Maize Journal (April 2026) 15(1): 91-100
OPINION PAPER

Breeding beyond boundaries: Transforming concern into genetic innovation

Bijendra Pal

Abstract: Plant breeding is a uniquely integrative scientific discipline that extends beyond conventional agriculture, wherein fundamental genetic principles are translated into practical solutions for crop improvement. At its core lies the strategic utilization and management of genetic diversity, sourced either from existing germplasm or deliberately generated to develop cultivars that serve as vital agricultural inputs to enhance productivity, stability, and resilience. A cultivar represents more than genetic novelty; it embodies a reliable promise to farmers by enhancing productivity while mitigating risks associated with variable field conditions. The development of such cultivars begins with genetic variability, the foundation of crop improvement which serves as the essential substrate for selection and recombination. Through systematic cycles of variation creation, selection, and evaluation, breeders convert genetic potential into agronomically superior and commercially viable outcomes. However, contemporary breeding faces critical concerns, including the erosion of genetic diversity, environmental uncertainty, phenotyping limitations, and misconceptions surrounding emerging technologies. This review advances the central thesis that such constraints are not merely limitations but can be transformed into drivers of innovation and cultivar development. This traditionally phenotype-driven process has undergone a paradigm shift in the 21st century, with the integration of molecular markers, genomic selection, doubled haploids, gene editing and advanced data-driven approaches, enabling greater precision, efficiency, and acceleration of genetic gain while maintaining long-term sustainability. Equally important is the role of the breeder's insight in interpreting complex genotype–phenotype interactions and aligning breeding objectives with real-world demands. It also addresses prevailing misconceptions and emerging concerns that may hinder progress, emphasizing the need to bridge genetic, technological, and commercial dimensions, recognizing that successful cultivars must meet both biological performance criteria and market expectations. Ultimately, breeding beyond boundaries requires a holistic, systems-oriented approach that converts scientific challenges into opportunities for creating superior, resilient, and widely adoptable crop varieties.

Keyword: Breeding • Genetic diversity • Selection index • Genetic gain • Breeder's eye • Climate resilience

Introduction

Plant breeding is a dynamic discipline that integrates fundamental biological principles with applied innovation to address the ever-evolving challenges of agriculture. It is both a science grounded in genetics, inheritance, and quantitative analysis and an art that relies on the breeder's intuition, experience, and ability to interpret complex biological systems. The philosophy of modern plant breeding extends beyond the mere development of new varieties; it encompasses the strategic transformation of biological variability into cultivars that are productive, resilient, and aligned with the needs of farmers and markets. A plant breeder operates at the interface of multiple scientific domains, including Mendelian genetics, quantitative genetics, physiology, and increasingly, genomics and data science. The breeder's role goes far beyond traditional agricultural practices; it involves designing crosses, managing genetic variability, and applying selection strategies to accumulate favorable alleles

✉ **Bijendra Pal**: bijendrapal127@gmail.com
Head R&D, Dayal Seeds, Meerut, Uttar Pradesh, India

Received: 25 December 2025/ Accepted: 04 April 2026

over successive generations (Falconer, 1996; Bernardo, 2002). In this context, the breeder is not merely selecting plants but engineering genetic combinations that can respond to present and future challenges. Innovation arises from the ability to integrate classical knowledge with emerging tools, enabling more precise and accelerated genetic improvement. A cultivar represents the ultimate product of plant breeding and serves as a tangible promise to farmers. It embodies enhanced productivity, stability across environments, and resilience to biotic and abiotic stresses. Beyond yield, modern cultivars are expected to minimize production risks and ensure consistent performance under variable climatic conditions (Ceccarelli, 2015). Thus, the success of a breeding program is measured not only by genetic gain but also by the reliability and adaptability of the cultivars delivered to end users. Genetic variability is the cornerstone of plant breeding, providing the raw material upon which selection acts. This variability may arise from natural sources, such as landraces and wild relatives, or be induced through hybridization, mutation, and advanced biotechnological interventions (Allard, 1999). The creation, maintenance, and strategic utilization of variability determine the long-term sustainability of genetic gain. Without sufficient diversity, breeding progress stagnates, underscoring the importance of continuously enriching the genetic base. Traditional plant breeding relied heavily on phenotypic selection following recombination through hybridization. While effective, this approach is often time-consuming and limited by environmental influences on trait expression. The advent of molecular markers, genomic selection, and gene editing technologies has revolutionized breeding by enabling precise manipulation and prediction of genetic outcomes (Lande & Thompson, 1990; Meuwissen *et al*., 2001). Modern breeding integrates these tools with conventional approaches, enhancing selection efficiency and accelerating cultivar development. Contemporary plant breeding is increasingly defined by its ability to convert constraints into opportunities. Challenges such as genetic erosion, climate variability, and technological limitations are no longer viewed solely as barriers but as catalysts for innovation. By leveraging advanced tools, strategic breeding designs, and a deep understanding of genotype–environment interactions, breeders can transform these concerns into pathways for creating superior cultivars. This paradigm shift highlights a systems-based approach where scientific challenges drive creative solutions, ultimately redefining the boundaries of plant breeding.

