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Systematic Review Article

Genomics-Assisted Breeding for Climate-Resilient Wheat: A Systematic Review

Ananya Mishra [1, *]

[1]*GIFT Engineering and Management College, GIFT Autonomous, Bhubaneswar, India*

Article History

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Abstract:

Introduction: Frequency, intensity, and co-occurrence of drought, heat, flooding, and disease stresses impacting wheat production are all on the rise, as is the demand for breeding strategies that will speed up wheat adaptation while remaining technologically prepared. The aim of this systematic review was to determine if there were any similarities or differences between empirical studies and simulation studies of Genomic Selection (GS), Genome-Wide Association Studies (GWAS), and Speed Breeding (SB).

Methods: A PRISMA 2020-guided systematic review searched PubMed, Scopus, and Web of Science for peer-reviewed wheat studies published from 2018 to 2025. Eligible studies evaluated Genomic Selection (GS) / Genomic Prediction (GP), Genome-Wide Association Studies (GWAS), Speed Breeding (SB) / Rapid Generation Advance (RGA), or partial combinations in bread or durum wheat for climate-relevant traits and reported at least one measurable breeding outcome. Two reviewers independently screened records and extracted data, and empirical and simulation evidence were analysed separately. Because of substantial heterogeneity in traits, populations, validation schemes, and outcome scales, findings were synthesised descriptively rather than meta-analytically.

Results: A moderate accuracy of prediction (approximately 0.45-0.51) was achieved in the empirical GS studies under stress, and these GWAS studies were mostly devoted to markers and candidate genes. Studies under controlled environments in SB have resulted in shorter generation times. The simultaneous use of GS and SB in the same study was found to be potentially higher gain per unit time, and gain estimates were determined by prediction accuracy, selection intensity, population size, recombination, and cycle management. For some data sets, the confidence level in predictions was increased by the use of models with environmental covariates or by multi-environment models. Since there were a wide variety of traits, populations, outcomes and reporting scales, a descriptive synthesis was carried out instead of a meta-analysis.

Conclusion: Speed breeding shortened generation intervals under controlled conditions and may facilitate faster advancement of climate-relevant traits, although evidence for realised field-level climate resilience remains limited. Multi-environment validation, diversity safeguards, economic analysis, interoperable data systems, and transparent benchmarking procedures in well-resourced and resource-limited programmes are needed.

Keywords: Genomic selection, genome-wide association studies, speed breeding, phenomics, climate resilience, and multi-environment models.

1. INTRODUCTION

The frequency, intensity, and overlap of abiotic and biotic stresses affecting wheat production, such as heat, drought, flooding, and disease, are increasing. Breeding for climate resilience cannot be reduced to identifying a limited number of 'resilience genes'. Wheat is produced in a wide variety of environments, and new cultivars must not only be highly adapted to their environments but also produce quality grain and have good agronomic fitness [1-4].

Long generation intervals and expensive field evaluation remain important constraints. However, these constraints limit the speed at which responses can be achieved in rapidly changing production environments through conventional crossing and phenotypic selection. Genomic Selection (GS)

*Address correspondence to this author at GIFT Engineering and Management College, GIFT Autonomous, Bhubaneswar, India; E-mail: ananyamishragift@gmail.com

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uses genome-wide markers to predict breeding values for complex traits; Genome-Wide Association Studies (GWAS) are used to find marker–trait associations and candidate regions, and Speed Breeding (SB) uses controlled photoperiod, temperature, and crop management to turn over generations [5-8]. These can be used at various stages of a breeding programme and selectively combined.

The evidence requirements differ across the three tools. Factors affecting GS accuracy include training population size and relatedness, trait architecture, phenotyping quality, environmental representation, model choice, and validation design. GWAS can identify loci associated with traits, but these associations need to be validated in other populations and under other environmental conditions before deployment. Operational and genetic bottlenecks can arise from inadequate field testing, excessive selection intensity, small effective population size, and/or loss of genetic diversity when SB reduces calendar time without necessarily increasing genetic gain.

Only bread and durum wheat were considered as evidence because these are large polyploid organisms, and wheat is largely self-pollinated, with a specific quality target and disease target for each crop, and supported by existing multi-environment testing networks. If other cereals were adopted into the evidence base, it would be more complex to evaluate the accuracy of prediction, generation intervals, and marker transferability. Only wheat was used for the synthesis, and maize, rice, or barley was not used as contextual material in the discussion.

Previously, there have been reviews on either of the three aspects of GS, GWAS, or SB separately. However, this review will concentrate on the real outputs of their empirical and simulation approaches and how they would have to be improved to show that they are better than traditional breeding. Prediction accuracy, environmental robustness, generation interval, realised or expected genetic gain, implementation constraints, and validation status are the focus of the analysis.

The review aimed to: (i) assess the empirical evidence for GS, GWAS, and SB in wheat and differentiate empirical results from simulated results; (ii) compare single-tool and partially integrated approaches; (iii) review G×E modelling, artificial intelligence and digital phenotyping, emerging tools, and diversity safeguards; and (iv) explore the methodological, infrastructural, and economic needs for operational application.

This review frames climate resilience as a multi-trait, multi-environment breeding objective rather than a single breeding outcome. The benefits of an integrated GS–GWAS–SB pipeline would have to be demonstrated by multi-cycle, head-to-head field comparisons with a managed conventional breeding programme.

2. METHODOLOGY

2.1. Study Design

This systematic review report follows PRISMA 2020. The review question focused on the measurable impact of GS, GWAS, and SB on the breeding of wheat for climate-relevant traits, either alone or in partial combinations. Only bread wheat (*Triticum aestivum* L.) and durum wheat (*Triticum turgidum* subsp. durum) were used as primary evidence. The following study designs were considered eligible: field trials, controlled-environment experiments, genomic prediction and association-mapping studies, and simulations reporting prediction, cycle, and/or genetic gains under a defined breeding scenario. Empirical and simulation evidence were extracted and analysed separately. Simulation results were not treated as direct evidence of realised changes in generation interval or genetic gain.

2.2. Search Strategy

Peer-reviewed papers from 2018 to 2025 were identified through a search of PubMed, Scopus, and Web of Science. Related terms were combined within the technology block (genomic selection/genomic prediction, GWAS, speed breeding/rapid generation), and the wheat and climate-relevant trait blocks were combined with AND. No included study assessed all three technologies. The full database-specific syntax, limits, dates, and retrieved counts are summarised in Appendix A. A targeted contextual update was performed to assess recent developments in Artificial Intelligence, pangenomics, genome editing, multi-omics, genomic foundation models, and multi-environment prediction. These background sources were used in the Discussion but were not included in the pre-specified 20-study dataset for analysis.

2.3. Eligibility Criteria

Peer-reviewed wheat studies were selected if they covered drought, heat, salinity, flooding, disease resistance, yield stability, phenology, or another well-defined climate-relevant trait, as assessed using GS, GWAS, and/or SB, and were published between 2018 and 2025. Each study was required to describe the population or data source, identify an empirical or simulation design, and report at least one measurable breeding outcome. Simulation studies were considered acceptable only if they reported their assumptions and breeding scenarios in sufficient detail to support interpretation of the results for accuracy, cycle reduction, and/or genetic gain. Conceptual articles, conference abstracts, protocols, non-peer-reviewed articles, articles without a genomic target or rapid cycling methodology, or articles with incomplete method and outcome data were excluded. Reviews were used only for background information and citation checking and were not considered primary evidence (Table **1**).

2.4. Search Transparency and Scope Control

The search was purposely targeted rather than comprehensive of all wheat genomics publications. Papers that did not include enough methodological details, or measurable breeding impact related to the question under review, or were general genomics papers, were excluded if they did not include marker diagnostic, physiology, or gene-function studies. These studies (n = 20) fulfilled the requirements for crop, technology, climate-relevance, design and outcome. Wheat evidence was not interwoven with evidence from other cereals, which were presented separately in the discussion as a clearly labelled "contextual comparison" with wheat evidence.

Table 1. Inclusion and exclusion criteria.

