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Narrative Review

Breeding Climate-Resilient Crops: Integrating Genomics, Phenomics, and Machine Learning for Heat and Drought Tolerance

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Abstract

Heat and drought increasingly co-occur and reduce yield, grain quality, and farmer income. This narrative review examines how genomics, phenomics, and machine learning can be integrated to breed heat- and drought-tolerant crops. Genomics provides genome-wide information for predicting breeding values. Phenomics provides high-throughput, repeatable measurement of stress traits that genomics alone cannot capture. Machine learning learns complex, non-linear patterns from large, multi-source data. Together, the three approaches can accelerate genetic gain, shorten breeding cycles, and improve selection for tolerance. However, gains depend on trait biology, data quality, validation in new environments, and seed systems that deliver varieties to farmers. The review provides an integrated breeding pipeline, a trait and data framework, and priorities for validation, equity, and policy.

Keywords: climate-resilient crops; breeding; genomics; phenomics; machine learning; heat tolerance; drought tolerance; genomic selection

1. Introduction

Climate change is increasing the frequency, duration, and co-occurrence of heat and drought stress during crop growth, flowering, and grain filling (IPCC, 2022; Lobell et al., 2011). Heat stress damages pollen viability, accelerates senescence, and shortens grain filling. Drought stress reduces water uptake, stomatal conductance, photosynthesis, and biomass. When heat and drought co-occur, their combined effect is often larger than the sum of each stress alone, because heat increases evaporative demand while drought limits water supply. For farmers, the result is lower yield, poorer grain quality, and greater income volatility, especially where irrigation is limited and seed systems are weak.

Breeding for heat and drought tolerance is therefore a central challenge for Seed Systems and Crop Improvement and for Climate-Smart Agriculture. Traditional breeding has made important gains by selecting for yield under stress, but it is slow, expensive, and limited by the low heritability of yield under stress, strong genotype by environment interaction, and the difficulty of measuring stress traits accurately in the field (Cooper et al., 2014; Araus et al., 2018). Three technologies promise to accelerate breeding: genomics, which measures DNA variation across the genome; phenomics, which measures plant traits at high throughput and high resolution; and machine learning, which learns complex, non-linear patterns from large, multi-source data (Crossa et al., 2017; Araus et al., 2018; van Dijk et al., 2021).

This review is a narrative review. It does not claim to be a PRISMA-guided systematic review, and it does not present a PRISMA screening flow, PICOT framework, or GRADE assessment. PRISMA-guided systematic reviews are included only when they are very necessary, for example when a journal or examiner requires a fully systematic search, screening, and grading process. For this educational review, a narrative synthesis is more appropriate, because it allows comparison across crops, technologies, and contexts, discussion of trade-offs, and a practical breeding framework, without pretending that a full systematic search was performed. The aim is to explain what each technology adds, how they fit together, when integration helps, and what must be done to turn prediction into farmer-adopted varieties.

Figure 1 shows when heat and drought hurt most across growth stages, illustrating why timing matters for trait selection and phenotyping.

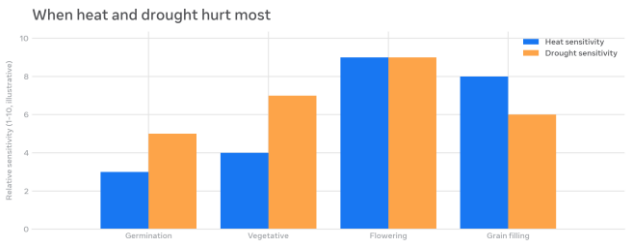


Figure 1. When heat and drought hurt most.

2. Biology of Heat and Drought Tolerance: Traits That Matter

Heat and drought tolerance are complex, polygenic traits. No single gene explains tolerance in most crops. Tolerance depends on many small-effect genes, on plant architecture, and on timing. Understanding which traits matter is essential, because genomics, phenomics, and machine learning are only useful if they predict traits that actually protect yield under stress.