Genetic diversity: The paradox of selection and sustainability

Genetic diversity is the fundamental resource that underpins all plant breeding efforts, yet it is inherently shaped and often constrained by selection, very process designed to exploit it. This creates a paradox in breeding systems, where the pursuit of genetic gain through selection can simultaneously erode the variability required for sustained long-term improvement. Understanding and managing this balance is central to modern breeding strategies.

Selection as a driver of genetic gain

Selection is the primary mechanism through which breeders achieve genetic improvement. By favoring individuals with superior phenotypic or genomic values, breeders increase the frequency of favorable alleles, thereby shifting the population mean in the desired direction (Falconer, 1996; Bernardo, 2002). This process has been instrumental in the remarkable yield gains observed in major crops over the past century. In quantitative genetics, the response to selection is directly proportional to selection intensity, heritability, and genetic variance, emphasizing the critical role of variability in enabling continued progress (Lynch & Walsh, 1998). Thus, selection serves as the engine of crop improvement, translating genetic potential into realized performance.

The hidden cost: Loss of genetic variability

Despite its benefits, selection imposes a significant cost by reducing genetic diversity over successive cycles. Directional selection leads to allele fixation, diminishing the pool of segregating alleles and narrowing the genetic base (Robertson, 1960). This reduction in variability not only limits future selection response but also contributes to declining prediction accuracy in genomic selection frameworks, as highlighted by recent studies demonstrating that selection-induced changes in allele frequency can disrupt marker–trait associations (Bernardo, 2025). Furthermore, reduced diversity increases vulnerability to biotic and abiotic stresses, potentially compromising crop resilience. Therefore, while short-term gains are achieved, the long-term adaptive potential of breeding populations may be jeopardized.

Managing the diversity–gain trade-off

To sustain long-term genetic progress, breeders must actively manage the trade-off between genetic gain and diversity. Strategies such as elite × elite crossing enable the accumulation of favorable alleles while maintaining high performance levels. Simultaneously, recycling germplasm—including the reintroduction of older or underutilized lines can reintroduce lost alleles and broaden the genetic base (Hallauer *et al*., 2010). In hybrid breeding systems, maintaining distinct heterotic pools is critical for preserving heterosis and ensuring continued hybrid vigor. These approaches collectively allow breeders to balance short-term gains with long-term sustainability by periodically replenishing genetic variability.

Sustainable breeding strategies

Sustainable breeding requires a shift from maximizing immediate genetic gain to optimizing long-term improvement. This involves designing breeding programs that conserve genetic diversity while delivering competitive cultivars. Approaches such as optimal contribution selection, genomic mating, and the integration of diverse germplasm sources have been proposed to achieve this balance (Gorjanc *et al*., 2018). Additionally, incorporating pre-breeding and introgression from wild relatives can expand the adaptive potential of breeding populations. Preventing breeding stagnation ultimately depends on maintaining a dynamic equilibrium between selection intensity and genetic diversity. By adopting such strategies, breeders can ensure continuous genetic gain while safeguarding the evolutionary potential of crop populations.

Breeding for emerging trait requirements

The increasing frequency of climate extremes, shifting agro-ecological zones, and evolving market demands necessitate a reorientation of plant breeding objectives toward emerging trait requirements. Modern breeding must not only enhance yield potential but also enable crops to perform under diverse and often adverse environments. This shift underscores the importance of understanding how selection, environmental pressures, and genetic mechanisms interact to shape adaptive traits.

Role of selection in trait evolution

Selection is the principal force driving trait evolution in breeding populations. Across successive generations, directional selection increases the frequency of favorable alleles associated with target traits, thereby reshaping the genetic architecture of populations (Falconer, 1996; Bernardo, 2002). This cumulative process enables the fixation of adaptive traits, whether related to yield, stress tolerance, or quality. In dynamic environments, selection not only improves existing traits but also facilitates the emergence of novel trait combinations through recombination. Over time, this leads to the evolution of genotypes better suited to specific environmental conditions, demonstrating the power of selection as a tool for both improvement and adaptation.

