Review

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Integrating Traditional Plant Breeding with Genomic Accelerators: Pathways for Scalable Crop Improvement

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Abstract

The traditional plant-breeding toolkit—controlled crosses, iterative phenotypic selection, and multi-environment testing—remains the core engine of crop improvement, reliably delivering field-validated varieties that scale in real farming systems. This review synthesizes how self-pollinating, cross-pollinating, and vegetatively propagated crops confront common constraints while highlighting high-impact accelerators and practical pathways for integration with genomics, cycle compression, digital phenotyping, and participatory approaches. We find that while traditional methods stay essential, accelerators such as phased marker-assisted and genomic selection, doubled haploids, speed breeding, off-season nurseries, and high-resolution field phenotyping markedly boost genetic gains. Crop-specific gains emerge from blending pedigree and genomic selection in self-pollinators, employing recurrent selection and heterotic management in outcrossers, and applying sanitation, indexing, and tissue culture in vegetatively propagated crops. Across crops, managing diversity, engaging farmers in testing, and thoughtfully designing seed systems to enhance scalability and quality are critical. A realistic near-term path integrates genomics, cycle compression, and participation with the enduring cycle of phenotypic evaluation, field testing, and seed-system development— contingent, of course, on seed-system maturation, breeder training, and enabling policy environments.

Keywords: conventional plant breeding; genomic selection; speed breeding; digital phenotyping; multi-environment trials; seed systems

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1. Introduction

Conventional plant breeding, when integrated with modern molecular tools and inclusive seed systems, remains the most reliable pathway for translating heritable variation into stress-resilient, high-performing cultivars that deliver measurable on-farm benefits. It is the foundational method for generating predictable genetic gains and farmer-validated cultivars. Conventional programs routinely introgress and combine desirable traits while subjecting candidates to rigorous field evaluation [1, 2, 3]. Through controlled crosses, backcrossing, and iterative selection cycles, breeders align heritable variation with target agronomic objectives. Multi-season, multi-site field trials then filter genotypes for stability, adaptation, and management compatibility. This process yields incremental, reliable gains in yield, stress tolerance, and quality that are demonstrable under farmer management. By coupling deliberate genetic manipulation with real-world validation, conventional breeding effectively translates genetic potential into cultivars that farmers will adopt.

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The effectiveness of breeding hinges critically on the seed and planting-material systems that deliver improved genetics to farmers. Functional seed systems, public–private partnerships (PPPs), community-based production, and farmer-led evaluation are essential for adoption, particularly in self-pollinating staples with uneven access to certified seed [4, 5]. Even the best genetics cannot impact livelihoods without robust distribution channels, quality assurance, and local testing. In such contexts, participatory evaluation ensures that new varieties align with farmer preferences and on-farm management realities, while institutional linkages among breeders, seed enterprises, and extension services determine reach and scale. Consequently, breeding, testing, and distribution must be treated as an integrated system to translate genetic gains into food security and livelihood improvements.

Conventional breeding pipelines deploy a suite of techniques tailored to crop biology and target environments. Methods such as selection within landraces, pedigree and bulk selection, backcrossing, recurrent selection, and hybrid and synthetic approaches, including clonal selection where appropriate, are often integrated within ideotype-driven programs [1.6]. The choice of method depends on the species' reproductive system (selfing, outcrossing, or asexual propagation), the architecture of the target traits, and the intended deployment strategy. Institutional frameworks established after the Green Revolution—testing networks, release procedures, and seed regulations—shape how multi-environment evaluations and formal releases operate across diverse agroecologies [7, 8]. Consequently, aligning the breeding method with crop biology and the relevant institutional context is central to producing varieties that perform reliably across target agroecologies.

Since the mid-2000s, conventional breeding programs have pragmatically incorporated molecular tools and cycle-compression strategies to enhance efficiency and accuracy. Breeders now deploy molecular diagnostics such as marker-assisted backcrossing, off-season nurseries, doubled haploids, speed breeding, and quantitative decision frameworks that explicitly account for heritability and genotype-by-environment interactions [6, 9, 10, 11]. These overlays shorten generation time, sharpen selection for major loci, and enable data-driven allocation of testing resources. Collectively, they bolster the robustness of conventional pipelines as platforms for genomics-assisted prediction of complex traits under field conditions [12, 13]. Integrating molecular tools with cycle compression thus preserves the strengths of traditional breeding while accelerating genetic gains.

A biology-aware, comparative review clarifies how breeding methods perform across self-pollinating, cross-pollinating, and asexually propagated crops. The analysis assesses classical line and mass selection, recurrent selection, synthetics, hybrids, and clonal strategies, and examines how these approaches interact with multi-environment testing, participatory evaluation, and seed-system constraints [2, 3, 6]. Each reproductive class imposes distinct constraints on genetic gain, seed multiplication, and dissemination. For instance, self-fertilizing species favor pure-line development and certified-seed pathways, while outcrossing species benefit from recurrent selection and hybrid strategies and clonally propagated crops, by contrast, require multiplication and phytosanitary practices tailored to vegetative propagation and disease management. Participatory evaluation and institutional factors further influence which pipeline elements yield farmer-relevant outcomes. Consequently, framing breeding choices by reproductive biology and delivery pathway reveals where specific methods are most appropriate and where system bottlenecks constrain impact.

This review delineates where conventional breeding pipelines remain indispensable, where modern overlays add the greatest value, and how policy and institutional contexts shape adoption. We evaluate trade-offs such as selection accuracy versus generation time, genetic risks (e.g., linkage drag and drift), and the resource demands of extensive multi-environment trial networks. The synthesis emphasizes pragmatic integration pathways—embedding speed breeding, doubled haploids, and genomic selection within participatory evaluation frameworks and inclusive seed systems—to accelerate adoption and enhance local relevance. It also examines policy levers that facilitate scaling, including regulatory flexibility, public–private partnerships (PPPs), and support for community seed systems. By combining rigorous conventional pipelines with targeted technological and institutional overlays, breeding programs can maximize genetic gain while ensuring that improved varieties reach and benefit farmers.

2. Methods and Current Applications

2.1. Inbreeding Crops

Conventional breeding for self-pollinating crops, when integrated with cycle compression strategies and targeted molecular overlays, remains the most reliable pathway to produce uniform, field validated cultivars while accelerating genetic gain and maintaining on farm relevance. This integrated approach encompasses a range of complementary techniques, including pure-line and mass selection, pedigree selection, bulk advancement, single-seed descent (SSD) method, marker-assisted backcrossing (MABC) and doubled haploids (DH) generation as well as population buffering, mutation, and ideotype-driven strategies.

Pure line selection isolates and fixates superior homozygotes to deliver the uniformity and predictability demanded by formal seed systems. Pure line development stabilizes elite genotypes from heterogeneous populations and landraces, yielding varieties well suited to mechanized seed production and reliable agronomic performance [1, 6]. Purified-line pipelines are particularly efficient for visually scorable, high-heritability traits, since selection directly targets homozygous phenotypes. They integrate smoothly with certification and quality-assurance processes; however, they reduce intra-line variation that can be advantageous for the incremental improvement of complex quantitative traits. While pure-line selection is indispensable in contexts where uniformity and certification are paramount, it should be complemented by other breeding strategies when the objective includes polygenic adaptation or broader environmental responsiveness.

Mass selection offers an accessible, low-cost pathway to shift population means within farmer-managed and participatory contexts. Repeated harvest and selection of seed from phenotypically superior plants can improve landraces and heterogeneous populations in low-input systems [3, 5]. Its simplicity and minimal infrastructure requirements render mass selection particularly well suited for community-level improvement and on-farm adaptation. The procedure preserves genetic heterogeneity, which enhances adaptability, but this same retained diversity can reduce uniformity, a characteristic often demanded by formal markets. Consequently, mass selection is most effectively deployed in contexts where farmer control and local adaptability are prioritized. In resource-limited settings, mass selection remains a pragmatic tool, provided programs are willing to accommodate trade-offs between adaptability and market uniformity.