Criterion	Inclusion	Exclusion	Reasoning and Justification
Study type	Field, controlled-environment, association-mapping, genomic-prediction, or wheat-specific simulation studies with defined breeding scenarios and measurable outcomes	Reviews as primary evidence, protocols, conference abstracts, and purely theoretical studies	Retains designs capable of informing wheat breeding outcomes while excluding nonprimary or nonoperational evidence.
Genomic or breeding tool	GS/genomic prediction, GWAS, SB/rapid generation advance, or partial combinations	No relevant genomic-prediction, association-mapping, or rapid-cycling method	A study could examine any one tool; the evaluation of all three tools was not required.
Crop	Bread wheat (Triticum aestivum L.) or durum wheat (Triticum turgidum subsp. durum)	Non-wheat crops, including allogamous-crop simulations	Maintains a wheat-only analytical dataset and avoids cross-crop pooling.
Climate relevance	Drought, heat, salinity, flooding, disease, yield stability, phenology, or another clearly defined climate-relevant trait	No climate-relevant stress, adaptation, or stability outcome	Aligns evidence with the review question.
Publication period	2018–2025	Before 2018 or after 2025 for the analytical dataset	Defines the pre-specified analytical window; later sources were only contextual.
Reporting	Population/data source, design, and at least one measurable breeding outcome were reported in the studies.	Insufficient methods or outcome information	This permits transparent interpretation and extraction.

2.5. Study Selection Process

Titles and abstracts were screened independently by two reviewers, and then the full texts were assessed based on the following criteria. Discussions were held in a structured manner with consensus building to resolve disagreements. Twenty studies were found that met all the criteria and were specific to wheat. During the title and abstract screening step, the reviewers concurred on 91% of the titles and abstracts, and Cohen's κ = 0.84 was computed.

Full-text exclusions were due to poor reporting of methods or outcomes, publication as a protocol only, or not meeting the wheat-only crop criterion. The small analytical sample should not be interpreted as representing the total body of wheat genomics research; it is instead a consequence of the defined scope. Retrospectively including other crops and/or other descriptive gene-function studies would have enhanced the volume of content but at the expense of consistency and comparability between prediction metrics, cycle effects, and claims of integration. This limitation affects generalisability and is discussed explicitly in the Discussion, but it remains important for within-crop interpretation.

Identification, screening, retrieval, eligibility assessment, and inclusion are summarised in Fig. (**1**). A total of 644 records were found in the database search. A total of 618 records were screened, with 26 being considered duplicates and 414 excluded. A total of 204 reports were sought for retrieval; all were retrieved and assessed for eligibility. A total of 184 reports were removed due to 88 insufficient methods and/or outcomes, 95 protocol-only, and 1 non-wheat allogamous-crop simulation study. A total of 20 studies, including [9-28], related to wheat were included in the qualitative synthesis of the results.

2.6. Data Extraction

The standardised extraction form recorded population size, target trait or stress, genomic or breeding tool, training and validation network design, geographic extent of tested conditions, reported accuracy or association metric, generation-interval effect, genetic-gain estimate, study limitations, and evidence type. Data were extracted independently by two reviewers, with consensus reached on any disagreements. Only reported effect sizes were extracted; missing effect sizes were not reconstructed.

2.7. Reporting and Methodological Appraisal

The included studies used association mapping, genomic prediction, multi-environment field evaluation, controlled-environment speed breeding, or stochastic simulation. None of the available and validated appraisal instruments were appropriate for all of these designs. We thus used an author-designed, five-domain reporting and methodological appraisal as follows: (i) population and diversity; (ii) specification of the genotyping platform or SB intervention; (iii) specification of phenotyping and environmental relevance; (iv) statistical rigour; and (v) validation. Each domain was coded as 1 (adequately reported) or 0 (absent or inadequately reported). The second domain examined for SB studies lacking a genotyping platform was the intervention protocol clarity and reproducibility. The checklist was designed as a transparency aid for describing evidence, but not as a validated risk-of-bias instrument or effect-size weight.

The overall categories were based on the number of adequately reported domains: high (4-5 domains), moderate (3 domains), and low (0-2 domains). All domains and designs were given equal weight solely to allow a clear overview of the characterised designs and did not reflect equal scientific value. The appraisal was conducted independently by two reviewers, with discrepancies resolved by consensus. In addition to the numerical category, study design, validation context, and type of evidence were considered when concluding (Tables **2** and **2A**).

Appraisal score = number of adequately reported domains ÷ 5.

The appraisal was used as a transparency aid. In particular, deficits in environmental validation, statistical rigour, or reproducibility were discussed qualitatively, even when studies received the same overall category.

Table 2A. Classification of included studies by evidence type.

Evidence Type	Studies	Nature of Evidence
Empirical / real-data studies (n = 19)	Juliana *et al.* [9]; Maulana *et al.* [16]; Nouraei *et al.* [17]; Vitale *et al.* [18]; Tyrka *et al.* [19]; Yannam *et al.* [10]; Alahmad *et al.* [13]; Javid *et al.* [20]; Rabieyan *et al.* [21]; Pang *et al.* [22]; Molero *et al.* [23]; Montesinos-López *et al.* [12]; Ghazy *et al.* [24]; Nawade *et al.* [25]; Cha *et al.* [14]; El Gataa *et al.* [26]; Tadesse *et al.* [27]; Devate *et al.* [28]; Liu *et al.* [11].	Field trials, controlled environment experiments, real phenotypic/genotypic datasets, GWAS, genomic prediction, or multi-environment evaluation.
Wheat-specific simulation study (n = 1)	Nannuru *et al.* [15]	Stochastic simulation of GS and SB for Fusarium head blight resistance in wheat

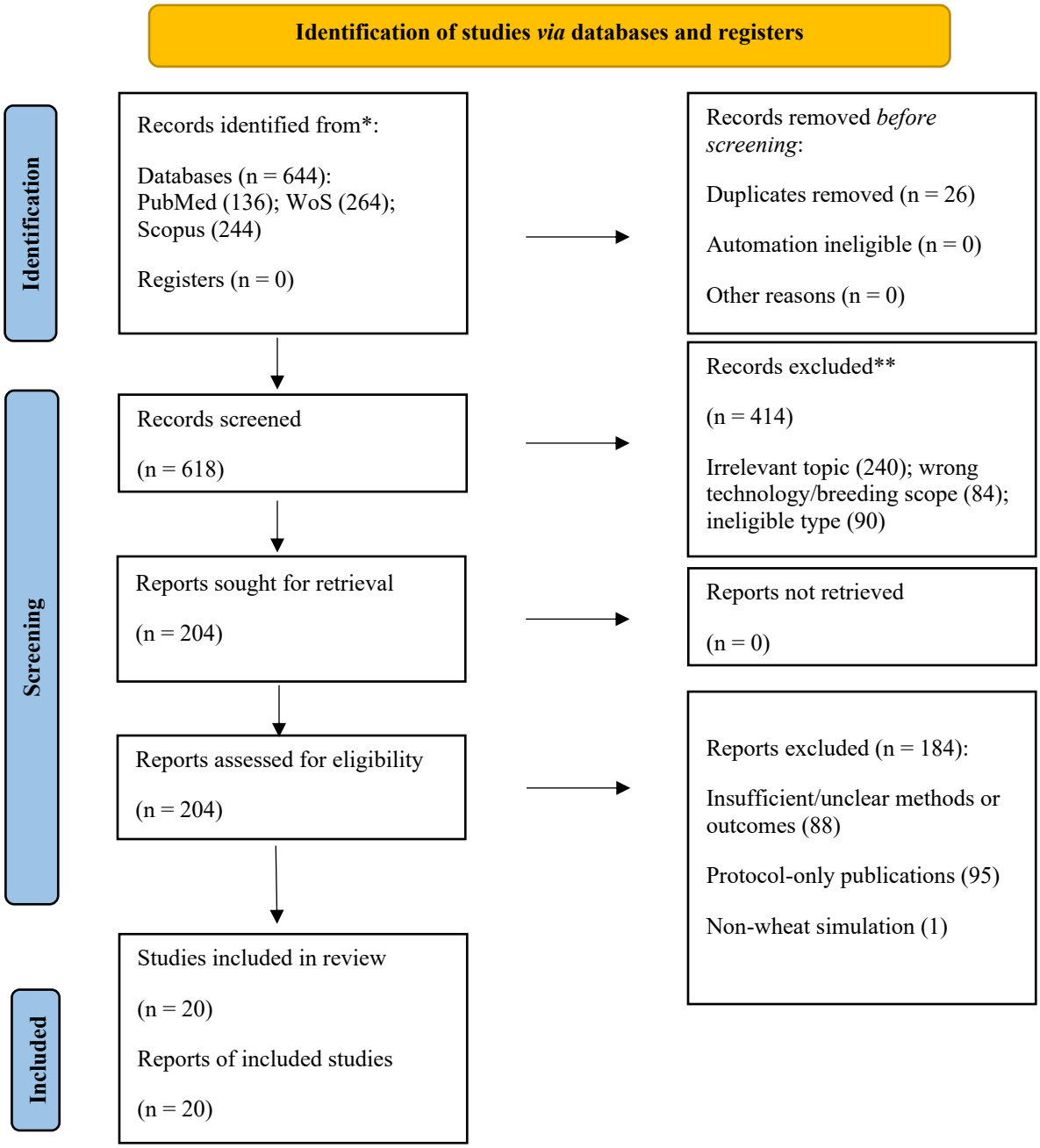


Fig. (1). PRISMA 2020 flow diagram.

