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Risk Analysis of Introducing Stable, High-Yielding Wheat Genotypes under Late-Season Drought Stress Conditions

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Article

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Abstracts

Bayesian probabilistic methods in multi-environment trials enable the simultaneous assessment of yield, stability, and both broad and specific adaptation of genotypes. More importantly, these methods incorporate estimation uncertainty into the decision-making process. To assess the probability and risk of selecting high-yielding and stable wheat genotypes under late-season water deficit, 20 genotypes were evaluated in a randomized complete block design with three replications across nine locations over two consecutive growing seasons. The Bayesian model estimated variance components of 0.008, 1.714, and 0.388 for genotype, environment, and genotype × environment interaction, respectively, indicating that environmental effects contributed most substantially to the observed variation. A selection intensity of 20% was applied to increase the mean grain yield of the selected genotypes. Overall, environmental conditions were the main source of yield variation, while the significant genotype × environment interaction indicated differential genotype responses across environments. Bayesian analysis facilitated decision-making under uncertainty by providing posterior distributions and probabilities of superior yield and stability. Although genotypes G3, G8, and G12 exhibited the highest posterior mean yields, their pairwise superiority probabilities indicated uncertainty in their superiority over some other genotypes. G16 showed the highest probability of superior yield, whereas G17 exhibited the greatest stability based on the probability of stability superiority. They were followed by G4, G9, and G3 in terms of yield. In contrast, the probability of pairwise stability superiority ranked G8, G7, G12, G10, and G20 as the most stable genotypes, respectively. G17 showed the highest joint probability of superior yield and stability (approximately 0.11), followed by G3, G4, G9, and G6. Despite the low absolute probabilities, the joint ranking of genotypes for yield and stability indicated that these genotypes had a greater likelihood of simultaneously meeting both breeding objectives than the other genotypes. Therefore, the final selection of genotypes should not be made based on yield or stability alone, but the simultaneous combination of yield, stability and probability of superiority should be the basis of breeding decisions. This approach can facilitate the identification of wheat genotypes with superior yield and broader adaptation across diverse environments.
Keywords: Stability, Uncertainty, Pairwise dominance probability, Genotype × Environment interaction, Wheat

1. Introduction

In crop breeding under stress conditions, selecting appropriate environments is crucial for identifying desirable genotypes. Given the substantial damage caused by environmental stresses to crops, particularly cereals, in recent years, evaluating crop responses to such stresses has received increasing attention (Passioura, 2007). In this context, grain yield and its stability across environments subject to environmental stresses are important criteria for cultivar selection and recommendation (Rajaram and Van Ginkel, 2001). Siddique et al. (2000) reported that improving yield and yield stability under drought stress, together with the adoption of drought-tolerant cultivars, is an effective strategy for enhancing crop productivity under water-limited conditions. Developing high-yielding and stable cultivars adapted to drought-prone environments, with desirable traits such as early maturity and resistance to pests and diseases, is essential.

Genotypes often differ in their yield across environments, resulting in changes in their relative ranking from one environment to another. These changes resulting from the interaction between genotype and environment are referred to as genotype × environment interactions (Najafi Mirak, 2018). Investigating genotype × environment interaction provides valuable information on cultivar yield across environments and is essential for assessing yield stability and adaptability (Karadavut et al., 2010). Reducing genotype × environment interaction and improving yield stability across

environments are key objectives in wheat cultivar development and recommendation (Yan and Rajcan, 2002). Genotype × environment interaction can alter genotype yield across environments, making it difficult to accurately estimate their true genetic value (Scapim et al., 2000). The presence of genotype × environment interaction reduces the correspondence between genotypic and phenotypic values, causing genotypes that perform well in one environment to perform poorly in another (Blanche and Myers, 2006). Genotype × environment interaction for important traits such as grain yield can hinder the efficient selection and release of new cultivars (Kang, 1988).

In addition to yield stability, cultivar adaptability is another important factor that should be considered. Although adaptability is a complex concept, it can be defined as the genetic capacity of a cultivar to achieve high and stable yield across diverse environments (Farshadfar, 1998). Given the considerable time and economic resources required to develop high-yielding, well-adapted cultivars, genotypes with broad adaptability and acceptable yield across diverse environments should be prioritized for selection and recommendation (Akcura et al., 2006).

Multi-environment trials (METs) are a key component of plant breeding programs, enabling the evaluation of genotype yield and adaptability across diverse climatic and management conditions. In these trials, genotype responses vary with environmental conditions, and genotype × environment interaction (GEI) can alter the relative ranking of cultivars across environments. This interaction complicates the selection and recommendation of superior genotypes for target environments; therefore, the simultaneous evaluation of yield and stability is a key objective in plant breeding. An ideal cultivar should not only have high yield potential but also maintain relatively stable yield across a wide range of environmental conditions (Crossa, 1990; Yan and Kang, 2003; Gauch et al., 2008).

Over the past decades, numerous methods have been developed to assess yield stability. Univariate methods, including Finlay–Wilkinson regression (Finlay and Wilkinson, 1963), the Eberhart–Russell model (Eberhart and Russell, 1966), and Shukla's stability variance (Shukla, 1972), were among the earliest statistical approaches used to assess genotype adaptability and stability. Although these methods provide valuable information on genotype responses to environmental variation, their reliance on single indicators limits their ability to capture the complexity of genotype × environment interaction. To address these limitations, multivariate approaches such as principal component analysis (PCA), the additive main effects and multiplicative interaction (AMMI) model (Gauch, 1992), site regression (SREG) (Crossa, 1990), GGE biplot (Yan et al., 2000), and factor-analytic models (Smith et al., 2001) have been developed to better characterize genotype × environment interaction and identify stable genotypes.

Despite advances in classical approaches to genotype × environment interaction analysis, these methods have limitations that may affect the accuracy of inferences from multi-environment trials. Methods such as AMMI and GGE biplot are primarily based on the frequentist framework and typically rely on point estimates of model parameters. In these approaches, the uncertainty surrounding the estimation of genotypic effects, environmental effects, and genotype × environment interaction is not explicitly accounted for, whereas reliable assessment of genotype stability requires this uncertainty to be incorporated into the analysis of multi-environment trial data (Van Eeuwijk et al., 2016). Another limitation is the strong dependence of these methods on data structure and the number of environments evaluated. In many breeding programs, multi-environment trial data may be unbalanced, for example, some genotypes may not be evaluated across all environments, or the number of replications may vary among environments. In such situations, frequentist methods, such as combined analysis of variance, may fail to fully capture the underlying variance–covariance structure across environments (Piepho et al., 2008). Moreover,

selecting the appropriate number of principal components in AMMI typically relies on statistical tests, such as the F-test, or variance-based criteria, which may lead to over- or under-selection of components in some cases (Gauch, 2013). REML/BLUP-based linear mixed models represent an important advancement in multi-environment data analysis by accounting for random genotype and environmental effects, enabling the estimation of variance components and prediction of genetic values (Resende, 2007). However, REML/BLUP methods still rely primarily on point estimates and may require probabilistic frameworks to more fully account for parameter uncertainty. This limitation is particularly important when the number of environments is limited, heritability is low, or the data structure is complex (Crossa et al., 2017).

The increasing complexity of multi-environment data and the need to predict genotype yield under new environmental conditions have driven a shift from classical point-estimation methods toward probabilistic and prediction-oriented models. Bayesian models have emerged as effective approaches for analyzing complex genotype × environment interactions by accounting for uncertainty, incorporating prior information with observed data, and estimating posterior parameter distributions (Gelman et al., 2013; Albert, 2020). In Bayesian analysis, model parameters are represented as probability distributions rather than fixed values, with prior information updated by observed data to obtain posterior distributions (Gelman et al., 2013). This framework enables direct quantification of parameter uncertainty, estimation of credible intervals, and calculation of the probability that one genotype outperforms others. A major advantage of this framework is the simultaneous estimation of genetic and environmental variance components, genotype × environment interaction, and error variance, together with their associated uncertainty. This feature enables Bayesian mixed models to provide more robust and reliable estimates than many classical methods when data are unbalanced, observations are missing, the number of environments is limited, or variances are heterogeneous across environments (Sorensen and Gianola, 2002).

The fundamental difference between Bayesian and frequentist approaches lies in their treatment of model parameters. In frequentist statistics, parameters are regarded as fixed but unknown quantities, whereas in the Bayesian framework, they are treated as random variables characterized by probability distributions. This framework enables simultaneous assessment of parameter estimates and their associated uncertainty, allowing decisions to be based on more than a single point estimate. For example, the probability of a genotype outperforming other genotypes or belonging to the most stable group can be directly estimated from posterior distributions, a capability not readily available in many classical methods (Hoff, 2009). Dias et al. (2022) investigated the theoretical and practical foundations of Bayesian probabilistic methods for reducing decision-making risk in breeding programs. In this study, Bayesian models were used to partition and evaluate genotype × environment interaction. The results showed good agreement between the Bayesian probabilistic approach and classical models for evaluating genotype × environment interaction. This finding indicates that, while retaining the information provided by conventional methods, the Bayesian approach can provide additional insights into parameter uncertainty and the probability of genotype superiority. Shiri et al. (2025) used a Bayesian approach to assess the probability of superior yield and stability among maize hybrids in a multi-environment trial. They identified several superior hybrids and showed that environmental effects contributed more to yield variation, indicating that mean yield alone is insufficient for genotype selection. The results indicated that probability- and risk-based approaches can improve the accuracy of cultivar selection and recommendation across diverse environments.