For drought, key traits include root depth and architecture, which determine water uptake; stomatal conductance, which balances water loss and photosynthesis; canopy temperature, which reflects transpiration and water status; stay-green, which reflects delayed senescence and continued photosynthesis; and osmotic adjustment, which helps cells retain water (Blum, 2011; Reynolds and Langridge, 2016). For heat, key traits include pollen viability and anthesis-silking interval in maize, which determine fertilisation under heat; canopy cooling, which reflects transpiration; membrane stability, which reflects cell damage; and grain-filling duration, which determines grain weight (Lobell et al., 2011; Reynolds et al., 2021). For combined heat and drought, traits that maintain water status while cooling the canopy are especially valuable, because heat increases demand while drought limits supply.

Table 1 summarises key heat- and drought-tolerance traits, how each is measured, and why it matters for yield.

Table 1. Key heat- and drought-tolerance traits.

Trait	Measured by	Why it matters
Canopy temperature	Thermal imaging, infrared	Lower means better transpiration and water status
Stomatal conductance	Porometer, gas exchange	Balances water loss and photosynthesis
Stay-green	NDVI, visual scoring	Longer photosynthesis, higher grain filling
Root depth / architecture	Root imaging, soil coring	Deeper roots reach more water
Pollen viability	Pollen assay, anthesis-silking	Determines fertilisation under heat
Grain-filling duration	Phenology, grain weight	Longer filling means heavier grain

Trait heritability matters. Yield under stress has low heritability, because it is influenced by many genes and by environment. Secondary traits such as canopy temperature, NDVI, and stay-green often have higher heritability and can be measured earlier and more cheaply, especially with phenomics. Selecting for these traits, in addition to yield, can accelerate genetic gain. However, a trait that helps in one environment can hurt in another: for example, high stomatal conductance helps when water is available but hurts when water is scarce. Trait selection must therefore be environment-specific and validated in the target population of environments.

3. Genomics: From QTL to Genomic Selection

Genomics has transformed breeding by allowing breeders to measure DNA variation across the genome and to predict breeding values without waiting for full phenotypic evaluation. Early work used quantitative trait loci (QTL) mapping to find large-effect loci for tolerance, but most heat and drought tolerance is controlled by many small-effect loci, so QTL alone was insufficient (Meuwissen et al., 2001; Crossa et al., 2017). Genomic selection, which uses genome-wide markers to predict breeding values, was a major advance because it captures small-effect loci together (Meuwissen et al., 2001).

Genome-wide association studies (GWAS) have identified loci for heat and drought traits in maize, wheat, rice, and other crops, including loci for canopy temperature, root traits, and grain yield under stress (Crossa et al., 2017; Juliana et al., 2019). Marker-assisted selection can be useful for large-effect loci, such as some disease-resistance genes, but for complex tolerance traits, genomic selection is generally more effective. Genomic selection has been shown to improve prediction accuracy and to shorten breeding cycles, especially when combined with rapid generation advance and speed breeding (Watson et al., 2018; Crossa et al., 2017).

Table 2 summarises genomic approaches, their strengths, and their limitations for heat and drought breeding.

Table 2. Genomic approaches.

Approach	Strength	Limitation
QTL mapping	Finds large-effect loci	Misses many small-effect loci
GWAS	Finds loci across diversity panels	Requires large panels, validation
Marker-assisted selection	Useful for large-effect loci	Limited for polygenic tolerance
Genomic selection (GBLUP)	Captures small-effect loci together	Needs large, well-phenotyped training data
Genomic selection + phenomics	Adds stress traits, improves accuracy	Needs phenomics infrastructure

Genomic selection depends on training data quality. If the training population is small, poorly phenotyped, or from a different environment than the target, prediction accuracy will be low. If markers are sparse or genotyping is expensive, small programmes may not be able to afford genomic selection. Low-cost genotyping, shared reference panels, and regional hubs can help, but they require coordination, data sharing, and capacity building.