Table 2. Reporting and methodological appraisal criteria.

Domain	Adequate Reporting (1)	Inadequate/Absent Reporting (0)	Rationale
Population and diversity	Population size, composition, and diversity are sufficiently described	Population or diversity is unclear	Supports interpretation and generalisability.
Genotyping or intervention specification	The marker platform/density or the SB intervention protocol was adequately specified.	Platform, density, or intervention protocol is insufficiently described	Supports technical reproducibility across the study designs.
Phenotyping and environment	Trait measurement and relevant environmental/stress conditions were adequately described.	Phenotyping or environmental context is insufficient	Climate-relevant traits are sensitive to the environment.
Statistical rigour	Models, corrections, and analytical procedures are appropriate and reported	Statistical methods are unclear or incomplete	It reduces false positives and overfitting.
Validation	Independent, external, multi-environment, or appropriate cross-validation was reported.	No adequate validation is reported	Supports robustness and transferability.

2.8. Data Synthesis and Analysis

Studies were categorised into evidence type (either empirical or simulation) and implementation category (GS; GWAS; SB; GS and environmental information; and GS and SB). A thematic synthesis analysed applications and limitations, and integration claims were evaluated using a structured quantitative comparison that summarised reported prediction accuracies, generation-interval effects, and genetic-gain projections. It was not possible to perform a formal meta-analysis due to heterogeneity of traits, populations, stress definitions, validation schemes, statistical scales, and outcomes reporting. A descriptive presentation of the reported values, without averaging, was therefore adopted; reported disagreement and uncertainty were likewise retained rather than averaged.

3. RESULTS

The 20 included studies evaluated GS, GWAS, and/or SB as individual tools or in partial combinations. Evidence was unevenly distributed across the three approaches: GWAS studies generally reported the marker–trait association, GS studies the prediction metrics, SB studies the generation acceleration, and few studies analysed integration. Each outcome reflects a component of a breeding programme and is not necessarily a direct measure of the same benefit.

Nineteen studies used association mapping, real-data multi-environment evaluation, genomic prediction, or field testing. One wheat-specific study used stochastic simulation to project GS–SB results. Therefore, the results are presented as either an empirical observation or a conditional simulation-based projection, which is then used throughout the Results and Discussion.

3.1. Quantitative Comparative Synthesis

Three outcome groups were compared: prediction accuracy, generation-interval effects, and genetic-gain projections. Reported values were extracted as presented, without recalculating effect sizes. Due to variation in traits, populations, comparators, population-validation designs, and reporting scales, the synthesis was limited to descriptive comparisons across studies. In many empirical GS studies conducted under stress, moderate prediction accuracy (~0.45–0.51) was obtained, and prediction accuracy differed depending on the trait under study, relationships between training and testing populations, the environments represented in the training sets, and the cross-validation design [9, 10]. For some datasets, environmental regressors led to either greater stability or lower prediction error, but the effect was not strong enough to provide a global estimate [11, 12]. Controlled-environment SB reduced generation time [13, 14]. Only one included wheat simulation combining GS and SB projected higher genetic gain per unit time; the projection depended on selection intensity, recombination level, prediction decay, population size, and similarity between controlled and field environments [15]. No study compared a complete GS–GWAS–SB pipeline with conventional wheat breeding repeatedly across field cycles (Table **3**). Thus, the evidence remains predominantly tool-specific or based on partial integration, with no definitive end-to-end pipeline advantage.

3.2. Theme 1: Genomic Selection in Wheat Breeding

GS, coupled with genome-wide markers, can be used for early selection, even before full phenotypic information is available. It is primarily useful for complex or low-heritability traits or for expensive-to-phenotype traits. However, it requires consideration of the training-population composition, the markers used, phenotyping quality, target-environment representation, model choice, and validation set design.

3.2.1. Wheat Breeding Strategies for Increased Climate Resilience

Climate-resilient wheat breeding is best viewed as a coordinated sequence of complementary decisions rather than a single technology. The evidence reviewed here supports broadening and characterising germplasm, phenotyping target traits under representative drought, heat, salinity, and disease conditions, using GWAS to prioritise potentially useful loci and

genomic selection to rank complex-trait candidates, advancing selected material rapidly with diversity safeguards, and confirming yield stability, quality, and stress response in multi-environment field trials [16]. Because the included studies reported different outcomes-marker discovery, prediction accuracy, generation acceleration, or field stress response-the most defensible strategy is stage-specific integration in which genomic and rapid-cycling tools inform, but do not replace, phenotypic selection and field validation [17-18].

3.2.2. Accelerating Breeding for Stress Tolerance

Secondary traits that can be repetitively assessed using high-throughput phenotyping (*e.g.,* canopy temperature, spectral response, biomass, and progression of stress) can complement GS. Under drought and heat conditions, Juliana *et al.* [9] reported moderate prediction accuracy, although performance differed across the populations and environments analysed. Further independent and forward-cycle validation, as well as external validation, is necessary.

3.2.3. Enhancing Yield Stability Under Climate Stress

GS can be useful for selecting yield stability by modelling performance under water and temperature regimes. However, a model developed in one environmental distribution may not perform reliably when applied to different germplasm, management conditions, or stress environments. Therefore, multi-environment and reaction-norm approaches play a role in utilising GS for climate adaptability.

3.3. Theme 2: Genome-Wide Association Studies (GWAS) for Identifying Resilience Traits

3.3.1. Identification of Stress Tolerance Markers

GWAS studies have detected SNPs or genomic regions associated with salinity, heat stress, drought, phenology, diseases, and yield [19]. While these findings provide markers and biological hypotheses, associations do not establish causality, functional relevance, portability across populations, or realised genetic gain. Before routine deployment, findings should be validated in independent populations, supported by functional evidence, and confirmed across multiple environments [20-22].

3.3.2. Salt Stress Tolerance Genetic Variation and Diversity

Alleles not found in elite germplasm can be found in landraces and in wild relatives as revealed by introgression and GWAS studies. Breeding value, linkage drag, adaptation penalties, and population-specific effects should all be considered separately because a favourable allele may exist which has breeding value, but also be associated with undesirable alleles ("linkage drag"), adaptation penalties, or population-specific effects. A field demonstration of the role of exotic alleles for heat tolerance was provided by Molero *et al.* [23]. This gives better support for deployment than discovery of markers alone, but needs to be tested further to confirm the stability of the alleles at different genetic backgrounds and target areas. Fig. (**2**) illustrates a high-level view of the steps from discovery to prediction, fast progression, testing at various locations, and deployment. Explicit decision gates consist of independent confirmation, uncertainty, population diversity, energy use, cost, and performance relevant to the farmer.

Javid *et al.* [20] reported candidate loci associated with salt-stress germination. Germination-stage associations can help prioritise alleles, but they should not be interpreted as evidence of adult-plant yield or stability unless confirmed under field salinity conditions.

3.3.3. Genetic Structure and Population Diversity

Rabieyan *et al.* [21] investigated population structure, marker associations, and genomic prediction in rain-fed and well-watered environments. The study illustrates how documented genetic diversity and environmental contrast can support prediction, while unmodelled population structure can confound association signals.

Table 3. Summary of findings.