Given the advantages of the Bayesian framework for analyzing multi-environment trials, this study aimed to assess genotype × environment interaction and simultaneously evaluate the yield, stability, and selection risk of wheat genotypes under terminal drought stress. The results are expected to improve selection accuracy and support the identification and recommendation of high-yielding, stable, and broadly adapted genotypes across diverse environments.

2. Materials and methods

2.1. Plant materials and experimental design

In this study, 20 wheat lines, including 18 genotypes selected from nationwide advanced yield trials representing winter and facultative growth types, along with the check cultivars Zarrineh and Heyran, were evaluated in a randomized complete block design with three replications at the research stations of Karaj, Mashhad, Miandoab, Tabriz, Arak, Jolgerok, Hamedan, Ardabil, and Zanjan during the 2021–2023 growing seasons under late-season water deficit (Table 1).

2.2. Crop management and late-season drought stresses

Agricultural management practices were largely consistent across the different experimental stations. At each experimental station, land preparation consisted of plowing, disc harrowing, two passes with a horizontal land leveler, fertilizer application, and furrow formation at 60 cm spacing. Potassium sulfate and ammonium phosphate were applied as basal fertilizers, while urea was applied in two split doses: at planting and as a topdressing. Each genotype was sown in a 6 m^2 plot at a density of 450 seeds m^{-2}, with the seeding rate adjusted based on the 1,000 seed weight. To control seed-borne fungal pathogens, the seeds were treated with carboxin–thiram fungicide at a rate of 2 g kg^{-1} seed before planting. To control weeds from tillering to stem elongation, a mixture of Puma Super and Granstar herbicides was applied at rates of 1 L ha^{-1} and 20 g ha^{-1}, respectively. Late-season water stress was imposed during the grain-filling stage by discontinuing irrigation from this stage onward, resulting in two fewer irrigation events than under normal irrigation conditions.

2.3. Statistical analysis

To evaluate genotype Yield, adaptability, and stability across multi-environment trials, a Bayesian linear mixed model implemented in the ProbBreed package in RStudio was used (Chaves et al., 2024). In this study, genotype, environment, and replication were included in the model as genetic, environmental, and experimental design effects, respectively. The effects of year and region were not included in the model, and homogeneous residual variance was assumed across environments. The observed yield of genotype *i* in environment *j* and replication *k* was modeled as follows:

$$Y_{ijk} = \mu + G_i + E_j + R_{k(j)} + GE_{ij} + \varepsilon_{ijk}$$

Where Y_{ijk} is the observed yield of genotype *i* in environment *j* and replication *k*; μ is the overall mean; G_i is the effect of genotype *i*; E_j is the effect of environment *j*; $R_{k(j)}$ is the effect of replication *k* nested within environment *j*; GE_{ij} is the genotype × environment interaction effect; and ε_{ijk} is the random residual error (Dias et al., 2022).

2.4. Bayesian inference and posterior analysis

SAS software was used for the combined analysis of the data and to test the homogeneity of experimental error variances across environments. The Bayesian model was fitted using the

bayes_met() function. Posterior sampling was performed using the No-U-Turn Sampler (NUTS), a Hamiltonian Monte Carlo (HMC) algorithm implemented in the Stan platform (Hoffman and Gelman, 2014; Carpenter et al., 2017). This approach eliminates the need to pre-specify the number of leapfrog steps. This approach mitigates random-walk behavior, thereby improving computational efficiency (Hoffman & Gelman, 2014; Nishio & Arakawa, 2019). Four independent Markov chains were run to fit the model, each consisting of 6,000 iterations. The first 3,000 iterations of each chain were discarded as warm-up, and the remaining samples were used for posterior inference.

2.5. Stability and genotype comparison

After model fitting and extraction of the posterior outputs, model adequacy was assessed using posterior predictive checks, while density plots and parameter diagnostic plots were examined to evaluate model fit and the posterior distributions. To compare genotypes, the posterior probability of superiority was calculated using a 90% credible interval for the probability estimates. Based on the posterior distributions, the mean genotypic effects, highest posterior density (HPD) credible intervals, and posterior probabilities of superiority were estimated for each genotype and used to rank genotypes according to their predicted yield. Genotype stability was also assessed using the posterior probability of stability. In addition to the posterior probability of stability across environments, the pairwise posterior probabilities of superiority and stability were estimated for comparisons among genotypes. The posterior probabilities of genotype yield and stability were also estimated separately within each environment to assess genotype-specific adaptation across environments.

To present the results, HPD credible interval plots, posterior probability of superiority and stability plots, pairwise probability matrices for yield and stability, the Joint yield –Stability Index, and environment-specific genotype yield results were generated and interpreted. These analyses enabled probabilistic comparisons among genotypes while explicitly accounting for uncertainty in the estimated parameters. All statistical analyses were performed in the R environment using RStudio (Posit Software, Boston, MA, USA). Bayesian model fitting for the multi-environment trials, posterior distribution extraction, model adequacy assessment, estimation of genotype superiority and stability probabilities, and generation of diagnostic plots were performed using the Prob Breed package.

Table 1. Wheat genotypes and their pedigrees, along with the locations where the experiments were conducted

Genotype No.	Pedigree
G1	Zarrineh(check1)
G2	Heyran (check2)
G3	EVWYT2/Azd//Rsh*2/10120/3/ Yan7578.128//Chil/2*Star
G4	Mihan/3/CMH79A.955/Bow//Pastor
G5	Mihan/3/CMH79A.955/Bow//Pastor
G6	Weizen/Mihan//Gaspard
G7	Weizen/Mihan//Gaspard
G8	Khalij/4/Ghk"s"/Bow"s"//90Zhong87/3/Shiroodi/5/Khalij/3/Yan7578.128//Chil/2*Star
G9	Catbird/Titona//Oroum
G10	Mo/4/Nd/WW15//Lee/Fn/3/N.5/Nac/5/2*Yan7578.128//Chil/2*Star
G11	Khalij/MV17
G12	Babaga/Fiocco
G13	DORADE-5/3/PROGRESS//PYN/BAU/4/TX71A983.4/TX69D4812//PYN/3/VPM/MOS83.11.4.8//PEW
G14	KINGBIRD/BILINMIYEN96.7
G15	BABAX/LR42//BABAX*2/3/KURUKU/4/TX96V2427/5/KAUZ//ALTAR 84/AOS/3/F10S-1
G16	MV22-2000/9/KLEIBER/2*FL80//DONSK.POLUK./8/KS82W409/STEPHENS/7/ NAI /HN7// BUC /5/ F59-71~
G17	PFAU/SERI.1B//AMAD/3/KRONSTAD F2004/4/SHARK-6/5/SHARK-6
G18	AP04T8531/KS04WKS-19//KS980554-12~9
G19	DORADE-5/3/SHI#4414/CROW//GK SAGVARI/CA8055

G20	EVEREST/CEDAR								
Year	Karaj	Hamedan	Ardabil	Arak	Miandoab	Mashhad	Jolge-Rokh	Zanjan	Tabriz
Year1	E1	E2	E3	E4	E5	E6	E7	E8	E9
Year2	E10	E11	E12	E13	E14	E15	E16	E17	E18

3. Results

3.1. Analysis of variance and variance components

To assess the homogeneity of error variances, separate analyses of variance were performed for grain yield in each environment, followed by Bartlett's and Hartley's F_{max} tests (Table 2). Because Hartley's F_{max} test was non-significant based on the error variances from the individual environmental analyses, the assumption of homogeneous error variances across environments was satisfied.

The combined analysis of variance revealed that the effects of location and the year × location, genotype × year, and genotype × year × location interactions were significant at the 1% probability level, whereas the effect of year was significant at the 5% probability level (Table 3). The significant genotype × year × location interaction, representing the genotype × environment interaction across years, indicated that genotype responses were not consistent across environments and that their yield varied with changes in environmental conditions. In other words, the genotypes evaluated exhibited differential yield across environments (Amini et al., 2023). The relatively small contribution of the genotype effect to the total sum of squares (1%) suggests limited genetic differentiation among the genotypes evaluated, which may reflect their prior selection within breeding programs (Golkari et al., 2016). In contrast, the main effect of environment and the genotype × environment interaction accounted for 69% and 22% of the total variation in grain yield, respectively (Table 3). The substantial contribution of the environmental effect indicates pronounced differences among the experimental environments, providing sufficient environmental diversity to assess the adaptability of the genotypes (Amini et al., 2023; Ehyaei et al., 2022). Moreover, the significant genotype × environment interaction indicates that selecting superior genotypes solely on the basis of their mean yield across environments may be misleading, as genotype yield depends on environmental conditions and genotype rankings may change across environments (Ehyaei et al., 2022). Based on mean grain yield, genotypes G3, G8, G12, G2, and G19 were the highest-yielding, whereas G16, G4, G13, G5, and G7 exhibited the lowest mean yields. Despite the superior mean yield of some genotypes, the significant genotype × environment interaction indicates that high yield alone is insufficient for identifying consistently desirable genotypes. Therefore, in addition to grain yield, measures of adaptability and stability should be considered to identify genotypes that combine high yield with greater consistency across environments (Olivoto et al., 2019).

The variance component associated with the replication effect was very small (0.009), indicating limited variability among replications (Table 4). This result indicates that the experiment was conducted with high experimental uniformity, with no appreciable differences among replications. The genotypic variance was also low (0.007), suggesting limited genetic variation among the evaluated genotypes for the trait under study. The 90% highest posterior density (HPD) credible interval for this variance component ranged from 0.002 to 0.025, further indicating that the genotypic variance was small and that variation attributable to genotype effects was limited. This finding was consistent with the results of the conventional analysis of variance, which showed that the genotype effect was not statistically significant. In contrast, the environmental variance was the largest among the estimated variance components. The 90% highest posterior density (HPD) credible interval for this variance component (0.915–2.995) was entirely above zero, indicating substantial variability among the experimental environments.