Breeding under stress environments

Breeding under stress conditions plays a critical role in developing resilient cultivars. Exposure to abiotic stresses such as drought, heat, salinity, and low nutrient availability imposes strong selection pressure, favoring genotypes capable of maintaining physiological and reproductive functions under adverse conditions (Chapman *et al*., 2012). Selection under adverse environments activates genomic regions that may remain silent under normal conditions. At the molecular level stress exposure can "switch on" specific genes/genomic regions that confer survival advantages, including osmotic adjustment, antioxidant activity, and stress-responsive signaling pathways. Conversely, non-essential metabolic pathways may be switched off/ downregulated, optimizing resource allocation for survival and reproduction. Recurrent selection under such environments reinforces these adaptive responses, leading to stable stress-tolerant phenotypes.

Environmental influence on genetic expression

The expression of genetic potential is profoundly influenced by environmental conditions, resulting in genotype × environment (G × E) interactions. These interactions complicate selection, as phenotypic performance may not consistently reflect genotypic value across environments (Cooper *et al*., 2014). Recent advances in genomics have revealed that environmental stimuli can induce dynamic changes in gene expression, often described as genomic reprogramming. Stress-induced transcriptional shifts, epigenetic modifications, and regulatory network adjustments enable plants to respond rapidly to environmental challenges (Nicotra *et al*., 2010). Understanding these mechanisms is essential for designing breeding strategies that capture stable and adaptive genetic effects across diverse environments.

Local adaptation and decentralized breeding

Local adaptation is a key outcome of sustained selection within specific agro-ecological conditions. Breeding programs conducted in target environments are more likely to identify genotypes with superior performance and stability under those conditions (Ceccarelli, 2015). Decentralized and participatory breeding approaches further enhance this process by incorporating farmer knowledge and real-world variability into selection decisions. Native environments provide unique selection pressures that shape genetic responses, allowing breeders to exploit location-specific advantages. As climate variability intensifies, regionally focused breeding strategies will become increasingly important for developing cultivars that are not only high-yielding but also resilient and context-specific.

Selection index: Bridging theory and field reality

The selection index provides a quantitative framework that integrates multiple trait values into a single decision criterion, enabling breeders to make balanced and objective selections. It effectively bridges theoretical genetic principles with field-level realities, ensuring that selection decisions translate into consistent and practical genetic gain.

Conceptual basis of selection index

The selection index is a cornerstone of quantitative genetics, providing a systematic framework to improve multiple traits simultaneously. It combines phenotypic or genomic information across traits into a single linear predictor of breeding value, with weights assigned based on economic importance and genetic parameters such as heritability and genetic correlations (Rahimi & Debnath, 2023). By integrating yield, quality, and stress tolerance traits into a unified metric, the selection index enhances decision-making efficiency and aligns breeding outcomes with production and market priorities (Bernardo, 2002).

Practical constraints

Despite its theoretical robustness, the practical implementation of selection indices is constrained by several factors. Accurate phenotyping remains a major bottleneck, as observed trait values are often confounded by environmental noise, reducing the correlation between phenotype and true genetic value (Alemu *et al*. 2024; Cooper *et al*., 2014). In addition, genotype × environment (G × E) interactions can destabilize index performance across locations and seasons. Recombination further limits the simultaneous improvement of multiple traits, particularly when unfavorable genetic linkages exist, making it difficult to assemble optimal allele combinations within a single genotype.

Numbers vs strategy debate

A longstanding debate in breeding programs concerns whether success is primarily a function of population size or strategic design. Larger populations increase selection intensity and the probability of identifying superior recombinants, supporting the notion of selection as a "numbers game" (Falconer, 1996). However, resource constraints often limit population size, particularly in public-sector breeding. From my experience, a reasonable number of individuals is indeed necessary but success also depends on choosing the right partners in the breeding population. Emerging perspectives emphasize that strategic choices such as selecting parents with complementary trait architecture and high combining ability can partially offset limitations in population size, improving selection efficiency without proportionally increasing costs.

Improving selection efficiency

Enhancing the effectiveness of selection indices requires a combination of biological insight and technological precision. Strategic parent selection, based on known trait expression and genetic diversity, increases the likelihood of generating superior recombinants. Equally important is the use of precision phenotyping platforms and well-managed testing environments that minimize environmental variance and improve trait measurement accuracy revealing true genetic potential (Araus & Cairns, 2014). Integrating genomic information into selection indices further refines prediction accuracy, enabling breeders to make more informed decisions early in the breeding cycle. Collectively, these approaches bridge the gap between theoretical potential and field-level realization.