Study (Reference)	Population/Data	Objective	Design and Methods	Tool/Intervention	Key Finding	Appraisal
Juliana *et al.* [9]	CIMMYT elite yield trial nurseries evaluated in drought-stressed (DS) and late-sown heat-stressed (HS) environments	Evaluated genomic selection and high-throughput phenotyping for predicting grain yield in DS and HS environments.	Genomic prediction with HTP; fivefold CV; reported mean prediction accuracies ~0.50 (DS) and ~0.51 (HS)	Genomic prediction integrating genomic + HTP data (prediction-focused, not a field "treatment")	Reported average genomic prediction accuracies around 0.50–0.51 in DS/HS environments	High
Yannam *et al.* [10]	Bread wheat was evaluated under well-watered (WW) and water-stressed (WS) conditions.	Evaluate/optimize GS models to enhance drought adaptation under contrasting water regimes.	Compare the performance of various GS models for agronomic traits under WW *vs* WS.	Genomic selection model comparison under WW/WS (no biological "treatment")	Reports the performance evaluation of GS models under contrasting regimes	Moderate

Liu *et al.* [11]	Wheat breeding population (genomic + transcriptomic datasets integrated with environmental covariates)	Evaluate whether incorporating gene expression and environmental data improves genomic prediction accuracy in wheat.	Genomic prediction models integrating SNP markers + gene expression data + environmental covariates	Genomic prediction with multi-omic and environmental integration	Integration of gene expression and environmental data improved prediction accuracy compared to genomic-only models; multi-source data enhanced predictive performance across environments	Low
Montesinos-López *et al.* [12]	Soft white winter wheat datasets: five datasets	Evaluate the impact of integrating environmental information alongside genomic and phenomic data for prediction.	Multi-environment prediction; integration of environmental information	Genomic + phenomic + environmental covariates in prediction models	Reported improvement in prediction accuracy when environmental information is integrated (NRMSE mentioned)	Moderate
Alahmad *et al.* [13]	Large segregating F2 durum wheat population (n = 1000) from Outrob4/Caparoi; selection evaluated in F3; traits include CR, LR, roots, height	Deploy speed breeding, multi-trait phenotyping, and a selection index for durum wheat.	Controlled-environment speed breeding; weighted selection index; compared selected *vs* unselected families	Speed breeding + selection index multi-trait selection	Selection improved means for CR tolerance, LR resistance, root traits; plant height did not improve significantly	Moderate
Cha *et al.* [14]	Wheat breeding materials under modified speed breeding (SV+mSB)	Establish energy-efficient generation acceleration system	Glasshouse 22-h photoperiod; SV+mSB system; 4-generation model	Speed vernalisation + modified speed breeding	Four generations/year achieved; breeding time reduced by >50%; 80% energy reduction *vs* conventional SB	Low
Nannuru *et al.* [15]	Two simulated datasets: one reflecting real-life genotypic data (MASBASIS) and one simulated breeding programme	Comparison of breeding schemes for improving Fusarium head blight (FHB) resistance using GS and speed breeding *vs.* phenotypic selection.	Stochastic simulations comparing schemes incorporating GS and speed breeding	Speed breeding + genomic selection (simulation of breeding cycles)	Simulations show advantages of GS-based programmes and further acceleration when combined with speed breeding (details depend on assumptions)	High
Maulana *et al.* [16]	Winter wheat; seedling-stage heat stress context	Map QTL/SNPs associated with seedling heat tolerance in winter wheat	GWAS using SNP markers for seedling heat tolerance	GWAS (marker discovery for MAS; no intervention)	SNP markers/QTL for seedling heat tolerance identified; stated usefulness for marker-assisted selection	High
Nouraei *et al.* [17]	Wheat (T. aestivum); traits include plant height, root length, root & shoot dry weight; genotyped using 90K SNP array	Identify genetic determinants (SNP markers/candidate genes) for drought tolerance–related traits.	GWAS using a 90K SNP array on drought-tolerance traits	GWAS (marker/candidate gene identification)	GWAS revealed genetic determinants for drought-related traits	Moderate
Vitale *et al.* [18]	CIMMYT historical grain-yield dataset (10 years; six selection environments)	Enhance genomic prediction accuracy for grain yield using historical data	Genomic prediction using an extended historical dataset; diversity–predictive-power trade-off assessed	Genomic selection modelling using an extended historical dataset	An extended historical dataset improved prediction in the evaluated context	Low

Tyrka *et al.* [19]	168 elite winter wheat lines from an ongoing breeding programme; DArTseq produced 19,350 SNP + PAV markers	Identify the main determinants of grain yield in elite winter wheat	GWAS using DArTseq SNP/PAV markers	GWAS	GWAS was performed to identify yield determinants	Moderate
Javid *et al.* [20]	292 Iranian bread wheat accessions (202 landraces + 90 cultivars) in the salt-stress germination context	Characterise the molecular basis of germination performance under salt stress using GWAS	GWAS on germination performance under salt stress; gene ontology/annotation used for candidate genes	GWAS (marker–trait + candidate gene discovery)	17 candidate genes identified *via* annotation/GO; findings improve understanding of germination under salinity	Low
Rabieyan *et al.* [21]	Iranian wheat: 208 landraces + 90 cultivars; genotyped *via* GBS	Determine population structure; detect MTAs by GWAS; perform genomic prediction of agronomic traits for drought-tolerance breeding	GWAS conducted using original phenotypes (pGWAS) and estimated breeding values (eGWAS); genomic prediction (GS) included	GWAS + GS (prediction of breeding values)	GWAS + GP used for agronomic traits/breeding values under rain-fed & well-watered farming	Moderate
Pang *et al.* [22]	768 wheat cultivars; 327,609 SNPs (GBS); evaluated across 7 environments; 395 QTLs for 12 traits	Large-scale high-resolution GWAS to dissect important agronomic traits in wheat	High-resolution GWAS using a dense SNP set across multiple environments	GWAS	Detected 395 QTLs for 12 traits across 7 environments (explicit)	High
Molero *et al.* [23]	149 spring wheat lines were tested in the field under yield potential and heat-stressed conditions	Assess how exotic-derived alleles/introgressions contribute to heat tolerance under field conditions	Field evaluation + MTAs/introgression overlap analysis	Use of exotic-derived material / introgressed alleles (breeding strategy; not an experimental "treatment")	Exotic-derived lines showed a significantly lower stress susceptibility index for some traits; introgressed segments overlapping MTAs were examined	Low
Ghazy *et al.* [24]	Twenty advanced wheat genotypes were evaluated under field heat stress for two years.	Assess phenotypic performance and genetic diversity; select heat-tolerant genotypes for desert environments.	Two-year field evaluation under heat stress; reports yield reduction and trait relationships (path analysis mentioned)	Phenotypic selection under field heat stress, with diversity and marker analyses	Heat stress reduced yield with ~53.8% average decline; heading date showed negative impact on grain yield under stress (path analysis)	Moderate
Nawade *et al.* [25]	Bread wheat; multi-locus GWAS + SNP effect analysis	Reveal genetic basis of heading, maturity, grain-filling duration	Integrative multi-locus GWAS + SNP effect analysis	GWAS (multi-locus)	Identifies loci underlying heading/maturity/grain-filling duration	High
El Gataa *et al.* [26]	198 elite bread wheat genotypes (Morocco; rainfed & irrigated; 15K SNPs)	Identify MTAs & perform genomic prediction for drought indices	GWAS + gBLUP genomic prediction; MLM model	GWAS and genomic prediction	39 significant MTAs; grain yield 0.34–2.57 t/ha (rainfed); LD decay 3.34–4.52 Mbp; genomic prediction performed	Low
Tadesse *et al.* [27]	252 elite ICARDA wheat genotypes; 10,173 SNPs	Identify MTAs & evaluate single/multi-trait genomic prediction	GWAS + GBLUP genomic prediction	GWAS and genomic selection	Significant MTAs on chr 1B & 2B for Zn & Fe; multi-trait GP improved predictive ability by 6.62% (Se) and 4.44% (Fe)	Low
Devate *et al.* [28]	282 advanced wheat breeding lines; 10,546 SNPs	Identify markers for drought & heat tolerance traits	Multi-location GWAS; BLINK model	GWAS under IR, RI, LS	57 significant markers; 23 stable; 9 pleiotropic; LD block size 7.15 Mb	Moderate

3.4. Theme 3: Speed Breeding for Accelerated Crop Development

3.4.1. Accelerating Breeding Cycles for Stress Tolerance

Under optimum plant density, nutrition and temperature, SB can help decrease the calendar time needed to produce crops. Rapid cycling can also help to make selection decisions earlier when used with GS [24]. However, generation turnover is only an input of the operation and not the actual climate gain or climate resilience. Understanding that large selection intensity and small effective population size, in conjunction with repeated rapid cycling and highly related material, can result in a reduction in allelic diversity and an increase in inbreeding. The following measures should be tracked in field programmes and monitored across programmes for programmes: coancestry, effective population size, rare favourable alleles, and trait diversity. Nannuru *et al.* [15] used a stochastic simulation study to predict benefits of using GS in combination with SB for FHB resistance, but no tests have been done in the field. This therefore does not involve an unguarded selection, but a protected selection, as illustrated in Fig. (**3**).

