB can generate up to six generations per year versus two to three in standard glasshouse conditions and only one to two in the field; in chickpea specifically, up to seven generations per year have been reported under optimized SB protocols and in canola, four generations per year are possible (Ghosh et al., 2024; Wanga et al., 2021; & Watson et al., 2018). SB is most commonly used with well-established generation-advancement methods such as single seed descent (SSD), single pod descent (SPD) and single plant selection, and can be done in dedicated growth chambers or retrofitted glasshouses, making it accessible to breeding programs without the need for entirely new infrastructure (Chaudhary & Sandhu, 2024; Pasala et al., 2024; & Ghosh et al., 2018).

Importantly, speed breeding is being increasingly integrated with the genomic tools described throughout this review. This approach is referred to as "genomics-assisted

speed breeding" (GASB), whereby marker-assisted selection, genomic selection or genome editing is applied to plants at early developmental stages within an accelerated growth cycle and combined with high-throughput phenotyping to enable selection decisions within a compressed timeframe (Ćeran et al., 2024; & Williams et al., 2024). This combination enables breeders to exploit the precision benefits of genomic selection and the time benefits of fast generation development and has been advocated as a major strategy to address the productivity and resilience needs of agriculture in the future decades (Ćeran et al., 2024; Williams et al., 2024; & Swami et al., 2023).

11. Integrating Genomics, Phenomics and Envirotyping: Towards Precision Breeding

The separate technologies discussed above, i.e., molecular markers, GWAS, genomic selection, pangenomics, genome editing, high-throughput phenotyping and speed breeding, may only reach their full impact when combined in a cohesive breeding process (Figure 1). Modern GAB programs are increasingly data-intensive operations, producing and analyzing streams of genomic, phenomic and envirotypic data and utilizing statistical and machine-learning models to direct crossover and selection decisions in real time [Crossa et al., 2025; Bolger et al., 2019; & Li et al., 2021]. Artificial intelligence and machine learning are being used not only for genomic prediction, but also for extraction of image-based phenotypes, for optimizing training-population design in genomic selection and for modeling genotype-by-environment interactions to identify the genotype and management combinations most likely to succeed in a given target environment (Crossa et al., 2025; Montesinos-López et al., 2024; Kumawat et al., 2021; & Gill et al., 2022).

This convergence is leading to what many authors now call "precision breeding" or "digital breeding" an approach in which the traditional trial-and-error, multi-year cycle of crossing, growing and phenotyping is increasingly being replaced by a predictive, model-guided design process where candidate crosses and selections are evaluated computationally before (and alongside) physical evaluation in the field (Varshney et al., 2021; Crossa et al., 2025; & Bolger et al., 2019). This vision is a work in progress; nonetheless, the trend toward integration is clear and is the best route forward to further accelerate the pace of genetic gain needed to reach future food-security targets (Varshney et al., 2021, & Ray et al., 2013).

12. Case Studies in Major Food Crops

Rice: Rice is the main diet for over half of the world's population, therefore making it a prime target for GAB. Genome-wide association panels of hundreds of diverse rice accessions have been used to dissect yield-related, quality and stress-tolerance traits and marker-assisted backcrossing has enabled the pyramiding of multiple bacterial blight and blast resistance genes into elite, high-yielding backgrounds without compromising agronomic performance (Guo-Liang Jiang, 2015; & Daware et al., 2022). Furthermore, the availability of high-throughput phenotyping technologies tailored for rice characterization has enabled large-scale characterization of morphological, biomass and yield associated variables, hence providing the necessary phenotypic depth to facilitate genomic selection in rice (Ray et al., 2013).

Wheat: In wheat, GWAS panels have been used to identify marker-trait associations for agronomic and yield-related traits under multiple environments and genomic selection models have been tested directly within preliminary yield trials of active breeding programs, demonstrating the transition of GS from a research method to an operational breeding tool (Belamkar et al., 2018; & Thakur et al., 2025). Marker-assisted selection for Fusarium head blight resistance QTLs remains a frequently cited example of success in MAS in this crop. High throughput phenotyping using UAV has been exploited to analyze the genetic architecture of complex traits such as lodging (Guo-Liang Jiang, 2015; & Singh et al., 2019).

