Received : 12-Jul-25 | Revised: 21-Aug-25 | Accepted: 10-Sep-25

REVIEW ARTICLE

Trends in Biotechnology and Plant Sciences

Enhancing Crop Improvement through Integration of Advanced Plant Breeding and Precision Agriculture

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Abstract

Precision agriculture, coupled with existing technologies in breeding plants, is a viable means of enhancing crop yields in the face of climate change, soil erosion, and the expanding and competing needs of food security. Contemporary breeders are therefore trying to find breeding approaches that would maximize genetic benefits and still preserve the plasticity of heterogeneous surroundings. This review explains how the combination of precision tools- UAV-based phenotyping, soil and canopy sensors, GIS-enabled mapping, and AI, along with genomic selection, CRISPR-Cas gene editing, speed breeding, and induced doubled haploid induction, will find application in agriculture. It is the combination of all these innovations that are fundamentally redefining breeding, with higher estimates of heritability with auto-controlled environments, better quality selection with predictive algorithms, high-throughput screening capable of selecting larger numbers, and higher rates of generational turnover. Breeders can close the gap between genomic potential and actual performance by creating digital twins and more advanced simulation models by developing ideotypes and predicting genotype-by-environment (G x E) interactions before plants are taken to the field. However, some regions can only scale to such integrated systems due to lack of the necessary infrastructure, rigid data interoperability and policy incompatibility, and resource constraints. In the meantime, potential moral concerns with gene-editing include fair access, personally stored data, and ethics. In the future, crop breeding will be centered on technological innovation, institutional change, cross-disciplinary research and international knowledge sharing. When directed at improving the productivity and sustainability of farming, precision-integrated breeding is a powerful, integrative paradigm.

KEYWORDS
Precision Agriculture**,** Crop improvement, Speed breeding, CRISPR-Cas, Genomic selection, High-throughput phenotyping, AI-driven agriculture, Sustainable crop improvement.

Citation: Murtaza A, 2025. Enhancing crop improvement through integration of advanced plant breeding and precision agriculture. Trends in Biotechnology and Plant Science, 3(3): 1-21. https://doi.org/10.62460/TBPS/2025.091

1 | INTRODUCTION

The current situation in agriculture is characterized by the convergence of environmental, demographic, and technological trends, which all exert pressure on the traditional crop-based production systems. Some of the relevant issues for global food security are net crop yield declines, soil erosion, increasing variability in climatic conditions, and the potential to produce food for a global population of 9.7 billion people in 2050 (Food & Nations, 2017). Although classical breeding has been the backbone of productivity gains over the years, the recurrent-selection model in its traditional form faces declining returns when applied to traits such as nitrogen-use efficiency, drought tolerance, or disease resistance due to the long time-scale requirements, relatively low throughput of a given trait at the phenotypic level, and low ability to capture context (Ceccarelli, 2015).

Molecular breeding has changed the paradigm of genomic characterization and manipulation of genotypes. Genomic selection (GS), as originally defined by (Meuwissen et al., 2001), enables prediction of breeding values prior to phenotype expression, and thus enables a reduction in cycle length and an increase in genetic gain (Crossa et al., 2017). At the same time, CRISPR-Cas9 and related gene-editing systems could be used to make more precise and heritable edits with less linkage drag, less regulatory complexity, and relative safety than transgenic approaches (Burgess, 2018). Speed breeding, which involves using controlled light and temperature conditions, enables up to four generations to be produced in a year in selected crops and can accelerate the process of selection in the greenhouse or under growth-chamber conditions (Watson et al., 2018). Despite these advances, it is still a challenge to deploy them at a large scale, as the development of a complex trait in a dynamic and field environment is still a major challenge (Tardieu et al., 2017).

Along with scientific discoveries of structure, precise agriculture has been adopted as an information method of crop management. Remote-sensing imagery, UAV-mounted sensors, in-situ weather and soil monitors, GPS infrastructure, and machine-learning paradigms enable site-specific intervention at unprecedented temporal resolutions not possible in traditional practice, reduce input misallocation, and enable ecological stewardship (Zhang & Kovacs, 2012). High-throughput non-destructive phenotyping is yet another challenge in conventional breeding; this is also addressed using the technological suite. Both appear to have an opportunity and a change factor in the joint synergies of precision-farming solutions and plant breeding (Kaya, 2025). The precision phenotyping platforms could serve as a link between genomic information and environment-specific factors, thereby characterizing the concept of genotype-environment interaction (Jarquín et al., 2014). By making machine-based decisions, trait performance can be better predicted in changing environments, breeding values can be better predicted in the future, and trial design can be more accurately performed than ever before (Berindean et al., 2024). Participatory breeding platforms also allow farmers to screen locally-defined candidate genotypes based on mobile applications and peer review (Rasmussen et al., 2020). However, there are a series of disadvantages that restrict the complete application of these innovations. In low-income settings, interoperability challenges include: weak infrastructures; limited dialogue and collaboration between disciplines; lack of resolution of ethics issues surrounding the privacy and stewardship of gene editing that could hinder integration; and non-equitable regulatory frameworks across borders (Anand et al., 2023).

Objective of this review is to critically assess the potential of emerging molecular breeding technologies, precision agriculture technologies and participatory approaches for addressing the multi-dimensional aspects of global food security. In particular, it will explore how the recent advances of genomic selection, CRISPR-Cas9, speed breeding and high-throughput phenotyping can complement precision farming as a tool to accelerate crop improvement. Moreover, this paper aims to shed light on opportunities and constraints for the scalability of these innovations in resource-poor territories, and to identify pathways to bridge the scientific and technological, as well as socio-regulatory, divides and move towards sustainable and climate resilient agro-ecosystems.

2: Tool and Trends in Modern Plant Breeding

Over the last few decades, the history of plant breeding based on Mendelian inheritance has transformed into the multidisciplinary practice of molecular biology, bioinformatics, gene editing and rapid generation (Buch et al., 2023). This is due to the increasing pressure for the development of climate adaptive high-yielding and high-quality cultivar that would be able to perform under variable environmental conditions and under resource constraints (Bhoite et al., 2024). The current breeding pipelines are based on the breeder equation to optimize the increment of genetic gain in terms of maximizing selection accuracy, minimizing cycle time, increasing selection intensity and preserving genetic variability (Alemu et al., 2024).

2.1 Genomic Selection (GS)

Genomic selection (GS) is a paradigm shift in quantitative breeding, particularly with respect to polygenic traits whose expression is controlled by many small-effect loci (Miedaner & Juroszek, 2021), and the methodology is fundamentally different from classical marker assisted selection (MAS) which targets the large-effect loci. In GS, the training population consists of individuals with both the genotypic and phenotypic data, from which the predictive models (GBLUP or Bayesian regressions) are developed (Abdul Aziz & Masmoudi, 2025). The models are then applied to a so-called selection population, which is genotyped but phenotypically untagged, thus allowing for earlier and cheaper selection (Zhang & Zhang, 2020).

The cereal crops in which GS has demonstrated potential include wheat, maize, rice, chickpea, and soybean, and understanding of GS has been reported to provide significant gain in precision (prediction accuracy) when combined with high-throughput phenotyping and well-designed training population (Crossa et al., 2017). Early generation selection increases breeding speed and reduces the need for extensive field testing. However, the GS tends to be less efficient when the training and testing populations differ, especially if the populations differ genetically, or if there are high G x E interactions (Vieira et al., 2025). The three above-mentioned flaws can be addressed by including environmental covariates and multi-environment trial information in the prediction model, thus increasing robustness even in heterogeneous agroecological environments (Szklarczyk et al., 2023).