Pedigree selection, bulk advancement, and single seed descent (SSD) constitute complementary pipelines that balance multi-trait control with rapid fixation and high throughput. Pedigree selection monitors family performance from segregation through advanced inbred lines and integrates effectively with marker data [6, 9]. Bulk and SSD strategies manage segregating generations under different resource constraints [10, 11]. Pedigree-based pipelines enable early culling for major genes and support systematic multi-trait improvement with detailed records. Bulk methods defer selection to preserve recombination and reduce early labor, whereas SSD rapidly fixes homozygosity and aligns well with off-season nurseries, speed breeding, and genomic screening. The choice among these approaches depends on program objectives, phenotyping capacity, and available resources. Consequently, integrating pedigree-based control with bulk or SSD fixation and cycle-compression platforms optimizes both selection precision and the speed of generating new lines.

Marker-assisted backcrossing (MABC) and doubled-haploid (DH) technologies are central to rapid, precise introgression and cycle compression in self-pollinating species. MABC enhances foreground and background selection to minimize linkage drag and expedite recovery of the recurrent-parent genome, while DH generates fully homozygous lines in a single generation, effectively compressing breeding cycles [10, 14]. By targeting specific loci and monitoring background recovery, MABC enables efficient trait transfer with minimized collateral genomic variation. DH, alongside other cycle-compression tools, shortens the interval to reliable phenotyping and cultivar release, thereby increasing throughput and accelerating time-to-market. Integrating these molecular tools with robust phenotyping yields faster and cleaner introgression. When paired with rigorous multi-environment field evaluation, MABC and DH substantially shorten breeding timelines while preserving elite agronomic backgrounds.

Population buffering, induced variation and ideotype-driven selection collectively expand resilience and align breeding with environment-specific performance goals. Multiline and composite

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populations broaden resilience to disease pressures and environmental variability, mutation breeding introduces novel alleles when natural variation is limited, and ideotypes articulate target architectures and physiological profiles to guide selection [15]. Multilines can enhance on-farm stability across heterogeneous pathogen landscapes, though they complicate certification and seed systems. Mutation breeding, when paired with molecular characterization, accelerates the discovery and stabilization of useful variants. Ideotype-based approaches shift selection toward traits such as root depth, phenology, and harvest index to bolster stress adaptation. Taken together, these strategies complement line-based methods by augmenting resilience, expanding the pool of alleles, and directing selection toward specific environmental challenges.

Multi-environment trials (METs) anchor breeding decisions, while molecular overlays and cycle-compression tools accelerate progress, each demanding careful resource planning. METs capture genotype-by-environment interactions and validate farmer-relevant performance using analyses such as AMMI and GGE biplots, providing essential evidence for deployment decisions, while marker-assisted backcrossing and genomic selection speed up selection when paired with dense phenotyping and well-designed training populations [9, 12 16]. METs move candidates from high-throughput screens to advanced yield trials and national testing, whereas molecular overlays enable early culling and targeted introgression, albeit at the cost of genotyping, data management, and breeder capacity. Cycle-compression platforms increase generation turnover but must be integrated with field validation to preserve agronomic relevance. A pragmatic strategy blends MET-based phenotypic selection with uniformity goals, layering MABC and cycle-compression tools to shorten development timelines while protecting elite backgrounds, contingent on investments in infrastructure and delivery pathways.

Generally, an effective conventional breeding program for self-pollinating crops combines field-validated phenotypic pipelines—encompassing pure-line, pedigree, mass selection, and bulk/SSD approaches—with targeted molecular overlays such as marker-assisted backcrossing (MABC) and genomic selection, and couples these with cycle-compression technologies like doubled haploids (DH) and speed breeding. When conducted within multi-environment trial (MET) anchored evaluation and integrated seed-system pathways, this approach preserves the field relevance and uniformity required for formal release while simultaneously accelerating genetic gain and enhancing on-farm impact.

2.2. Outbreeding Crops

Conventional breeding for cross-pollinating crops should be conducted as an integrated population-improvement enterprise that deliberately exploits heterosis by melding mass and recurrent selection with quantitative combining-ability analyses, synthetic and hybrid strategies, and targeted genomic overlays—each aligned with seed-system realities—to deliver resilient, high-yielding cultivars across diverse farmer contexts.

The essence of cross-pollinated crop breeding lies in population improvement aimed at generating and exploiting heterosis for farmer-relevant gains. Classical programs integrate recurrent phenotypic selection in open-pollinated populations with structured hybrid development and controlled pollination to deliver reliable hybrid seed and sustained mean performance [17, 18]. Recombination and recurrent selection elevate favorable allele frequencies across cycles, while controlled pollination and male-sterility systems enable scalable hybrid seed production. Multi-environment testing (MET) and replicated testcross networks quantify genotype-by-environment (G×E) interactions and validate heterotic performance prior to scaling seed production [19]. Consequently, population improvement coupled with strategic hybridization constitutes the methodological backbone that translates genetic potential into stable, farmer-relevant performance in cross-pollinating crops.

Mass selection represents a pragmatic, low-cost entry point for population improvement in open-pollinated systems, particularly for simple, highly heritable traits. Through repeated phenotypic selection and intercrossing of superior individuals, population means can be shifted at scale with minimal infrastructure, making mass selection broadly accessible in farmer-managed contexts [17]. Its strengths lie in simplicity, scalability, and suitability for broad adaptation goals and decentralized seed systems. Yet, the absence of a controlled family structure reduces precision for complex traits and risks the loss of rare favorable alleles unless population size and management intensity are adequately maintained. Mass selection remains valuable where resources are constrained, but programs must carefully manage population size and structure to conserve genetic diversity and mitigate erosion of useful alleles.

Recurrent selection schemes overcome the limitations of mass selection by recombining superior individuals to increase quantitative gains and to build heterotic pools for hybrid exploitation. Family-based recurrent designs (half-sib, full-sib, S1/S2) and reciprocal recurrent selection (RRS) are established approaches to elevate favorable allele frequencies and maximize hybrid performance [20]. RRS advances complementary populations in parallel to capture specific combining abilities, while family designs enable estimation of additive and dominance components to inform selection decisions. Moreover, recurrent schemes balance short-term gains with the maintenance of genetic variance, thereby preserving long-term selection potential. Consequently, recurrent selection lies at the core of sustained improvement and in creating the structured diversity that underpins high-performing hybrids.

Quantitative combining-ability analyses and staged evaluations are essential for identifying productive parents and validating hybrid performance across environments. Diallel and line-by-tester designs partition additive (GCA) and non-additive (SCA) variance to guide parent choice, while stability and adaptation analyses (AMMI and GGE) distinguish broadly adapted hybrids from niche entries [18, 19]. Use GCA to select parents with broad additive value and SCA to identify specific, high-heterosis crosses. This, in turn, should be followed by population-improvement steps and multi-location testcross trials within METs to confirm performance across diverse environments. Stage-gated evaluation ensures that only hybrids with validated G×E stability advance to seed production scaling. Collectively, combining-ability metrics and MET-anchored evaluation concentrate resources on crosses most likely to yield stable, farmer-adoptable hybrids.

Synthetics and hybrids play complementary roles in breeding and seed systems: synthetics preserve farmer seed autonomy while hybrids maximize mean performance where seed systems can reliably produce and disseminate them. Synthetic varieties—intercrossed, complementary genotypes maintained by open pollination—tend to elevate mean performance above parental averages while enabling farmer seed saving and reuse. In contrast, hybrids (single-, double-, and three-way) can deliver larger yield gains but require inbred parental lines, controlled pollination, and robust seed-production infrastructure [18, 21]. Synthetics are particularly valuable where hybrid seed systems are weak or farmer autonomy is prioritized, whereas hybrids demand specialized seed production capacity, market arrangements, and quality-assurance mechanisms to be viable. Controlled pollination and male-sterility platforms can reduce labor and containment requirements for hybrid seed production in contexts where these investments are economically justified [22]. Consequently, the choice among synthetics, open-pollinated varieties (OPVs), and hybrids should be tailored to crop biology, seed-system capabilities, and farmer preferences, balancing potential yield gains with accessibility and resilience.