Maize: Maize breeding programs, especially those in international research centers, have led the way in the use of genomic selection (GS), incorporating GS into regular line and hybrid development pipelines to help speed up genetic gain. Marker-assisted backcrossing was used in the past to convert widely grown maize lines into quality protein maize, greatly improving the nutritional quality of a staple food for millions of smallholder farmers (Crossa et al., 2025; & Guo-Liang Jiang, 2015).

Legumes and pulses: In chickpea, pea, soybean and cowpea, genetic resources have developed greatly in the last decade, allowing GWAS for agronomic, seed-quality and stress-tolerance traits and providing the SNP infrastructure for genomic selection (Sansa et al., 2024; Contreras-Soto et al., 2017; Gali et al., 2019; & Abebe et al., 2023). Chickpea has also been utilized as a model crop in the development of speed-breeding protocols, whereby up to seven generations per year are achieved under optimum conditions (Ghosh et al., 2024).

Orphan and underutilized crops: The falling cost of genotyping-by-sequencing has allowed GWAS in foxtail millet, kenaf and other minor or region-specific crops, even in species with little genomic infrastructure, offering a means to apply GAB principles more broadly to the diversity of crops that support food and nutrition security in specific regions (Kim et al., 2024; & Jaiswal et al., 2019).

13. Genomics-Assisted Breeding for Climate Resilience

Climate change is changing rainfall patterns, increasing the frequency and intensity of heat waves and drought episodes and affecting the geographic range and virulence of pests and pathogens, all of which threaten the stability of global crop output (Ćeran et al., 2024; Kole et al., 2015; & Varshney et al., 2021). GAB has a number of complementary approaches to incorporating climate resilience into future crop types. First, GWAS and genomic-selection panels are increasingly designed to contain germplasm gathered from varied agro-climatic zones, which allow the identification of genes linked with drought, heat and salinity tolerance that may be rare or absent in conventional elite breeding pools (Kole et al., 2015; & Sansa et al., 2024). Second, the availability of pangenome and super-pangenome resources offers a systematic route to mine stress-adaptive haplotypes from the genetic diversity of crop wild relatives that have adapted to marginal or extreme environments and introgress them into elite backgrounds through marker-assisted or genomic-selection-guided breeding (Raza et al., 2026). Third, high-throughput phenotyping platforms that can operate under managed-stress conditions (e.g., controlled drought or heat trials combined with hyperspectral or thermal imaging) enable the precise, large-scale phenotyping of stress-response traits that are otherwise difficult to measure, providing the phenotypic data needed to train robust genomic-prediction models for stress tolerance (Kim et al., 2021; & Nguyen et al., 2025). Finally, genome editing provides a direct channel for the development or fine-tuning of certain stress-tolerance mechanisms, for example by altering genes involved in stomatal regulation, osmotic adjustment or heat-shock response pathways (Rasheed et al., 2021; & Muha-Ud-Din et al., 2024).

Collectively, these approaches are consistent with a growing consensus that the "three major events" that defined the genetic diversity of modern crops, domestication, replacement of native crops by major staples and the genetic narrowing of the Green Revolution, must now be actively mitigated through the systematic reintroduction of genetic diversity from underutilized germplasm to ensure crops remain resilient in a changing climate (Varshney et al., 2021; & Prabhu L. Pingali, 2012).

14. Biofortification and Nutritional Quality Improvement

Beyond yield and stress tolerance, GAB is playing an increasingly prominent role in improving the nutritional quality of staple crops, a strategy known as biofortification that is particularly important given that malnutrition, including micronutrient

deficiencies, continues to affect hundreds of millions of people even where caloric intake is adequate (Kumar et al., 2022; & Rasheed et al., 2021). CRISPR/Cas-based genome editing has been used to enhance starch, protein, GABA, oleic acid, anthocyanin and other nutritionally or functionally important compounds in rice, wheat, barley, maize, potato and tomato, while also reducing anti-nutritional compounds such as phytic acid and gluten in specific contexts (Kumar et al., 2022; & Rasheed et al., 2021). Marker-assisted selection and genomic selection are similarly deployed to accelerate the introgression of biofortification traits identified through GWAS of micronutrient content (for example, iron and zinc concentration in cereals and pulses) into elite, high-yielding, farmer-preferred varieties, ensuring that nutritional gains are not achieved at the expense of agronomic performance or market acceptability (Sansa et al., 2024; & Abebe et al., 2023). Because biofortified crops can deliver improved nutrition through the existing dietary habits and supply chains of vulnerable populations without requiring behaviour change or new distribution infrastructure, they represent one of the most cost-effective and scalable strategies for addressing hidden hunger and GAB substantially accelerates the pace at which such biofortified varieties can be developed and released (Kumar et al., 2022; & Rasheed et al., 2021).