4. Phenomics: Measuring Stress Traits at Scale

Phenomics is the high-throughput, high-resolution measurement of plant traits using sensors, imaging, drones, satellites, and automated platforms (Araus et al., 2018; van Dijk et al., 2021). Phenomics can measure canopy temperature, NDVI, canopy cover, plant height, and senescence repeatedly, non-destructively, and at scale, which is impossible with manual phenotyping alone. This matters for heat and drought breeding, because stress traits change over time and must be measured at the right growth stage.

Thermal imaging can detect canopy temperature differences that reflect water status and transpiration. Multispectral imaging can measure NDVI and other indices that reflect greenness, biomass, and senescence. RGB imaging can measure canopy cover, height, and architecture. Drones can cover large trials quickly, while satellites can cover regional trials, though with lower resolution. Controlled phenotyping

platforms can measure root traits, stomatal conductance, and photosynthesis under managed stress, but they must be validated in the field, because controlled conditions do not always predict field performance (Araus et al., 2018).

Table 3 summarises phenomic tools, what each measures, and the main trade-off for each.

Table 3. Phenomic tools.

Tool	Measures	Trade-off
Thermal imaging	Canopy temperature, water status	Sensitive to wind, time of day
Multispectral / NDVI	Greenness, biomass, senescence	Saturates at high biomass
RGB imaging	Canopy cover, height, architecture	Needs calibration, lighting control
Drones	Large trials, repeat measures	Cost, regulation, data processing
Satellites	Regional trials, large scale	Lower resolution, cloud cover
Root imaging	Root depth, architecture	Expensive, field validation needed

Phenomics adds value in three ways. First, it measures traits that genomics alone cannot capture, such as canopy temperature at flowering under heat. Second, it measures traits repeatedly, so breeders can capture dynamic stress responses, not just final yield. Third, it can increase heritability by reducing measurement error and by measuring traits at the right time. However, phenomics requires investment in sensors, drones, data storage, and analysis, and it can generate large, messy data that need quality control. Low-cost phenomics, using smartphones, handheld thermal cameras, and community-based scoring, can help small programmes, but it must be validated against standard methods.

5. Machine Learning: When It Helps, When It Overfits

Machine learning learns complex, non-linear patterns from data, including interactions between genes, traits, and environments (Crossa et al., 2017; van Dijk et al., 2021; Montesinos-Lopez et al., 2021). Common models include random forest, gradient boosting, support vector machines, and deep learning models such as convolutional neural networks (CNN) and long short-term memory (LSTM) networks. Machine learning can integrate genomic, phenomic, environmental, and management data, which is difficult with linear models alone.

In the literature, machine learning improved prediction accuracy for yield under stress, especially when data were large, multi-environment, and included phenomic traits. Deep learning performed well for image-based phenomics, such as detecting stress from canopy images, while ensemble models that combined genomic selection with machine learning and phenomics gave the highest accuracy in several studies (Montesinos-Lopez et al., 2021; Crossa et al., 2017). However, machine learning can overfit, especially when data are small, when validation is only cross-validation within the same environment, or when models are not tested on new genotypes or environments. Overfitting means a model appears accurate in training but fails in the field, which is the worst outcome for a breeding programme.

Figure 2 presents an illustrative comparison of predictive accuracy by approach, showing why integration tends to outperform single approaches in the literature.

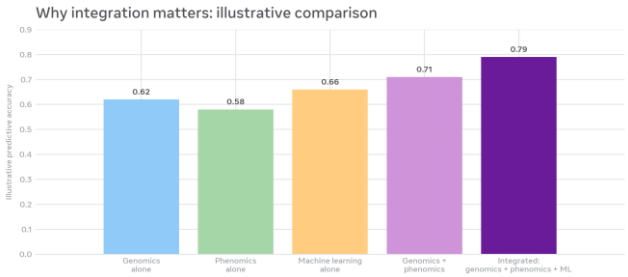


Figure 2. Why integration matters: illustrative comparison.