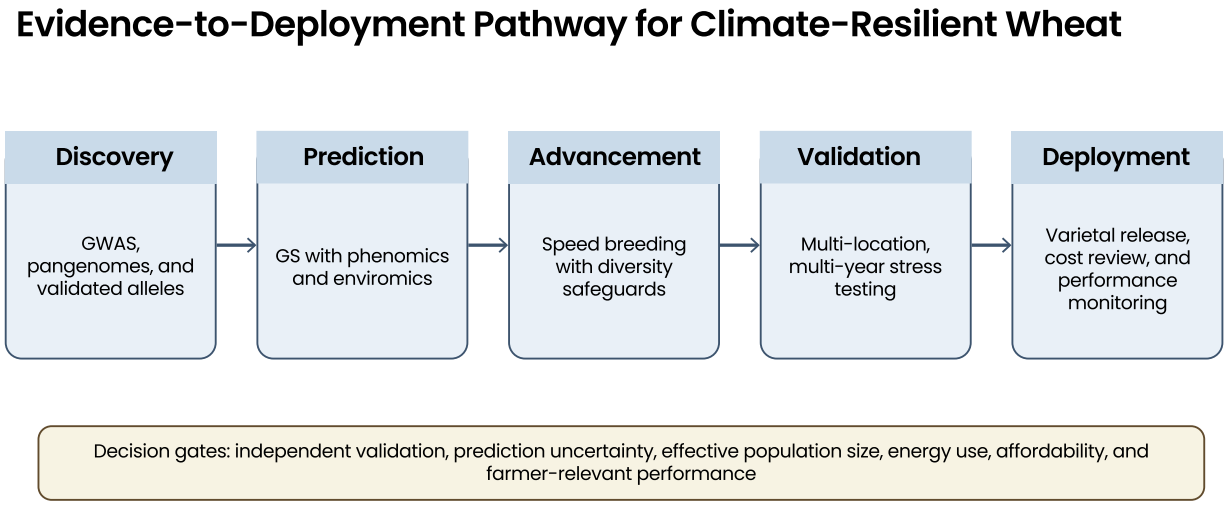


Fig. (2). Original conceptual synthesis developed for this review using basic geometric shapes and text. It integrates the evidence-to-deployment stages discussed in references [5, 9-15, 18, 23, 41] and [52–59] and is not adapted from a single published image. This pathway has not been validated as an end-to-end pipeline.

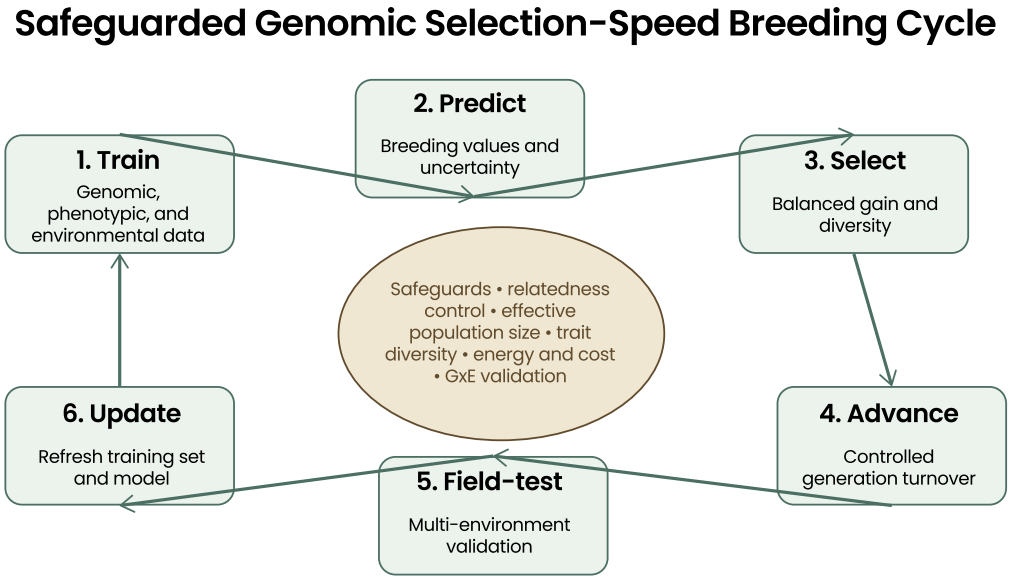


Fig. (3). Original conceptual synthesis developed for this review using basic geometric shapes and text. The cycle emphasises model updating, field validation, population diversity, and resource constraints.

3.4.2. Integration of SB with GS for Disease Resistance

SB can facilitate accelerated breeding for disease resistance by producing more generations per year and advancing segregating material before field testing. However, disease presence and expression may be influenced by adult-plant development, pathogen population, humidity, temperature, and inoculation method [25]. Controlled-environment screening should therefore be followed by field validation, as demonstrated in wheat Fusarium head blight screening [26].

3.5. Theme 4: Integration of Genomic Selection, GWAS, and Speed Breeding

3.5.1. Synergies Between Genomic Tools

Integrating genomic, phenomic, environmental, transcriptomic, and other omics data improves predictions; however, more data does not always lead to better decisions [27]. High dimensionality can increase overfitting, opacity, and computational costs when individual modalities are not biologically relevant, sufficiently sampled, or harmonised; targeted integration can be more effective when the included modalities are biologically relevant, adequately sampled, and harmonised [28]. Studies should therefore use parsimonious baseline models for comparison, quantify each modality's contribution in ablation analyses, and perform external/forward-cycle validation [29-31].

3.5.2. Overcoming Environmental Variability with Genomic Data

Environmental variables include stress timing, temperature, precipitation, VPD, soil variables, and management. Computational approaches for G×E include reaction-norm models, marker × environment kernels, multi-trait/multi-environment Bayesian models, factor-analytic mixed models, enviromic similarity matrices, crop-growth-model covariates, random forests, gradient boosting, and deep neural networks [32-33]. Models can also cluster and weight environments in the target population and stress-test models under future climate scenarios [34]. Their value depends on temporal resolution, biological relevance to the crop's agronomic stage, representation of the target environment, and validation in new, real-world environments and future cycles. Leave-one-environment-out and forward prediction are thus more informative than random cross-validation alone [35].

3.5.3. Stepwise Integration Model for Genomic Selection, GWAS, and Speed Breeding

Table **4** presents a sequence of planned implementation steps derived from the reviewed evidence, not a validated pipeline. It links discovery, prediction, rapid progress, and field confirmation, but acknowledges that each stage can introduce error, cost, bias, and loss of diversity [36]. The framework should be prospectively evaluated against a conventional breeding comparator.

No included study implemented this complete model across repeated breeding cycles with a conventional breeding comparator (Table **5**). Therefore, the framework is a testable research agenda, not evidence of operational effectiveness.

In general, the prediction performance of GS was moderate but was context-dependent; the discovery evidence from GWAS was evident; the cycle time under controlled conditions was decreased by the use of SB; and, in some cases, the combination of GS with environmental information gave better robustness [37]. There was a Wheat simulation that indicated that gains were possible using GS–SB integration, but no study was found that actually simulated a full pipeline. The prediction accuracy, realised response to selection, multi-environment yield stability, generation interval, genetic diversity, energy use, and cost per line selected should be reported jointly by prospective trials. Simulations must be used to plan, and should be clearly distinguished from empirical testing [38].

Quantitative reporting was uneven: GS studies emphasised accuracy, GWAS studies emphasised significance and marker discovery, and SB studies emphasised calendar acceleration. This outcome heterogeneity is the principal reason why a pooled meta-analysis was not performed and why Table **6** uses a structured comparative format.

