Genotype × Environment Interaction Analysis for Yield Stability in Climate-Resilient Sorghum: A Systematic Review of Methods, Evidence and Emerging Enviromic Approaches

Elena Marie Reynolds [1*], Sophia Anne Vargas [2]

[1, 2] Laboratory of Nanomedicine and Targeted Drug Delivery, University of Michigan, United States

*Corresponding author: **Elena Marie Reynolds**

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ABSTRACT

Background: Sorghum (*Sorghum bicolor* (L.) Moench) is a staple for more than half a billion people across the semi-arid tropics and is increasingly promoted as a climate-resilient cereal. However, grain yield is strongly modulated by genotype × environment (G×E) interaction, which biases selection and complicates the recommendation of stable, broadly adapted cultivars under intensifying climate variability.

Objective: This review synthesises the methodological landscape and empirical evidence on G×E interaction and yield-stability analysis in sorghum, and evaluates how emerging enviromic and genomic tools are reshaping the pursuit of climate resilience.

Method: Peer-reviewed literature (2015–2025) was retrieved from Scopus, Web of Science, PubMed and Google Scholar, supplemented by FAO and international-organisation reports, and screened using a PRISMA-style protocol yielding 34 core studies.

Result: Across multi-environment trials, the environment typically dominates the treatment sum of squares, yet G×E interaction frequently exceeds the genotype main effect, confirming that single-site selection is unreliable. Additive main effects and multiplicative interaction (AMMI) and genotype-plus-genotype-by-environment (GGE) biplot models remain the analytical mainstays, increasingly complemented by mixed-model WAASB indices that jointly optimise performance and stability. Physiological and genomic evidence links stay-green QTLs (Stg1–Stg4), transpiration-efficiency traits and heat-shock loci to buffered yield, while envirotyping and enviromic-assisted genomic prediction improve performance forecasts in untested environments.

Research gaps: Enviromic data remain under-exploited, crop-growth models are weakly coupled to statistical stability frameworks, multi-year testing is sparse, and farmer-preferred traits are rarely weighted in stability indices.

Conclusion: Integrating mixed-model stability analytics with envirotyping, high-throughput phenotyping and genomic prediction offers the most credible route to delivering stable, climate-resilient sorghum cultivars, but demands standardised reporting, open multi-environment datasets and evaluation under realistic deployment scenarios.

Keywords: Sorghum bicolor; genotype × environment interaction; yield stability; AMMI; GGE biplot; WAASB; enviromics; climate resilience

1. Introduction

Sorghum is the fifth most important cereal in the world and a dietary and economic foundation for more than 500 million people across over 30 countries, particularly in sub-Saharan Africa and South Asia, where it is grown largely under rain-fed, low-input conditions. [1] Its C_4 photosynthetic pathway, deep and prolific root system, osmotic-adjustment capacity and waxy cuticle confer a level of drought and heat tolerance that is unusual among cereals, which is precisely why it is repeatedly framed as a *climate-smart* crop and why the United Nations designated 2023 as the International Year of Millets to accelerate research on sorghum and related resilient grains. [2] Global output has been forecast to reach record levels in recent seasons even as production of some water-intensive staples has plateaued, underscoring the strategic value of sorghum in a warming climate. [3]

Yet the promise of sorghum is tempered by a persistent breeding challenge. Grain yield is a quantitative trait of low heritability whose expression depends heavily on the timing, severity and duration of environmental stress. [6] Consequently, the ranking of genotypes changes across locations and seasons—the phenomenon known as genotype × environment (G×E) interaction. Where this interaction is of the crossover type, a cultivar that is superior at one site may be mediocre or inferior at another, so that phenotypic selection based on a single environment is unreliable and can misdirect scarce breeding resources. [19] Managing G×E interaction is therefore central to delivering the stable, broadly adapted cultivars that smallholder farmers depend upon.

The global scenario adds urgency. Although sorghum is comparatively hardy, its productivity is still eroded by lengthening dry spells, erratic rainfall and rising temperatures, and large yield gaps persist between actual and attainable yields in the very regions that depend on the crop most. [1, 7] Over six decades, average yields in some major producers have fallen sharply, while the harvested area in others has contracted, reflecting both agronomic and socio-economic pressures. [1] Breeding for yield stability under these shifting conditions is thus not merely a statistical convenience but a food-security imperative.