Table 4 summarises machine learning models, their strengths, and their risks for breeding.

Table 4. Machine learning models.

Model	Strength	Risk
Random forest / boosting	Handles non-linear, mixed data	Can overfit if data small
Support vector machine	Good for small to medium data	Needs tuning, scaling
Deep learning (CNN)	Excellent for images, phenomics	Needs large data, compute
LSTM / time-series	Captures dynamic stress over time	Needs repeated measures
Ensemble GS + ML + phenomics	Highest accuracy in several studies	Complex, needs validation

Table 5 summarises how crop, stress, validation, and data size change prediction accuracy in the literature.

Table 5. What changes prediction accuracy.

Factor	Direction	Interpretation
Large data vs small data	Large: ML advantage larger	ML needs data to learn patterns
External validation vs cross-validation only	External: accuracy lower, more honest	Cross-validation overstates field accuracy
Multi-environment vs single environment	Multi: accuracy lower, more robust	Single environment overstates stability
Combined heat + drought vs single stress	Combined: accuracy lower	Combined stress is more complex
Phenomics included vs genomics only	Phenomics: accuracy higher	Phenomics adds stress traits

Validation is the most important safeguard. Models should be validated on new genotypes, new environments, and new seasons, not only on random cross-validation within the same trial. Data leakage, where information from the test set leaks into training, must be avoided. Code, data, and model details should be shared so that other programmes can reproduce and test the model. Without strong validation, machine learning is a promising tool that can mislead breeding decisions.

6. Integrated Pipeline: Genomics + Phenomics + Machine Learning

Integration is the core contribution of this review. Genomics tells us what DNA a line carries. Phenomics tells us how that line behaves under stress, at the right time, in the right environment. Machine learning learns how genomic, phenomic, and environmental data together predict tolerance and yield. No single technology is sufficient: genomics without phenomics misses stress traits, phenomics without genomics

cannot predict new lines, and machine learning without good data overfits.

Figure 3 shows conceptual genetic gain trajectories by breeding approach, illustrating why integrated breeding diverges from conventional breeding over time.