Therefore, a substantial proportion of the observed variation in genotype yield can be attributed to differences in environmental conditions. The genotype × environment interaction variance was also relatively large, with its 90% highest posterior density (HPD) credible interval (0.332–0.453) entirely above zero. This result indicates a substantial genotype × environment interaction, demonstrating that genotypes responded differently across environments and that their relative yield rankings changed among environments. The presence of such an interaction underscores the need for stability analysis approaches, such as AMMI and GGE biplot, to identify genotypes with broad or environment-specific adaptation. The residual error variance (0.243) was considerably lower than the genotype × environment (G×E) interaction variance, suggesting that G×E interaction accounted for a greater proportion of the observed variation than random experimental error. This finding supports the quality and reliability of the experimental data for subsequent stability analysis. The relative contributions of the variance components showed that the environment accounted for approximately 72% of the total phenotypic variance. This result confirms that genotype yield was primarily influenced by environmental conditions, whereas the direct contribution of genotype effects was relatively limited. Nevertheless, the substantial variance associated with the genotype × environment interaction highlights the need to evaluate genotypes across diverse environments and assess the stability of their yield to identify superior and widely adapted genotypes.

Table 2. Variance of experimental error in different environments along with the Hartley F_{max} and Bartlett's tests to evaluate the uniformity of variances

Year	df	Karaj	Hamedan	Ardabil	Arak	Miandoab	Mashhad	Jolge-Rokh	Zanjan	Tabriz
Year1	38	0.281	0.212	0.245	0.227	0.339	0.264	0.242	0.234	0.185
Year2	38	0.24	0.282	0.239	0.19	0.208	0.278	0.174	0.313	0.188
Hartley's F_{max} = 1.95 ^{ns}										
Bartlet's statistic = 128.1**										

**: Significant at 1% probability levels,

Table 3. Combined analysis of variance of grain yield of bread wheat genotypes

Source of variation	Digree of freedom	Sum of square	Mean square	Percentage of total sum of square
Year	1	190.49	190.49**	9
Location	8	1097.2	137.15**	52
Year×Location	8	180.39	22.55**	8
Block (Year×Location)	36	14.88	0.413	1
Genotype	19	26.99	1.42	1
Year×Genotype	19	58.02	3.052**	3
Location×Genotype	152	186.65	1.23	9
Year×Location×Genotype	152	209.24	1.38**	10
Error	684	164.95		8
CV(%)	8.97			

* and **: Significant at 5% and 1% probability levels, respectively.

3.2. Genotypic effects and posterior distributions

To assess how well the fitted model reproduced the observed data-generating process, samples were drawn from the model's conditional joint distribution using posterior predictive sampling and compared graphically with the observed data. The generated and observed data were compared using key descriptive statistics, including the minimum, maximum, median, mean, and standard deviation, with posterior predictive probability values used to assess the agreement between the model-generated and observed distributions (Gelman et al., 2013). Bayesian p-values were used to assess the agreement between the observed data and the data generated by the fitted model by

calculating the proportion of replicated datasets in which the test statistic was equal to or more extreme than that observed in the original data. When the model adequately reproduces the observed data, the Bayesian posterior predictive p-values are expected to be close to 0.5 and, more generally, to remain away from the extreme values of 0.01 and 0.99 (Gelman et al., 2013). Therefore, Bayesian posterior predictive p-values close to 0.5 are generally considered desirable, as they indicate good agreement between the observed data and those replicated from the fitted model (Dias et al., 2022). In this study, the model-fit diagnostics also provided evidence of an adequate fit of the Bayesian model to the observed data. Comparison of the observed and model-generated data yielded Bayesian posterior predictive p-values ranging from 0.277 to 0.429 for the evaluated statistics (minimum, maximum, median, mean, and standard deviation) (Table 4). These values, being well above the extreme tails of the posterior predictive distribution, indicate good agreement between the observed and model-generated data and provide evidence of an adequate model fit. The p.val-mean value was close to 0.5, providing further evidence that the model adequately reproduced the distributional characteristics of the observed data. In addition, the mean R-hat (potential scale reduction factor), a diagnostic used to assess MCMC convergence, was equal to 1.00, indicating that the Markov chains had converged and that the posterior estimates were stable. This diagnostic compares within-chain and between-chain variability to assess the consistency of the chains and the convergence of the posterior distributions for the model parameters. Specifically, R-hat is based on the ratio of the estimated marginal posterior variance to the within-chain variance; values approaching 1 indicate that the within- and between-chain variances are similar, providing evidence of satisfactory convergence and consistent exploration of the parameter space across chains (Fabreti & Hohna, 2022). Conversely, R-hat values substantially greater than 1 indicate inadequate mixing and incomplete convergence of the MCMC chains, suggesting that the posterior distribution has not yet been reliably explored (Gelman et al., 2013). Moreover, a high effective sample size (ESS) indicates efficient sampling and satisfactory mixing of the MCMC chains, with a greater proportion of effectively independent posterior draws, thereby enhancing the precision and reliability of the resulting parameter estimates. Inspection of the posterior distributions of the model parameters provided further evidence of adequate model fit and satisfactory posterior sampling (Figure 1a). With the exception of the posterior distribution for the environmental effect, which was broader owing to the substantial heterogeneity among the experimental environments, the remaining posterior distributions were unimodal and well-behaved, with no pronounced skewness or irregular tails. This pattern further supports satisfactory posterior convergence and efficient yield of the MCMC sampling algorithm. Moreover, the relatively narrow posterior distribution of the genotype effect indicates lower uncertainty in its estimation, thereby increasing confidence in the discrimination and comparison of genotypic yield. It should be noted that when the posterior distribution of a variance component is approximately symmetric, the resulting estimates and inferences are generally insensitive to the choice of central tendency measure, such as the mean or median. Finally, the posterior predictive check showed a strong overlap between the distributions of the observed and model-generated data, with their density curves closely coinciding, further supporting the adequacy of the fitted model. This close agreement demonstrates the model's ability to capture the underlying structure of the observed data and further supports the suitability of the Bayesian framework for analyzing data from multi-environment experiments (Figure 1b).

Table 4. Table 4. Posterior means of variance components, cumulative percentage of total variance, 95% highest posterior density (HPD) intervals, posterior predictive p-values, and Bayesian model diagnostic statistics.

Effect	Variance	cumulative percentage of total variance	$HPD_{0.05}$	$HPD_{0.95}$	Parameter	Value

					p.val-max	0.7727
REP	0.009	0.4%	0.002	0.02	p.val-min	0.429
GEN	0.008	0.3%	0	0.027	p.val-median	0.4249
ENV	1.714	72.5%	0.9	3.065	p.val-mean	0.4878
GEN:ENV	0.388	16.5%	0.331	0.451	p.val-sd	0.5048
error	0.243	10.3%	0.223	0.265	Eff-No-parameters	157.7745
					WAIC2	2268.6882
					Mean-Rhat	1
					Eff_sample_size	1.1155

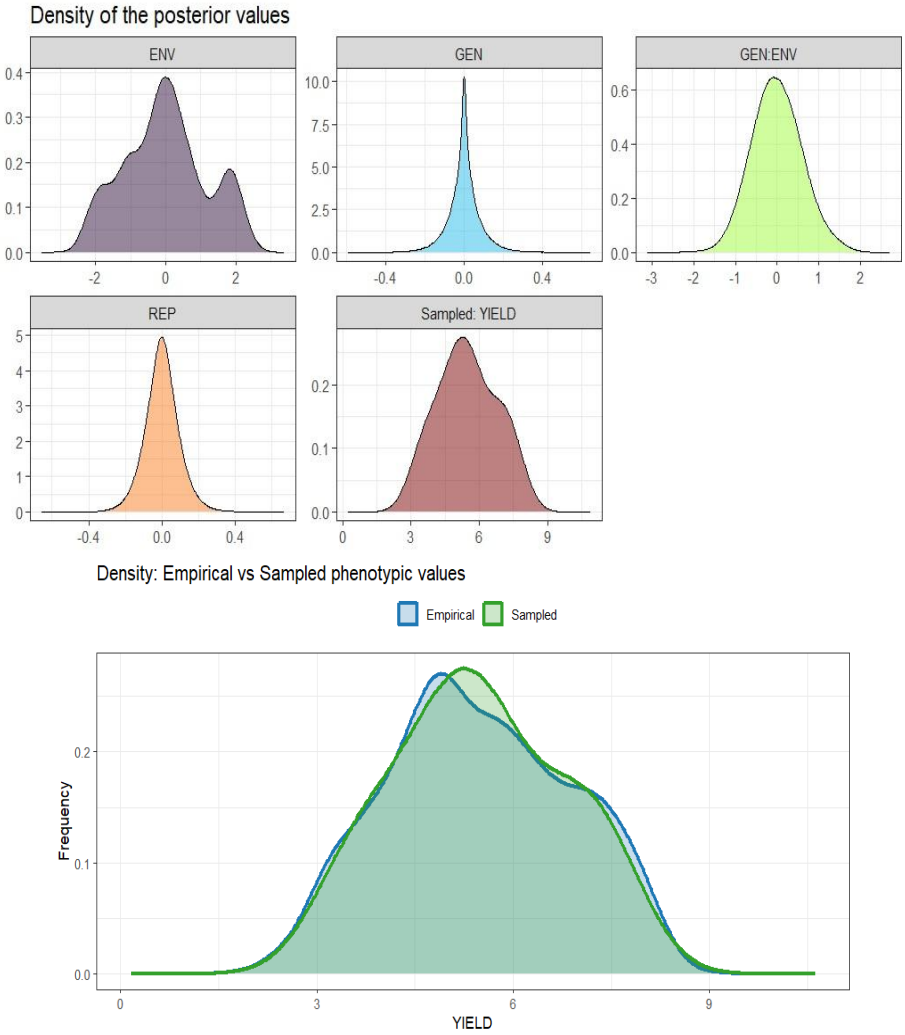


Fig. 1. (a) Posterior density distributions of the estimated model parameters, illustrating the uncertainty associated with the Bayesian estimates. (b) Posterior predictive check comparing the observed data with data simulated from the fitted Bayesian model.