Genomic selection (GS) has so far been highly successful in a small number of cereal and legume crops, including wheat, rice, maize, chickpea and soybean. The prediction performance of GS has been significantly improved by the combination with high-throughput phenotyping and optimal design of the training population (Garg et al., 2025). Moreover, due to the cost efficiency of breeding, the intensity of the breeding schedules is constrained by the selection of early generations. However, GS performance is vulnerable when there is a difference between training and testing population genes or strong genotype-by-environment (G x E) interactions. Some of these limitations can be partly offset by incorporating environmental covariates and multi-environment trial information in the prediction model, which will make the model more robust across agroecological conditions (Alemu et al., 2024).

Overall, GS is a revolution in modern breeding practice. With the recent availability of genome-wide data and high-quality predictive modeling, GS provides a scalable, accurate, and valuable approach to enhance complex traits in crop species in a time frame that has never been seen before (Johnston et al., 2024).

2.2 Genome Editing with CRISPR-Cas Systems

CRISPR-Cas genome editing is a gamechanger in trait development in plants because it does not need pre-designed gene editing; instead, gene editing can be done very specifically, efficiently and with precision (Table 1)(Bhuyan et al., 2023) by guiding Cas9 enzyme into the desired loci of the genome where it triggered a pair of double-strand breaks using synthetic RNA. The cellular machinery fixes these breaks by non-homologous end joining (NHEJ) (similar to gene knockout), or homology-directed repair to introduce gene insertions or substitutions (Kagan et al., 2022). This is already evident in agricultural applications: knockout of OsERF922 in rice made it resistant to blast disease; ARGOS8 in maize made them more tolerant to drought (Xie et al., 2017). A combination of genes coding for oil in soybeans was also successfully bred for higher nutritional value (Chakravarty et al., 2025). In some countries, CRISPR is more specific (fewer transgenes, fewer regulatory requirements) than transgenic approaches (Garg et al., 2025). However, it still has technical limitations such as the dependence on tissue culture, low transformation efficiency and off-target effect. Several new technologies such as base editing, prime editing, and pathogen-free delivery devices are helping to overcome these limitations, thus leading to increased and broader acceptability (Taning et al., 2021).

CRISPR-Cas genome editing has introduced a level of control, precision, and programmability to plant breeding at multiple levels that has fundamentally altered the current reality of plant breeding by enabling specific and precise plant genome modification with a wide range of crop choices (Chakravarty et al., 2025). Unlike previously engineered systems, e.g. ZFNs and TALENs, a single guide RNA directs the Cas9 nuclease to a Cas9-binding site in the genome, resulting in DNA double-strand breaks (Cordeiro et al., 2024). Then, the plant cell repairs these DSBs either non-homologous (end joining), which often introduces small deletions or insertions, or in a homology-dependent manner, which allows biological constructs to make specific genomic additions or substitutions (Garg et al., 2025).

CRISPR can be used in a broad manner for crop traits improvement like disease resistance, abiotic stress tolerance, crop nutrition etc. (Hasan, 2024). As such, rice OsERF922 editing has conferred enhanced resistance to blast disease. Further, maize MoArg8 knock-out model animals also showed increased drought stress resilience and water-use efficiency (Irkham et al., 2024). Genes for fatty acid biosynthesis were manipulated in soybean to produce oleic acid and linolenic acid reduced oilseed lines with improved oil stability and nutritional quality of the oil (Khan et al., 2025). The CRISPR system is more target specific than traditional transgenic techniques, has a lower risk of random insertion of foreign DNA and a lower regulatory burden in some jurisdictions if foreign DNA is not inserted (Misra et al., 2024). CRISPR-based editing is an even more popular technique in many breeding programs because it can be approved quickly in most regulatory applications (Yang et al., 2025) (Fig. 2).

Table 1: CRISPR-Cas Application in Key Crops

CROP	Target Gene	Modified Trait	Improvement	References
Rice	OsERF922	Blast disease resistance	40-60% reduction in infection	(Shah et al., 2024; Wang et al., 2016)
Maize	AGROS8	Drought tolerance	30% higher yield under water stress	(Shi et al., 2017)
Soybean	FAD2/FAD3	Oil composition	85% oleic acid (25% in wild type); improved stability	(Bhati et al., 2021)
Wheat	Pm3	Powdery mildew resistance	Near complete immunity	(Wang et al., 2023)

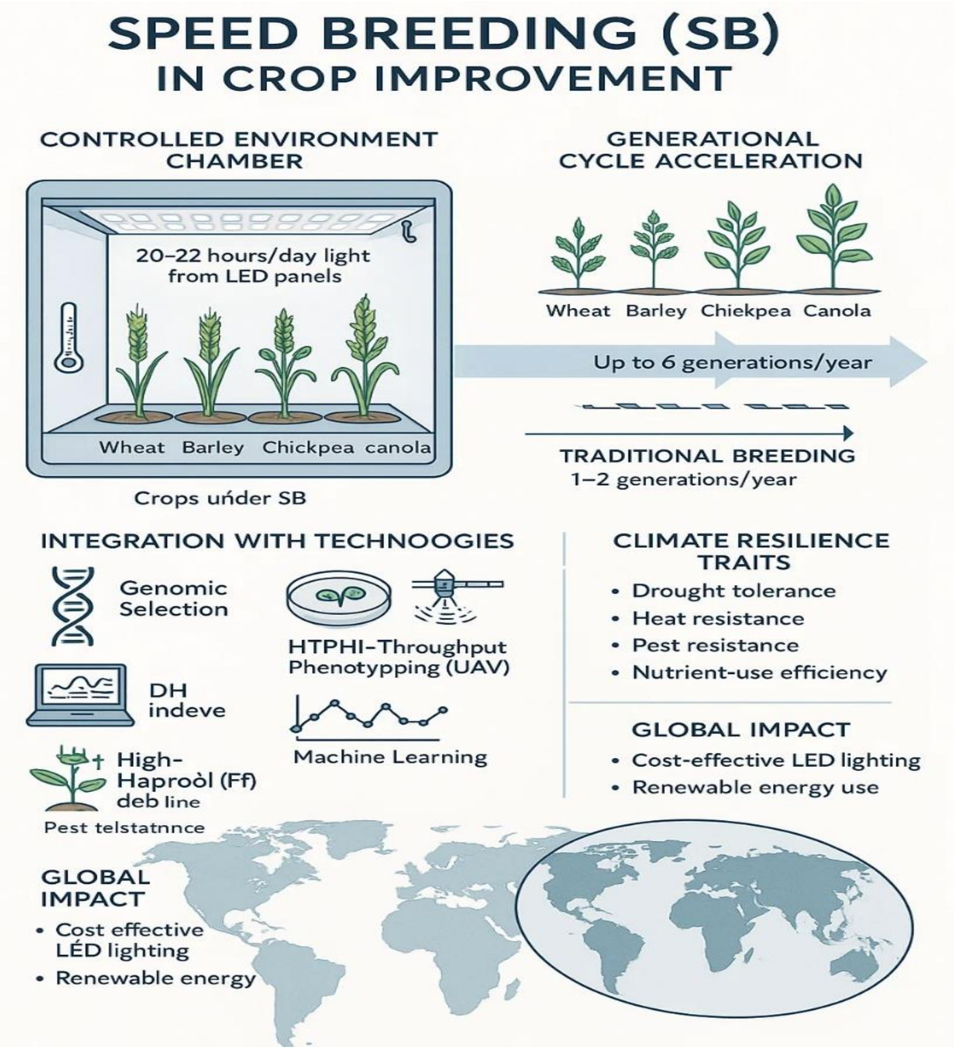

Fig. 1: Integrated Speed Breeding Framework for Climate-Resilient Trait Development.