Advanced breeding tools empowering plant breeders in the 21st century

The 21st century has brought new hope for crop improvement, with advanced molecular and data-driven tools guiding breeders to make more precise selections and handle the complex "numbers game" of genetic values more efficiently

Marker assisted backcrossing and the value of EDVs

Marker assisted selection (MAS), especially marker assisted backcrossing, has become a core strategy for improving existing varieties by introgression of major genes or quantitative trait loci (QTLs) governing specific traits, especially those associated with disease resistance and quality (Miedaner & Korzun, 2012). The foundational work of Lande and Thompson (1990) underscored the effectiveness of MAS in backcross breeding, establishing its role in modern crop improvement programs. This approach has led to many successful releases of essentially derived varieties (EDVs) in crops such as wheat, barley, rice, tomato, and maize (Cerrudo *et al*., 2018). Yet, a fundamental question emerges: does this approach deliver meaningful long-term value? Rather than relying solely on incremental enhancement, could greater gains be achieved by developing entirely new cultivars that integrate these traits within more competitive genetic backgrounds? This perspective does not diminish the importance of essentially derived varieties (EDVs), but instead encourages breeders to look beyond incremental improvements toward more transformative breeding strategies.

From Quantitative Trait Loci (QTL) mapping to Genomic Selection (GS)

QTL mapping and GWAS have identified numerous loci for yield, adaptation and disease resistance, but many explain only a small fraction of phenotypic variance and can be highly background specific, limiting broad application (Wang *et al*., 2016). The difficulty lies in estimating genetic values, which depend on phenotypic data often clouded by environmental noise (Alemu *et al*., 2024). In response, genomic selection has emerged as a more powerful framework for polygenic traits. Instead of focusing on a few mapped QTL, GS uses dense markers across the genome to predict genomic estimated breeding values and select individuals based on genome wide effects (Cerrudo *et al*., 2018).

Simulation and empirical studies show that GS generally outperforms MAS for complex, low heritability traits such as grain yield, particularly when many loci of small effect are involved (Cerrudo *et al*., 2018). In maize, for example, GS models applied to doubled haploid (DH) populations achieved higher prediction accuracy than the variance explained by mapped QTL, confirming the polygenic nature of yield and related physiological traits. Nevertheless, GS depends critically on high quality, multi environment phenotyping for training, and its accuracy can decline when applied across very diverse germplasm or changing target populations. A pragmatic path is to combine QTL based MAS with GS: use MAS to introgress or fix major QTL for key traits while relying on GS to capture the numerous small effect loci and optimize overall performance (Miedaner & Korzun, 2012).

Gene editing: Promise and bottleneck

CRISPR/Cas mediated gene editing technology has opened new frontiers in precision breeding by enabling targeted modification of specific genes (Chen *et al*., 2019). Early successes in crops such as rice and maize demonstrate the potential to improve yield, stress tolerance, and quality traits. However, several challenges remain. Most plant genome editing workflows depend on tissue culture–based, genotype-dependent transformation systems, which constrain efficiency, limit species coverage, and require specialized facilities. In addition, identifying appropriate gene targets demands deep functional genomic knowledge, further complicating the application of these technologies (Wang *et al*., 2023; Yu *et al*., 2024). Moreover, regulatory frameworks and public acceptance continue to influence the deployment of edited crops. Recent work stresses that expanding tissue culture independent or reduced culture transformation methods, and improving delivery systems (e.g. RNPs, viral vectors, nanomaterials), is crucial to mainstream editing in diverse crops. Equally important is deciding what to edit. True breeding impact depends on tight integration between field breeders and molecular scientists to define priority traits, identify causal genes or alleles, and validate edited phenotypes under realistic environments (Cardi *et al.,* 2023).

Doubled haploids and their integration with genomics

Doubled haploid (DH) technology allows rapid production of fully homozygous lines, shortening breeding cycles and increasing selection intensity. DH populations are particularly useful for QTL discovery and for implementing GS, as demonstrated in maize and barley (Wang *et al*., 2016; Cerrudo *et al*., 2018). However, DH pipelines can generate very large numbers of fixed lines, creating challenges in phenotyping, managing genetic diversity, and ensuring adaptation across target environments. A practical way forward may lie in combining DH with GS, offers a powerful system that generate many DHs, genotype them, and use GS to prioritize the most promising lines for extensive field testing, thereby accelerating line recycling while maintaining genetic diversity and adaptability (Wang *et al*., 2016; Cerrudo *et al*., 2018).