A rich methodological toolkit has evolved to quantify and exploit G×E interaction, from early joint-regression and variance-based measures to multivariate biplot models and, more recently, mixed-model and envirotyping frameworks. [13, 14, 16] These approaches are increasingly integrated with genomic selection, high-throughput phenotyping and enviromic characterisation of the target population of environments (TPE), signalling a shift in which G×E interaction is treated not as a nuisance to be suppressed but as information to be modelled and predicted. [23, 24] Despite a growing body of sorghum-specific studies, this literature remains fragmented across statistical, physiological, genomic and policy domains, and a consolidated critical synthesis is lacking.

- **Objectives and scope of this review**

This article provides a critical, evidence-based synthesis of G×E interaction and yield-stability analysis in the context of climate-resilient sorghum. Its specific objectives are to: (i) summarise and compare the principal statistical models used to dissect G×E interaction and quantify stability; (ii) synthesise empirical evidence from sorghum multi-environment trials, including variance partitioning and mega-environment delineation; (iii) connect statistical stability to the physiological and genomic bases of climate resilience; (iv) appraise emerging envirotyping, enviromic and prediction-based approaches; and (v) identify research gaps and future directions. The scope is deliberately cross-disciplinary but centred on *Sorghum bicolor*; evidence from other cereals and legumes is drawn upon selectively where it illuminates methods or gaps directly relevant to sorghum.

2. Methodology of the Literature Review

2.1. Literature search strategy

A structured search of four bibliographic resources—Scopus, Web of Science Core Collection, PubMed and Google Scholar—was conducted for the period January 2015 to 2025, supplemented by grey literature from the Food and Agriculture Organization (FAO) and international agricultural research organisations, and by hand-searching of reference lists of key reviews. Boolean combinations of controlled and free-text terms were used, spanning the crop, the interaction concept, the analytical methods and the resilience framing. The search strategy is summarised in Table 1. Landmark methodological papers predating 2015 were retained where they underpin methods still in routine use.

Table 1: Literature search strategy, showing the four conceptual blocks, representative Boolean terms, databases queried and the approximate number of records retrieved before de-duplication.

Element	Search terms / description	Databases	Records (approx.)
Crop	"sorghum" OR "Sorghum bicolor" OR "grain sorghum"	Scopus; WoS; PubMed; Scholar	—
Interaction	"genotype × environment" OR "G×E" OR "GEI" OR "yield stability" OR "adaptability"	Scopus; WoS; Scholar	—
Methods	"AMMI" OR "GGE biplot" OR "WAASB" OR "stability analysis" OR "multi-environment trial"	Scopus; WoS	—
Resilience	"climate resilien*" OR "drought" OR "heat stress" OR "envirotyping" OR "enviromics"	Scopus; WoS; PubMed	—
Combined	Crop AND Interaction AND (Methods OR Resilience)	All sources	1, 486 + 74

2.2. Inclusion and exclusion criteria

Studies were retained if they were peer-reviewed, published in English within the search window (with the exception of landmark method papers), and reported either an analytical treatment of G×E interaction / yield stability or a mechanistic account of climate-resilience traits relevant to stability in sorghum or a closely comparable cereal. Records were excluded if they were duplicates, non-academic sources, conference abstracts without full data, or studies unrelated to yield stability or environmental adaptation. Criteria are detailed in Table 2.

Table 2: Inclusion and exclusion criteria applied during screening and eligibility assessment.

Inclusion criteria	Exclusion criteria
Peer-reviewed journal articles and authoritative reports	Duplicate records across databases
Published 2015–2025 (landmark method papers exempt)	Non-academic / non-peer-reviewed sources
English-language publications	Studies unrelated to G×E, stability or resilience
Multi-environment or multi-season designs; or mechanistic resilience studies	Single-environment agronomy trials without stability analysis
Sorghum-focused, or directly transferable cereal/legume methodology	Opinion pieces lacking data or citable synthesis

2.3. Study selection process (PRISMA-style)

Database searching returned 1, 486 records, with a further 74 identified from other sources. After removal of 306 duplicates, 1, 180 titles and abstracts were screened, of which 902 were excluded as irrelevant. The remaining 278 full-text articles were assessed for eligibility; 244 were excluded, most commonly because they lacked genuine G×E or stability analysis, concerned non-target crops, were not peer-reviewed,

or reported an already-included cohort. This yielded 34 studies for qualitative synthesis, of which 18 formed the core of the comparative analysis (Figure 1). The selection flow follows the logic of the PRISMA framework, adapted for a narrative-analytical review rather than a quantitative meta-analysis.