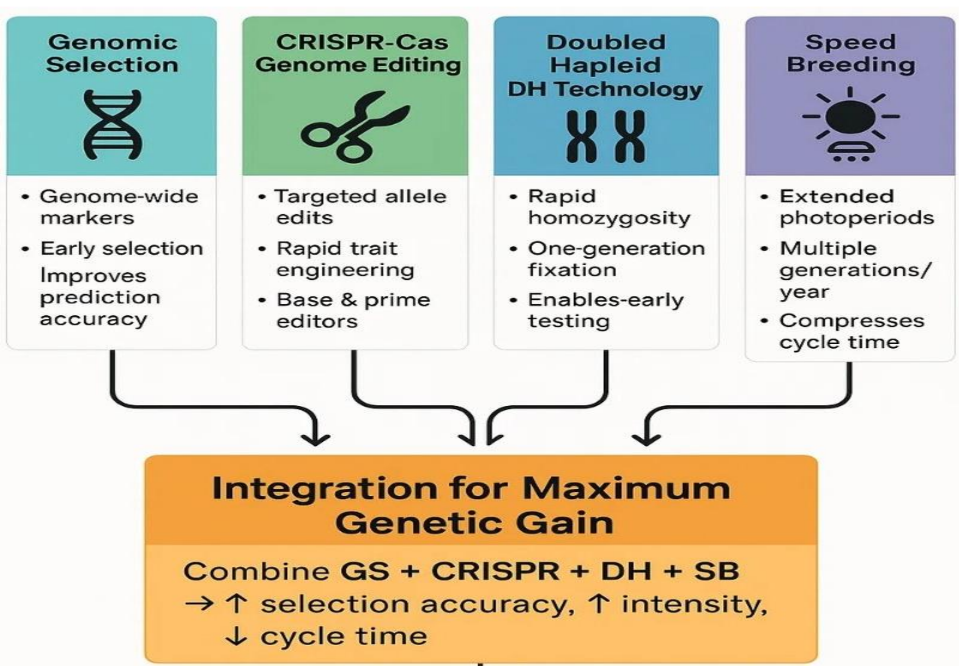

Fig. 2: Integrated Framework of technologies to Revolutionize Crop Improvement.

2.3 Doubled Haploid Technology

Doubled haploidy is a plant breeding technique that accelerates haploid breeding lines by growing faster, by inducing chromosome doubling, producing a homozygous individual in one generation instead of the traditional selfing (six to eight generations) (Shariatpanahi et al., 2021). Doubled haploid systems are being increasingly used in crops to rapidly freeze genotypes as in maize, wheat and barley, so that early stage testing can be conducted and the time lag between a discovery in a breeding program and eventual cultivar release can be shortened (Taning et al., 2021).

Doubled haploid lines are generated either by in vitro anther or microspore culture or by the in vivo method of male-sterile induced haploid production. However, these systems are not universal, are not very responsive and have complicated protocols in legumes, oilseeds and trees (Forster & Thomas, 2005). Despite the trend towards greater genetic homogeneity and genetic stability in some cases, the use of double haploids in hybrid breeding programs and QTL analysis remains the current trend (Zaidi et al., 2023). Doubled haploid technology, in combination with genomic selection or genome editing, allows the desired alleles to be fixed in a short time, ensuring the robustness of the implementation of the traits, while making them more accessible (Yassue et al., 2021).

2.4 Speed Breeding (SB)

Speed breeding (SB) is a controlled manipulation of environmental conditions with the goal of shortening the number of generations and the number of breeding cycles during the growing season (Wanga et al., 2021). Long day-length (20–22 hours of light per day), optimized temperature regime, and efficient solid-state LED lighting has enabled control of up to half a dozen generations per year in several key crops in the agricultural landscape, including wheat, barley, chickpea and canola (Watson et al., 2018). The advent of genomic selection (GS) or double haploid (DH) lines and the combination of both will dramatically speed up the time required to release new varieties (Miedaner & Juroszek, 2021) (Fig. 1).

It allows rapid introgression of useful alleles, rapid pyramiding of complementary traits and rapid turnover of segregating populations. On the other hand, indoor conditions are unnaturally free of disease or drought stress, so environment-sensitive traits may be limited by the indoor environment (Wang et al., 2023). Furthermore, some contexts (e.g., growth chambers, controlled-environment facilities, energy-intensive lighting) might raise some questions about the need for scalability and affordability in resource-limited environments (Samantara et al., 2022). However, SB cannot be neglected as a basic tool in the modern pre-breeding activities and in early generation selection systems.

At present, crop breeding, selection, and evaluation (SB) have moved from conventional slow selection to high-throughput phenotyping (HTP) systems as well as machine-learning models for real-time monitoring of plant growth, phenology, and other physiological features (Chen et al., 2025). The integration increases the accuracy of selection under accelerated cycles for continuous and non-destructive measurement of key parameters (canopy temperature, chlorophyll fluorescence, biomass accumulation, and fluorescence); SB and GS pipelines intersect to enable early data-driven breeding decisions and reduce the % of low-potential genotypes that pass through the breeding funnel (Dhanyalakshmi et al., 2024). This plasticity of SB also allows for the development of germplasm that can be screened quickly for traits related to climate resilience, including heat and drought tolerance, pest resistance and nutrient-use efficiency. Although the scalability issue has not been completely resolved, the use of efficient and cost-effective LED technologies, modular expansion units, and the operation of a renewable energy plant is making it more accessible worldwide. Such SB-induced controlled conditions allow for the specific study of gene-environment interactions. Thus, some adaptive phenotypes can be introgressed into elite backgrounds (Duan et al., 2025). With the modern trend of intensified climate change and food-security issues advocated in modern agriculture worldwide, SB is one of the key strategies for genetic acceleration in combination with multi-environment tested methods, which are emerging in the breeding programs of today (Hafeez et al., 2023).

2.5 Integration for Maximum Genetic Gain

The combination of genomic selection (GS), clustered regularly interspaced short palindromic repeats (CRISPR), double haploid (DH) production, and single-step genomic synthesis are especially strong breeding platform (Zhang & Kovacs, 2012). The breeder equation states that genetic progress, or what is denoted as genetic gain, depends on the intensity of selection, accuracy of selection, the genetic variance and the cycle time (He et al., 2023). When such technologies are combined, each of the corresponding components will be optimized: GS will accelerate and refine selection, CRISPR will introduce allele-specific specificity of modification, DH will anchor desirable genotypes in a very short time, and SB will collapse the overall breeding cycle, allowing multiple favorable alleles to be accumulated within a limited period of time (Li et al., 2023). Despite these benefits, an inescapable limit presents itself to the present architecture: phenotyping (Zhang & Kovacs, 2012). Unless we can demonstrate phenotypic measurements that are accurate, with a spatial resolution and scalable to real-world conditions, then assumed or designed molecular advantages can fail when it is time to roll out designs to the field (Vincent et al., 2022). Accordingly, the burden of obvious interest in such breeding interventions is therefore coupled with the precision-agriculture platforms that are following suit as being able to capture contemporaneous phenotypic and environmental data is not just a desirable extension but a pre-condition. The proposed integration constitutes the foundation of the future, precision-integrated crop-improvement systems (Ghavi Hossein-Zadeh, 2024).