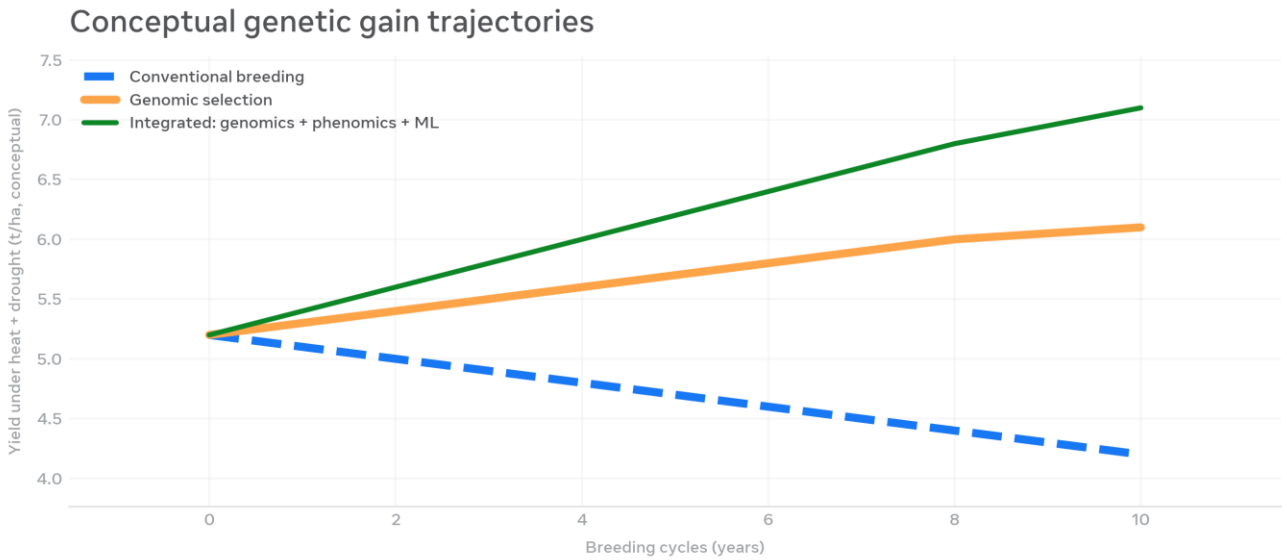


Figure 3. Conceptual genetic gain trajectories.

Table 6 summarises the integrated breeding pipeline, from defining the target environment to delivering seed.

Table 6. Integrated breeding pipeline.

Step	Question	Tool	Output
1. Target environment	Where will variety be grown?	Climate, soil, farmer knowledge	Target population of environments
2. Trait definition	Which traits protect yield?	Physiology, farmer traits	Priority traits
3. Population	Which lines to test?	Diversity, landraces, elite lines	Training population
4. Genotyping	What DNA do lines carry?	SNP, low-cost genotyping	Marker data
5. Phenotyping	How do lines behave under stress?	Phenomics, field trials	Trait and yield data
6. Modelling	How to predict tolerance?	GS, ML, ensemble	Prediction model
7. Validation	Does it work in new environments?	External validation	Validated model
8. Selection	Which lines to advance?	Selection index, farmer traits	Selected lines
9. Seed systems	How to reach farmers?	Seed multiplication, extension	Adopted variety

Speed breeding and rapid generation advance can shorten cycles, especially when combined with genomic selection and early phenomic screening (Watson et al., 2018). Instead of waiting for full yield trials, breeders can screen seedlings for genomic breeding values and for early phenomic traits, then advance only the best lines to field trials. This saves time and cost, but it requires that early traits predict field yield under stress, which must be validated. Participatory breeding, where farmers evaluate lines on farm and for traits they value, such as grain quality, cooking quality, and market traits, can improve adoption and ensure that tolerance does not come at the cost of traits farmers care about.

7. Crop Examples

Maize is highly sensitive to heat and drought at flowering, when pollen viability and anthesis-silking interval determine fertilisation. Genomic selection plus phenomics for canopy temperature and anthesis-silking interval has improved prediction for maize yield under drought in several studies (Crossa et al., 2017; Juliana et al., 2019). Wheat is sensitive to heat during grain filling, when high temperature shortens filling and reduces grain weight. Phenomics for stay-green, canopy temperature, and NDVI has helped select wheat lines with longer grain filling under heat (Reynolds et al., 2021). Rice is sensitive to heat at flowering and to drought at vegetative and reproductive stages. Genomics plus phenomics for root traits, canopy temperature, and grain filling has improved rice tolerance in several programmes.

Table 7 summarises crop examples, showing the key stress, key traits, and what integration added.

Table 7. Crop examples.

Crop	Key stress	Key traits	What integration added
Maize	Heat + drought at flowering	Pollen, anthesis-silking, canopy temp	Early screening, faster cycles
Wheat	Heat at grain filling	Stay-green, canopy temp, NDVI	Longer filling, stable yield
Rice	Heat at flowering, drought	Root traits, canopy temp, grain filling	Root + canopy traits together

Legumes / sorghum	Drought, heat	Root, stay-green, canopy	Low-cost phenomics, farmer traits

Legumes, sorghum, and millet are important for food security and nutrition, but they have less genomic and phenomic evidence than maize, wheat, and rice. This is a gap: these crops are often grown in the most stress-prone environments, by the most vulnerable farmers, with the least investment in breeding. Low-cost genotyping, low-cost phenomics, and participatory breeding are especially important for these crops, and programmes should prioritise them for equity, not only for commercial value.