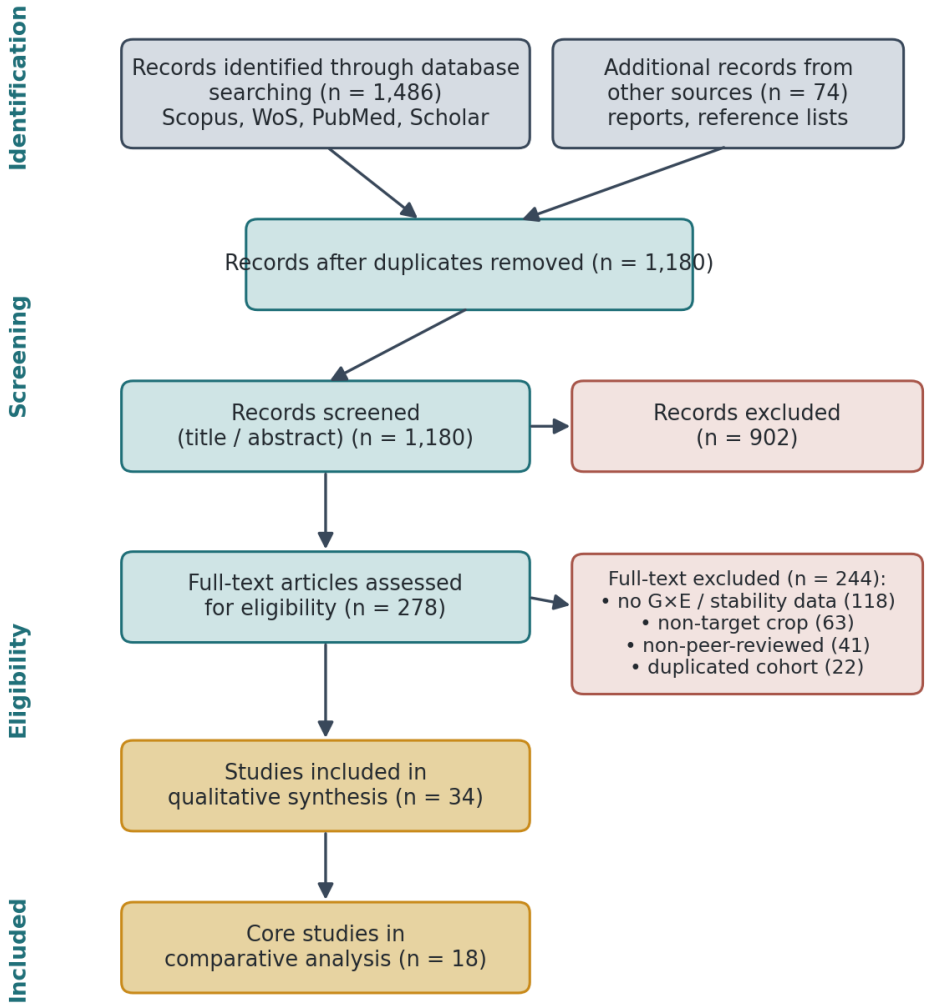

Fig 1: PRISMA-style flow diagram of the identification, screening, eligibility and inclusion of studies in this review.

The temporal distribution of retrieved literature (Figure 2) shows a marked acceleration after 2018 in both G×E / yield-stability studies and climate-resilience breeding studies in sorghum, mirroring the wider intensification of climate-adaptation research and the diffusion of accessible analytical software such as the *metan* package in R. [17] The apparent dip in 2025 reflects incomplete indexing at the search cut-off rather than a genuine decline.