3.3. Probability of superiority

Examination of the posterior means of the genotypic effects indicated that G3, G8, G12, G2, and G19 had positive genetic effects, suggesting that these genotypes were expected to perform above the overall population mean. In contrast, the remaining genotypes exhibited negative posterior estimates of genotypic effects, indicating that their expected yields were below the overall mean (Table 5). However, the 95% highest posterior density (HPD) intervals for the genotypic effects of all genotypes included zero (Figure 2), indicating that the estimated deviations

from the overall mean were not sufficiently supported by the posterior distributions. Therefore, the posterior evidence was insufficient to establish a definitive difference between the genotypic effect of any genotype and zero. This result is fully consistent with the estimated variance components, as the posterior estimate of genotypic variance was very small, indicating limited variation in mean yield among the genotypes. In contrast, most of the variation in genotypic yield was attributable to environmental effects and genotype × environment interaction. The posterior-based Probability of Superiority analysis indicated that G3, G8, G12, and G2 exceeded the overall mean by at least 20% in 50%, 43%, 32%, and 31% of the posterior samples, respectively, corresponding to a 20% selection intensity. These findings indicate that, despite the relatively small genotypic variance, these genotypes had the highest posterior probability of attaining the target yield level, highlighting their potential value as promising candidates for further evaluation in breeding programs (Table 5; Figure 3). The results further indicated that, despite the relatively small differences in mean genotypic yield, the substantial environmental variance and pronounced genotype × environment interaction resulted in considerable variation in the probability of superior genotypic yield across environments. These finding highlights one of the key advantages of the Bayesian framework: genotype selection is not based solely on posterior mean yield, but also incorporates the uncertainty associated with the parameter estimates, thereby providing a more comprehensive basis for genotype evaluation. The stability probability of each genotype was also estimated from the posterior distribution of the genotype × environment interaction effects. Higher posterior probabilities indicate greater confidence that a genotype exhibits consistent and stable yield across different environments. In this study, genotype G17 was identified as the most stable genotype, with a posterior probability of stability of 86%. This was followed by G4, G9, and G3, with posterior probabilities of stability of 80%, 40%, and approximately 20%, respectively (Table 5; Figure 4). Accordingly, G17 and, to a lesser extent, G4 can be classified as stable genotypes, whereas G9 exhibited intermediate stability and G3 was characterized as relatively unstable. Notably, although genotype G3 exhibited the highest probability of superior yield, it had a relatively low posterior probability of stability. This finding indicates that a genotype with superior yield potential is not necessarily the most desirable genotype in terms of yield stability across environments. Therefore, the selection of genotypes for release or incorporation into breeding programs should consider yield, stability, and the uncertainty surrounding their estimates simultaneously, representing a major advantage of the Bayesian framework over conventional approaches.

Table 5. Posterior means of genotypic effects, predicted yield, 90% highest posterior density (HPD) intervals, probability of superiority, and probability of stability for the evaluated genotypes.

Genotype	Yield	Posterior Mean of Genotypic Effect	$HPD_{0.95}$	$HPD_{0.05}$	Probability of Superiority	Predicted Yield	$HPD_{0.95}$	$HPD_{0.05}$	Probability of stability
G1		0.0023	0.1291	-0.1134	20	5.482	5.33	5.641	16
G2		0.0166	0.1771	-0.0714	31	5.508	5.38	5.696	10
G3		0.0458	0.2594	-0.0336	50	5.548	5.424	5.784	20
G4		-0.0176	0.0685	-0.1785	10	5.443	5.252	5.572	80
G5		-0.0112	0.0834	-0.1551	12	5.455	5.28	5.59	14
G6		-0.0048	0.1009	-0.1369	16	5.466	5.297	5.609	34
G7		-0.0111	0.0846	-0.1559	12	5.454	5.278	5.589	0.1
G8		0.0354	0.2309	-0.0458	43	5.535	5.411	5.755	0
G9		-0.0020	0.1070	-0.1249	16	5.471	5.317	5.615	40
G10		-0.0085	0.0909	-0.1544	13	5.458	5.281	5.6	0.1
G11		-0.0006	0.1116	-0.1220	17	5.473	5.322	5.62	12
G12		0.0193	0.1831	-0.0715	32	5.511	5.376	5.7	0
G13		-0.0152	0.0730	-0.1741	10	5.446	5.259	5.576	31
G14		0.0023	0.1217	-0.1122	19	5.481	5.33	5.634	8
G15		-0.0046	0.1016	-0.1380	15	5.466	5.301	5.614	17
G16		-0.0290	0.0506	-0.2140	7	5.426	5.214	5.55	5

G17	-0.0096	0.0893	-0.1501	13	5.457	5.29	5.595	86
G18	-0.0021	0.1107	-0.1262	16	5.472	5.315	5.621	13
G19	0.0154	0.1724	-0.0771	30	5.506	5.371	5.687	14
G20	-0.0003	0.1203	-0.1228	18	5.475	5.316	5.632	0.1

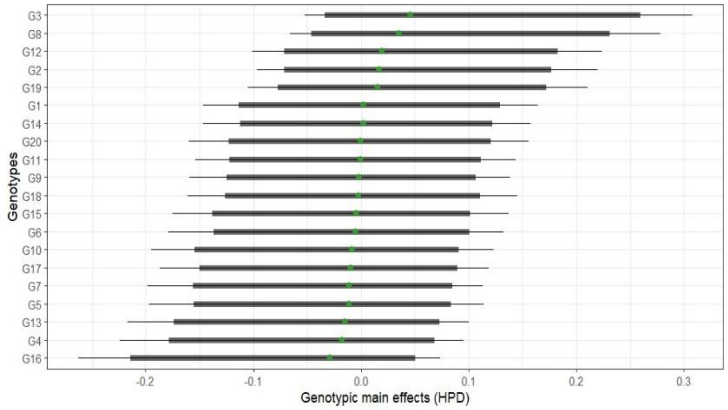


Fig. 2. Posterior means of genotypic main effects with 90% highest posterior density (HPD) intervals for the evaluated genotypes. Green diamonds represent posterior mean estimates, and horizontal bars indicate the corresponding 90% HPD intervals.

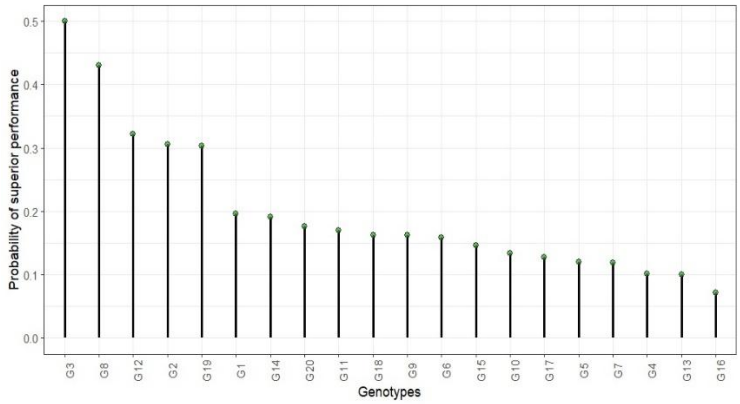


Fig. 3. Posterior probability of superiority for the evaluated genotypes based on the Bayesian mixed model. Higher probabilities indicate a greater likelihood that a genotype outperforms the remaining genotypes across the target environments.

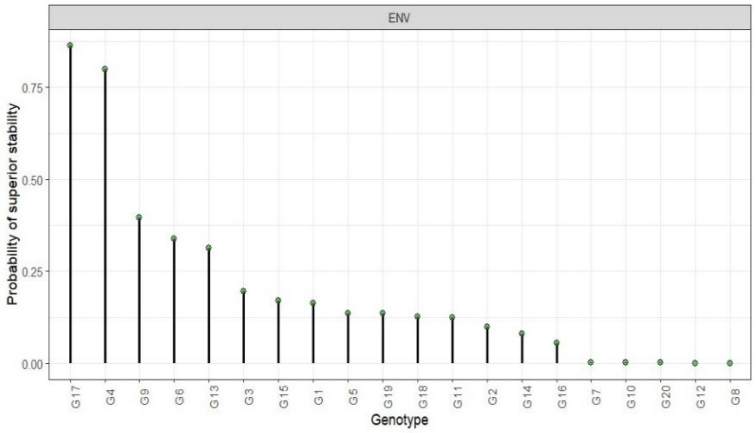


Fig. 4. Posterior probability of stability for the evaluated genotypes based on the Bayesian mixed model. Genotypes are ranked in descending order according to their probability of exhibiting stable

3.4. Pairwise probability of superiority comparisons

The pairwise probability of superiority matrix represents the posterior probability that each genotype outperforms every other genotype in terms of yield yield (Table 6). Pairwise comparisons among genotypes provide valuable insight into their relative yield and the probability of one genotype outperforming another. This information is particularly valuable during the advanced stages of breeding programs, when the primary objective is to identify superior genotypes for potential variety release. Pairwise comparisons enable the direct assessment of the relative strengths and weaknesses of each genotype against other genotypes or control cultivars, thereby providing a more informative basis for selecting superior genotypes with greater confidence. Because these probabilities are derived from posterior samples, the uncertainty associated with parameter estimation is inherently incorporated into the comparisons. Consequently, this approach provides a more comprehensive and realistic assessment of genotypic yield across diverse environments. Rather than imposing a definitive ranking, the Bayesian framework quantifies the posterior probability of superiority or stability for each genotype, enabling breeders to incorporate the degree of uncertainty and their confidence in each selection decision (Dias et al., 2022). Unlike conventional approaches that rank genotypes solely according to their mean yield, this Bayesian framework enables all genotypes to be compared pairwise using their posterior distributions. In other words, each entry in the matrix represents the posterior probability that the genotype in the corresponding row outperforms the genotype in the corresponding column.