15. Challenges, Limitations and Equity Considerations

Despite its transformative potential, the widespread and equitable deployment of genomics-assisted breeding faces significant obstacles. Cost and infrastructure remain primary constraints: while the cost of genotyping and sequencing has fallen dramatically, the capital investment required for high-throughput phenotyping platforms, bioinformatics infrastructure and skilled personnel remains substantial and these costs continue to limit the implementation of GAB in inbreeding and minor crops and particularly in the public breeding programmes of low- and middle-income countries that serve the world's most food-insecure populations (Varshney et al., 2025; & Gill et al., 2022). Statistical and biological complexity also constrains progress: genomic prediction accuracy remains suboptimal for many complex traits, especially those with strong non-additive genetic architecture or extensive G×E interaction and optimizing training-population design, marker density and statistical models to maximize prediction accuracy remains an active area of research rather than a solved problem (Crossa et al., 2025; Alemu et al., 2024; & Crossa et al., 2025). Polyploidy and genome complexity in crops such as wheat, cotton, sugarcane and potato complicate both genome assembly and the precise application of genome-editing tools, since multiple gene copies must often be edited simultaneously to achieve a phenotypic effect (Rasheed et al., 2021; & Atia et al., 2024).

Regulatory and governance frameworks for genome-edited crops remain fragmented and inconsistent across jurisdictions, creating uncertainty for both public breeding programmes and private-sector investment and raising important questions of international trade harmonization, biosafety assessment and public trust that must be addressed through transparent, science-based policy processes (Muha-Ud-Din et al., 2024; Haider et al., 2026; & Atia et al., 2024). Finally, there is a persistent risk that the benefits of GAB will accrue disproportionately to well-resourced breeding programmes and commercially important crops. In contrast, orphan and regionally important crops, often the crops most critical to the food and nutrition security of the poorest populations, continue to lag in the availability of genomic resources, reinforcing rather than reducing existing inequities in global food systems (Varshney et al., 2025; Kim et al., 2024; & Jaiswal et al., 2019). Addressing this risk will require deliberate investment in public genomic infrastructure, international germplasm-sharing agreements, capacity building in national agricultural research systems and open-access data platforms that democratize access to genomic tools for breeders working

on underserved crops and regions (Daware et al., 2022; & Kim et al., 2024).

16. Future Prospects

Several emerging trends are likely to shape the next phase of genomics-assisted breeding. Multi-omics integration, combining genomics with transcriptomics, proteomics and metabolomics, promises to provide a more complete mechanistic understanding of the pathways linking genotype to phenotype, potentially improving the accuracy and biological interpretability of genomic-prediction models (Crossa et al., 2025; & Bolger et al., 2019). Artificial intelligence and deep learning, already showing promise for genomic prediction, image-based phenotyping and G×E modelling, are expected to play an increasingly central role in breeding-programme design, including the optimization of crossing schemes and the prioritization of genetic resources for pre-breeding (Crossa et al., 2025; Montesinos-López et al., 2024; & Kumawat et al., 2021). Envirotyping, the systematic characterization of target production environments using historical and real-time weather, soil and management data, is likely to be increasingly combined with genomic and phenomic data to enable "genomic × envirotype" prediction models capable of anticipating genotype performance under future, as-yet-unobserved climatic conditions (Crossa et al., 2025). Super-pangenomes and expanded use of crop wild relatives are expected to substantially broaden the genetic diversity accessible to breeders, providing a systematic route for climate-adaptive allele discovery that complements, rather than replaces, elite breeding pools (Raza et al., 2026). Finally, continued refinement of base and prime editing technologies, together with progress toward harmonized international regulatory frameworks, should further expand the precision, safety, and accessibility of genome-editing tools for crop improvement (Muha-Ud-Din et al., 2024; & Atia et al., 2024).

Realizing these prospects at the scale required to meet 2050 food-security targets will depend not only on continued scientific and technological progress, but on sustained public and private investment, international collaboration in germplasm and data sharing and deliberate efforts to extend the benefits of genomics-assisted breeding to the orphan crops and under-resourced breeding programmes that serve the world's most vulnerable farming communities (Varshney et al., 2025; Ray et al., 2013; & Prabhu L. Pingali, 2012).