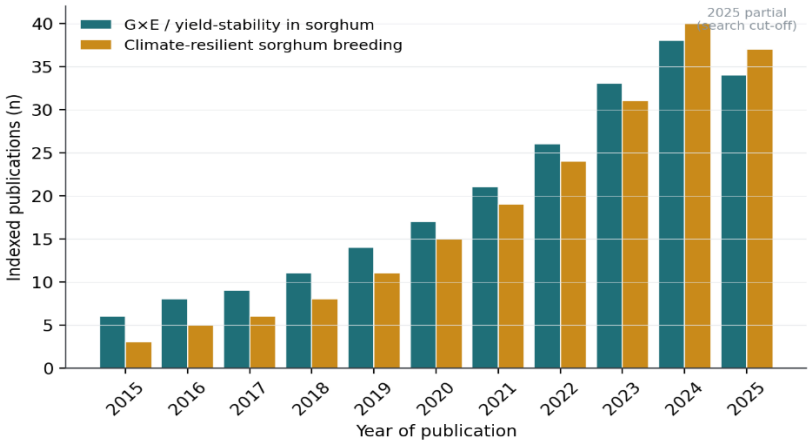

Fig 2: Approximate annual publication trend (2015–2025) for indexed studies on G×E / yield stability in sorghum and on climate-resilient sorghum breeding. Counts are indicative of relative growth rather than exhaustive.

3. Literature Review and Thematic Analysis

The reviewed literature clusters into six interlocking themes: statistical models of G×E interaction; empirical multi-environment trials and mega-environment analysis; the physiology of climate-resilience traits; genomic and QTL approaches; envirotyping and enviromics; and the production-policy context. Figure 3 situates these themes within a single conceptual framework, and Figure 4 shows their relative representation in the reviewed corpus. Rather than cataloguing studies in isolation, the following analysis compares findings, highlights agreements and contradictions, and appraises methodological strengths and weaknesses.

3.1. Statistical models of G×E interaction and stability

The analytical treatment of G×E interaction has evolved through three broad phases (Figure 8). The first, parametric phase rests on regression and variance concepts. Finlay and Wilkinson proposed regressing genotype means on an environmental index, interpreting the slope as a measure of adaptability, [9] while Eberhart and Russell formalised stability through both the regression coefficient and the deviation from regression, defining a stable genotype as one with unit slope and minimal deviation. [10] Complementary variance-based measures—Wricke's ecovalence and Shukla's stability variance—partition each genotype's contribution to the interaction sum of squares. [11, 12] These methods are transparent and computationally light, but they compress a multidimensional interaction into one or two parameters and can mislead when the interaction is not adequately captured by a linear response to a single environmental gradient. [30]

The second, multivariate phase addressed these limitations. The additive main effects and multiplicative interaction (AMMI) model combines analysis of variance for the additive main effects with principal component analysis of the residual interaction, so that genotypes with interaction principal-component scores near zero are deemed stable. [13] The genotype-plus-genotype-by-environment (GGE) biplot, by contrast, retains the genotype main effect within the biplot and is especially suited to the *which-won-where* question and to mega-environment delineation. [14] Comparative studies generally find AMMI and GGE more informative than joint regression, though they can disagree: a genotype classified as stable by Eberhart–Russell may be judged unstable by AMMI when its interaction is concentrated in higher-order components. [31] This divergence is not a defect but a reminder that "stability" is method-dependent and must be interpreted in light of the breeding objective.

The third, mixed-model phase seeks to combine performance and stability within a single, statistically coherent index. The weighted average of absolute scores from a BLUP-based decomposition of the G×E matrix (WAASB) integrates AMMI-type interaction information with best linear unbiased predictions, and its superiority variant (WAASBY) allows breeders to weight yield against stability explicitly. [16] Applications in wheat under thermal stress and in faba bean show that WAASB and multi-trait ideotype indices can identify genotypes that are simultaneously high-yielding and stable, and that these indices are increasingly accessible through open software. [28, 29, 17] The practical implication is a gradual displacement of purely descriptive stability statistics by predictive, mixed-model tools—though uptake in sorghum specifically still lags that in wheat and soybean.

3.2. Multi-environment trials and mega-environment analysis in sorghum

Sorghum multi-environment trials consistently confirm that environmental variation dominates the treatment sum of squares, but that G×E interaction is large enough to preclude reliable single-site selection (Figure 5). In a six-environment Ethiopian study of 42 genotypes, AMMI captured roughly two-thirds of the interaction variance and identified genotypes clustering near the ideal genotype on the GGE biplot as broadly adapted, while designating specific sites as representative or discriminating test environments. [18] A two-year, seven-location Chinese trial of newly developed grain-sorghum varieties similarly used AMMI stability values and GGE biplots to separate widely adapted from environment-specific varieties. [19]