Stratified selection, multi-parent populations, and carefully designed genomic overlays can raise mean performance while conserving diversity and accelerating genetic gains. Stratified schemes and multi-parent populations enhance recombination and mapping resolution, enabling targeted improvement for agroecological niches. When integrated within population frameworks, marker-assisted recurrent selection and genomic prediction can speed selection without compromising long-run potential [20, 23]. Stratification and subpopulation recurrent selection help manage inbreeding and genetic drift while preserving sufficient variance for future cycles. Genomic selection can increase selection intensity and shorten breeding cycles, provided training populations and phenotyping depth are adequate; however, marker-based approaches must be compatible with mating structures that generate heterosis. Implementing genomic overlays also requires investment in genotyping, data management, and breeder capacity, and must be aligned with downstream seed systems to ensure adoptable outcomes. Consequently, a thoughtful integration of stratified population designs with genomic tools can accelerate heterotic gains while safeguarding the population processes that underlie those gains.

Overall, a robust breeding program for cross-pollinating crops combines accessible methods (mass selection) with structured recurrent schemes and combining-ability analyses, intermediate options (synthetics), and hybrid systems, each selected to align with seed-system realities. Selective integration of genomic tools, coupled with investments in seed-production infrastructure and MET-anchored validation, can accelerate heterotic gains while enhancing resilience and farmer adoptability.

2.3. Vegetatively Propagated Crops

Conventional breeding of vegetatively propagated crops integrates rigorous clonal selection, clean-stock sanitation, targeted induction of variation, and, where feasible, sexual introgression followed by re-clonalization. These components are consistently anchored in multi-environment, farmer-oriented evaluations to preserve heterozygous trait complexes and to deliver stable, scalable benefits.

Clonal selection serves as the principal driver of genetic improvement in asexually propagated crops because it preserves farmer-preferred heterozygous trait complexes and enables evaluation of whole-plant performance under real management conditions. The process typically begins with identifying superior genotypes within landraces or segregating populations and maintaining them through vegetative propagation. Selection criteria focus on integrated performance metrics—yield, quality, storability, and agronomic behavior under representative management regimes. To capture the fixed, heterozygous trait complexes that characterize clonally propagated crops, breeders rely on robust phenotyping and multi-site, multi-season trials that assess stability across environmental gradients and management intensities. Practical examples abound in root-and-tuber systems (e.g., potato, cassava, sweet potato), where advanced clones are advanced through replicated clonal trials to verify adaptation and farmer acceptance. Consequently, clonal selection must be buttressed by extensive field validation to ensure that selected genotypes deliver consistent, farmer-relevant gains across target environments.

Sanitation and certified clean-stock pipelines are foundational to productivity and the successful deployment of improved clones, because pathogen-free planting material preserves accumulated genetic gains and mitigates yield erosion. The process rests on systematic elimination of diseased or virus-infected plants, routine indexing using serological and molecular assays, and tissue-culture–based multiplication to support certified propagation and nursery programs. In crops such as potato, banana, and cassava, access to pathogen-free planting material is often the single most influential determinant of on-farm performance, and international protocols formalize evaluation and nucleus-seed production to safeguard health status [24, 25]. Where formal pipelines function effectively, they enable reliable downstream multiplication; where they falter, disease pressure rapidly erodes breeding gains. Consequently, investment in clean-stock production, routine diagnostics, and certification is essential for any robust clonal-breeding and dissemination program.

When natural genetic variation falls short of breeding goals, induced mutagenesis offers a pragmatic route to novel alleles that can be fixed through clonal propagation. Both physical (gamma and X-ray) and chemical (EMS) mutagenesis can yield immediate, clonally fixable changes in traits such as quality, disease tolerance, or phenology. Yet mutation breeding often generates numerous neutral or deleterious events and can introduce pleiotropy, somaclonal variation, or off-target effects. To manage these risks, mutation programs require large-scale screening, rigorous phenotypic and molecular characterization, and multi-year, multi-location clonal trials to confirm trait stability and exclude adverse side effects [26]. Consequently, mutagenesis should be applied strategically and only when targeted gaps in germplasm cannot be addressed through existing variation or by sexual introgression.

Artificial ploidy manipulation serves as a potent tool to modulate vigor, organ size, fertility, and metabolite profiles, yet it demands rigorous cytogenetic confirmation and extensive clonal testing because polyploidy can unpredictably alter gene expression and physiology. Chromosome-doubling agents such as colchicine or oryzalin are employed to restore fertility in sterile hybrids, enlarge organs, or shift secondary metabolite concentrations. These changes can, in turn, enhance biomass quality or enable breeding strategies that rely on altered fertility. Given that polyploid induction often yields complex and unpredictable phenotypic shifts, breeding programs must incorporate cytogenetic verification, molecular assays, and long-term clonal performance evaluations before any release. Consequently, ploidy manipulation is a powerful but high-risk lever that requires thorough validation to ensure consistent, beneficial outcomes.

In crop systems where sexual reproduction is feasible, the strategic integration of targeted introgression into elite clonal backgrounds, followed by re-clonalization, offers a powerful synthesis of genetic precision and phenotypic stability. Through backcrossing or alternative sexual introgression methodologies, breeders can effectively transfer specific alleles conferring desirable traits, such as disease resistance, enhanced quality attributes, or abiotic stress tolerance, into well-adapted clonal genotypes. Subsequent re-clonalization then permanently fixes these favorable allelic combinations, ensuring their faithful propagation for agricultural deployment. However, the success of this hybrid breeding strategy hinges on meticulous management of key genetic parameters, including the preservation of heterozygosity, minimization of linkage drag, and comprehensive recovery of the recurrent parental genome. Moreover, to safeguard the integrity of genetic gains throughout the multiplication and distribution pipeline, this approach must be embedded within robust clean stock programs and formal certification systems [1, 6]. When implemented with rigor and foresight, the coupling of sexual introgression with re-clonalization enables incremental yet transformative improvements that remain largely inaccessible through conventional clonal selection alone.

Contemporary clonal breeding prioritizes integrated trait portfolios that blend superior agronomic performance with tangible end-user value, pairing accelerated evaluation with certification and farmer-led multiplication to shorten the path from genetic gains to on-farm impact. Target traits encompass yield stability, durable disease resistance, dry matter and starch content, provitamin A biofortification, postharvest resilience, and organoleptic quality, with particular emphasis on durability and postharvest performance in perennials and fruit crops due to their extended production cycles [27, 28, 29]. Formal certification standards (e.g., seed potato schemes, cassava inspection protocols) generate high-health nucleus material for multiplication, while decentralized approaches—rapid propagation techniques, community seed enterprises, and quality-declared planting material—expand access where formal systems are limited [30, 31, 32]. Consequently, effective deployment relies on a synergistic integration of centralized clean stock production and rigorous indexing with locally adaptive, farmer-oriented multiplication and quality assurance to scale benefits without compromising health status.

Practical breeding programs sequence methods in a deliberately pragmatic order: prioritizing sanitation and rigorous multi-environment clonal evaluation, reserving mutagenesis and polyploidy for clearly justified needs, and employing sexual introgression only when it demonstrably enhances trait portfolios. Operational priorities center on investing in nucleus-stage molecular diagnostics and clean-stock pipelines to safeguard genetic integrity, while accelerating clonal selection and conducting multi-location trials to shorten release timelines without compromising stability. Aligning multiplication pathways—whether formal certification or community-based systems—with farmer needs and market requirements maximizes adoption; however, scaling necessitates robust training, monitoring, and quality assurance to prevent disease spread and preserve varietal identity [25, 29]. In sum, sequencing technical choices within certified clean-stock networks and farmer-oriented dissemination channels is essential to translate breeding gains into reliable, scalable benefits for growers.