Table 4. Conceptual stepwise integration model (not yet experimentally validated end-to-end).

Step	Action	Objective	Tools / Methods
1	Define the target and characterise germplasm.	Specify climate-relevant traits and identify candidate alleles or regions in wheat.	Product profile; GWAS; pangenomics
2	Collect connected phenotype and environment data.	Measure target traits across representative stress, site, season, and management conditions.	Multi-environment phenotyping; envirotyping
3	Develop and validate prediction models.	Rank candidates while quantifying uncertainty and transferring to new environments and cycles.	GS; G×E models; transparent ML benchmarks
4	Advance selected material rapidly with safeguards.	Shorten the generation turnover while maintaining family representation and genetic diversity.	SB; coancestry and effective-population-size monitoring
5	Benchmark in multi-environment field trials	Compare the realised gain, stability, quality, cost, energy, and diversity to those of conventional breeding.	Prospective field trials; matched conventional comparator

Table 5. Comparative integration outcomes across genomic-assisted breeding studies.

Study	Tools and Stress Focus	Prediction Metrics Reported	Cycle and Genetic-Gain Outcome	Study Type
Juliana *et al.* [9]	GS + HTP Stress: Drought, heat	Mean prediction accuracy ≈0.50 (DS) and ≈0.51 (HS)	Not reported Genetic gain: Not reported	Empirical
Maulana *et al.* [16]	GWAS Stress: Heat	SNP/QTL discovery; no prediction benchmark	Not applicable Genetic gain: Not reported	Empirical
Nouraei *et al.* [17]	GWAS Stress: Drought	SNP/candidate-gene discovery; no prediction benchmark	Not applicable Genetic gain: Not reported	Empirical
Vitale *et al.* [18]	GS + historical data Stress: Yield stability	Historical data improved genomic prediction; context-specific values reported.	Not reported Genetic gain: Not reported	Empirical
Tyrka *et al.* [9]	GWAS Stress: Yield traits	Marker-trait associations	Not applicable Genetic gain: Not reported	Empirical
Yannam *et al.* [10]	GS Stress: Drought	GS models compared under contrasting water regimes	Not explicitly quantified Genetic gain: Not reported	Empirical
Nannuru *et al.* [15]	GS + SB Stress: Fusarium head blight	Stochastic comparison of breeding schemes	Accelerated cycles in simulation Genetic gain: Higher projected gain per unit time; assumption-dependent	Simulation
Alahmad *et al.* [13]	SB + selection index Stress: Multiple quantitative traits	Not a prediction study	Reduced generation interval under controlled conditions Genetic gain: Not reported	Empirical
Javid *et al.* [20]	GWAS Stress: Salinity	17 candidate genes reported	Not applicable Genetic gain: Not reported	Empirical
Rabieyan *et al.* [21]	GWAS + GS Stress: Drought	Genomic prediction under rain-fed and well-watered conditions	Not reported Genetic gain: Not reported	Empirical
Pang *et al.* [22]	GWAS Stress: Multiple agronomic traits	395 QTLs across seven environments	Not applicable Genetic gain: Not reported	Empirical
Molero *et al.* [23]	Association mapping + introgression Stress: Heat	Field stress-susceptibility and marker-trait evidence	Not applicable Genetic gain: Not reported	Empirical
Montesinos-López *et al.* [12]	GS + phenomics + environment Stress: Multi-environment	Environmental information improved prediction in evaluated datasets	Not reported Genetic gain: Not reported	Empirical
Ghazy *et al.* [24]	Field evaluation Stress: Heat	Yield declined by ≈53.8% under heat stress	Not applicable Genetic gain: Not reported	Empirical
Nawade *et al.* [25]	Multi-locus GWAS Stress: Phenology	Loci for heading, maturity, and grain-filling duration	Not applicable Genetic gain: Not reported	Empirical
Cha *et al.* [14]	SB Stress: Generation acceleration	Not a prediction study	Four generations/year; >50% time reduction reported Genetic gain: Not reported	Empirical
El Gataa *et al.* [26]	GWAS + GS Stress: Drought	39 MTAs; genomic prediction reported	Not reported Genetic gain: Not reported	Empirical
Tadesse *et al.* [27]	GWAS + multi-trait GS Stress: Drought; micronutrients	Multi-trait prediction improved predictive ability for selected traits	Not reported Genetic gain: Not reported	Empirical
Devate *et al.* [28]	GWAS Stress: Drought, heat	57 significant markers; 23 stable and 9 pleiotropic	Not applicable Genetic gain: Not reported	Empirical
Liu *et al.* [11]	GS + transcriptomics + environment Stress: Multi-environment	Multi-source models improved prediction over genomic-only models	Not reported Genetic gain: Not reported	Empirical

Table 6. Comparative advantages, disadvantages, quantitative evidence, cycle effects, and practical limitations of genomic-assisted approaches.

Approach	Main Advantages	Main Disadvantages	Quantitative Evidence and Cycle Effect	Practical Limitations
GS	Early ranking of candidates for complex traits	Accuracy may decline in unrelated populations or unrepresented environments.	Stress studies reported accuracy of ~0.45-0.51. Earlier selection may shorten decisions, but cycle reduction has not been consistently quantified.	Representative training sets, reliable phenotypes, computing, and regular model updating.
GWAS	Marker-trait associations and candidate regions were identified.	These associations may be population-specific and miss rare or small-effect variants.	Mainly locus discovery, direct prediction, realised gain, and generation reduction were rarely benchmarked.	Population structure control, independent validation, and a clear marker-deployment pathway are needed.
SB	It shortens generation turnover under controlled conditions.	Rapid cycling alone does not ensure gains and may narrow diversity.	Generation acceleration was demonstrated; however, trait-level realised gain was reported less consistently.	Energy, facilities, genotype-specific protocols, disease screening, and field equivalence.
GS + environmental data	Models G×E and can improve environment-specific rankings.	Environmental variables may be noisy, collinear, or weakly transferable to future climate conditions.	Some studies report lower prediction error and greater cross-environment stability, with prediction quality the main benefit rather than cycle time.	Harmonised envirotyping, spatial data, biological alignment, and external validation.
GS + SB	It combines rapid prediction and rapid generation turnover.	The projected gains depend on assumptions and may erode diversity.	Mainly simulation or partial-integration evidence; potentially higher per-year gain but no complete multi-cycle field comparator.	Population-size safeguards, recombination management, field testing, and cost and energy accounting.
Full GS + GWAS + SB pipeline	This can connect discovery, prediction, selection, and rapid advancement.	Complexity and errors can propagate across stages, and superiority remains unproven.	No end-to-end empirical benchmark against conventional breeding was included, and the cycle advantage was not operationally established.	Data integration, expertise, capital, governance, validation, and equitable access require significant investment.

4. DISCUSSION

4.4. Strengths and Limits of the Empirical Evidence

There is empirical evidence for useful but limited roles for them, according to the tool they are used with. Wheat GS results have shown that candidate rankings (in drought or heat or across water regimes) may differ depending on the validation set, the quality of the phenomes, the environmental representativeness, and the training population [5, 9, 12]. In the absence of causal function and deployment value, wheat GWAS results yield marker–trait associations and candidate regions [16, 17, 22, 25]. Controlled-environment SB may also decrease generation intervals, but it does not always increase realised genetic gain [36]. The prediction accuracy of GS (~0.45–0.51) reported here might be enough for some operations, but if used as a breeding tool, it relies on the heritability of the traits, selection pressure, cost, relatedness to the population of interest, and environmental stability [39-40].

4.5. Simulation Evidence and Inference Boundaries

Simulation can make comparisons between breeding designs which would take years to test empirically. However, the expected gain is dependent on several assumptions relating to genetic architecture, recombination, effective population size, prediction decay, cost, and selection intensity. The wheat evidence set used in this review had potential for use in together using GS and SB as a way to improve resistance against Fusarium head blight; however, it provided no long-term field validation [17]. Other aspects of the breeding design literature also emphasise the need to avoid loss of accuracy, selection intensity, genetic variation, and the cost of operations, to achieve more rapid cycles leading to larger annual gains [41-43]. It would be beneficial in future studies for pre-registration of assumptions, comparing models with field trials, and model updating based on the results of field trials to be performed.