According to the results, G16 was the most prominent genotype in terms of its posterior probability of superiority in pairwise comparisons. Compared with G3, G8, G2, G12, G4, G13, G15, G19, and the other genotypes, G16 exhibited a high posterior probability of superiority. For example, the posterior probability that G16 outperformed G3 was 0.83, while the corresponding probability relative to G8 was 0.80. These values indicate that, according to the posterior distribution, G16 had a high probability of outperforming both G3 and G8. In contrast, G3 and G8 exhibited relatively low posterior probabilities of superiority in pairwise comparisons with many of the other genotypes. For example, the posterior probability that G3 outperformed G16 was only 0.17, while its corresponding probability relative to G13 was 0.20. Likewise, G8 had a posterior probability of superiority of only 0.20 relative to G16. Thus, although these genotypes may exhibit relatively favorable yield based on their posterior mean genotypic effects, the pairwise comparisons provide limited evidence that they outperform the leading genotypes. Genotypes G13 and G4 also exhibited relatively favorable yield in the pairwise comparisons. For example, the posterior probability that G13 outperformed G3 and G8 was 0.80 and 0.76, respectively, whereas the corresponding probabilities for G4 were 0.80 and 0.77, respectively. These findings indicate that G13 and G4 were relatively favorable genotypes, exhibiting a high posterior probability of superiority in pairwise comparisons. Although G16 did not necessarily exhibit the highest posterior mean genotypic effect, it showed the strongest evidence of pairwise superiority over the other genotypes. This finding highlights the value of pairwise superiority probabilities within the Bayesian framework, as this criterion not only reflects relative genotypic yield but also explicitly incorporates uncertainty into the comparisons among genotypes. Although G3, G8, and G12 exhibited the highest posterior mean yields, their pairwise superiority probabilities indicated considerable uncertainty in their relative advantage over certain genotypes. This discrepancy suggests that ranking genotypes solely according to posterior mean estimates may not fully capture the uncertainty surrounding their relative yield. Therefore, incorporating posterior probabilities provides complementary information that can improve the discrimination, comparison, and selection of genotypes under uncertainty. Accordingly, final genotype recommendations should

be based on a joint assessment of posterior mean yield, stability probabilities, and integrated yield–stability criteria, thereby accounting for both expected yield and the uncertainty surrounding these estimates in the selection decision.

For ease of interpretation, the results of the pairwise comparisons are also presented as a heatmap in Figure 5, where the color intensity represents the posterior probability of one genotype outperforming another. However, the magnitude of these probabilities should also be considered when interpreting the evidence for genotypic superiority. Probabilities close to 50% indicate only a marginal advantage and substantial uncertainty, providing limited evidence that one genotype is superior to the other. Probabilities between 60% and 80% may be interpreted as moderate evidence of genotypic superiority, whereas probabilities exceeding 80% provide strong evidence that one genotype outperforms the other. G16 occupied the uppermost position on the vertical axis, and its color pattern indicated a high posterior probability of superiority over many of the other genotypes. In particular, the pairwise comparison matrix showed that the posterior probability of G16 outperforming G3 and G8 was 0.83 and 0.80, respectively. Thus, G16 exhibited the strongest overall evidence of pairwise superiority among the evaluated genotypes, followed by G13 and G4. It should be emphasized that this figure does not represent a simple ranking based on mean yield; rather, it reflects the posterior probability that one genotype will outperform another. Thus, the pattern of the pairwise probabilities also convey information about the uncertainty associated with the comparisons. For example, a probability of 0.83 for G16 relative to G3 indicates that, according to the posterior distribution, there is an 83% probability that G16 outperforms G3. In contrast, the posterior probability that G3 outperforms G16 is only 17%. Thus, Bayesian inference incorporates not only the relative ranking of genotypes but also the degree of uncertainty surrounding their superiority into the decision-making process, representing a major advantage of the Bayesian framework over conventional methods.

Table 6. Pairwise posterior probabilities of superior yield among wheat genotypes estimated from the Bayesian mixed model.

	G1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12	G13	G14	G15	G16	G17	G18	G19	G20
G1	0	0.59	0.72	0.37	0.41	0.45	0.40	0.67	0.46	0.42	0.48	0.60	0.38	0.50	0.44	0.32	0.41	0.46	0.59	0.48
G2	0.41	0	0.63	0.29	0.32	0.36	0.32	0.59	0.37	0.34	0.38	0.51	0.30	0.40	0.35	0.25	0.33	0.38	0.50	0.39
G3	0.28	0.37	0	0.20	0.22	0.25	0.22	0.45	0.25	0.23	0.27	0.37	0.20	0.29	0.25	0.17	0.23	0.26	0.35	0.27
G4	0.63	0.71	0.80	0	0.54	0.58	0.54	0.77	0.60	0.56	0.60	0.72	0.51	0.63	0.58	0.44	0.55	0.60	0.71	0.61
G5	0.59	0.68	0.78	0.46	0	0.54	0.50	0.75	0.56	0.51	0.57	0.69	0.47	0.60	0.54	0.40	0.51	0.55	0.68	0.57
G6	0.55	0.64	0.75	0.42	0.46	0	0.45	0.71	0.52	0.47	0.53	0.65	0.43	0.55	0.50	0.37	0.47	0.52	0.64	0.53
G7	0.60	0.68	0.78	0.46	0.50	0.55	0	0.75	0.57	0.51	0.57	0.69	0.47	0.59	0.54	0.41	0.51	0.56	0.68	0.58
G8	0.33	0.41	0.55	0.23	0.25	0.29	0.25	0	0.30	0.27	0.31	0.42	0.24	0.33	0.28	0.20	0.26	0.29	0.40	0.31
G9	0.54	0.63	0.75	0.40	0.44	0.48	0.43	0.70	0	0.46	0.51	0.64	0.41	0.54	0.48	0.35	0.45	0.50	0.62	0.51
G10	0.58	0.66	0.77	0.44	0.49	0.53	0.49	0.73	0.54	0	0.56	0.68	0.46	0.58	0.53	0.39	0.49	0.55	0.67	0.56
G11	0.52	0.62	0.73	0.40	0.43	0.47	0.43	0.69	0.49	0.44	0	0.63	0.40	0.52	0.47	0.34	0.44	0.49	0.61	0.51
G12	0.40	0.49	0.63	0.28	0.31	0.35	0.31	0.58	0.36	0.32	0.37	0	0.29	0.40	0.34	0.25	0.32	0.37	0.48	0.38
G13	0.62	0.70	0.80	0.49	0.53	0.57	0.53	0.76	0.59	0.54	0.60	0.71	0	0.62	0.57	0.43	0.54	0.59	0.70	0.60
G14	0.50	0.60	0.71	0.37	0.40	0.45	0.41	0.67	0.46	0.42	0.48	0.60	0.38	0	0.44	0.32	0.41	0.46	0.59	0.48
G15	0.56	0.65	0.75	0.42	0.46	0.50	0.46	0.72	0.52	0.47	0.53	0.66	0.43	0.56	0	0.36	0.47	0.52	0.64	0.53
G16	0.68	0.75	0.83	0.56	0.60	0.63	0.60	0.80	0.65	0.61	0.66	0.75	0.58	0.68	0.64	0	0.61	0.65	0.75	0.66
G17	0.59	0.67	0.77	0.45	0.49	0.53	0.49	0.74	0.55	0.51	0.56	0.68	0.46	0.59	0.53	0.39	0	0.55	0.67	0.56
G18	0.54	0.62	0.74	0.40	0.45	0.48	0.44	0.71	0.50	0.45	0.51	0.63	0.41	0.54	0.48	0.35	0.45	0	0.63	0.51
G19	0.41	0.50	0.65	0.29	0.32	0.36	0.32	0.60	0.38	0.33	0.39	0.52	0.30	0.41	0.36	0.25	0.33	0.37	0	0.40
G20	0.52	0.61	0.73	0.39	0.43	0.47	0.42	0.69	0.49	0.44	0.49	0.62	0.40	0.52	0.47	0.34	0.44	0.49	0.60	0

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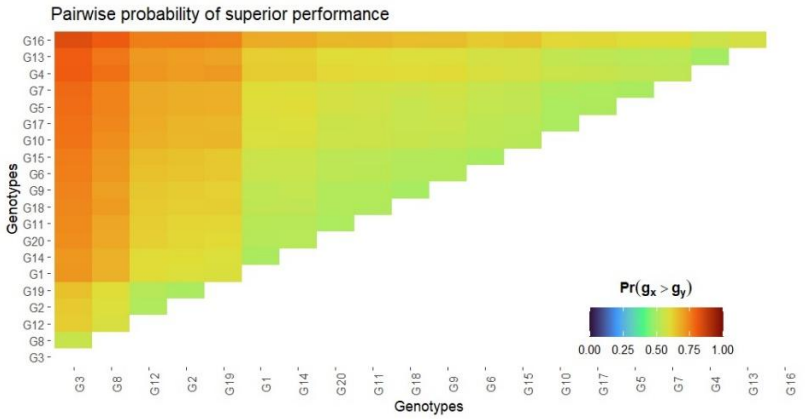


Fig. 5. Heatmap of pairwise posterior probabilities of superior yield among the evaluated wheat genotypes. Cell colors represent the posterior probability that the genotype in each row outperforms the genotype in the corresponding column [$Pr(g_x > g_y)$].