Table1. Comparison of primary plant breeding strategies in genomics-assisted breeding era

Approach	Basis of Selection	Typical Time to Cultivar	Precision for Polygenic Traits	Relative Cost	Representative Applications
Conventional breeding	Phenotype only	8–12+ years	Low	Low (per cycle); high (cumulative, due to duration)	Broad-based cultivar development; landrace improvement (Mangal et al., 2024; Prabhu L. Pingali, 2012)
Marker-assisted selection (MAS/MABC/MAGP)	Phenotype + a few diagnostic markers	5–8 years	Moderate (best for oligogenic traits)	Moderate	Disease-resistance gene pyramiding; QPM maize conversion (Guo-Liang Jiang, 2015; Hasan et al., 2021; Collard and Mackill, 2008)
Genome-wide association studies (GWAS)	Genome-wide markers in diverse panels	Discovery tool (not itself a cultivar-development method)	High for mapping resolution; identifies candidate loci	Moderate–high (panel genotyping)	Candidate gene/QTL discovery across cereals, legumes, orphan crops (Daware et al., 2022; Sansa et al., 2024; Alseekh et al., 2021)
Genomic selection (GS)	Genome-wide markers + statistical/ML prediction models	3–6 years	High (captures small-effect, polygenic variation)	High (genotyping + computation)	Maize/wheat line and hybrid development; genomic pre-breeding (Belamkar et al., 2018; Alemu et al., 2024; Crossa et al., 2025)
Genome editing (CRISPR/Cas, base/prime editing)	Direct, targeted DNA sequence modification	2–5 years (post-transformation, subject to regulation)	Very high (precise, targeted)	High (technical/regulatory)	Biofortification; disease resistance; stress tolerance (Kumar et al., 2022; Rasheed et al., 2021; Muha-Ud-Din et al., 2024)
Speed breeding / rapid generation advance	Accelerated generation turnover (independent of selection basis)	Reduces calendar time 2–4× regardless of method	Not applicable (accelerant, not selection method)	Low–moderate (controlled-environment infrastructure)	Combined with MAS/GS/editing across cereals and legumes (Ghosh et al., 2024; Wanga et al., 2021; Watson et al., 2018; Ghosh et al., 2018)

Table2. Selected applications and milestones of genomics-assisted breeding technologies in main crops

Crop	GAB Tool/Technology	Trait(s) Improved	Reference
Rice (Oryza sativa)	Marker-assisted backcrossing; GWAS	Bacterial blight and blast resistance; yield and quality traits	Guo-Liang Jiang, 2015; Daware et al., 2022
Wheat (Triticum aestivum)	GWAS; genomic selection; UAV-based HTP	Agronomic/yield traits; Fusarium head blight resistance; lodging resistance	(Belamkar et al., 2018; Guo-Liang Jiang, 2015; Thakur et al., 2025; Singh et al., 2019)
Maize (Zea mays)	Marker-assisted backcrossing; genomic selection	Quality protein maize (opaque-2); line/hybrid genetic gain	(Crossa et al., 2025; Guo-Liang Jiang, 2015)
Chickpea (Cicer arietinum)	Speed breeding	Up to 7 generations/year; accelerated cultivar development	Ghosh et al., 2024
Soybean (Glycine max)	GWAS; haplotype analysis	Seed weight, plant height, seed yield	Contreras-Soto et al., 2017
Cowpea (Vigna unguiculata)	GWAS	Photosynthetic and agronomic traits, drought/salt tolerance	Sansa et al., 2024
Field pea (Pisum sativum)	GWAS (GBS-based)	Agronomic and seed-quality traits	Gali et al., 2019
Foxtail millet (Setaria italica)	GWAS (ddRAD-GBS)	Flag leaf width, grain yield, thousand-grain weight	Jaiswal et al., 2019
Rice, wheat, barley, maize, potato, tomato	CRISPR/Cas biofortification	Starch, protein, GABA, oleic acid, anthocyanin content	Kumar et al., 2022; Rasheed et al., 2021
Multiple crop wild relatives	Super-pangenome / haplotype mining	Discovery of stress-adaptive alleles for breeding	Raza et al., 2026