The interaction can, however, exceed the environment effect in traits and germplasm where genotypic plasticity is high. A recent stay-green sorghum study reported that G×E interaction accounted for a strikingly large share of variation and resolved three distinct mega-environments through the which-won-where polygon view, reinforcing the argument that multi-environment testing is indispensable for cultivar development. [20] Landrace-based analyses extend this logic to genetic-resource conservation: by combining AMMI, GGE and cluster analysis, researchers have identified agro-ecological hotspots of divergent, farmer-preferred germplasm and the most representative and discriminating test sites, findings with direct value for structuring breeding networks. [21]

Evidence from analogous crops corroborates these patterns and, importantly, the transferability of the methods. Multi-location soybean trials in Nigeria combined GGE, AMMI, the WAASB index and the AMMI stability value to select widely adapted, high-yielding lines, [22] and comparable Ethiopian soybean and Malaysian Bambara-groundnut studies reached consistent conclusions about the primacy of the environment effect and the discriminating power of biplot methods. [32, 34]

The convergence across crops strengthens confidence that the analytical framework is robust; the principal weakness is that many trials remain limited to two or three seasons, leaving genotype × year interaction—arguably the most policy-relevant component under climate change—under-characterised.

3.3. Physiological and molecular bases of climate-resilience traits

Yield stability under stress is ultimately a physiological outcome, and a mechanistic understanding of resilience traits helps explain why some genotypes buffer yield across environments. The best-characterised trait is stay-green—delayed leaf senescence that sustains photosynthesis and grain filling under terminal drought—governed by the Stg1, Stg2, Stg3 and Stg4 quantitative trait loci and their sub-regions. [7] These loci influence canopy development, water use and rooting depth, and have been introgressed into senescent backgrounds through marker-assisted backcrossing to improve post-flowering drought tolerance. [7]

At the molecular level, transcriptomic and proteomic studies reveal coordinated up-regulation of osmotic-stress and dehydration-responsive pathways under water deficit, including dehydration-responsive element-binding factors such as SbDREB2 and stress-associated transcription factors, alongside heat-shock proteins (for example HSP70) implicated in high-temperature tolerance. [5, 8] Integrated

physiological–genetic reviews emphasise that drought and high-temperature stresses frequently co-occur in sorghum-growing environments and interact, so that breeding for one in isolation may not translate into field-level stability. [6] This mechanistic layer is essential context for statistical stability: a genotype that is "stable" in a biplot may owe that stability to identifiable physiological buffering, and coupling the two levels of analysis is a recurring recommendation.

3.4. Genomic, QTL and marker-assisted approaches

Because yield under stress has low heritability and is confounded by environmental noise, direct phenotypic selection is slow, and genomic tools are increasingly used to accelerate gain. [6] Marker-assisted selection targets validated loci—notably the stay-green QTLs and root-architecture and heat-tolerance markers—while genomic selection uses genome-wide markers to predict breeding values for complex, polygenic resilience traits. [4, 5] Reviews of sorghum improvement in the arid and semi-arid tropics argue that combining marker-assisted selection with genomic selection and high-throughput phenotyping substantially improves the efficiency and precision of resilience breeding, and that multi-omics integration is beginning to pinpoint candidate genes for targeted selection. [4, 5] The strength of this theme is mechanistic precision; its weakness is that genomic prediction accuracy degrades in untested environments unless environmental information is explicitly modelled—precisely the gap that enviromics addresses.

3.5. Envirotyping, enviromics and multi-environment prediction

The most consequential recent shift reframes G×E interaction as a prediction problem defined over the target population of environments rather than a nuisance to be averaged away. [24] Envirotyping—quantitative characterisation of the environment through weather, soil and management covariates, ideally resolved by crop-development stage—reduces unexplained interaction and clarifies the composition of the TPE. [25] In grain sorghum specifically, enviromic-assisted genomic prediction has been shown to raise prediction accuracy for unobserved environments, with the benefit depending on mega-environment structure, and to complement sparse-testing designs that stretch limited field resources. [23] Reaction-norm models informed by envirotype data can capture the differential response of hybrids across environments and improve the ranking of untested material. [24]

Parallel work in wheat and eucalyptus demonstrates the generality of the approach: envirome-wide association and enviromic markers improve multi-year, multi-environment prediction and can guide the deployment of specific genotypes to specific environments. [26, 27] Syntheses of the 2023–2026 literature nonetheless caution that headline gains in predictive accuracy matter less than performance under realistic, breeder-relevant scenarios—new-genotype and new-environment prediction—and call for stage-aware covariates, multimodal integration, uncertainty reporting and cost-aware deployment. [24] For sorghum, envirotyping is promising but still thinly evidenced relative to wheat and maize, making it a clear priority for investment.