3. Precision Agriculture: Enabling Technologies and Applications

Precision agriculture (PA) is a paradigm in crop management which integrates digital technologies with sensor networks and data analytics to make the decision-making spatially and temporally acute. In essence, inputs, such as water, fertilizers, pesticides, and labor, are to be employed when and where they are proved to be necessary and with the help of current field-level data.

3.1 Remote Sensing and High-Throughput Phenotyping

Remote sensing and high-throughput phenotyping are two of the most powerful components of the data-intensive precision agriculture ecosystem (Wang & Ahmad, 2025). Plant phenotype can be remotely sensed with high temporal and spatial resolution (representing the heterogeneous environment) by non-destructive quantification of canopy temperature, height, biomass, chlorophyll concentration, and vegetation indices (especially the Normalized Difference Vegetation Index, NDVI) (Nigon et al., 2020). These measurements are strongly correlated with stress responses, growth rate and productivity, and thus provide good relationships to the genotypes performance under abiotic and biotic stresses (Yuan et al., 2021).

At the same time, HTP is emerging through the automation of phenotypic recording of thousands of genotypes in breeding nurseries. Thermal, hyperspectral, multispectral and LiDAR-enabled platforms are now being deployed at regular intervals to characterize plant architecture, water-use efficiency, disease progression and photosynthetic activity (Moroni et al., 2022). Such systems are used on UAVs, tractors, gantries or as fixed camera systems in controlled environments (Rui et al., 2024). Machine-learning algorithms have been applied to the processed data to mine quantitative traits information at larger and faster scales than ever before, accelerating selective cycles to improve the clarity of genotype by environment (G x E) interactions and, by extension, the predictive power of genomic-selective memory (LSTM) networks (Cravero et al., 2022). According to Miedaner, "algorithms can be trained to perform yield prediction, disease detection, crop classification and phenological stage identification based on multisource inputs, UAV imagery, soil sensors and climate variables" (Miedaner & Juroszek, 2021).

As an example of the application, the use of CNN-LSTM models to decode UAV time series of images that led to the estimation of crops flowering and maturity stages, in particular soybean maturity stage, is presented. This type of analysis will help the breeders to choose appropriate genotypes and the best harvesting time (Zhang & Zhang, 2020). In addition to the phenology focus, real-time environmental feedback is being used to generate agronomic management (with increased relevant genotype-specific advice on such tasks as irrigation scheduling or nitrogen application) that is increasingly under dynamic control by AI models (Liakos et al., 2018). The platforms able to integrate these outputs of the AI are those of a decision-support system (DSS) aggregating and synthesizing sensor, weather and soil data, as well as information on past management (Sarker & Jahan, 2025). In so doing, they maximize breeding decisions by selecting genotypes that are conserved through variable field environments, allowing for the development of general adapted and stable cultivars (Gazoulis et al., 2022).

3.2 Artificial Intelligence and Decision-Support Systems

With the growing data streams of high-density sensor networks, unmanned aerial vehicle (UAV) imagery, satellite data and Internet of Things (IoT) devices, artificial intelligence (AI) has emerged as a revolutionary tool in modern farming (Chen et al., 2025). Precision agriculture can be achieved by querying, analyzing, and acting on large data streams in real time (Ghazal et al., 2024). Some of these architectures (e.g., convolutional neural networks (CNNs) and long short-term memory (LSTM) networks) have been shown to achieve impressive results in the detection of crop diseases, plant species, crop health monitoring, and even forecasting weather and crop yields using historical and real-time data (Goldenits et al., 2024). Such models can be applied to high-resolution multispectral and hyperspectral imagery to identify physiological changes in crops that are so minute as to be invisible to a human observer or conventional sensors (Mohamad Zaki et al., 2025).

The application of AI plays a key role in the optimization of resource-use through decision-support systems (DSS).

Farmers use these systems, which combine AI algorithms with agroecological, meteorological, and management information to jointly enable informed and timely decisions on irrigation dates, fertilizer application, pest management, and crop harvesting (Mushtaq et al., 2025). Other examples are reinforcement learning for dynamic irrigation optimization dependent on predicted evapotranspiration rate and soil moisture to improve the water-use efficiency (Sun et al., 2020).

AI-based DSS platforms have acquired some user-friendly interface and real-time alerts that are accessible via mobile applications, making them even more useful for smallholder farmers in developing regions. As the technologies continue to evolve, AI is likely to expand its collaboration with robotics, autonomous tractors, and remote diagnostics to automate end-to-end processes on farms (Zhang et al., 2025). Thus, AI, together with powerful DSS models, will form a new powerful tool that will help to create more data-based, sustainable and resilient agricultural systems (in particular under greater climate uncertainty) (Mălinaș et al., 2025).

3.3 In-field Environmental Monitoring and Integration

Precision agriculture also extends to in-situ environmental monitoring where a network of ground-based sensors continuously record real-time changes in soil moisture, electrical conductivity, pH, nutrient availability and microclimatic parameters (Sleep et al., 2022). It is this infinite data stream that is the particular environmental context in which the genotypes are being assessed; for breeders, the perceived instantaneous feedback enables the rapid real-time adjustment of the selection pressure to the changing abiotic stress in the real world (Sampath et al., 2023). In tandem, participatory plant breeding has been provided with mobile applications and cloud-based platforms at reduced cost to encourage more use of their facilities to collect farmer-generated data on plant performance and preference. This two-way digital communication provides breeders with the chance to be in sync with the needs of the end-users of the new varieties in terms of agronomic feedback as well as economic and social preferences (Nordey et al., 2020). Seed Tracker is an open source platform enabling farmers to provide geo-referenced answers to questions regarding new seed qualities, including taste, pest resistance, and market demand. This feedback, together with the metadata of the sensors about the environmental conditions, can lead to a co-evaluation paradigm which will multiply the amount of data that can be fed into breeding analytics, and bring the innovation closer to what the field needs (Meque et al., 2021).

3.4 Synergies with Genomics and Breeding Pipelines

The second and equally realistic breeding enhancement and acceleration concept is the concept of precision agriculture to complement the genomic-based technologies (Voss-Fels et al., 2019). Genomic selection is therefore a concept that yields theoretical benefits in the form of DNA-based genotypes and statistical modeling of those genotypes but practically preconditions the transformation of these theoretical benefits into practical applications in the real world via precision-agriculture platforms. For example, if a particular genotype is predicted to be drought stress tolerant and can be validated in a real-world scenario using sensor-controlled irrigation and drone-based canopy temperature indices, then this is empirical data of resilience (Araus et al., 2018)(Table 2).

The integration of genotypic, phenotypic, and environmental data can now be used to develop machine-learning models to construct dynamic selection indices that allow priorities to be reallocated as environmental conditions change or breeding goals change (Shen et al., 2022). Now, this is exactly the dynamic process that allows this intensity of selection and requirements to be time-varying (against trait-based selection lock-in) and a highly continuous-feedback system that can enable the rate of genetic gain to be accelerated and cultivars stabilized across locations and years (for a rapidly changing climate) (Davis et al., 2024). With the advent of precision-agriculture tools (thanks to cloud-computing, edge-device infrastructure, and open-source software capabilities), it is only a matter of time before they become more integrated into breeding pipelines (Halubanza, 2024). It is also anticipated that genetic innovations like CRISPR and GS will be integrated with adaptive, sensor-based systems in breeding systems of the future to ensure that the traits selected will be functional in the complex and non-homogeneous nature of crop production environments (Javadiyan et al., 2017). The synergy is a great guideline and roadmap for an efficient, communicating and resilient agriculture in the future (Mălinaș et al., 2025).