Toward integrated breeding pipelines

No single technology can address the multifaceted challenges of modern plant breeding. Future breeding progress will depend less on any single technology and more on integrated pipelines that combine:

- Marker-assisted selection (MAS) and QTL-informed strategies remain essential for tracking major genes and disease resistance.
- Genomic selection (GS) enables prediction of performance for complex traits such as yield across diverse environments.
- Doubled haploid (DH) systems accelerate breeding cycles by rapidly fixing recombinants and strengthening GS training populations.
- Gene editing provides the capability to precisely introduce or fine-tune alleles once their functional relevance is established.

The coordinated deployment of these tools within well-designed breeding schemes requires close collaboration among breeders, molecular biologists, geneticists, and data scientists. Ultimately, the effectiveness of these tools depends not only on technological advancement but also on their alignment with biological complexity and field-level realities, supported by robust phenotyping. A systems-based, interdisciplinary approach is therefore essential to fully harness their collective potential. When effectively integrated, these technologies enable breeders to develop cultivars that are not merely incrementally improved, but truly competitive, resilient, and transformative for global agriculture (Miedaner & Korzun, 2012; Cerrudo *et al*., 2018; Wang & Doudna, 2023).

Commercial plant breeding: Challenges beyond the breeder's eye

The contemporary agricultural landscape is increasingly shaped by a value-conscious and well-informed customer who demands high and consistent performance from seed. This evolving expectation has introduced a critical challenge in modern plant breeding: bridging the gap between label claims and field realization across diverse and variable environments. Consequently, breeding is no longer driven solely by the breeder's perspective but is increasingly structured around market demand, explicit product profiles, and value-chain requirements. The foremost priority for breeders today is therefore to precisely understand customer needs and translate them into measurable breeding objectives (Bassi *et al*., 2023; Cobb *et al.,* 2019). A major hurdle in this context is the ability to deliver stable performance under heterogeneous and unpredictable environmental conditions. This pressure is transforming breeding programs into highly structured, efficiency-driven systems akin to a "breeding factory" capable of developing products tailored to specific customer requirements while minimizing environmental variability. Advances in quantitative genetics, genomic prediction, phenomics, and enviromics, supported by big data and artificial intelligence, have enhanced selection accuracy and accelerated breeding cycles. However, challenges such as genotype × environment interactions and local adaptation continue to limit predictability and performance stability. Such a shift necessitates a redefinition of the traditional concept of the *breeder's eye* (Bassi *et al*., 2023; Xu *et al*., 2022; Cobb *et al*., 2019).

Historically, the breeder's eye was considered as the ultimate authority in identifying superior plant types with promise. While phenotypic evaluation remains essential, it is no longer sufficient in isolation. Indeed, in well-conducted trials, top-performing entries are often consistently recognized, regardless of the evaluators, indicating that performance is reproducible rather than dependent solely on individual intuition (Glenn *et al*., 2017). However, in today's commercial framework, a superior plant must go beyond visual or phenotypic appeal. It must meet the expectations of multiple stakeholders across the value chain, including production teams, processing units, and sales and marketing groups. This evolution raises an important question: where does the breeder's unique role now reside?

The answer lies in a broader and more strategic function. The breeder's role is no longer confined to visual selection but extends to:

- Translating market and stakeholder feedback into quantitative product profiles that incorporate agronomic, quality, and sensory traits.
- Strategically identifying and combining genetic diversity to meet these profiles while preserving key economic traits and long-term adaptability.
- Designing efficient, cost effective breeding strategies and data architectures that integrate molecular tools, envirotyping, and advanced analytics.
- Ensuring that label claims are consistently realized under field conditions.
- Embedding seed economics (cost of goods, production feasibility, hybrid systems) into trait prioritization and product advancement.

In this context, commercial plant breeding is emerging as a discipline that demands the integration of scientific rigor with market intelligence. Breeders must act as architects of tailored solutions, balancing genetic potential, environmental adaptability, and customer expectations. Additionally, there is a growing need to incorporate traits that enhance commercial value, such as high germinability, early vigor, extended seed shelf life, and overall seed quality, which influence stand establishment, logistics, and marketability. Ultimately, the breeder's eye is no longer limited to identifying a visually superior plant. It now represents an integrative capability: anticipating market and societal needs, mobilizing appropriate germplasm, and orchestrating a technology-rich breeding process that consistently delivers varieties whose on farm performance, quality attributes, and economic profile match their commercial promise. The future of plant breeding, therefore, lies in developing programs that are not only technically robust but also commercially relevant, ensuring that every released variety reliably delivers on its promise in farmers' fields (Bassi *et al*., 2023; Xu *et al*., 2022; Cobb *et al*., 2019).