3.5 Pairwise probability of superior stability comparisons

The pairwise probability of superior stability matrix represents the posterior probability that each genotype exhibits greater stability than the other genotypes, based on the posterior distribution of genotype × environment interaction effects (Table 7). The stability criterion was defined based on the variance of the genotype × environment (G × E) interaction effect. A lower G × E interaction variance indicates greater stability of the corresponding genotype across environments. In this matrix, each entry represents the posterior probability that the genotype in the row is more stable than the genotype in the corresponding column. Values close to 1 indicate strong posterior evidence that the row genotype is more stable than the column genotype, whereas values close to 0 indicate greater stability of the column genotype. The overall pattern of the results indicated that G7, G8, G10, G12, and G20 exhibited relatively greater stability than most of the other genotypes. Among these genotypes, G8 exhibited the strongest evidence of stability, with posterior probabilities of superiority over G1, G2, G3, G5, G6, G9, G11, G13, G14, G15, G16, G17, G18, G19, and G20 generally ranging from 0.95 to 1. These results provide very strong posterior evidence that G8 is more stable than most of the evaluated genotypes. G7 also exhibited a highly favorable stability profile, with posterior probabilities of superiority ranging from 0.88 to 0.98 relative to G1, G2, G3, G5, G6, G9, G11, G13, G14, G15, G16, G18, and G19. However, the posterior probability that G7 was more stable than G8 was only 0.28, indicating that G8 had a substantially higher probability of being the more stable genotype. Compared with G10 and G20, G7 had posterior probabilities of superiority of approximately 0.48, indicating considerable uncertainty in the relative stability of these genotypes. G12, G10, and G20 were also among the genotypes exhibiting relatively high stability across environments. For G12, the posterior probability of greater stability than G1, G2, G3, G5, G6, G9, G11, G13, G14, G15, G16, G18, and G19 was consistently high, ranging from 0.93 to 0.99. G10 also showed a high posterior probability of greater stability than many of the evaluated genotypes. For example, the corresponding probabilities relative to G1, G2, and G3 were 0.96, 0.94, and 0.97, respectively. A similar pattern was observed for G20, with posterior probabilities of greater stability than G1, G2, G3, G5, and G6 of 0.96, 0.93, 0.96, 0.94, and 0.98, respectively. In contrast, G4 and G17 exhibited the least favorable stability profiles among the evaluated genotypes. For example, the posterior probability that G4 was more stable than G8 or G7 was essentially zero, whereas the corresponding probability for G8 relative to G4 was 1. G17 exhibited an even less favorable stability profile, with very low posterior probabilities of being more stable than many of the evaluated genotypes. In contrast, G7, G8, G10, G12, and G20 each had a posterior probability of 1.00 of being more stable than G17.

Accordingly, based on the overall pattern of pairwise posterior probabilities, the genotypes can be broadly classified into three stability groups. The first group, comprising G8, G7, G12, G10, and G20, exhibited a high posterior probability of greater stability than most of the other genotypes. The second group, including G16, G14, G2, G6, G11, G18, G19, G1, G3, G5, G13, G15, and G9, showed intermediate stability, whereas the third group, consisting of G4 and G17, was characterized by a low posterior probability of superior stability.

Figure 6 provides an important visual representation for interpreting the posterior probabilities of superior stability, graphically illustrating the patterns presented in Table 7. The red, orange, and yellow color ranges correspond to probabilities close to 1, indicating strong posterior evidence that the row genotype has a lower G × E interaction variance than the column genotype and is therefore more stable. This pattern was particularly evident for G8, G7, G12, G10, and G20. Blue and purple color ranges correspond to probabilities close to zero, indicating strong posterior evidence that the row genotype has a greater G × E interaction variance than the column genotype and is therefore less stable. This pattern was observed for G16, G14, G2, G6, G11, G18, G19, G1, G3, G5, G13, G15, and G9. In contrast, green and yellow shades represent probabilities close to 0.50, indicating substantial uncertainty and insufficient posterior evidence to establish a clear stability advantage of one genotype over another, as observed for G4 and G17. It should be noted that, because of the triangular structure of the heatmap, genotypes G3, G8, and G12 appear at one end of the stability spectrum, whereas G13 and G16 appear at the opposite end. However, determining which end represents greater stability requires careful consideration of the direction of the pairwise probabilities and the corresponding numerical values presented in Table 7. These results demonstrate that superior yield is not necessarily associated with greater stability, emphasizing that genotype selection should be based on a simultaneous assessment of both yield and stability. This finding represents a major advantage of the Bayesian framework, as it considers not only posterior mean yield but also the uncertainty surrounding the estimates and the posterior probability of superiority for each genotype in the decision-making process.

Table 7. Pairwise posterior probabilities of superior stability among wheat genotypes estimated from the Bayesian mixed model.

	G1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12	G13	G14	G15	G16	G17	G18	G19	G20
G1	0	0.41	0.51	0.89	0.46	0.66	0.05	0.02	0.69	0.04	0.43	0.03	0.62	0.38	0.49	0.31	0.93	0.45	0.46	0.04
G2	0.59	0	0.6	0.93	0.55	0.73	0.08	0.02	0.77	0.06	0.52	0.05	0.7	0.46	0.57	0.38	0.95	0.54	0.54	0.07
G3	0.49	0.4	0	0.9	0.45	0.63	0.04	0.01	0.66	0.03	0.42	0.02	0.6	0.37	0.48	0.29	0.91	0.45	0.44	0.04
G4	0.11	0.07	0.1	0	0.08	0.19	0	0	0.23	0	0.09	0	0.18	0.06	0.11	0.04	0.57	0.09	0.09	0
G5	0.54	0.45	0.55	0.92	0	0.69	0.05	0.02	0.72	0.05	0.47	0.04	0.65	0.42	0.53	0.35	0.93	0.49	0.49	0.06
G6	0.34	0.27	0.37	0.81	0.31	0	0.02	0.01	0.54	0.02	0.29	0.01	0.47	0.25	0.35	0.2	0.85	0.31	0.31	0.02
G7	0.95	0.92	0.96	1	0.95	0.98	0	0.28	0.98	0.48	0.94	0.38	0.98	0.91	0.95	0.88	1	0.93	0.94	0.48
G8	0.98	0.98	0.99	1	0.98	0.99	0.72	0	1	0.7	0.98	0.61	0.99	0.97	0.99	0.95	1	0.98	0.98	0.68
G9	0.31	0.23	0.34	0.77	0.28	0.46	0.02	0	0	0.01	0.26	0.01	0.44	0.21	0.31	0.17	0.83	0.26	0.28	0.01
G10	0.96	0.94	0.97	1	0.96	0.98	0.52	0.3	0.99	0	0.94	0.4	0.97	0.91	0.95	0.88	1	0.94	0.94	0.49
G11	0.57	0.48	0.58	0.91	0.53	0.71	0.06	0.02	0.74	0.06	0	0.03	0.68	0.45	0.56	0.37	0.94	0.53	0.52	0.06
G12	0.97	0.95	0.98	1	0.96	0.99	0.62	0.39	0.99	0.6	0.97	0	0.99	0.95	0.97	0.93	1	0.96	0.97	0.59
G13	0.38	0.3	0.4	0.82	0.35	0.53	0.02	0.01	0.57	0.03	0.32	0.01	0	0.25	0.38	0.2	0.88	0.33	0.34	0.02
G14	0.62	0.54	0.63	0.94	0.58	0.75	0.09	0.03	0.79	0.09	0.55	0.05	0.75	0	0.62	0.42	0.96	0.58	0.58	0.07
G15	0.51	0.43	0.52	0.89	0.47	0.65	0.05	0.01	0.69	0.05	0.44	0.03	0.62	0.38	0	0.31	0.92	0.46	0.46	0.04
G16	0.69	0.62	0.71	0.96	0.65	0.81	0.12	0.05	0.83	0.12	0.63	0.07	0.8	0.58	0.69	0	0.97	0.66	0.65	0.1
G17	0.07	0.05	0.09	0.43	0.07	0.15	0	0	0.17	0	0.06	0	0.12	0.04	0.08	0.03	0	0.06	0.06	0
G18	0.55	0.46	0.55	0.91	0.51	0.69	0.07	0.02	0.74	0.06	0.47	0.04	0.67	0.42	0.54	0.34	0.94	0	0.5	0.05
G19	0.55	0.46	0.56	0.91	0.51	0.69	0.06	0.02	0.72	0.06	0.48	0.03	0.66	0.42	0.54	0.35	0.94	0.5	0	0.05
G20	0.96	0.93	0.96	1	0.94	0.98	0.52	0.32	0.99	0.51	0.94	0.41	0.98	0.93	0.96	0.9	1	0.95	0.95	0

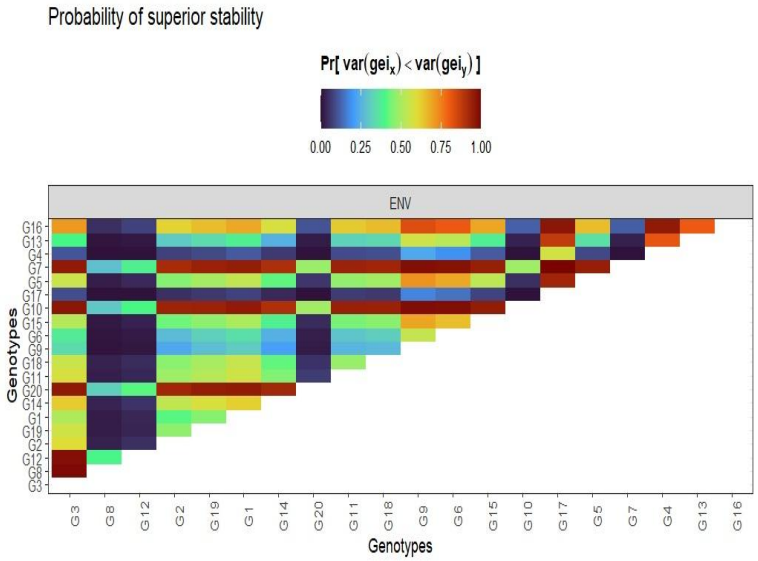


Fig. 6. Heatmap of pairwise posterior probabilities of superior stability among the evaluated wheat genotypes. Cell colors represent the posterior probability that the genotype in each row is more stable than the genotype in the corresponding column, expressed as $Pr[var(GEI_x) < var(GEI_y)]$.