4. Synergies between Traditional Breeding and Precision Agriculture

This convergence of precision crop production with traditional breeding may be called its historic compositional verse, paradigmatic change of methodology and philosophy of breeding of crops and plant improvement, in which precision can provide digital selection instruments that can increase its effectiveness, accuracy and scope. In this complementary ecosystem, the discipline generates genetic possibilities, and this information is being collected in real-time and the environment is being observed to generate and optimise the information, which in turn determines the action and its effectiveness (Shavit et al., 2022).

Table 2: Synergistic Applications and Tools in Genomics and precision agriculture

Technology	Key Tools & Methods	Applications
Remote Sensing & HTP	UAV multispectral imaging, LiDAR, thermal sensors, NDVI analytics	Phenotyping without destruction, G×E interaction mapping, stress response quantification
AI/ML-Driven Analytics	CNN-LSTM architectures, reinforcement learning algorithms, cloud-based DSS	Yield forecasting, pest disease detection, and irrigation scheduling as well as when to harvest
IoT Sensor Networks	Soil moisture/EC/pH sensors, microclimate monitors, edge computing devices	Real time abiotic stress monitoring, precision nutrient management, differential resource allocation
Integrated Data Platforms	Mobile DSS (e.g., Seed Tracker), farmer-participatory apps, genotype-phenotype databases	Prioritize trait, market driven varieties, co-evaluation systems
Genomics-PA Integration	GS + UAV phenotyping, CRISPR validation via sensor networks, dynamic selection indices	Climate-resilient cultivar development, real-time trait pyramiding, target environment adaptation

4.1 Complementary Strengths of Traditional Breeding and Precision Agriculture

The primary mode of agriculture is conventional plant breeding which is founded on a number of known strategies (phenotypic selection, recurrent selection, and pedigree breeding) (Farooq et al., 2009) which do not depend on the non-observable traits but on the observable traits which contribute to the accumulation of optimum genotypes across generations. Local practitioners operating within this framework are well aware of the agroecological environment, genotype-environment interactions, and adaptive capacity of germplasm reservoirs. However, they are not very effective due to the complexity of quantitative traits and environmental resources and costly selection cycles (White et al., 2011).

Precision agriculture is able to overcome most of these constraints by integrating data-intensive, spatially explicit and sensor-based applications into the crop breeding cycle (Araus & Cairns, 2014). The use of technological solutions such as artificial intelligence, GPS field mapping, soil and crop sensors, and drone monitoring is enabling the monitoring of crop health in various environments in real time. Use of these tools leads to an increase in the granularity of the phenotypic information, and a reduction in the human component of subjectivity, since producers can now make selection decisions based on highly accurate and repeatable data. For example, conventional breeder measures on drought response could be supplemented with more information from normalized difference vegetation index (NDVI) imaging and soil moisture sensors to provide quantitative measures of water-use efficiency and canopy vigor (Kamilaris & Prenafeta-Boldú, 2018). As a result, the integration of subjective and objective criteria improves the capability of a breeder to develop ideal genotypes in complex stress conditions.

4.2 Technological Integration for Enhanced Breeding Pipelines

Technology has already begun to revolutionise modern breeding, in the context of precision agriculture (Nordey et al., 2020); the judicious application of precision technologies is perhaps increasingly prevalent in breeding pipelines; it will also serve to accelerate and improve the accuracy of crop improvement programs. Complex traits of large populations may be characterized in real time by means of high-throughput phenotyping (HTP), remote sensing, machine learning, and simulation modelling (Crain et al., 2018). New data resolution and fast velocities are now available to breeders to characterize traits such as drought resistance, nitrogen use efficiency, and disease tolerance that cannot be resolved by on-the-ground data collection through automation (mainly through the use of drones, multispectral imaging systems, and soil sensors) (Li et al., 2020).

At the same time, genomic prediction models when combined with environmental and health-related phenotypic (HTP) data result in more accurate predictions of breeding values and on a per-individual selection basis (Cobb et al., 2019). Moreover, an integrative model of this nature would reduce the time taken to breed better cultivars, especially when used in conjunction with speed-breeding or doubled haploid methods. These technological synergies are transforming the breeding work: the paradigm is shifting to a proactive one, where now it is possible to simulate genotype-by-environment interaction and then test in the field. Collectively these technologies have increased the speed and accuracy of crop-improvement initiatives and the principles of climate-resilient agriculture.

4.3 Data-Driven Decision Support for Breeding

Data-based decision support system (DSSs) have emerged as the highest radical co-evolution factor at the converging frontier of modern breeding and precision agriculture evolution (Yuan et al., 2021). All future genetics models will be built on the latest big-data analytics and real-time sensor data to develop predictive models that can be used to inform breeding decisions across a range of applications. Genomic, phenotypic, and environmental data will be integrated into unified platforms to allow systematic interrogation of trait-environment interactions to improve environmental stability and adaptability of selected genotypes (Liu et al., 2022).

Some of the most noticeable advances in this space include training cutting-edge machine-learning architectures, e.g., CNN-LSTM model, on high-resolution imagery captured by unmanned aerial vehicles (UAVs), e.g., (Peng et al., 2022) to be extremely precise in predicting crop-related events such as flowering and maturity during crop development. Such predictions would allow breeding nurseries to be better managed, and thus losses after harvest reduced. Additional background for the expression of traits in certain stress conditions is given by environmental monitoring systems in combination with weather stations and soil diagnostics, so that the expression of the traits can be specifically interpreted in the given stress conditions (Zhang et al., 2025). The resulting data set can be used to drive selection decisions, but also allows goal-directed fine-tuning of breeding targets towards real-world condition in the field (Zheng et al., 2024).

4.4 Accelerating Genetic Gain through Integrated Platforms

The absorption of precision modalities intensifies and concentrates the essence of traditional plant breeding, that is, the accuracy of selections, the power of selections, the heterostasis of heredities, and the generation period of breeding turnovers (Peng et al., 2022). The high-throughput phenotyping data has the potential to significantly complement the breeding values via calibration of genomic selection. In addition, DH technologies, speed breeding technologies, and genome editing accelerate the rate of phenotype testing and genetic fixation. Precision agriculture provides the confidence that such changes will be successful in agro-ecological settings (Zaidi et al., 2023)(Fig. 3).

Low and high throughput phenotyping play a vital role during the first seasons of the breeding pipeline to bring the best genetics through to the discards as fast as possible. These systems can measure phenotypic values on single plants in the thousands, i.e. highly resolved and able to detect small changes in traits (Valenzuela-Aragon et al., 2025). The datasets allow identifying the landscape of complexity of the attributes, which would be challenging to observe using other tools with machine-learning algorithms. The data can be used to make a more intensive selection without losing character diversity due to the additional accuracy. Additional optimization of the breeding cycle is achieved through the introduction of real-time environmental feedback that mimics future environmental and nutritional stress. In a field setting, selection pressure can be exerted to generate resilience that will be adapted to the present climate, and the future climate, when breeders are actively informed of drought or high heat stress through in situ sensor data, or nutrient limitation. Parliamentary plant breeding may therefore be characterized as a combination of conventional plant breeding and precision agriculture, where breeding aims are highly sensitive to biological knowledge and technological constraints: environmentally friendly, data-driven, and genetics-driven (Waaswa et al., 2024).