Integrative framework: Transforming concerns into innovation

Modern plant breeding operates within a landscape of interconnected constraints that challenge both scientific progress and practical deployment. A systems-oriented framework is therefore essential to transform these concerns into pathways for innovation and sustainable genetic gain.

Key concerns identified

One of the most critical concerns is the progressive loss of genetic diversity due to repeated cycles of directional selection, which can limit long-term improvement and adaptive potential (Bernardo, 2002). Environmental variability further complicates breeding outcomes through strong genotype × environment (G × E) interactions, reducing the predictability of cultivar performance across locations and seasons (Cooper *et al.,* 2014). In parallel, technological limitations–such as incomplete understanding of complex trait architecture, dependence on high-quality phenotypic data, and constraints in deploying advanced tools, restrict the full realization of modern breeding approaches (Crossa *et al.,* 2017). Additionally, increasing market pressures demand cultivars that are not only high-yielding but also stable, cost-effective, and tailored to specific value chains, adding another layer of complexity to breeding objectives.

Transforming pathways

Transforming major constraints in commercial breeding into opportunities requires a strategic re framing of how variation, environment, technology, and markets are used to drive genetic gain. Genetic diversity, rather than being depleted, must be actively created, conserved, and mobilized as the primary engine of long term innovation. Elite lines, landraces and wild relatives provide alleles for yield, quality, and biotic/abiotic stress tolerance, which can be harnessed through recombination and systematic introgression into commercial backgrounds. Environmental stress, instead of being viewed solely as a limitation, can act as a selective force that drives adaptation and reveals beneficial allelic variation. Multi environment testing, genome–environment association and landscape/functional genomics reveal loci and haplotypes associated with drought, heat, salinity and other stresses, enabling targeted deployment of climate adaptive variation in breeding pipelines (Swarup *et al*., 2021; Dwivedi *et al*., 2017). Technological advancements ranging from genomic selection to gene editing, enable greater precision in selection and trait manipulation, converting complexity into predictability. Similarly, customer demand can be leveraged to refine breeding targets, ensuring that selection decisions are aligned with real-world needs and economic value.

Proposed integrative breeding model

An integrative breeding model must combine genetic, technological, and commercial dimensions into a unified, data-driven system. Such a model integrates diverse germplasm resources, high-throughput phenotyping, genomic prediction, and precision breeding tools within a coordinated framework. Decision-making is guided by predictive analytics and continuous feedback from multi-environment testing and market performance. This approach aligns with emerging concepts of "modernized breeding programs," where interdisciplinary collaboration and digital integration enhance efficiency and impact (Hickey *et al.,* 2017). Ultimately, by embedding flexibility, diversity management, and customer orientation into breeding pipelines, this framework enables the systematic conversion of constraints into innovation, delivering cultivars that are resilient, competitive, and sustainable.

Future perspectives

Integration of AI and data science

The future of plant breeding will be increasingly shaped by the integration of artificial intelligence (AI) and data science into breeding pipelines. Predictive breeding, enabled by machine learning algorithms and large-scale genomic and phenotypic datasets, allows for the estimation of breeding values with greater accuracy and speed (Crossa *et al.,* 2017). AI-driven models can capture complex, non-linear interactions among genes and environments, thereby improving selection decisions under variable conditions. The convergence of high-throughput phenotyping, environmental data, and genomics is expected to transform breeding into a predictive and decision-support-driven discipline.

Multidisciplinary collaboration

As breeding challenges become more complex, interdisciplinary collaboration is essential. The integration of expertise from plant breeders, molecular biologists, geneticists, and data scientists enables the effective utilization of advanced tools such as genomic selection and gene editing. Collaborative frameworks enhance the translation of genomic discoveries into field-level applications, ensuring that innovations are both scientifically robust and practically relevant (Hickey *et al.,* 2017). Such partnerships are critical for bridging gaps between laboratory research and breeding program implementation.

Sustainable and resilient breeding systems

Future breeding systems must prioritize sustainability and resilience in the face of climate change and resource constraints. Climate-smart breeding approaches focus on developing cultivars with enhanced tolerance to abiotic stresses, improved resource-use efficiency, and stable performance across diverse environments. Incorporating diverse germplasm, leveraging genomic tools, and adopting decentralized breeding strategies will be key to achieving long-term sustainability. Ultimately, breeding programs must balance productivity with environmental stewardship, ensuring that crop improvement contributes to resilient agricultural systems and global food security.