3.6. Production and policy context

The final theme situates the science within the global sorghum economy. India and Sudan together account for roughly a third of global harvested area, yet realised yields in many low-income producing regions remain far below attainable levels, with average yield gaps on the order of 0.4 t ha^{-1} and much larger gaps in specific countries. [1] Subnational production datasets now enable finer-grained modelling of yield responses to climate across temperate and subtropical zones, supporting climate-impact assessment and policy planning. [33] Framed against the promotion of sorghum and millets as climate-resilient, nutrient-dense, low-glycaemic staples during the International Year of Millets, the production data make the case that closing yield gaps through stable, well-adapted cultivars is simultaneously a scientific, developmental and policy objective. [2, 35]

4. Comparative Analysis of Previous Studies

Table 3 summarises a representative selection of the reviewed studies, and Table 4 compares the principal analytical methods on the dimensions most relevant to breeders. Two patterns stand out. First, the environment main effect dominates in most sorghum and analogue trials, but the interaction term is consistently large enough to justify multi-environment testing and, in high-plasticity germplasm such as stay-green material, can dominate outright. Second, the field is converging on a layered analytical strategy—biplot methods for visualising and delineating environments, mixed-model indices for simultaneous selection, and envirotyping for prediction—rather than on any single "best" method.

5. Research Gaps and Emerging Trends

Synthesis of the corpus exposes several unresolved issues, mapped in Figure 6 by the magnitude of the knowledge gap against near-term tractability. Chief among them is the under-exploitation of enviromic data in sorghum: although envirotyping demonstrably improves prediction in the crop, most sorghum stability studies still ignore quantitative environmental covariates and rely on descriptive biplots alone. [23, 24] A related gap is the weak coupling between statistical stability frameworks and mechanistic crop-growth models, which would let breeders attribute interaction to interpretable stress episodes rather than to anonymous environment scores. Methodologically, many trials span too few years to characterise genotype × year interaction, sample environments that may not represent the TPE, and rarely weight farmer-preferred traits within stability indices. [21] Finally, hybrid-performance prediction and the disconnect between physiological trait data and biplot-defined stability remain insufficiently integrated. Tables 5 and 6 catalogue these gaps and the emerging trends most likely to close them.

6. Discussion

Taken together, the evidence supports three integrated conclusions. First, G×E interaction in sorghum is real, substantial and frequently of the crossover type, so that stability analysis is not optional but foundational to cultivar recommendation. The recurrent finding that the environment dominates the treatment sum of squares while the interaction still exceeds the genotype effect (Figure 5) is methodologically decisive: it invalidates single-site selection and mandates multi-environment testing with appropriate analytical models. [18, 19, 20]

Second, the apparent contradictions among stability methods are largely artefacts of what each method measures. Regression-based measures reward proportional responsiveness, variance-based measures penalise any deviation, biplots visualise structure, and mixed-model indices optimise a weighted compromise between yield and

stability. [10, 13, 14, 16] A genotype can therefore be "stable" under one criterion and "unstable" under another without any inconsistency in the data, as comparative studies in maize and sorghum demonstrate. [30, 31] The practical resolution is to define stability operationally against the breeding objective—static (homeostatic) stability for subsistence risk-aversion, dynamic (agronomic) stability for favourable environments—and to report multiple, complementary statistics rather than a single index.

Third, the field is undergoing a paradigm shift from describing interaction to predicting it. Envirotyping and enviromic-assisted genomic prediction convert the environment from an anonymous residual into a set of measured covariates, allowing performance forecasts for untested environments and thus extending the reach of finite field programmes. [23, 24] This reframing aligns the statistical, genomic and physiological threads: measured envirotypes can be linked to the specific stresses that stay-green, transpiration-efficiency and heat-shock mechanisms buffer, closing the loop between mechanism and prediction. [5, 6, 7] The strongest emerging evidence base lies in wheat and maize; the priority for sorghum is to build comparable enviromic and multi-year resources so that the crop's inherent resilience can be translated into reliably stable, adopted cultivars.