Conventional breeding for vegetatively propagated crops operates as an integrated, field-anchored enterprise that harmonizes clonal selection with sanitary systems, purposeful induction of genetic variation, ploidy management, and selective sexual introgression. Its success hinges on rigorous multi-environment evaluation, robust diagnostic and certification frameworks, and dissemination pathways that preserve health status while aligning with farmer priorities.

3. Future Directions

3.1. Inbreeding Crops

Conventional breeding for self-pollinating crops should be reframed as an integrative enterprise that maintains field-validated selection logic while systematically layering modular genomic tools, accelerated generation cycles, targeted multi-trait portfolios, and farmer-led evaluation to deliver faster, locally relevant genetic gains.

Genomic tools should augment, not replace, pedigree-based pipelines, thereby preserving established selection logic while enhancing precision and velocity. Marker-assisted backcrossing (MABC) serves as the most immediate molecular mechanism for precise introgression and background recovery, whereas genomic selection (GS) scales the prediction of polygenic performance when training populations and phenotyping depth are adequate [11, 33]. Treat genomics as a modular overlay that is embedded at decision points within pedigree and backcross workflows by incorporating markers and genomic estimated breeding values. Apply MABC for single-gene or major-effect introgressions and leverage GS to prioritize candidates for complex trait architectures, while continuing to rely on conventional, field-based multi-environment testing (MET) to validate performance and guard against prediction bias. The integration of MABC and GS into existing pipelines preserves breeder intuition and MET validation while enhancing accuracy and shortening segments of the selection cycle.

Reducing generation time is essential for accelerating annual genetic gain and hinges on integrating speed breeding, doubled-haploid (DH) production, and off-season (shuttle) nurseries. Standardized speed-breeding regimes increase generational throughput, while DH systems yield fully homozygous lines in a single step. Off-season nurseries expose material to diverse environments, accelerating selection and broadening testing envelopes [34-37]. Implement controlled-environment speed breeding to shorten generation intervals, employ DH or single-seed descent (SSD) to fix lines rapidly, and utilize off-season or shuttle nurseries to amplify selection intensity and induce early-stress responses. Crucially, accelerated advancement should be tightly linked to downstream multi-environment testing (MET) validation to prevent selection that is driven solely by controlled-environment phenotypes. When these accelerated-generation approaches are integrated and anchored to field validation, they elevate throughput and shorten the interval from cross to release without compromising real-world performance.

Breeding objectives should be broaden beyond yield to encompass systemic resilience and end-user traits, including stress tolerance, nutritional quality, and processing characteristics. Clear ideotype definitions and refined selection indices can assign appropriate weights to stress adaptation and nutritional components alongside yield, while high-throughput phenomics and marker data enable monitoring of component traits without compromising elite agronomic backgrounds [33]. Explicit trait portfolios should integrate responses to heat, drought, salinity, and nutrient deficiencies with micronutrient density and cooking/processing attributes. Multi-trait selection indices can quantify trade-offs and inform the targeted deployment of marker-assisted or genomic approaches to retain yield while enhancing quality and bioavailability. Operationalizing these multi-trait frameworks ensures breeding delivers agronomic performance together with nutritional and processing value that matter to both farmers and consumers.

Embedding breeder outputs within farmer realities requires participatory evaluation and decentralized seed pathways so development and delivery advance in parallel. Farmer-led selection, community trials, and local seed enterprises enhance trait relevance and accelerate varietal turnover in smallholder contexts. Implement stage-gated pipelines that integrate on-farm participatory trials at early and advanced stages, and partner with quality-declared seed multiplication systems and local enterprises to scale seed production and shorten adoption lags. Leverage farmer feedback to refine trait priorities—such as taste, maturity, and processing characteristics—with iterative loops that continuously align breeding goals with user needs. Collectively, coupling participatory evaluation with decentralized seed systems harmonizes varietal development with local preferences and speeds adoption while preserving local adaptation.

Technical and social innovations introduce constraints that breeding programs must anticipate and manage through targeted investments and governance. Genomic overlays and doubled-haploid (DH) platforms demand robust genotyping capacity, data management, and analytical expertise, whereas speed breeding carries the risk of bias toward controlled-environment phenotypes and

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necessitates coordinated participatory testing and stringent quality assurance [11, 34]. Plan upfront investments in genotyping infrastructure, comprehensive data pipelines, and breeder training; design multi-environment testing (MET) anchored validation to counteract controlled-environment selection bias, and establish protocols and training for participatory trials and decentralized multiplication to safeguard varietal identity and data integrity. On this basis, proactive investments in infrastructure, capacity building, and institutional linkages mitigate risk and enable the sustainable integration of new technologies into breeding programs.

Successful integration hinges on pragmatic, evidence-driven deployment and institutional arrangements that bridge breeding pipelines with seed-system actors. Programs that layer genomic prediction with marker-assisted introgression, demonstrated to increase accuracy or speed, and that couple these technical advances with participatory deployment, offer greater potential for locally relevant impact. Employ pilot studies and cost–benefit analyses to determine where genomics or doubled-haploid production adds value, and implement stage-gated decision rules that require multi-environment testing (MET) confirmation before release. Formalize partnerships with extension services, seed enterprises, and farmer organizations to ensure delivery and establish feedback loops. Institutionalized decision rules and collaborative arrangements translate technical gains into equitable, locally adapted varietal adoption.

Overall, a pragmatic integration strategy preserves the field-grounded strengths of conventional selection and multi-environment testing (MET) validation while selectively incorporating genomic tools, accelerated generation systems, multi-trait selection frameworks, and participatory delivery mechanisms. This synergistic approach compresses breeding cycles, enhances the accuracy of both genomic prediction and introgression, and ensures that genetic gains are not only accelerated but also contextually relevant and aligned with local agroecological and socio-economic conditions.

3.2. Outbreeding Crops

Conventional breeding for cross-pollinating crops must expand its heterotic resource base and deliberately integrate classical recurrent selection with marker-assisted approaches, physiology-informed phenotyping, and seed-system-aware deployment. This integrated framework aims to deliver stress-resilient, multifunctional hybrids that are adoptable within smallholder contexts.

Breeding programs should systematically broaden parental diversity to uncover novel heterotic patterns and reduce vulnerability associated with narrow genetic bases. Purposeful sampling of diverse germplasm—including landraces, underutilized species, wild relatives, and neglected crops—creates opportunities to identify heterotic groups beyond classical crop pools [38]. Implement stratified germplasm surveys that prioritize geographic, agroecological, and farmer-preferred diversity, while explicitly considering cross-compatibility constraints. Test novel parental combinations in representative target environments using factorial designs or partial diallel screens to reveal emergent or unexpected combining ability. Concurrently, monitor allele-frequency shifts and maintain core diversity panels to prevent genetic bottlenecks, thereby safeguarding diversity while expanding the space of potential heterotic sources. Collectively, this approach enlarges the pool of viable parents for constructing superior heterotic hybrids and enhances system resilience.

Future breeding objectives should explicitly prioritize multifunctionality, ensuring hybrids meet food, feed, and processing needs while remaining compatible with decentralized seed distribution. Hybrids that blend grain quality, fodder value, processing traits, and seed-system compatibility are more likely to be adopted within mixed farming systems [32]. Integrate milling behavior, oil composition, fodder digestibility, and post-harvest stability into selection indices alongside yield and stress tolerance. Weight traits to reflect local value chains and farmer priorities, and employ multi-trait selection indices that quantify trade-offs among yield, quality, and seed cost. Design hybrid release and seed-pricing strategies that permit partial farmer seed saving or community multiplication where appropriate. Embedding multifunctional objectives and seed-system constraints into breeding and deployment increases the likelihood that hybrids will be useful and accessible to smallholders.