Conclusion

Plant breeding, at its core, represents the transformation of concern into innovation where constraints such as genetic erosion, environmental variability, and technological limitations are converted into opportunities for innovation. This philosophy underscores the dynamic nature of breeding as both a scientific and creative discipline. The future of crop improvement depends on the effective integration of classical genetic principles with advanced tools, including genomic selection, gene editing, and data-driven decision systems, while simultaneously aligning outcomes with market and farmer needs. Such integration ensures that breeding programs remain both biologically robust and commercially relevant. Moving forward, plant breeding will increasingly evolve as a precision-driven and purpose-oriented science, guided by predictive analytics, interdisciplinary collaboration, and sustainability goals. By embracing this holistic approach, breeders can deliver cultivars that not only enhance productivity but also ensure resilience, adaptability, and long-term agricultural sustainability in a rapidly changing world.

References

Alemu, A., Åstrand, J., Montesinos-Lopez, O. A., Sanchez, J. I., Fernandez-Gonzalez, J., Tadesse, W., Vetukuri, R. R., Carlsson, A. S., Ceplitis, A., Crossa, J. & Ortiz, R. (2024). Genomic selection in plant breeding: key factors shaping two decades of progress. *Molecular Plant*, **17**(4): 552–578.

Allard, R. W. (1999). *Principles of plant breeding*. John Wiley & Sons.

Araus, J. L. & Cairns, J. E. (2014). Field high-throughput phenotyping: the new crop breeding frontier. *Trends in Plant Science*, **19**(1): 52–61.

Bassi, F., Sanchez-Garcia, M. & Ortiz, R. (2023). What plant breeding may (and may not) look like in 2050? *The Plant Genome*, **17**.

Bernardo, R. (2002). *Breeding for quantitative traits in plants*. Woodbury, MN: Stemma Press.

Bernardo, R. (2025). Why does genomewide prediction become ineffective after several cycles of recurrent selection? *Crop Science*, **65**(5): 70164.

Cardi, T., Murovec, J., Bakhsh, A., Boniecka, J., Bruegmann, T., Bull, S. E., Eeckhaut, T., Fladung, M., Galovic, V., Linkiewicz, A. & Lukan, T. (2023). CRISPR/Cas-mediated plant genome editing: outstanding challenges a decade after implementation. *Trends in Plant Science*, **28**(10): 1144–1165.

Ceccarelli, S. (2015). Efficiency of plant breeding. *Crop Science*, **55**(1): 87–97.

Cerrudo, D., Cao, S., Yuan, Y., Martinez, C., Suarez, E.A., Babu, R., Zhang, X. & Trachsel, S. (2018). Genomic selection outperforms marker assisted selection for grain yield and physiological traits in a maize doubled haploid population across water treatments. *Frontiers in Plant Science*, **9**: 366.

Chapman, S. C., Chakraborty, S., Dreccer, M. F. & Howden, S. M. (2012). Plant adaptation to climate change–opportunities and priorities in breeding. *Crop and Pasture Science*, **63**(3): 251–268.

Chen, K., Wang, Y., Zhang, R., Zhang, H. & Gao, C. (2019). CRISPR/Cas genome editing and precision plant breeding in agriculture. *Annual Review of Plant Biology*, **70**(1): 667–697.

Cobb, J. N., Juma, R. U., Biswas, P. S., Arbelaez, J. D., Rutkoski, J., Atlin, G., Hagen, T., Quinn, M. & Ng, E. H. (2019). Enhancing the rate of genetic gain in public-sector plant breeding programs: lessons from the breeder's equation. *Theoretical and Applied Genetics*, **132**(3): 627–645.

Cooper, M., Messina, C. D., Podlich, D., Totir, L. R., Baumgarten, A., Hausmann, N. J., Wright, D. & Graham, G. (2014). Predicting the future of plant breeding: complementing empirical evaluation with genetic prediction. *Crop and Pasture Science*, **65**(4): 311–336.

Crossa, J., Pérez-Rodríguez, P., Cuevas, J., Montesinos-López, O., Jarquín, D., De Los Campos, G., Burgueño, J., González-Camacho, J.M., Pérez-Elizalde, S., Beyene, Y. & Dreisigacker, S. (2017). Genomic selection in plant breeding: methods, models, and perspectives. *Trends in Plant Science*, **22**(11): 961–975.