3.6 Joint yield–stability analysis

The joint posterior probability of yield and stability, representing the probability that a genotype simultaneously achieves superior yield and desirable stability, was calculated for all evaluated genotypes, and the results are presented in Figure 7. This index provides a more comprehensive criterion for identifying desirable genotypes than evaluating yield yield or stability separately, because its estimation requires the simultaneous fulfillment of both criteria. Relatively low values of the joint probability are also expected in this context, because the probability of simultaneously achieving two desirable characteristics is generally lower than the probability of achieving either characteristic individually. Among the evaluated genotypes, G17 exhibited the highest joint probability, with a value of approximately 0.11. Therefore, G17 had the highest posterior probability of simultaneously achieving high yield and desirable stability across the studied environments. This was followed by G3, G4, G9, and G6, with joint posterior probabilities of 0.10, 0.08, 0.064, and 0.054, respectively. These results indicate that these genotypes have a relatively greater probability of simultaneously achieving superior yield and desirable stability, highlighting their potential as promising candidates for selection. At the next level, G19 had a joint posterior probability of approximately 0.04, while G1, G13, and G2 each showed a probability of approximately 0.03. Although these genotypes also showed a non-negligible probability of achieving a favorable combination of yield and stability, the posterior evidence supporting their simultaneous superiority over genotypes with higher joint probabilities was more limited. The remaining genotypes exhibited lower joint probabilities, indicating a lower likelihood of simultaneously achieving high yield and desirable stability. These results highlight the importance of using joint probability in breeding programs, as selection based solely on yield or stability may identify genotypes that possess only one of these two desirable attributes. In contrast, the joint probability criterion enables the identification of genotypes with greater potential to simultaneously combine high yield and desirable stability across different environments.

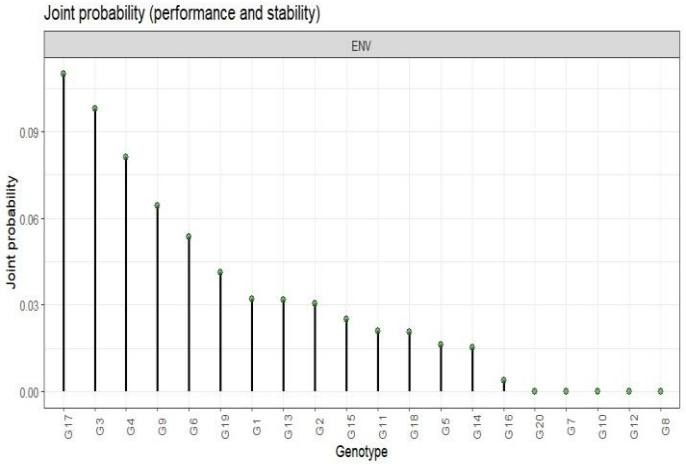


Fig. 7. Joint posterior probabilities of superior yield and stability among wheat genotypes

3.7. Environment-specific genotype performance

Table 8 and the heatmap presented in Figure 8 illustrate the posterior probability of superior yield of each genotype across the different experimental environments. This heatmap illustrates the posterior probabilities of yield superiority and serves as a graphical complement to the table of genotype-specific superiority probabilities across the experimental environments. In the combined analysis of variance, the genotype × environment interaction was significant, and the pattern shown in this heatmap provides a clear explanation for this finding by demonstrating substantial differences in the relative yield of genotypes across environments. In the heatmap, the color intensity of each cell represents the posterior probability that the corresponding genotype will exhibit superior yield in that environment. Dark colors indicate a low posterior probability of superiority, whereas yellow, orange, and red shades indicate a high posterior probability of superiority. The color pattern clearly demonstrates that the responses of the genotypes varied across environments, indicating a lack of uniformity in genotype yield across the tested environments. Some genotypes exhibited a high posterior probability of superiority in certain environments, whereas this probability decreased considerably in other environments. Overall, this pattern provides clear evidence of genotype × environment interaction, indicating that the relative yield of genotypes changed across environments. In other words, a genotype that performs well in one environment is not necessarily the best-yield genotype in another environment. For example, G8 had a posterior probability of superiority of 1in E18, whereas its probability of superiority was below 0.25 in some other environments, demonstrating substantial changes in its relative ranking across environments. This pattern illustrates the concept of yield instability across different environments, reflecting the differential response of the genotype to environmental conditions.

G3, shown in the first row of the heatmap with numerous bright yellow, orange, and red cells corresponding to environments E10, E12, E13, E14, E16, E17, and E6, exhibited a high posterior probability of superior yield in these environments. This result is also consistent with the posterior mean estimates, where G3 exhibited the highest posterior mean genotypic effect (0.0458), indicating a high genetic potential for yield. G8 also exhibited a highly favorable yield pattern across the evaluated environments. This genotype exhibited a high posterior probability of superiority in environments E10, E11, E13, E14, E16, E17, and E18. G12 exhibited a high posterior probability of superiority in environments E10, E11, E13, E17, and E18, while G19 showed a high probability of superiority in environments E2, E9, E15, and E18.

Some genotypes also exhibited superior yield in specific environments, indicating a degree of environment-specific adaptation. G7 exhibited a high posterior probability of superiority in environments E17, E6, and E5, but showed a lower probability of superiority across many of the other environments, indicating relatively specific adaptation to certain environmental conditions. Similarly, G16 exhibited a higher posterior probability of superior yield in environment E4, suggesting relatively favorable adaptation to this specific environment. However, their probability of superior yield across environments was generally lower. Therefore, G7 and G16 can be considered to exhibit relatively specific adaptation rather than broad adaptation. Environments in which genotypes exhibit markedly different posterior probabilities of superiority have greater discriminatory power, allowing more effective differentiation among genotypes. For example, in environment E10, genotypes G8, G12, and G14; in E13, G15, G12, G8, G20, and G3; in E18, G8, G12, and G19; and in E17, G7, G8, G12, and G3 showed substantial differences in their posterior probabilities of superior yield relative to the other genotypes. Therefore, these environments exhibited greater discriminatory power for differentiating among genotypes.

Table 8. Posterior probabilities of genotype superiority within each environment estimated from the Bayesian mixed model.

	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	E11	E12	E13	E14	E15	E16	E17	E18
G1	0.852	0.380	0.271	0.021	0.289	0.090	0.126	0.514	0.802	0.000	0.000	0.173	0.000	0.003	0.135	0.169	0.000	0.000
G2	0.075	0.219	0.720	0.007	0.010	0.058	0.643	0.842	0.022	0.012	0.916	0.461	0.000	0.505	0.532	0.325	0.000	0.000
G3	0.030	0.012	0.000	0.353	0.008	0.679	0.118	0.062	0.207	0.464	0.053	0.796	0.653	0.938	0.002	0.864	0.835	0.287
G4	0.007	0.017	0.000	0.004	0.000	0.021	0.041	0.000	0.006	0.001	0.295	0.058	0.000	0.693	0.044	0.008	0.013	0.000
G5	0.009	0.001	0.010	0.057	0.008	0.351	0.173	0.000	0.726	0.000	0.212	0.665	0.000	0.231	0.000	0.379	0.012	0.000
G6	0.074	0.208	0.147	0.071	0.000	0.745	0.188	0.015	0.097	0.000	0.198	0.663	0.000	0.211	0.116	0.018	0.000	0.000
G7	0.685	0.000	0.000	0.002	0.861	0.866	0.002	0.000	0.340	0.455	0.132	0.045	0.000	0.000	0.000	0.000	0.979	0.000
G8	0.541	0.000	0.000	0.000	0.000	0.083	0.013	0.561	0.057	0.968	0.868	0.121	0.787	0.772	0.000	0.727	0.810	1.000
G9	0.007	0.030	0.932	0.278	0.038	0.000	0.006	0.429	0.029	0.005	0.008	0.174	0.000	0.008	0.228	0.371	0.000	0.000
G10	0.297	0.000	0.056	0.000	0.000	0.284	0.258	0.553	0.045	0.000	0.504	0.270	0.000	0.631	0.000	0.325	0.298	0.003
G11	0.191	0.000	0.228	0.004	0.388	0.499	0.625	0.754	0.088	0.000	0.011	0.321	0.022	0.001	0.000	0.000	0.002	0.126
G12	0.063	0.000	0.570	0.021	0.006	0.000	0.136	0.053	0.007	0.908	0.023	0.032	0.855	0.002	0.000	0.010	0.937	1.000
G13	0.002	0.351	0.000	0.174	0.614	0.012	0.380	0.000	0.005	0.042	0.333	0.000	0.000	0.000	0.003	0.016	0.000	0.433
G14	0.437	0.589	0.000	0.140	0.005	0.011	0.244	0.000	0.458	0.998	0.015	0.037	0.000	0.000	0.837	0.000	0.000	0.089
G15	0.006	0.000	0.327	0.000	0.016	0.098	0.029	0.001	0.002	0.000	0.004	0.022	0.948	0.000	0.322	0.375	0.000	0.034
G16	0.072	0.000	0.000	0.984	0.133	0.142	0.314	0.000	0.026	0.146	0.015	0.066	0.002	0.000	0.000	0.000	0.000	0.027
G17	0.076	0.189	0.000	0.039	0.008	0.003	0.052	0.185	0.155	0.000	0.333	0.009	0.000	0.002	0.546	0.017	0.000	0.035
G18	0.204	0.235	0.739	0.900	0.861	0.006	0.460	0.032	0.025	0.000	0.004	0.004	0.000	0.001	0.092	0.035	0.000	0.000
G19	0.170	0.776	0.000	0.524	0.143	0.000	0.072	0.000	0.877	0.000	0.021	0.020	0.004	0.001	0.895	0.029	0.114	0.911
G20	0.202	0.993	0.000	0.420	0.610	0.051	0.123	0.000	0.025	0.001	0.056	0.064	0.730	0.000	0.249	0.334	0.000	0.056