Delivering hybrids that perform under water limitation and heat stress requires physiology-informed parental screening and test networks that mirror farmers' stress profiles. Implement managed stress screening and test-cross networks that capture timing, intensity, and stress combinations to improve the probability of achieving high yield potential with stability under concurrent abiotic stresses [39]. Employ managed drought and heat trials that simulate critical stress windows—such as flowering and grain filling—and incorporate precise timing and intensity controls. Integrate traits such as root architecture, transpiration efficiency, phenology, and stay-green into selection decisions and test-cross evaluation. Advance promising hybrids through extensive multi-environment trials that reflect farmer landscapes and cropping systems. Ensure robust male-sterility platforms, isolation protocols, and quality-control measures so stress-resilient hybrids can be produced reliably at scale. Thus, physiology-guided selection, coupled with realistic test networks and dependable seed production logistics, is essential to generate hybrids that sustain yield under real-world abiotic stresses.

Marker-enabled recurrent selection can substantially accelerate population improvement when tightly integrated with structured mating designs and high-quality phenotyping. Marker-assisted recurrent selection (MARS) and marker-enabled reciprocal recurrent selection shorten cycles and improve the accuracy of hybrid performance predictions when calibrated against robust field data [23]. Embed genotyping within planned mating schemes (e.g., recurrent selection strategies) so markers track alleles without disrupting the mating structures that generate heterosis. Employ early genotypic culling to reduce field testing load and refine parental selection via marker-informed estimates of combining ability, while monitoring allele trajectories across cycles. Maintain iterative calibration of marker effects using multi-environment phenotypes to mitigate prediction drift and to capture G×E interactions. Thus, when markers are used as tools within recurrent selection designs rather than as replacements for them, they can accelerate genetic gains while preserving the population processes that generate heterosis.

Scaling these innovations requires a realistic appraisal of costs, institutional capacity, and close alignment with seed-system actors. Investments in germplasm characterization, genotyping infrastructure, and multi-location test-cross networks must be weighed against anticipated genetic gains and socioeconomic returns, with participatory evaluation and partnerships with community seed enterprises helping to lower adoption barriers [32, 38]. Conduct formal cost–benefit analyses for genotyping platforms, phenotyping networks, and seed-production investments to prioritize interventions with the highest expected return. Invest in breeder training, data-management systems, and local seed-enterprise development to sustain pipelines and ensure quality assurance. Furthermore, design evaluation and deployment pathways in collaboration with farmers, producer organizations, and extension services to harmonize trait priorities with seed-access models. Consequently, realistic financing, capacity-building, and institutional partnerships are prerequisites for translating technical advances into widely adopted locally relevant hybrids.

A pragmatic integration strategy should preserve the population processes that generate heterosis while delivering short-term gains through targeted genomic and operational innovations. Genomic tools ought to complement, not replace, classical recurrent selection, and marker-based schemes must include periodic infusion of novel germplasm alongside explicit diversity monitoring to sustain long-term genetic variance [23]. Define stage-gated decision rules that require multi-environment testing (MET) confirmation and diversity checks prior to fixation or release. Schedule periodic introgression of landrace or exotic alleles and maintain core diversity panels to preserve long-term selection potential. Subsequently, couple these technical pipelines with seed-system design, quality assurance, and participatory deployment to ensure that gains are durable and equitably shared. Success depends on coupling technical acceleration with deliberate diversity stewardship and seed-system integration, so faster genetic gains remain sustainable and locally relevant.

In conclusion, future directions for breeding cross-pollinating crops should emphasize: expanding heterotic resources, prioritizing multifunctionality, implementing physiology informed stress selection, embedding marker technologies within recurrent selection frameworks, and investing in institutional capacity and seed-system infrastructure for scalable deployment. Together, these elements constitute a pragmatic, stewardship-oriented strategy to deliver resilient, multifunctional hybrids that are accessible and adoptable by smallholder farmers.

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3.3. Vegetatively Propagated Crops

Conventional breeding of vegetatively propagated crops should integrate classical clonal selection and sanitation with controlled tissue culture, pragmatic genomic monitoring, strengthened clean-seed systems, and market-driven quality targets to deliver resilient, farmer-preferred planting material at scale.

Meristem culture and micropropagation compress the interval between selection and farmer access by enabling rapid, pathogen-free multiplication of elite clones. These in vitro technologies achieve multiplication rates far exceeding field cuttings, allowing breeders to advance promising genotypes from nucleus to foundation stages in months rather than years—an advantage that is especially important where demand and disease pressure are high. Controlled tissue-culture protocols also facilitate early elimination of systemic pathogens through thermotherapy and meristem excision, markedly improving the phytosanitary status of downstream material. When tightly controlled and linked to downstream certification, tissue culture therefore functions as a high-leverage tool for rapid, health-preserving dissemination [40].

Adoption of tissue culture must be accompanied by rigorous quality assurance to prevent somaclonal drift and preserve clonal fidelity. In vitro propagation can introduce somaclonal variation and epigenetic changes that alter agronomic or quality traits, so programs should implement standardized culture protocols, routine molecular fidelity checks (e.g., SSR/SNP fingerprinting), and staged field validation. Multi-year, multi-site clonal trials are necessary to distinguish stable, beneficial variants from transient or deleterious changes and to ensure farmer acceptance under real management conditions. In short, controlled tissue-culture protocols combined with molecular and field validation capture useful novelties while excluding unstable or harmful variants [41].

Low-cost genomic assays and DNA barcodes make clone identity and trait monitoring practical across multiplication chains. Targeted SNP panels or barcodes enable routine identity testing that prevents mislabeling, supports traceability from nucleus stock to farmer fields, and documents varietal purity during decentralized multiplication. Where sexual introgression is used, genomic pedigree reconstruction can quantify introgression and background recovery before re-clonalization, increasing precision in trait transfer while protecting elite heterozygous backgrounds [40, 42]. Consequently, scalable genomic monitoring strengthens both quality assurance and the precision of breeding interventions as programs scale.

Sustained yield gains depend on pairing genetic improvement with robust sanitation, indexing, and certified clean-seed pipelines. Routine virus indexing using serology and PCR at nucleus and foundation stages, combined with meristem culture and thermotherapy, reduces pathogen load and preserves the productivity of improved clones [24, 25]. International and CGIAR-aligned protocols provide operational guidance for inspection, nucleus production, and release, and empirical experience shows that health status is often the single largest determinant of on-farm performance in potato, cassava, and banana systems. Thus, investment in clean-stock pipelines and routine diagnostics is among the most cost-effective strategies to sustain breeding gains.

Breeding objectives should explicitly integrate market and end-user quality traits alongside agronomic targets to drive adoption. Texture, processing suitability, storability, provitamin A retention, frying quality, and dry-matter content are examples of traits that determine farmer and consumer uptake; incorporating food-science assays into selection indices and participatory on-farm trials ensures clones meet production and value-chain requirements. Multidisciplinary phenotyping—combining sensory panels, biochemical assays, and agronomic evaluation—shortens the path from selection to marketable product [43]. Embedding end-user quality metrics in selection therefore accelerates adoption and aligns breeding outcomes with value-chain demand.

Programs must manage somaclonal variation, capacity constraints, and costs as they adopt genomic and in vitro technologies. Somaclonal variation can erode clonal fidelity even as it occasionally yields useful novelty, so routine molecular fingerprinting and extensive clonal trials are essential before release [41, 42]. Rollout of genomic approaches should follow a pragmatic trajectory: begin with low-density marker panels for identity and key-trait monitoring, then scale to higher-resolution assays as infrastructure and expertise grow. A staged, capacity-aware adoption pathway minimizes risk while enabling progressive gains from genomic and tissue-culture tools.