Dwivedi, S. L., Scheben, A., Edwards, D., Spillane, C. & Ortiz, R. (2017). Assessing and exploiting functional diversity in germplasm pools to enhance abiotic stress adaptation and yield in cereals and food legumes. *Frontiers in Plant Science*, **8**: 1461.

Falconer, D. S. (1996). *Introduction to quantitative genetics*. Pearson Education India.

Glenn, K. C., Alsop, B., Bell, E., Goley, M., Jenkinson, J., Liu, B., Martin, C., Parrott, W., Souder, C., Sparks, O. & Urquhart, W. (2017). Bringing new plant varieties to market: plant breeding and selection practices advance beneficial characteristics while minimizing unintended changes. *Crop Science*, **57**(6): 2906–2921.

Gorjanc, G., Jenko, J., Hearne, S. J. & Hickey, J. M. (2016). Initiating maize pre-breeding programs using genomic selection to harness polygenic variation from landrace populations. *BMC Genomics*, **17**(1): 30.

Hallauer, A. R., Carena, M. J. & Miranda Filho, J. D. (2010). *Quantitative genetics in maize breeding*. Springer Science & Business Media.

Hickey, J. M., Chiurugwi, T., Mackay, I. & Powell, W. (2017). Genomic prediction unifies animal and plant breeding programs to form platforms for biological discovery. *Nature Genetics*, **49**(9): 1297–1303.

Lande, R. & Thompson, R. (1990). Efficiency of marker-assisted selection in the improvement of quantitative traits. *Genetics*, **124**(3): 743–756.

Lynch, M. & Walsh, B. (1998). *Genetics and analysis of quantitative traits*. Sunderland, MA: Sinauer Associates.

Meuwissen, T. H., Hayes, B. J. & Goddard, M. (2001). Prediction of total genetic value using genome-wide dense marker maps. *Genetics*, **157**(4): 1819–1829.

Miedaner, T. & Korzun, V. (2012). Marker-assisted selection for disease resistance in wheat and barley breeding. *Phytopathology*, **102**(6): 560–566.

Nicotra, A. B., Atkin, O. K., Bonser, S. P., Davidson, A. M., Finnegan, E. J., Mathesius, U., Poot, P., Purugganan, M. D., Richards, C. L., Valladares, F. & van Kleunen, M. (2010). Plant phenotypic plasticity in a changing climate. *Trends in Plant Science*, **15**(12): 684–692.

Rahimi, M. & Debnath, S. (2023). Estimating optimum and base selection indices in plant and animal breeding programs by development new and simple SAS and R codes. *Scientific Reports*, **13**(1): 18977.

Robertson, A. (1960). A theory of limits in artificial selection. *Proceedings of the Royal Society of London Series B: Biological Sciences*, **153**(951): 234–249.

Swarup, S., Cargill, E. J., Crosby, K., Flagel, L., Kniskern, J. & Glenn, K.C. (2021). Genetic diversity is indispensable for plant breeding to improve crops. *Crop Science*, **61**(2): 839–852.

Wang, J. & Doudna, J. (2023). CRISPR technology: a decade of genome editing is only the beginning. *Science*, **379**(6629).

Wang, S. B., Wen, Y. J., Ren, W. L., Ni, Y. L., Zhang, J., Feng, J. Y. & Zhang, Y. M. (2016). Mapping small-effect and linked quantitative trait loci for complex traits in backcross or DH populations via a multi-locus GWAS methodology. *Scientific Reports*, **6**(1): 29951.

Wang, S., Wang, G., Li, H., Li, F. & Wang, J. (2023). *Agrobacterium tumefaciens*-mediated transformation of embryogenic callus and CRISPR/Cas9-mediated genome editing in 'Feizixiao' litchi. *Horticultural Plant Journal*, **9**(5): 947–957.

Xu, Y., Zhang, X., Li, H., Zheng, H., Zhang, J., Olsen, M. S., Varshney, R.K., Prasanna, B.M. & Qian, Q. (2022). Smart breeding driven by big data, artificial intelligence, and integrated genomic-enviromic prediction. *Molecular Plant*, **15**(11): 1664–1695.

Yu, L., Zou, J., Hussain, A., Jia, R., Fan, Y., Liu, J., Nie, X., Zhang, X. & Jin, S. (2024). Systemic evaluation of various CRISPR/Cas13 orthologs for knockdown of targeted transcripts in plants. *Genome Biology*, **25**(1): 307.