4.6. Genotype × Environment Interaction and Computational Approaches

GxE is not just a statistical "noise," but a change in performance and ranking of genotypes and environments, which depends on the developmental stage, soil, management, and intensity and timing of stresses. There are several computer-based methods that are relevant, such as reaction-norm models, marker × environment kernels, factor-analytic mixed models, multi-trait/multi-environment Bayesian models, enviromic similarity matrices, crop-growth-model covariates, and machine-learning ensembles [44-46]. Deep learning may represent interactions that are not linear and not just one type of

data, but may be successful depending on the trait and data. Leave-one-environment-out, leave-one-year-out, and forward-cycle validation should be used to evaluate the models, and uncertainty should be reported for the calibrated point predictions. There also needs to be biological synchrony with environmental variables. For instance, a short heat period during anthesis or drought during grain filling could be covered by the seasonal means. Data in these areas in particular, such as meteorology data, soil data, management data and crop state data, should therefore be specifically harmonised if there are missing data and data imprecision [47-48]. Future climate scenarios are not observations but extrapolations and should be viewed as sensitivity analysis and/or stress testing.

4.7. Speed Breeding Trade-offs and Diversity Safeguards

The major advantage of SB is reduced calendar time. However, controlled-environment infrastructure, electricity and cooling requirements, genotype-specific protocol optimisation, space constraints, altered plant morphology, and microclimate-dependent disease expression create important trade-offs [49-51]. Rapid cycling can also cause genetic bottlenecking through repeated use of a small group of parents or reuse of genomic rankings without updated field information. Diversity safeguards should include maintaining a minimum number of families, applying optimum-contribution selection, limiting coancestry, monitoring effective population size, and establishing mechanisms for transferring tested foreign material when appropriate [52-53]. Recent contextual literature similarly concludes that speed breeding is most effective when combined with stress-aware protocols, genomics-assisted selection, and multi-location field testing, rather than used as an isolated substitute for conventional evaluation [54-56].

4.8. Artificial Intelligence, Digital Phenotyping, and Prediction Algorithms

Machine learning (ML) and deep learning may leverage markers, imagery, spectral measurements, weather, management, and omics data. They may also capture nonlinear interactions that simpler linear models cannot [57]. Candidate algorithms include random forests; gradient boosting models for structured covariate time series; models for images and spectra, including CNNs; models for longitudinal weather or phenology time series (recurrent or transformer); and models for genomic, pathway, or environmental relationships (graph models) [58-59]. These should be evaluated against approaches of well-known transparency, such as GBLUP, Bayesian genomic regression, and factor-analytic approaches. Evaluation of models should be done with nested cross-validation for hyperparameter tuning and leave-environment-out and forward-cycle tests to determine the transferability of operation. Important aspects are calibration, uncertainty quantification, ablation analysis, interpretability, data leakage checks, and reporting of computational and energy costs. Digital phenotyping may decrease some of the measurement costs yet increase a few measurement biases, such as from sensor drift and inconsistencies in platforms, missing data, and unequal access [60]. AI should be used within a model that is under the supervision of a human or a breeder and for which the changes in the model are documented, and there are clear acceptance/rejection criteria for breeding lines.

4.9. Climate Resilience as a Dynamic Multi-trait Target

Climate resilience comprises yield stability, recovery, phenology, and eventually root and canopy traits, disease resistance, quality, and adaptation to compound or sequential stresses. Trade-offs may occur between improvements in different components; for example, early maturity may reduce yield potential or grain quality under favourable conditions but help avoid stress. Selection indices and multi-trait models should therefore account for the target population of environments, farmer/market preferences, and/or the probability of compound events [61]. The identification of a marker or demonstration of stress tolerance under controlled conditions should not be used alone as evidence of the climate resilience of a cultivar.

4.10. Economic Feasibility, Equity, and Resource-Limited Programmes

The implementation costs are related to skilled personnel, electricity and cooling, genotyped and phenotyped plants, locations, equipment and data engineering, and logistic seed. The best design in terms of economic impact is not always the most technologically sophisticated, but one that maximises the realised benefit over time and investment, and maintains genetic diversity and relevance of the product [62-63]. Other challenges that occur in developing country programmes are unreliable electricity and internet connection, few cold chains, less laboratory capacity, high import prices for consumables, small and scattered networks of tests, weak quantitative genetics and data-engineering skills, limited access to cloud computing and proprietary platforms. A phased approach may start with smaller phenotyping sets, low-cost phenotyping panels, and types of genotyping platforms that are broadly available. Reducing recurrent costs might then be achieved *via* the establishment of regional phenotyping networks, open-source pipelines, interoperable data standards, local training and coordinated procurement and maintenance. Programmes should include capital and operating costs and cost per cycle, cost per candidate advanced, energy wastage, man-hours, opportunity cost, scale sensitivity and uncertainty in economic evaluation. Governance arrangements should ensure that germplasm and data are openly available at the local level and do not place too many restrictions on climate-adapted germplasm, and should be freely available to vulnerable farming systems [64-65].

4.11. Genome Editing, Pangenomics, Multi-Omics, and Genomic Foundation Models

The Wheat Genome Initiative is transitioning towards a multi-linear reference genome. Structural and presence–absence variation is captured by multiple assemblies and/or pangenomes, which may be missed by SNP-only analyses [62, 63, 64, 66]. Multi-omics integration can link sequence variation to gene expression, proteins, metabolites, epigenetic states, and physiological responses, and genome editing can test candidate-gene function and introduce defined alleles [39, 65]. Transformation capacity, off-target assessment, trait complexity, regulation, intellectual property, and access remain constraints for these tools; however, they could shorten the pathway from discovery to validation. More recently, large sequence, graph, or multimodal architectures have been

pretrained on large quantities of genomic and functional information (called foundation models) and customised to specific tasks. Wheat applications include prediction and transfer learning for traits with limited labelled data, prediction of wheat variants, annotation of regulatory regions, imputation, and prioritisation of causal alleles. However, polyploid homoeology, biased reference panels, lack of phenotype labels, limited population representativeness, high computational demands, and lack of interpretability may generate high-confidence, non-transferable predictions. Evaluation should include wheat-specific benchmarks, held-out populations and chromosomes, forward-cycle testing, calibrated uncertainty, comparison to simpler models, and wheat germplasm and farmer-linked data-governance safeguards. Foundation models should currently be used as research tools to prioritise hypotheses and should not be treated as validated substitutes for breeding trials.

4.12. Transferable Lessons from Maize, Rice, and Barley

Data from other cereals provided context but were not added to the wheat data set. The allogamous-crop SpeedGS simulation by Jighly *et al.* [67] was not included in the analytical evidence set and is discussed here only as modelling evidence from a different context. Maize studies show the usefulness of integrating genetic data with environmental information from multi-environment (ME) trials, but performance can also be unstable due to environmental effects. In barley, clear evidence shows that explicit G×E genomic prediction and the pangenome can uncover genomic variation that a single reference genome can mask [50, 68]. Interconnected programmes for variety testing, rapid variety replacement, and development of product profiles in rice and maize also highlight the importance of these priorities [60-61]. Wheat transfer must consider polyploidy, self-pollination, disease ecology, grain-quality goals, transformation effectiveness, and programme size. These comparisons support methodological transfer only; they are not directly comparable evidence of wheat performance.

4.13. Evidence Gaps and Benchmarking Priorities

The primary knowledge issue is whether an integrated system can provide continuous, low-cost realised gains compared with a powerful conventional comparator; it is not about whether the parts can work. Such a credible benchmark would include multiple cycles of iteration, similar population sizes and budgets, evaluation in target environments, documentation of failures as well as successes, and explicit management of genetic diversity. Current pipeline-integrated and component-level evidence therefore does not support categorical claims about pipeline superiority.