5. Accelerating Genetic Improvement through Integrated Technologies

5.1 Precision Agriculture as a Driver of Component-Specific Genetic Advancement

5.1.1 Advancing Early-Generation Selection

Lastly, GS can be combined with HTP to enable early generation selection that is much faster. It, as stated, decreases the staged growth of breeding values and as such, GS may estimate the breeding values of zero or minimal steps, which is my benefit and observed in released genome wide markers and a workload that is decreased to a few field tests of the season (Sarkar et al., 2024). At the same time, HTP infrastructures (UAV-based multispectral or chlorophyll fluorescence sensors, canopy thermal imager) allow non-destructive and rapid measurements of such key parameters as biomass, plant height, stomatal conductance, and canopy temperatures (Crusiol et al., 2022). By integrating all these strategies, the predictive power of tensions that are poorly inherited or highly susceptible to the environment (e.g. yield, root architecture, grain filling under heat stress) is enhanced (Singh et al., 2023). Furthermore, the ability to integrate machine learning for aggregation of the phenotypic and genotypic data and construction of complete genomic proprietary models that are dynamically updated in a wide range of environments (Abdul Aziz & Masmoudi, 2025).

5.1.2 Accelerating Breeding Cycles by Speed Breeding Protocols

A system of speed breeding has been developed in which the photoperiod, temperature and nutrient environment is controlled to reduce the generation time to a very short period. In some crops, six generations per year have been completed, thus the use of photoperiod extension, temperature control and vernalization avoidance have been introduced in crops such as wheat, chickpea, and barley (Watson et al., 2018). Such systems coupled with in-situ imaging and artificial stress regimes can mimic seasonal variation and many stressing episodes under the controlled weather regime, and thus enable high-throughput selection for heat tolerance, salinity response and disease resistance (Sanhueza et al., 2022). Furthermore, the combination of environmental monitoring in real time with tight climate control enables an increased genetic gain per unit time, particularly if combined with genomic selection pipelines (Arif et al., 2025).

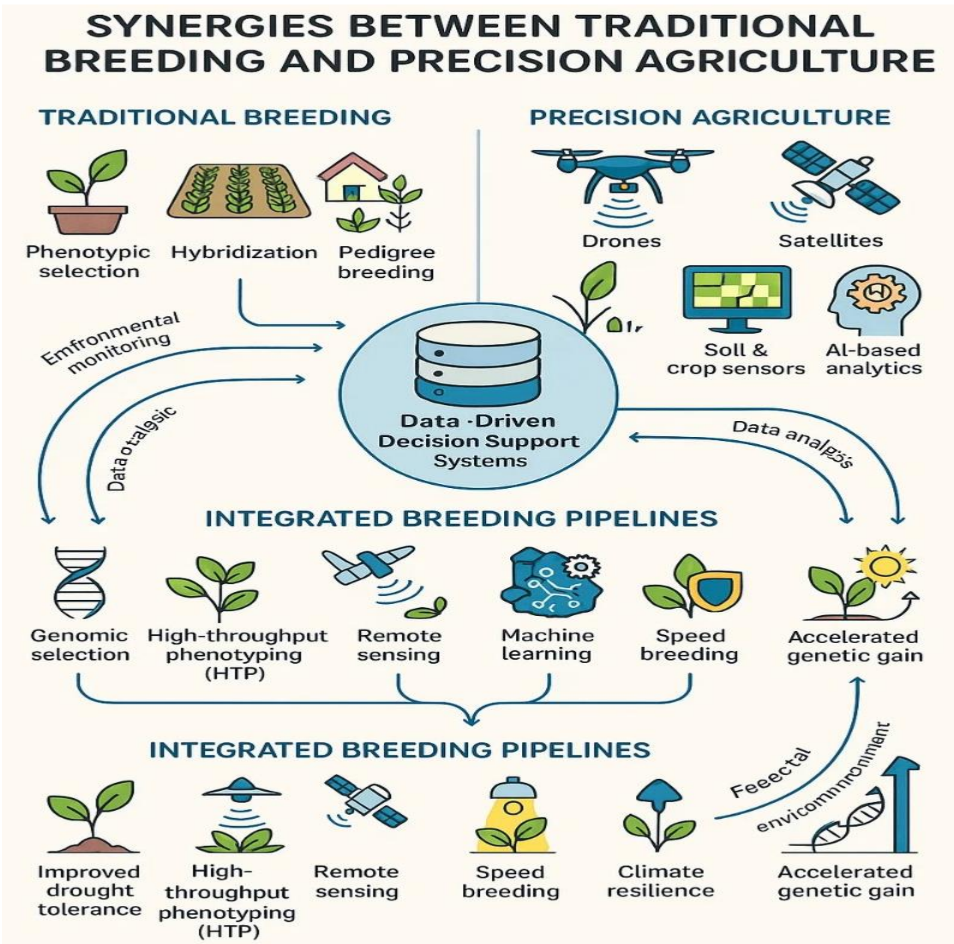

Fig. 3: Interlocking Traditional Breeding Wisdom with Precision Agriculture Technologies

5.1.3 Enhancing Selection Intensity

Precision agriculture boosts the intensity of selection, thanks to the availability of digital agricultural infrastructures that make possible high-definition screening procedures. The number of plots that can be phenotyped in heterogeneous environments in a relatively short time has now been enlarged to many thousands of plots, using automated drones and sensors mounted on robots and fixed-field phenotyping platforms (Sanhueza et al., 2022). Such imaging-based algorithms offer the potential for low-level phenotypic evidence, such as early wilting, decline in canopy vigor or chlorophyll degradation, of stress-tolerance and stress-related yield components (Zhou et al., 2025). Because bulk phenotyping increases the number of genotypes evaluated, selection stringency increases significantly without a large increase in resources (Zhang et al., 2025). Also, AI-based systems eliminate human bias and ensure environmental consistency; e.g., breeders can identify the elite line picked up in the traditional test (Zhang et al., 2024), and provide sensor-based information on nutrient use and irrigation regime on experimental plots, eliminating environmental noise and improving heritability estimation (Zatsu et al., 2024).

5.2 Simulation Models and Digital Twin Platforms in Breeding Pipelines

Digital twinning and predictive simulation are an emerging trend in the precision-integrated breeding industry. In modern applications, a digital twin can be defined as a virtualized and dynamic replica of a genotype that is grown in a laboratory environment or as a simulation in a virtual field, its state kept in active and real-time synchrony with sensor measurements acquired by UAVs, weather stations and soil probes (Li et al., 2025; Zhang et al., 2024). These systems can simulate G × E interactions and make predictions of trait expression in a range of stress conditions, offering breeders a tool to test hypotheses, make predictions and optimize cross design without the cost and time of physical experiments. Operational platforms (APSIM, DSSAT, etc.) have also become interactive platforms to combine genomic information to test scenarios for the climate resilience and ideotype optimization (Banerjee et al., 2024; Caian et al., 2024).

The strategy is to take the expanding use of reinforcement learning and apply it to the decision problem in situ, using the digital twins as the foundation for more trait predictions as additional field and phenotypic information becomes available. By converting breeding into a feedback loop carried out in silico, this will make the process data-driven and iterative; promising to enable well-informed and fast decision-making to be made in silico and then validated in the field (Feng et al., 2024; Gholizadeh Vazvani et al., 2025). As predictive environmental technologies continue to advance, breeders will be increasingly expected to use them to meet all of those goals, to further optimize breeding approaches and achieve higher genetic returns at lower costs and lower risk (Crossa et al., 2025).