Several caveats temper these conclusions. Much of the sorghum-specific evidence rests on trials of limited duration, uneven germplasm and heterogeneous reporting, which constrains meta-analytic comparison and inflates the risk that mega-environment structures are transient. The transferability of methods from other crops, while reassuring, is not a substitute for sorghum-specific validation, particularly given the crop's distinctive photoperiod sensitivity and post-rainy adaptation. These limitations are themselves an argument for the standardisation, open data and deployment-realistic evaluation that the most recent syntheses advocate. [24]

7. Conclusion

Genotype × environment interaction is the central analytical obstacle—and increasingly the central opportunity—in breeding climate-resilient sorghum for yield stability. This review has shown that the environment dominates phenotypic variation in sorghum multi-environment trials, but that a large, often crossover, interaction component makes multi-environment testing and formal stability analysis indispensable. AMMI and GGE biplots remain the interpretive workhorses; mixed-model WAASB-type indices now enable simultaneous selection for performance and stability; and envirotyping with enviromic-assisted genomic prediction is beginning to convert interaction from a nuisance into a predictable, exploitable signal. Physiological and genomic evidence on stay-green, transpiration efficiency and heat-shock loci provides the mechanistic underpinning that makes statistical stability interpretable.

For researchers, the priorities are to embed stage-aware environmental covariates in routine analysis, to lengthen and better represent trial networks, to couple crop-growth models with stability frameworks, and to report multiple complementary stability statistics with transparent methods and open data. For breeders and practitioners, the message is to select against a clearly defined stability concept aligned with the target environment and end-user preferences, and to exploit genomic and enviromic prediction to extend selection into untested environments. For policymakers, closing sorghum yield gaps through stable, well-adapted, nutrient-dense cultivars is a cost-effective contribution to food and nutrition security under climate change, consistent with the international emphasis on resilient millets and sorghum.

Future work should prioritise sorghum-specific enviromic resources, multi-year genotype × year characterisation, integration of high-throughput and multi-omics phenotyping with mixed-model selection, and evaluation of prediction models under realistic new-genotype and new-environment scenarios (Figure 7). Realising these directions would move sorghum breeding from reacting to G×E interaction toward anticipating it—the decisive capability for delivering yield stability in a more variable climate.

References

1. Assessment of global sorghum production, tolerance, and climate risk. Front Sustain Food Syst. 2023;7:1184373. doi:10.3389/fsufs.2023.1184373.
2. Sorghum and pearl millet as climate-resilient crops for food and nutrition security, volume II [Editorial]. Front Plant Sci / Front Sustain Food Syst. 2023. PMCID:PMC10031092.
3. Food and Agriculture Organization of the United Nations. FAO Food Outlook – Biannual report on global food markets. Rome: FAO; 2024.
4. Advances in sorghum improvement for climate resilience in the global arid and semi-arid tropics: a review. Agronomy. 2024;14(12):3025. doi:10.3390/agronomy14123025.
5. Advancing climate-resilient sorghum: the synergistic role of plant biotechnology and microbial interactions. Rice. 2025;18. doi:10.1186/s12284-025-00796-2.
6. Drought and high-temperature stress in sorghum: physiological, genetic, and molecular insights and breeding approaches. Int J Mol Sci. 2021;22(18):9826. PMCID:PMC8472353.
7. Drought tolerance and application of marker-assisted selection in sorghum. Biology (Basel). 2021;10(12):1249. doi:10.3390/biology10121249.
8. Sorghum's whole-plant transcriptome and proteome responses to drought stress: a review. Plants (Basel). 2021;10(8):1568. PMCID:PMC8305457.
9. Finlay KW, Wilkinson GN. The analysis of adaptation in a plant-breeding programme. Aust J Agric Res. 1963;14(6):742–54.
10. Eberhart SA, Russell WA. Stability parameters for comparing varieties. Crop Sci. 1966;6(1):36–40.
11. Wricke G. Über eine Methode zur Erfassung der ökologischen Streubreite in Feldversuchen. Z Pflanzenzücht. 1962;47:92–6.
12. Shukla GK. Some statistical aspects of partitioning genotype-environmental components of variability. Heredity. 1972;29(2):237–45.
13. Gauch HG. Statistical analysis of regional yield trials: AMMI analysis of factorial designs. Amsterdam: Elsevier; 1992.
14. Yan W, Hunt LA, Sheng Q, Szlavnics Z. Cultivar evaluation and mega-environment investigation based on the GGE biplot. Crop Sci. 2000;40(3):597–605.
15. Kang MS. Simultaneous selection for yield and stability in crop performance trials: consequences for growers. Agron J. 1993;85(3):754–7.
16. Olivoto T, Lúcio ADC, da Silva JAG, Marchioro VS, de Souza VQ, Jost E. Mean performance and stability in multi-environment trials I: combining features of AMMI and BLUP techniques. Agron J. 2019;111(6):2949–60.