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Scaling improved clonal materials requires a hybrid model linking centralized clean-stock production with decentralized, quality-assured multiplication. Centralized tissue-culture production of nucleus material ensures high health standards, while community-level rapid multiplication and quality-declared planting material expand farmer access; success depends on training, monitoring, and institutional coordination to prevent pathogen spread. Where formal certification is limited, well-designed decentralized systems—backed by periodic molecular checks and extension support—can deliver improved clones at scale without sacrificing health status [24, 25]. Combining centralized clean-stock pipelines with decentralized multiplication and strong quality assurance thus translates laboratory gains into reliable on-farm impact.

In sum, conventional clonal breeding that couples clonal selection and sanitation with controlled tissue culture, pragmatic genomic monitoring, and market-oriented trait targets can deliver resilient, farmer-preferred planting material at scale. Success requires staged adoption, rigorous quality assurance, and integrated dissemination pathways that preserve health and varietal identity.

4. Cross-Cutting Themes

Conventional breeding increasingly rests on three interdependent pillars—targeted induced variation, pragmatic molecular and phenomic overlays, and farmer and seed-system co-design—operating within an imperative to secure equitable access and rigorous quality assurance so that genetic gains translate into locally relevant and durable impact.

Induced mutation is a pragmatic, targeted strategy when existing germplasm lacks alleles for resistance, quality, or abiotic tolerance, but it should be invoked only after exhaustive sampling of natural diversity and followed by rigorous validation. Large-scale mutation screens (physical or chemical mutagens) expand the allelic space available to breeders and can generate single-gene changes useful for disease resistance or quality traits. Contemporary workflows pair high-throughput phenotypic screens with molecular characterization to accelerate candidate discovery and to flag off-target or deleterious events early [44]. Because mutagenesis produces many neutral or harmful variants, programs require multi-environment trials, molecular validation, and careful curation to exclude pleiotropy and unstable effects. For these reasons, induced mutation should be applied as a last resort and embedded within molecular and field-validation pipelines to fill critical genetic gaps without compromising long-term varietal stability.

Embedding farmers and seed-system actors in program design and evaluation is essential to ensure that genetic gains meet local preferences and diffuse rapidly. Participatory selection and on-farm validation integrate local priorities—taste, maturity, processing behavior, labor requirements, and management practices—directly into selection indices. Early, iterative farmer feedback reduces adoption lags by revealing context-specific trade-offs (e.g., yield versus culinary quality) and by identifying the management regimes under which candidate varieties perform [45]. In smallholder and under-utilized crop contexts, participatory approaches have repeatedly increased the likelihood of rapid diffusion and sustained use. Consequently, systematic, iterative farmer engagement converts breeder outputs into locally relevant products and shortens the path from release to adoption.

Molecular markers and calibrated phenomics should augment, not replace, robust field selection to increase precision and speed for both simple and complex traits. Marker-assisted backcrossing secures foreground alleles and accelerates background recovery in introgression programs; genomic prediction can hasten selection for polygenic traits when applied in later-generation evaluation; and genome-wide association studies (GWAS) help prioritize candidate loci for functional follow-up. High-throughput phenotyping platforms increase throughput, but they must be field-aligned and trait-relevant so measurements reflect breeder priorities and farmer management. Cost-sensitive deployment—starting with low-density marker panels for identity and key traits and scaling to higher resolution as capacity grows—balances predictive gain with affordability [46, 47]. Thus, when used as pragmatic overlays and calibrated to field relevance, molecular and phenomic tools materially raise selection efficiency without undermining breeder judgment.

Equity, affordability and ethical governance must shape breeding priorities and delivery mechanisms from the outset to ensure broad, fair access to benefits. Benefit-sharing arrangements,

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gender-responsive trait prioritization and explicit alignment with local culinary and market needs, help ensure that improved varieties serve diverse users. Policy instruments—access and benefit-sharing frameworks, intellectual property regimes and seed laws—have direct effects on smallholder access and on the distribution of breeding benefits [48], and therefore require ex-ante evaluation and, where necessary, adaptation to local contexts. Embedding social scientists and legal expertise in breeding programmes improves the design of equitable dissemination pathways. Thus, ethical stewardship and deliberate policy design are prerequisites for translating accelerated breeding into inclusive, sustainable gains.

Maintaining varietal identity and health across multiplication chains requires rigorous DUS (distinctness, uniformity and stability) testing, molecular traceability, and clear operational rules that prioritize validation, cost-sensitive genomics and iterative participatory trials. DUS testing, purity standards and traceability reduce admixture and protect farmer trust; integrating low-cost molecular identity checks into nucleus and foundation stages strengthens stewardship. Operational rules should include prioritizing targeted mutation only after exhaustive germplasm sampling followed by molecular and field validation, embedding participatory trials early and iteratively, adopting staged genomic strategies that begin with low-density panels, and focusing phenomics investments on reliably measurable, breeder-relevant traits. Community-based quality-declared seed schemes can complement formal channels where they are weak, provided they are supported by clear protocols, periodic molecular checks and extension support. Consequently, clear, actionable rules and integrated quality assurance across breeder-seed to farmer-field pathways are essential to manage trade-offs and to ensure that breeding advances are durable, traceable and accessible.

5. Evaluation and Deployment Pathways

Effective evaluation and deployment of conventionally bred varieties require an integrated framework that links rigorous experimental design, quantitative inference, staged advancement, seed-system planning, and embedded monitoring so that genetic gains observed in trials translate into measurable and durable on-farm benefits.

Reliable selections begin with well-replicated trials and multi-environment testing that control local variance and represent the target agroecological domain. Randomized complete-block or alpha-lattice layouts, stratified sampling across agroecologies, and spatial mixed-model analyses (e.g., spatial autoregressive residuals; REML/BLUP) increase precision and improve heritability estimation. Adequate replication reduces local noise and raises the signal-to-noise ratio for genetic effects, stratified METs ensure trial environments reflect farmer conditions, and spatial mixed models correct for field heterogeneity—together strengthening the statistical basis for culling and advancement decisions. Investing in robust trial design and modern quantitative analyses therefore yields clearer estimates of genetic merit and greater confidence that trial gains will persist under farmer conditions.

Predicting genetic gain and defining recommendation domains depends on explicit parameters for heritability and selection intensity together with rigorous decomposition of G×E interaction. Narrow-sense heritability predicts additive response to selection, while regression-based stability metrics, AMMI and GGE biplot analyses separate main effects from interaction structure and identify broadly versus specifically adapted genotypes. Use narrow-sense heritability to set realistic expectations for additive gain and choose selection intensity consistent with program capacity; triangulate regression stability, AMMI and GGE to quantify crossover interactions and inform staged release strategies. Quantitative framing of gains combined with multiple G×E methods thus clarifies which genotypes will deliver reliable benefits across intended domains.

Stage-gated pipelines balance throughput and accuracy by progressively narrowing candidate pools while refining performance estimates. Early-generation nurseries (bulks, F4–F6) and high-throughput screens reduce candidate numbers; preliminary and advanced yield trials increase plot size and replication; and pre-release national trials provide regulatory and agronomic evidence for release and seed multiplication. Early bulks and rapid screens prioritize traits and remove poor performers quickly; larger, replicated trials improve precision under realistic management; and later participatory on-farm trials validate farmer-relevant traits and management responses for adoption

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planning. Stage gating therefore concentrates resources where they most improve decision accuracy and ensures released varieties combine robust trial performance with farmer-validated relevance.

Deployment pathways must be planned in parallel with breeding so seed-system capacity does not become a bottleneck to impact. Self-pollinated crops require progression from foundation to registered and certified seed chains, hybrids require parental-line integrity and controlled seed production, and asexually propagated crops combine centralized clean stock (e.g., tissue culture and indexing) with decentralized multiplication and quality-declared planting material schemes. Preserving genetic purity across seed classes maintains varietal identity; hybrid programs must protect parental lines to ensure heterosis at scale, while clean-stock systems plus rapid multiplication expand access without compromising phytosanitary status. Parallel planning of seed systems and breeding therefore secures the pathway from genetic improvement to farmer access and preserves the quality needed for on-farm benefits.