5.3 Optimizing Heritability, Selection Accuracy, and Breeding Cycle Duration

For genetic gain to be fast, it is necessary to intervene in appropriate ways in the breeder equation which is the result of selection intensity, heritability (h^2), selection accuracy (r), time of breeding cycle (L) (Gorjanc et al., 2018). As a result of technological developments, breeders have been able to increase selection accuracies and selection magnitudes to reduce the number of generations and increase the estimates of heritability under conditions of field variability (Araus & Cairns, 2014). The new breeding architecture at large increases the number of parameters multi-dimensionally, using for example genomic selection in conjunction with high-throughput phenotyping and new types of environmental perturbation. Through such integration, modern crop improvement pathways benefit from a more stable and accelerated yield gain of both simple and complex traits that are drought-tolerant, N-use efficient, and climate-proof in terms of yield stability (Chen et al., 2025).

The relative magnitude of traditional breeding and integrated technological inputs to the four large variables in the breeder equation; selection intensity, heritability (h^2), selection accuracy and breeding cycle time, is illustrated in Fig. 5. The results show clear benefits of integrated technologies for speeding up the rate of genetic gain. Conventional breeding is shown to have relatively low efficiency rates for all parameters, the lowest being the selection intensity (20%) and reduction in cycle time. For the integration methods compared to the singular ones, the genomic selection, speed breeding, UAV-based phenotyping, and artificial intelligence-based prediction can achieve a much higher result with 95% selection intensity and 70% combined heritability, 80% accuracy, and a significant time reduction in the breeding cycle. The findings demonstrate the increase in accuracy and heritability estimates with the combined technology in the variable field conditions and also enable breeders to perform more rapid and more severe selection to eventually provide more robust and climate-resilient genetic gain.

6. Challenges and Knowledge Gaps

Despite the potential of precision agriculture and modern plant breeding, there are still knowledge gaps and challenges that need to be overcome before mass conversion can be realized. These will be technical, infrastructural, ethical, and human resource based, especially in low- and middle-income countries where scarcity of resources continues to exist. Boundaries are a significant part of the effort to establish breakthrough, growthable and sustainable new structures of innovation (Naseer et al., 2024)(Fig. 5).

6.1 Data Interoperability and Standardization

The extreme heterogeneity of data goods, e.g., genomic sequences, unmanned aerial vehicle imagery, environmental sensor records, and agronomics, adds the problem of interoperability to that of being both large in individual dimension and manifold (Garg et al., 2025). Often, data is stored in proprietary or siloed formats, lacks standardized metadata and documentation and therefore has little to no ability to be directly shared among platforms and institutions (Kushwaha et al., 2022). Such a restriction hampers the very essence of integrative analyses, adoption of AI-based algorithms, and design of multi-source predictive models. That is why the adoption of the open-source standards, the cloud-based infrastructures and the FAIR (Findable, Accessible, Interoperable, Reusable) paradigm are presented as the most important basis for the reduction of these problems (Gacenga et al., 2024; Katharria et al., 2025).

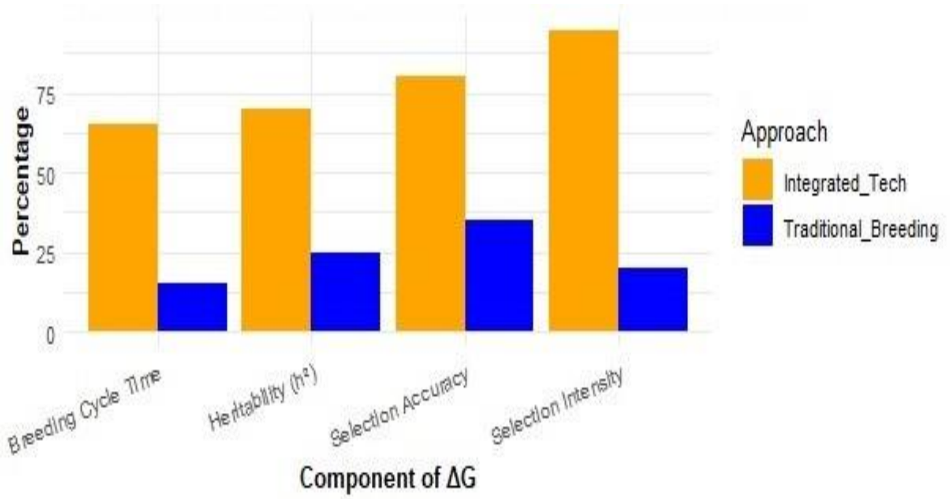

Fig. 5: Impact of integrated technologies on components of the breeder's equation.

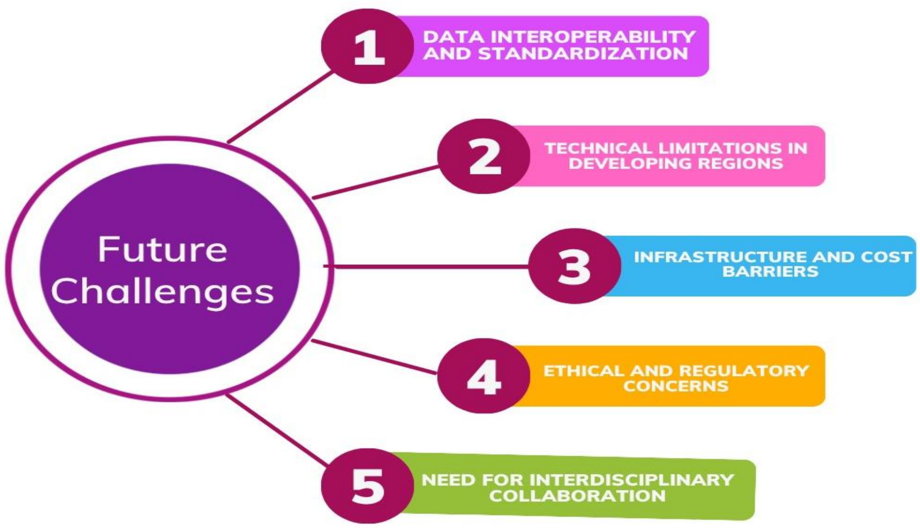

Fig. 5: Five Critical Barriers to Scalable Adoption of precision agriculture.

6.2 Technical limitations in Developing Regions

In addition, technical competence is a long-standing constraint in plant breeding programs of most developing countries, where access to high technologies, computing facilities, and highly trained personnel is severely limited (Mwadzingeni et al., 2025). The latter also exacerbates pre-existing inequality in genetic development by widening further the gap between well-resourced institutions in the Global North and under-resourced initiatives in the Global South (Cuce et al., 2022). This can be achieved by concrete measures for the long-term funding of specific training programs, research consortia, and investment models for long-term technology transformation. Virtual training web sites and partnerships with CGIAR centers are just some of the several options which have demonstrated success for transferring skills and infrastructure to lower resource environments (Tao et al., 2023). This absence of interventions helps to perpetuate lags in modernising breeding tool use and reducing the capacity of breeding programmes to respond sustainably to acute needs for climate change, food security, and agriculture intensification (Singh et al., 2025).