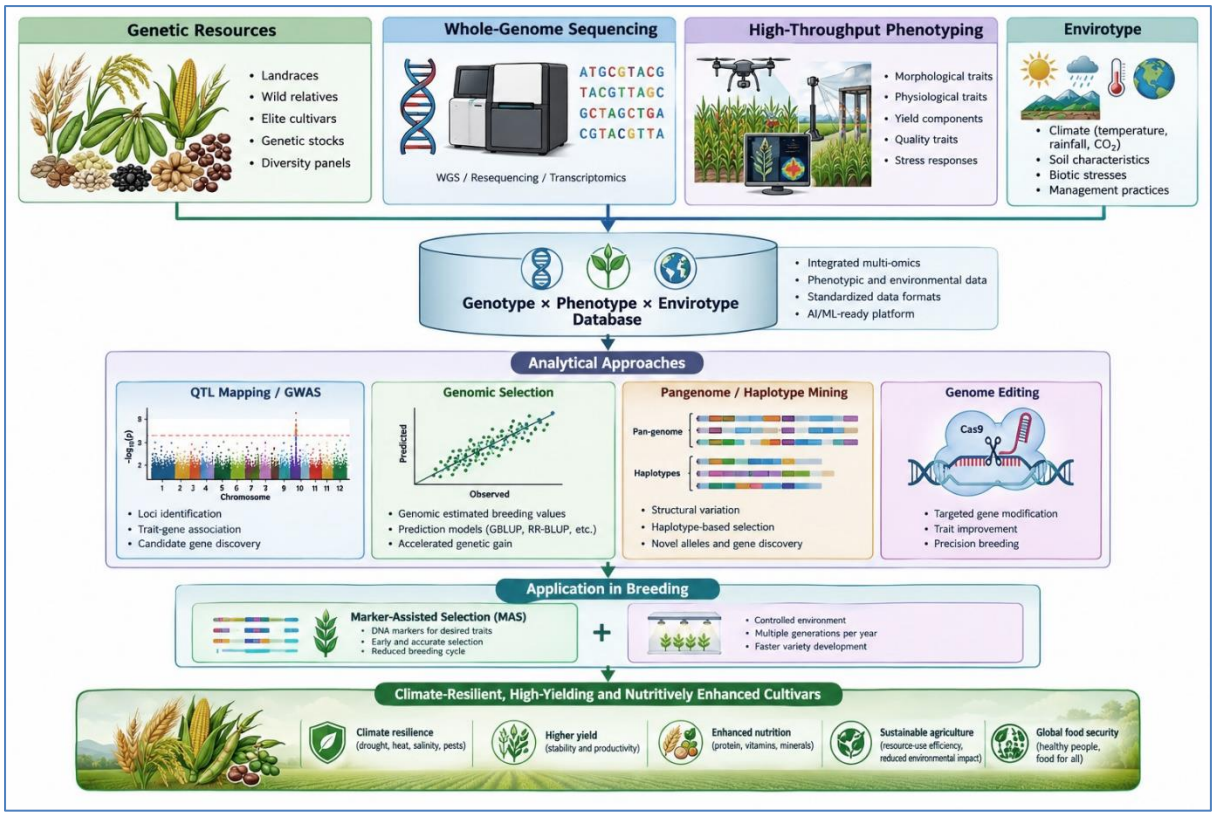

Figure1. Genomics-assisted breeding pipeline integrating genomic, phenotypic and environmental data for accelerated development of climate-resilient and nutritionally enhanced cultivars

CONCLUSION

Genomics-assisted breeding represents one of the most significant methodological transformations in the history of plant breeding, shifting the discipline from a predominantly phenotype-driven enterprise to one increasingly guided by genotype-based prediction. Through the integration of molecular markers, genome-wide association studies, genomic selection, pangenomics, genome editing, high-throughput phenotyping and speed breeding, GAB has demonstrably increased both the precision and the pace at which new crop varieties can be developed, with documented applications spanning yield improvement, disease and pest resistance, climate resilience and nutritional biofortification across cereals, legumes and orphan crops alike. Yet the technology's full potential remains unevenly realized: cost, infrastructure, statistical complexity, regulatory fragmentation and persistent inequities in access to genomic resources continue to constrain its deployment, particularly for the crops and breeding programmes that serve the world's most food-

insecure populations. Ensuring that genomics-assisted breeding fulfils its promise for sustainable agriculture and global food security will require not only continued technical innovation, but also deliberate, coordinated investment in infrastructure, capacity building, data sharing and inclusive governance, so that the benefits of the genomics era in plant breeding reach every crop and every farming community that depends on it.

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