Embedding monitoring and evaluation from the outset enables measurement of adoption, varietal turnover and yield-gap closure, and informs iterative refinement of breeding and dissemination strategies. Household surveys, seed-sales and certification records, and remote sensing can be triangulated to estimate area planted, productivity changes and adoption dynamics. Combine survey data on farmer preferences and management with administrative seed records to estimate turnover and market fit; use remote sensing where feasible to validate area planted and yield trends; and track time to adoption and livelihood indicators (income, food security, nutrition) to assess socioeconomic outcomes. Integrated, multi-source monitoring therefore provides the evidence base needed to judge impact and iteratively align breeding objectives with farmer and market realities.

Anticipating methodological and system risks and building mitigation into design preserve selection accuracy and increase the likelihood of durable, farmer-relevant impact. Poor experimental design can be countered by spatial mixed models and adequate replication; misclassification of G×E is reduced by triangulating AMMI, GGE and regression stability metrics; and seed-system misalignment is addressed by co-designing multiplication and distribution with stakeholders. Adopt spatial mixed models from the outset and ensure replication to protect selection accuracy, use complementary G×E methods to reveal interaction structure and avoid inappropriate recommendation domains, and engage seed producers, regulators and distributors during advanced trials to confirm multiplication, certification and logistics are feasible. Proactive design choices and stakeholder alignment thus create an evidence-based, deployment-aware framework that maximizes the probability that varietal improvements translate into sustained, on-farm benefits.

6. Challenges and Limitations

Conventional plant breeding is constrained by interrelated limits—prolonged breeding cycles and limited program capacity, genetic narrowing with linkage drag, escalating climate and biotic complexity, and persistent adoption barriers. Only integrated, simultaneous responses that compress cycles, broaden and steward genetic diversity, target stress-relevant evaluations, and align seed systems can sustain and accelerate farmer-level genetic gain.

Long breeding cycles and limited program capacity dampen responsiveness and lower annual genetic gain. The interval from cross to release typically spans multiple years—often six to twelve years in many programs—placing heavy demands on field infrastructure, nurseries, and skilled personnel [12]. Extended cycles constrain throughput and hinder timely responses to emergent pests, diseases, or market opportunities. Programs lacking off-season nurseries, doubled haploid (DH) platforms, speed-breeding facilities, or stable funding cannot compress cycles, reducing selection intensity and delaying impact. Targeted investments in speed breeding, DH technologies, expanded off-season capacity, and breeder training are therefore essential to shorten time to impact and elevate annual genetic gain [10, 12]. Thus, without deliberate efforts to compress cycles and expand capacity, breeding programs remain slow and reactive, limiting the pace at which improved varieties reach farmers.

Reliance on a narrow elite parent base and backcross recovery creates bottlenecks and linkage drag that constrain long-term adaptability. Persistent use of a limited set of elite parents produces genetic bottlenecks observed across crop systems, and backcrossing to recover elite backgrounds can carry undesirable alleles alongside target loci [6, 16]. Such bottlenecks reduce standing variation and increase vulnerability to novel threats, while linkage drag complicates the stacking of complex traits and slows pre-breeding progress. Practical responses include systematic introgression from landraces and wild relatives, structured pre-breeding pipelines to replenish variation, and marker-assisted background selection to minimize linkage drag while preserving elite performance. These measures require coordinated, long-term investment and careful prioritization of donor sources. Therefore, expanding and managing genetic diversity through pre-breeding and marker-guided strategies is essential to restore adaptive potential and enable durable trait stacking.

Rapidly shifting pest, disease, and climatic pressures amplify G×E complexity and diminish the predictive value of historical trial data. More frequent and severe climatic extremes, coupled with evolving pest and disease regimes, complicate selection and undermine assumptions based on past environments [11]. Consequently, breeders must prioritize stability across concurrent stresses rather than performance under a single stress, a shift that complicates phenotyping, trial design, and selection models. Recommended strategies include expanding managed-stress screening, integrating physiological selection criteria with genomic prediction to capture complex adaptive responses, and broadening multi-environment trial (MET) networks to sample environments that reflect likely future conditions. These approaches enhance the robustness of selection but demand more sophisticated trial infrastructure and analytic capacity. Therefore, addressing climate and biotic complexity requires stress-aware evaluation networks and a combined physiological–genomic selection framework to preserve predictive power under changing conditions.

Technical success in breeding does not guarantee farmer impact if seed access, affordability, extension support, or trait fit are lacking. Even technically superior varieties may fail to be adopted if breeder priorities diverge from farmer preferences (e.g., taste, processing, and labor requirements) or if seed systems and extension services cannot deliver seed and knowledge to farmers [5, 49]. Barriers include limited multiplication capacity, high seed costs, weak certification or decentralized distribution, and insufficient participatory evaluation that captures farmer trait priorities. Overcoming these barriers requires embedding participatory selection and market-driven trait definition early in pipelines, co-designing multiplication and distribution pathways with stakeholders, and monitoring adoption metrics to iteratively refine breeding targets and dissemination strategies. Consequently, aligning breeding objectives with seed-system design and farmer preferences is essential to translate genetic gains into widespread, equitable on-farm benefits.

The four constraints interact synergistically, so isolated fixes yield limited returns; integrated strategies are required to accelerate and sustain impact. Slow cycles reduce responsiveness to new threats, narrow genetic bases amplify vulnerability, shifting environments complicate selection, and seed-system mismatches impede delivery—together constraining the rate at which genetic gains reach farmers [12, 16]. The most effective approach combines cycle compression (e.g., speed breeding and DH), diversity management (pre-breeding and marker-assisted background selection), stress-relevant METs with combined physiological–genomic selection, and seed-system strengthening through participatory deployment. Coordinated investments in infrastructure, pre-breeding, evaluation networks, and dissemination pathways generate mutually reinforcing gains that shorten time to adoption and enhance durability of impact. Thus, only an integrated, programmatic response—simultaneously addressing cycles, diversity, evaluation, and delivery—can overcome the compounded limitations of conventional breeding and translate scientific advances into durable farmer-level benefits.

7. Future Directions and Integration

Integrating genomic overlays, accelerated generation systems, digital phenotyping, strengthened seed-system models, and enabling policy can pragmatically shorten time to release and increase farmer-relevant genetic gain within conventional breeding pipelines. Yet each acceleration innovation introduces technical, infrastructural, and socio-institutional constraints that must be managed through coordinated, field-anchored workflows.

The objective of integration is to reconfigure, not replace, field-based selection so that cycle compression, genomic augmentation, high-throughput phenotyping, field-aligned evaluation, and deployment planning function as a single, coordinated workflow. Combining complementary technologies and planning steps preserves the validation and multiplication stages that underpin reliable release and adoption [10, 12]. A coordinated workflow aligns accelerated generation methods with METs and on-farm validation to avoid advancing lines that perform only under controlled conditions. It requires explicit gating rules, data flows that link genomic predictions to field observations, and parallel seed-system planning so that multiplication and certification capacity are available when varieties are ready for release. Institutional coordination among breeding, seed production, extension, and policy actors is necessary to operationalize this alignment. For these reasons, reconfiguring to a single, coordinated workflow preserves the strengths of field-based selection while enabling faster, evidence-based advancement.