6.3 Cost and Infrastructure Barriers

The use of precision crop farming platforms, particularly the ones involving hyperspectral cameras, drone data, automated phenotyping devices, and climate regulating systems, is expensive and is beyond the budget of smallholder-based projects (Singh et al., 2025). Additionally, the systems are frequently wired to produce at an intensive farm level and therefore are frequently inappropriate for limited or scattered farm configurations. There is an urgent need for low-cost modular and open access technologies which can be adapted to the heterogeneous agroecological and economical settings (Singh et al., 2025).

6.4 Ethical and Regulatory Concerns

Today, genome editing and big data have become essential tools for plant breeding and have raised ethical concerns about data privacy, genetic ownership and similar issues of informed consent (Mmbando, 2024). At the same time, continued regulatory uncertainty regarding the treatment of CRISPR-derived cultivars or phenotype recommendations developed using AI creates additional layers for breeder and developer decision-making models (Roth et al., 2025). These problems can only be solved by concerted international policy-making and the design of clear and inclusive governance and governing systems for the digital and genomic world to build a large community of trust and implementation (Ruder & Wittman, 2025).

6.5 Need for Interdisciplinary Collaboration

Precision agriculture can be implemented by integrating data-rich precision agriculture with trait-based breeding, which, in turn, requires additional interdisciplinary communication between plant scientists, data scientists, agronomists, and social scientists (Shavit et al., 2022). Such collaboration is still constrained by silos of science. These would be solved by institutional incentives through the formation of transdisciplinary research networks; through the design of new programs of study which would produce what the author would call hybrid professionals whose specialization would not be simply limited to biology and AI but would be constituted by agronomy and ethics (Zhang & Kovacs, 2012).

7. Future Directions

The modern, unitary development of crop improvement is a precondition of the current manifestation of biological innovation and the computerization of precision. As climate variability and food security is a common issue around the world, plant breeding must evolve to utilize real-time environmental and artificial intelligence (AI) data and multi-omics as novel inputs to inform selection decision-making. The goal of future breeding systems should be to deliver efficiencies and evidence-based effectiveness, scalable, inclusive and based on multi-sectoral partnerships.

7.1 Breeding for Dynamic Traits: Resilience to Climate Variability

While traditional breeding tries to encode a trait according to a fixed environmental niche, the changing nature of the climate poses a serious challenge to breeding. In place, breeding in the future must be directed at the dynamic trait that exhibit adaptive plasticity in changing field environments. Special characters of heat dissipation, delayed senescence, root plasticity and flexible synchronization of flowering time were translated into basic characters of climate resistant varieties (Yin et al., 2024).

"If we are to breed such characters, we will need to use integrated platforms that will apply high-frequency UAV imaging, consistent ground sensors, and time-series modeling." With such tools, genotype-by-environment-by-management (GxE by M) guided selection can be performed by characterizing phenotypic plasticity in a space and time context (Sharma & Kumar, 2025). A further area of improvement for genomic selection is the inclusion of stress-sensitive markers to estimate realistic models of resilience from prediction models to be implemented in real variable environments determined by transcriptomics and metabolomics (Ruder & Wittman, 2025).

7.2 AI-Guided Selection and Propagation

For these reasons, and within a novel and integrated infrastructure, AI-driven selection, genetic multiplication, and manual agronomic control, robotic breeding farms, are a feasible and increasingly feasible goal (Pandey & Mishra, 2024). These systems would include fleets of drone devices, robotic phenotyping platforms and automated data capture modules that are managed by cloud-based decision engines (Roy & Medhekar, 2025). Continuous monitoring of vegetative progress, control of specialized intervention, and modeling of reaction to the environment in real time will decrease human error and dramatically increase throughput (Ruder & Wittman, 2025).

Non-disappearing phenotypic data from devices will be used in addition to genomic and environmental data to make selection decisions. A combined dataset will allow machine learning models to find genotypes on multi-trait indexes that summarize simultaneously the phenotypic, genotypic, and environmental dimensions of the data (Selim et al., 2025). At the same time, a process can be AI-optimized for both regeneration in vitro and development of a double haploid, where machine-learning algorithms identify optimal conditions for a specific genotype. Though in early stages, these systems are expected to modify the breeding process through continuous feedback-based selection loops with minimal excess concurrence (Pandey & Mishra, 2024; Wang & Mendes, 2024).

7.3 Integration of Multi-Omics with Field-Level Intelligence

The integration of multi-omics data (genomics, transcriptomics, proteomics, metabolomics) with environmental or phenotype information, at high spatial and temporal resolution, represents a further step towards an integrative basis to explain trait architecture at the molecular level and its causal relation to agronomic performance in the field (Kumar et al., 2025; Mmbando, 2024).

For example, to determine genes for resiliency, gene responses to drought stress based on transcriptomic changes can be correlated with NDVI images (Meque et al., 2021). Furthermore, metabolomic profiling of root exudates combined with pest surveillance information obtained by UAV can assist resistant breeding initiatives. These datasets, as part of the AI system, allow unprecedented accuracy in predicting complex trait expression and in protecting molecular innovations at the field level (Musavi et al., 2022).

7.4 Institutional and Policy Support for Integrated Breeding Systems

In addition, given that breeding systems have become increasingly technologically intensive, it is necessary to develop institutional and policy frameworks for accessibility, equity, and ethical use (Singh et al., 2023). The emerging tools, especially genome editing, must be shown to be regulatory clear. The state apparatus along with the research, for their part, works on drafting the homogenous principles based on which the application of CRISPR-based solutions will take place in a sensible and harmless manner (Irkham et al., 2024).

There should also be incentives provided through policies to share open data and create partnerships between the government and the private sector. Beyond that, the government will also fund the construction of the cyber infrastructure in the long-term, which will in turn be needed to support the national breeding programs, especially in the global south (Batan, 2025). To provide the plant breeders with the training they would need to Integrate training module in the broad-based data science, artificial intelligence, and sensor technology (Bhuiyan et al., 2023). At the same time, participatory models need to be institutionalized to capture the needs of the smallholders and to match breeding goals with local demand. The second case can be defined as trying to go to the agencies such as CGIAR and NARS to improve the ground infrastructure because of its support in trying to facilitate the changes on the ground technology (Wanyama et al., 2024).

8. Conclusion

The convergence of precision agriculture technologies with molecular breeding technologies is a paradigm shift in the field of plant breeding that enables breeders to address the increasing needs of the world. Genome-editing technologies, doubled haploid genotyping technologies, and genomic breeding are all rational ways to obtain genetically higher rates of gain by accelerating improvement rates, targeting new genetic gains in target environments, and improving environmentally relevant gains. The synergistic architecture is a combination of the optimum components of the breeder equation. Genomic selection reduces the phenotypic expression distance to competitive genotypes; rapid breeding or controlled stay strategies shorten generation cycles; and enhanced sensing captures minor character variation in diverse field backgrounds. Digital twins and simulation models provide a novel level of predictive power, enabling performance prediction under simulated stresses and significantly speeding ideotype development iterations. This paradigm shift moves breeding from a generation-based approach to an adaptive, continuous feedback-driven model. Developing countries, especially those with low and middle incomes where precision breeding technologies are underutilized, require efficient institutional and policy frameworks to close yield gaps.

Funding: This study was not supported by any public, commercial, or non-profit funding agency.

Conflicts of Interest: The authors confirm no conflicts of interest

Authors' Contribution: GM designed the study, conducted the literature review, wrote, prepared the associated figures and graphs and critically revised the manuscript, and approved the final version.

Generative AI Statement: The authors declare that this manuscript has been written without the use of generative artificial intelligence tools.

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