FUTURE DIRECTIONS

Future programmes will need to be staged and forward-looking. First, specify the target population of environments and create a multi-trait product profile that lists farmer/market and climate-risk priorities. Second, standardise phenotyping and envirotyping across linked field sites. Third, compare transparent GS baselines with G×E, ML, deep-learning, and multimodel approaches *via* leave-environment-out and forward-cycle validation, uncertainty calibration, and breeder review. Fourth, prioritise alleles using GWAS, pangenomes, multi-omics, genome editing, and outputs from foundation models; however, use alleles only after independent functional validation and field testing. Fifth, introduce SB only with diversity thresholds, energy accounting, disease-screening equivalence, and contingency plans for facility failure. Operational systems should specify data standards, model-version control, retraining triggers, decision-making thresholds, staff responsibilities, cybersecurity, and audit trails. Finally, benchmark the full life cycle of this workflow against conventional breeding across multiple breeding cycles, incorporating multiple co-primary outcomes: realised response, stability, quality, diversity, time, cost, and energy. These tests would be more reproducible and applicable to programmes with limited resources if they use common protocols, open metadata, regional infrastructure, and tiered steps toward adoption.

STRENGTHS OF THE REVIEW

This review is wheat-specific, distinguishes empirical results from simulation projections, and compares the results of these methods: GS, GWAS, SB, environmental integration, and GS plus SB. It also flags the lack of end-to-end benchmarks, elaborates on the reasons for the unsuitability of meta-analysis, and links methodological evidence to computational, diversity, economic, equity, and implementation constraints.

LIMITATIONS

Limitations of the review include the possibility of publication bias, the restriction to English-language studies, restriction to studies analysed in the period between 2018 and 2025, and restriction to studies of wheat where a technique or tool used to address climate change was tested, and a measurable impact on the outcomes was reported. For no outcome was it possible to perform a formal meta-analysis because of heterogeneity. A five-domain tool developed by the author and not yet validated was used for the methodological appraisal. One simulation study performed on wheat was included along with 19 empirical/real data studies. To account for more recent developments, contextual sources between 2024 and 2026 were added to the source list to provide a more recent update, but not to alter the pre-specified 20-study analytical data set. The recommendations on cost, equity, AI governance, and operational aspects are based on evidence, given that limited economic evidence was available.

CONCLUSION

These methods of Speed Breeding (SB), Genomic Selection (GS) and Genome-Wide Association Studies (GWAS) are complementary, with each having its own strengths to tackle the challenges in wheat improvement. Moderate context-specific accuracy of empirical GS studies, potentially useful loci identified by GWAS studies, and faster cycling time in controlled-environment SB. In some of the datasets, the addition of environmental covariates and/or partial integration led to better prediction, and in some cases, the gain per unit time (time) was greater for the GS plus SB projections. This does not

suggest that the GS-GWAS-SB pipeline is more efficient than traditional breeding; rather, it demonstrates that the steps to establish this pipeline are feasible. When appropriate field data and independent validation support it, diversity safeguards are included, cost and energy accounting are implemented, AI governance is transparent, and the models are continually updated, staged integration may be warranted. For claims of faster adaptation or better realised gain, prospective, multi-cycle trials of the technology are required to be used as a basis for comparison to matched conventional technology in the target environments.

LIST OF ABBREVIATIONS

GS	=	Genomic Selection
GWAS	=	Genome-Wide Association Studies
ML	=	Machine Learning
SB	=	Speed Breeding

AUTHOR'S CONTRIBUTION

A.M. has contributed to the study conceptualization, methodology, data analysis, interpretation of results, and manuscript writing.

CONSENT FOR PUBLICATION

Not applicable.

AVAILABILITY OF DATA AND MATERIALS

The data will be made available on reasonable request by contacting the corresponding author [A.M.].

FUNDING

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CONFLICT OF INTEREST

The author declares that there is no conflict of interest regarding the publication of this article.

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DECLARATION OF AI

During the preparation of this manuscript, the author used ChatGPT for language editing and refinement purposes. Following the use of this tool, the author carefully reviewed and revised the content where necessary and accept full responsibility for the final published version of the article.

APPENDICES

Appendix A: Database search strategy

Database	Database-Specific Boolean Search String	Results Retrieved	Publication Window / Exact Search Date
PubMed	(("genomic selection"[Title/Abstract] OR "genomic prediction"[Title/Abstract] OR "genome-wide association study"[Title/Abstract] OR GWAS[Title/Abstract] OR "speed breeding"[Title/Abstract] OR "rapid generation advance"[Title/Abstract]) AND (wheat[Title/Abstract] OR "Triticum aestivum"[Title/Abstract] OR "Triticum turgidum"[Title/Abstract] OR "durum wheat"[Title/Abstract]) AND ("climate resilience"[Title/Abstract] OR "climate change adaptation"[Title/Abstract] OR drought[Title/Abstract] OR heat[Title/Abstract] OR salinity[Title/Abstract] OR flood*[Title/Abstract] OR disease[Title/Abstract] OR "yield stability"[Title/Abstract])) AND ("2018/01/01"[Date - Publication] : "2025/12/31"[Date - Publication])	136	Publication window: 2018–2025. Search executed
Scopus	TITLE-ABS-KEY (("genomic selection" OR "genomic prediction" OR "genome-wide association stud*" OR GWAS OR "speed breeding" OR "rapid generation advance") AND (wheat OR "Triticum aestivum" OR "Triticum turgidum" OR "durum wheat") AND ("climate resilien*" OR "climate change adapt*" OR drought OR heat OR salinity OR flood* OR disease OR "yield stability")) AND PUBYEAR > 2017 AND PUBYEAR < 2026 AND DOCTYPE (ar)	244	Publication window: 2018–2025. Search executed
Web of Science	TS=(("genomic selection" OR "genomic prediction" OR "genome-wide association stud*" OR GWAS OR "speed breeding" OR "rapid generation advance") AND (wheat OR "Triticum aestivum" OR "Triticum turgidum" OR "durum wheat") AND ("climate resilien*" OR "climate change adapt*" OR drought OR heat OR salinity OR flood* OR disease OR "yield stability")) AND PY=(2018-2025) AND DT=(Article)	264	Publication window: 2018–2025. Search executed

Search update note: A targeted contextual update was conducted on 20 June for literature published during 2024–2026 on AI-enabled prediction, pangenomics, genome editing, multi-omics, genomic foundation models, and multi-environment modelling. These sources updated the Discussion and reference base but were not added to the pre-specified 20-study analytical dataset.

Appendix B: Screening stages

PRISMA Stage	Total (n)
Records identified from databases	644
Duplicate records removed before screening	26
Records screened (title and abstract)	618
Records excluded at title-and-abstract screening	414
— Irrelevant topic	240
— Wrong technology or breeding scope	84
— Non-original or ineligible publication type	90
Full-text reports assessed for eligibility	204
Full-text reports excluded	184
— Insufficient or unclear methods/outcomes	88
— Protocol-only publications	95
— Non-wheat allogamous-crop simulation	1
Wheat studies included in qualitative synthesis	20

Appendix C: Reporting and Methodological Appraisal

Study	Pop. /div.	Genotype/SB	Pheno./env.	Stats.	Valid.	Score/Category
Juliana *et al.* [9]	1	0	1	1	1	4/5 (High)
Yannam *et al.* [10]	1	0	1	0	1	3/5 (Moderate)
Liu *et al.* [11]	0	1	0	1	1	3/5 (Moderate)
Montesinos-López *et al.* [12]	0	1	0	1	1	3/5 (Moderate)
Alahmad *et al.* [13]	1	0	1	1	0	3/5 (Moderate)
Cha *et al.* [14]	1	0	1	0	0	2/5 (Low)
Nannuru *et al.* [15]	1	1	0	1	1	4/5 (High)
Maulana *et al.* [16]	1	1	1	1	0	4/5 (High)
Nouraei *et al.* [17]	1	1	0	0	1	3/5 (Moderate)
Vitale *et al.* [18]	1	0	0	0	1	2/5 (Low)
Tyrka *et al.* [19]	1	0	1	1	0	3/5 (Moderate)
Javid *et al.* [20]	1	0	0	0	1	2/5 (Low)
Rabieyan *et al.* [21]	1	0	1	0	1	3/5 (Moderate)
Pang *et al.* [22]	1	1	1	1	0	4/5 (High)
Molero *et al.* [23]	1	0	0	0	0	1/5 (Low)
Ghazy *et al.* (24)	1	0	1	1	0	3/5 (Moderate)
Nawade *et al.* [25]	0	1	1	1	1	4/5 (High)
El Gataa *et al.* [26]	0	1	0	0	1	2/5 (Low)
Tadesse *et al.* [27]	0	0	0	1	1	2/5 (Low)
Devate *et al.* [28]	1	0	1	0	1	3/5 (Moderate)

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