8. Economics, Seed Systems, Equity, and Scaling

Prediction accuracy alone does not ensure impact. A variety that is tolerant in trials but not available as seed, not affordable, or not liked by farmers will not be adopted. Seed systems determine whether a variety reaches farmers: formal seed systems, community seed banks, and informal farmer-to-farmer exchange all matter, and each has strengths and limitations. For example, hybrid maize seed must be bought each season, while open-pollinated varieties and legumes can be saved, which affects cost and adoption.

Table 8 summarises economics and adoption factors for climate-resilient varieties.

Table 8. Economics and adoption factors.

Factor	Effect on adoption	Who is most affected
Seed cost and availability	High cost delays adoption	Smallholders, remote farmers
Grain quality / market traits	Poor quality reduces adoption	Women, market sellers
Labour / input demand	High demand reduces adoption	Labour-poor households
Extension + demo trials	Increases adoption and learning	Remote, low-literacy farmers
Credit / subsidy	Increases adoption if targeted	Poorest, most stressed areas

Gender and equity deserve explicit attention. Women farmers often grow food crops for household consumption, yet they may have less access to land, seed, credit, and extension, even though they are key to household nutrition. Breeding programmes should include traits that women value, such as cooking time, taste, and market quality, and should measure adoption by gender. Similarly, youth and tenants need varieties with short-term benefits if they are to invest in new seed. Programmes should measure adoption, not only yield in trials, and should design seed systems that reach the poorest and most remote farmers, not only large, commercial farms.

9. Challenges, Limitations, and Future Priorities

Several challenges remain. First, data quality and sharing are uneven: genomic, phenomic, and environmental data are often in different formats, with different standards, and are not shared. Second, validation is often weak: many models are tested only by cross-validation within the same trial, not on new genotypes and environments. Third, costs are high: genotyping, phenomics, and data infrastructure require investment that small programmes may not have. Fourth, combined heat and drought is less studied than single stresses, even though it is the most damaging in the field. Fifth, legumes, sorghum, and millet are under-studied relative to maize, wheat, and rice.

Table 9 summarises challenges and practical responses for breeding programmes.

Table 9. Challenges and practical responses.

Challenge	Practical response
Data quality / sharing	Common standards, open data, shared panels
Weak validation	External validation on new genotypes and environments
High cost	Low-cost genotyping, low-cost phenomics, regional hubs
Combined stress understudied	Managed combined-stress trials, multi-environment trials
Under-studied crops	Prioritise legumes, sorghum, millet for equity

Future priorities should include: (i) long-term, multi-environment trials that measure genomic, phenomic, yield, and adoption together, especially for combined heat and drought; (ii) low-cost genotyping and phenomics for small programmes and for legumes, sorghum, and millet; (iii) external validation, data sharing, and open code so that models can be tested by other programmes; (iv) participatory breeding that includes farmer-valued traits, including grain quality, cooking, and market traits; and (v) seed systems, economics, and equity research, including how to reach women, remote households, and the poorest farmers.

10. Conclusion

Heat and drought tolerance are complex, polygenic traits that require integrated breeding. Genomics, phenomics, and machine learning each add value, but together they can accelerate genetic gain more than any one alone. Genomics predicts breeding values, phenomics measures stress traits at the right time, and machine learning learns how genomic, phenomic, and environmental data together predict tolerance. Success depends on good data, strong validation, farmer participation, and seed systems, not only on model accuracy. For breeders, the message is to integrate the three technologies, validate externally, and measure farmer-valued traits. For policymakers, the message is to invest in genotyping, phenomics, data infrastructure, seed systems, and long-term breeding programmes, so that climate-resilient varieties can reach the farmers who need them most.

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Conflict of Interest

The authors declare no conflict of interest.

Data Availability

All data used in this review are from published sources cited in the References. No new primary data were generated.

Author Contributions

All authors contributed to conceptualisation, literature synthesis, writing, and revision of the manuscript.

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