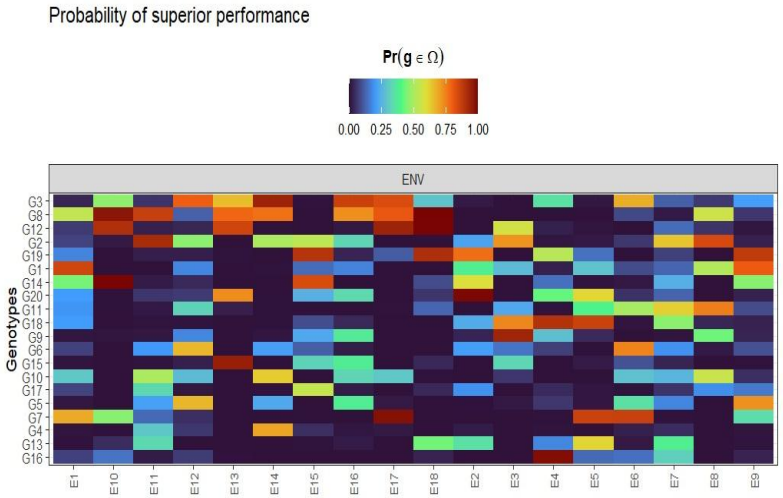


Fig. 8. Heatmap of posterior probabilities of genotype superiority within each environment estimated from the Bayesian mixed model.

4. Conclusion

The results of the Bayesian analysis indicated that most of the variation in yield in this study was attributable to environmental effects and genotype × environment interaction, rather than to direct differences among genotypes. Environmental variance accounted for approximately 72.5% of the total variance, whereas genotypic variance contributed only about 0.3%, indicating a relatively small direct genetic contribution to the observed variation in yield. This finding indicates that environmental conditions played a dominant role in determining yield yield, while the differences among genotypes in terms of their overall yield were relatively small. However, the relatively high variance of the genotype × environment interaction, together with an HPD interval entirely above zero, indicates that genotypes responded differently to changes in environmental conditions. Therefore, evaluating genotype yield based solely on overall mean yield is insufficient for selecting superior genotypes, and simultaneous consideration of yield consistency and stability is essential. The good fit of the Bayesian model further supports the validity and reliability of the inferences drawn from this study. Posterior predictive probabilities for various summary statistics, including the mean, median, standard deviation, minimum, and maximum, fell within acceptable ranges, further supporting the adequacy of the model. Therefore, the posterior distributions and estimated probabilities can be interpreted with reasonable confidence for genotype comparisons and informed breeding decisions.

In terms of yield, G3, G8, G12, G2, and G19 exhibited positive posterior mean genotypic effects, with G3 showing the highest posterior mean genotypic effect. The probabilities of achieving a yield at least 20% higher than the overall mean were estimated at 0.50, 0.43, 0.32, and 0.31 for G3, G8, G12, and G2, respectively. However, the HPD intervals for the genotypic effects of all evaluated genotypes included zero. Therefore, the superiority of any genotype cannot be established with high certainty based solely on the posterior genotypic effects. This finding underscores the importance of incorporating uncertainty into the decision-making process and indicates that observed differences among genotypes should be interpreted with caution. The results of the pairwise comparisons further supported this finding, highlighting the importance of accounting for uncertainty when evaluating differences among genotypes. Although G3, G8, and G12 showed favorable positions in terms of posterior mean genotypic effects and the probability of superior yield, G16 exhibited a higher posterior probability of superiority in many pairwise comparisons. Genotypes G13 and G4 also showed relatively strong posterior evidence of superiority over several other genotypes in the pairwise comparisons. This discrepancy between rankings based on posterior mean yield and pairwise posterior probabilities of superiority indicates that reliance on a single criterion may not provide a complete representation of the relative position of the genotypes. In fact, pairwise posterior probability of superiority incorporates not only the magnitude of the estimated effect but also the uncertainty associated with genotype comparisons into the selection process.

From the perspective of stability, a different pattern of results was observed. G8, G7, G12, G10, and G20 exhibited higher posterior probabilities of stability than the majority of the evaluated genotypes. Among these genotypes, G8 showed the strongest posterior evidence of favorable stability, with probabilities close to one in comparisons with most other genotypes. G7, G12, G10, and G20 were also classified among the relatively stable genotypes, showing favorable posterior probabilities of stability compared with most of the other genotypes. In contrast, G4 and, particularly, G17 exhibited a less favorable stability profile, with lower posterior probabilities of being more stable than the other genotypes. These results demonstrate that high-performing genotypes are not necessarily the most stable genotypes, and vice versa. Therefore, selection based

solely on yield yield may result in the identification of genotypes with limited adaptability across environments.

The posterior probabilities of superior yield across individual environments also provided clear evidence of genotype × environment interaction, confirming that the relative yield of genotypes varied substantially across environments. The differing patterns of posterior probabilities across environments demonstrated that genotype rankings were not fixed; a genotype with a high probability of superiority in one environment may perform less favorably in another environment. For example, G8 had a posterior probability of superiority of 1.00 in environment E18, whereas its probability of superiority was considerably lower in some other environments, further demonstrating the presence of genotype × environment interaction. G3 also exhibited a high posterior probability of superiority in environments such as E12, E14, E16, and E17, whereas its probability of superiority was substantially lower in some other environments, further highlighting its differential response to environmental conditions. G16 also showed a high posterior probability of superiority in environment E4, but had a relatively low probability of superiority across many of the other environments, indicating more specific rather than broad adaptation. This pattern indicates the presence of specific adaptation among some genotypes and further emphasizes the importance of genotype × environment analysis in genotype selection.

According to these results, high yield and stability can be considered two distinct but complementary characteristics that should be evaluated simultaneously in genotype selection. G3 occupied a highly favorable position in terms of genetic yield potential, but its probability of favorable stability was only about 20%. In contrast, G8 showed a favorable profile for both yield yield and, particularly, stability, suggesting a more desirable balance between productivity and consistency across environments. G17 also showed the highest stability probability according to the criterion used, with a stability probability of 86%; however, it ranked only at an intermediate level in terms of the probability of superior yield. Therefore, no genotype can be considered the best option based on a single criterion alone, highlighting the need for a multi-criteria approach that jointly considers yield yield, stability, and their associated uncertainty. Under these circumstances, the joint posterior probability of superior yield and desirable stability provides a more comprehensive criterion for decision-making, as it evaluates the probability of simultaneously achieving both desired attributes. Based on this criterion, G17 ranked first, with a joint posterior probability of 0.11, followed by G3, G4, G9, and G6, indicating their relatively greater potential to simultaneously achieve high yield and desirable stability. Despite the relatively low absolute values of these joint probabilities, the resulting ranking indicates that these genotypes had a greater probability of simultaneously achieving the two desired objectives than the other genotypes. Therefore, these genotypes can be considered promising initial candidates for further evaluation and validation in subsequent breeding trials.

Overall, the findings of this study demonstrate that the Bayesian framework provides a more comprehensive approach to genotype evaluation than methods based solely on average yield. In addition to estimating genotype yield and stability, the Bayesian framework incorporates the uncertainty associated with these estimates and the posterior probability of superiority of each genotype into the decision-making process. Integrating information from variance components, genotypic effects, probabilities of superiority and stability, pairwise comparisons, environment-specific yield, and the joint probability of superior yield and stability demonstrated that superior genotype selection should be based on a multi-criteria approach rather than a single indicator. Based on these findings, G3 and G8 can be considered promising genotypes in terms of yield potential; G8, G7, G12, G10, and G20 showed more favorable stability profiles; and G17, G3, G4,

G9, and G6 emerged as relatively promising genotypes when yield and stability were considered jointly.

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Author contributions
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Data Availability
The data supporting the findings of this study are available from the corresponding author upon reasonable request.

Declarations
Competing Interests: The authors declare that they have no competing interests.
Ethics Approval: This study did not involve human participants or animals and therefore did not require ethical approval.

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