17. Olivoto T, Lúcio ADC. metan: an R package for multi-environment trial analysis. Methods Ecol Evol. 2020;11(6):783–9.
18. Genotype-by-environment interaction, AMMI, GGE biplot and mega-environment analysis of elite Sorghum bicolor genotypes in humid lowland areas of Ethiopia. Heliyon. 2024;10. PMCID:PMC10907745.
19. Assessment of yield performances for grain sorghum varieties by AMMI and GGE biplot analyses. Front Plant Sci. 2023;14:1261323. doi:10.3389/fpls.2023.1261323.
20. Analyzing genotype-environment interactions and identifying stable, high-yielding stay-green sorghum genotypes using different stability models. Res Sq [Preprint]. 2025. doi:10.21203/rs.3.rs-7893237/v1.
21. Genotype-by-environment interaction, correlation, AMMI, GGE biplot and cluster analysis for grain yield and agronomic traits in sorghum. BMC Plant Biol / PMCID:PMC8491923. 2021.
22. Abebe AT, Adewumi AS, Adebayo MA, Shaahu A, Mushoriwa H, Alabi T, *et al*. Genotype × environment interaction and yield stability of soybean genotypes in multi-environment trials in Nigeria. Heliyon. 2024;10(18):e38097. doi:10.1016/j.heliyon.2024.e38097.
23. Winans ND, *et al*. Envirotyping can increase genomic prediction accuracy of new environments in grain sorghum trials depending on mega-environment. Crop Sci. 2024;64(2). doi:10.1002csc2.21213.
24. Integrating envirotyping and phenomics for AI-enabled multi-environment genomic prediction in crop breeding. Agronomy. 2026;16(10):1019. doi:10.3390/agronomy16101019.
25. Envirotyping facilitates understanding of genotype × environment interactions and highlights the potential of stay-green traits in wheat. bioRxiv [Preprint]. 2025. doi:10.1101/2025.03.11.642575.
26. Envirome-wide associations enhance multi-year genome-based prediction of historical wheat breeding data. bioRxiv [Preprint]. 2022. doi:10.1101/2022.08.14.503901.
27. Integrating enviromics to predict performance and guide clonal deployment in Eucalyptus spp. bioRxiv [Preprint]. 2025. doi:10.64898/2025.12.01.691191.
28. Selection of suitable wheat genotypes under thermal stress and complex genotype-environment interaction using stability analyses and selection indices. PMCID:PMC12476864. 2025.
29. Dissection of genotype-by-environment interaction and simultaneous selection for grain yield and stability in faba bean (Vicia faba L.). bioRxiv [Preprint]. 2022. doi:10.1101/2022.09.08.507215.
30. Finlay and Wilkinson model vs. AMMI model in the analysis of genotype-environment interaction in sorghum. Rev Fac Agron / ResearchGate. 2015.
31. A comprehensive comparison between Eberhart and Russell joint regression and GGE biplot analyses to identify stable, high-yielding maize hybrids. Field Crops Res. 2010;118(3):218–25. doi:10.1016/j.fcr.2010.05.006.
32. Adaptability and stability for soybean yield by AMMI and GGE models in Ethiopia. Front Plant Sci. 2022;13. PMCID:PMC9727298.
33. Global sorghum production dataset for temperate to subtropical regions at subnational scale over 2000–2020. Data Brief. 2025. PMCID:PMC12356385.
34. AMMI and GGE biplot analysis for yield performance and stability of Bambara groundnut genotypes under multi-environmental trials. Sci Rep. 2021;11:22791. PMCID:PMC8611061.
35. Teferra TF, Awika JM. Sorghum as a healthy global food security crop: opportunities and challenges. Cereal Foods World. 2019;64(5). doi:10.1094/CFW-64-5-0052.