Reducing generation time is the most direct lever to raise annual genetic gain, but it requires targeted infrastructure and careful validation. Doubled-haploid (DH) technology, off-season and shuttle nurseries, and speed breeding increase the number of effective generations per year and enable earlier, more reliable phenotyping [10, 12]. DH fixes homozygosity in a single generation, accelerating trait fixation and earlier selection; off-season and shuttle nurseries expose segregating material to diverse environments; speed breeding manipulates photoperiod and temperature to compress generation time. Combining DH with speed breeding or off-season nurseries maximizes yearly cycles, but METs and on-farm testing must be retained as gating steps to validate candidate lines under farmer management and environmental variability. Investments in facilities, trained personnel, and stable funding are prerequisites for realizing these gains. Consequently, cycle compression raises potential genetic gain rapidly, but only when paired with rigorous field validation and sustained infrastructure investment.

Genomic tools should augment phenotypic METs through calibrated, phased deployment rather than supplanting field evaluation. Marker-assisted backcrossing (MABC) effectively enables targeted introgression and background recovery, while genomic selection performs best when phased into later generations with robust training populations (6, 10). Use markers for foreground and background selection to reduce linkage drag during introgression, where low-density marker panels streamline parental selection and identity checks. Genomic selection pilots should begin after sufficient phenotypic depth exists so predictions are reliable. Continuous calibration—validating genomic predictions against MET outcomes—prevents disconnection between genotypic scores and farmer-relevant performance. Data management, well-constructed training populations, and high-quality phenotyping are critical enablers. Therefore, phased, calibrated genomic overlays can shorten cycles and improve accuracy only when tightly integrated with and validated by field data

Digital phenotyping and analytics can increase throughput and sharpen selection when explicitly aligned with breeder field workflows and validated under realistic management. Low-cost sensors, mobile data capture, and cloud analytics yield plot-level indices (e.g., NDVI, canopy temperature) and standardized scoring that accelerate candidate triage. Automated pipelines that flag promising candidates reduce bottlenecks and enable rapid scaling of phenotyping; however, bias can arise if measurements derive from controlled environments or if sensors capture proxies that poorly correlate with farmer priorities. Integration requires standard protocols, training for field teams, and cross-validation of sensor indices against manual measurements and farmer assessments. Data pipelines must be robust, interoperable, and designed to feed METs and genomic training sets. Therefore, digital tools amplify breeder capacity when field-tested, standardized, and embedded in existing selection and validation workflows.

Strengthening seed systems and aligning policy are essential to convert accelerated breeding outputs into accessible, affordable seed and equitable impact. Models such as public–private partnerships (PPPs) for hybrid seed, Quality-Declared Seed (QDS) and community seed banks for marginal areas, and centralized clean-stock systems for vegetatively propagated crops broaden reach while preserving quality. Policy levers—institutionalized release procedures, targeted investment, and balanced intellectual-property frameworks—shape incentives for scaling [5, 49]. Designing multiplication and distribution pathways in parallel with selection anticipates certification requirements and logistical constraints. QDS and community multiplication can extend access where formal systems are weak; PPPs can scale production for commercial crops; and regulatory harmonization and funding for national breeding capacity encourage private investment while protecting farmer seed rights and benefit sharing. Policy alignment with accelerated cycles reduces temporal mismatches between release and market readiness. Accordingly, seed-system design and enabling policy are as important as technical acceleration for ensuring that faster breeding translates into widespread, equitable adoption.

Accelerations introduce risks—selection bias toward controlled environments, data and infrastructure gaps, and seed-system misalignment—that require explicit mitigation and phased operationalization. Speed breeding and DH can bias selection toward controlled-environment performance; genomic approaches demand data infrastructure and high-quality phenotypes; and seed-system misalignment can block adoption unless addressed during advanced trials [6, 10, 49]. Mitigations include mandatory MET and on-farm validation as gating criteria, phased genomic rollouts starting with low-density marker panels, and co-design of multiplication and distribution mechanisms (QDS, PPPs, community banks) during advanced trials. Operational rules should require continuous calibration of genomic predictions, standardized digital-phenotyping protocols, and explicit investment plans for seed multiplication and certification. These interlocking actions preserve external validity while enabling accelerated throughput. Consequently, a pragmatic, phased implementation—anchored in MET validation, incremental genomic adoption, and parallel deployment planning—balances the benefits of acceleration with the practical realities of field performance, seed access, and farmer priorities, increasing the likelihood of durable, locally relevant impact.

8. Conclusions

Conventional plant breeding remains indispensable because it yields field-validated, scalable, and contextually adapted varieties. Accelerating its impact requires integrating calibrated genomic tools, cycle compression, high-throughput field-aligned phenotyping, strengthened seed systems, and enabling policy—while preserving multi-environment validation and farmer priorities.

The core strength of conventional pipelines lies in their field-based integration of crossing, staged selection, and multi-environment testing (METs), which preserves breeders' ability to manage complex trait trade-offs and to deliver certified seed at scale. Staged advancement and METs generate agronomic, stability, and management evidence that underpins national release systems and farmer trust. By prioritizing replicated field evaluation and seed-chain integrity, conventional programs produce uniform, verifiable varieties whose performance is credible to regulators, seed producers, and farmers; this credibility undergirds adoption and varietal turnover. Retaining field validation and seed-system realism is essential to ensure that technical gains translate into measurable on-farm benefits.

Molecular tools and accelerated generation systems should be introduced incrementally and pragmatically to augment, not replace, field-based decision making. Marker-assisted backcrossing (MABC) and low-density marker panels help protect elite backgrounds, while phased genomic selection improves predictions for polygenic traits once training populations and phenotypic depth exist. Use MABC to identify panels for parental selection and background recovery to reduce linkage drag. Apply genomic selection in later generations where MET data support reliable models. Combine doubled-h haploid (DH) technology, speed breeding, and off-season nurseries to compress cycles, while retaining METs and on-farm trials as gating criteria. This calibrated, phased rollout preserves external validity while capturing the cycle-compression and accuracy benefits of molecular and accelerated methods.

Future breeding programs must explicitly target climate resilience and end-user value so that varieties meet both biophysical and socio-economic needs. Breeding for heat and drought stability alongside nutritional and processing quality increases the likelihood of sustained adoption and livelihood impact. Design selection indices in collaboration with farmers to embed taste, processing, labor, and seed-cost considerations, and embed stability metrics and multi-stress screening within MET networks to select broadly resilient genotypes. Integrate nutritional and value-chain traits into early-stage priorities to avoid late-stage trade-offs. Centering resilience and farmer priorities in breeding objectives enhances relevance, accelerates uptake, and amplifies socio-economic returns.

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Accelerations introduce predictable risks—selection bias from controlled environments, premature genomic deployment, and seed-system misalignment—that require explicit safeguards. Speed breeding and doubled-haploid (DH) approaches can favor controlled-environment performance, whereas genomic methods demand high-quality phenotypes and data infrastructure to avoid biased predictions. Mitigations include mandatory MET and on-farm validation gates, phased genomic adoption beginning with low-density panels linked to existing METs, standardized digital-phenotyping protocols, and co-design of multiplication pathways from foundation to certified or QDS/community systems developed during advanced trials. Policy measures—streamlined release procedures and balanced intellectual property (IP) frameworks—further align incentives for scaling while protecting farmer access. Clear operational rules and parallel investments in validation, data, seed systems, and policy reduce acceleration risks and preserve farmer-relevant outcomes.

The most effective route to durable, locally relevant genetic gain is an integrated pathway that compresses cycles and deploys calibrated genomic overlays while keeping field validation, seed-system design, and farmer priorities central. Combining cycle compression, diversity management, stress-aware METs, and deployment planning results in mutually reinforcing gains that shorten time to adoption and increase impact. Operationalizing this pathway requires: (1) gating accelerated advancement on MET and on-farm performance; (2) phasing genomic tools from identity checks to full genomic selection as training sets mature; (3) embedding seed-system and policy planning from project inception; and (4) co-designing objectives with end users to ensure fit and equity. When calibrated acceleration is paired with rigorous field evidence, robust seed systems, and participatory priorities, conventional breeding can deliver faster, more equitable and measurable benefits for producers and value chains.

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