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Deciphering Yield Stability in Wheat Under Drought via Integrative Multi-Model Genotype × Environment Analysis

Shivashankaragouda Patil
UNIVERSITY OF AGRICULTURAL SCIENCES, DHARWAD https://orcid.org/0009-0003-0720-5199
Abhishek V. Karadagi
abhivk71@gmail.com
UNIVERSITY OF AGRICULTURAL SCIENCES, DHARWAD https://orcid.org/0009-0008-7756-621X
Bobochand Singh Oinam
UNIVERSITY OF AGRICULTURAL SCIENCES, DHARWAD https://orcid.org/0009-0008-7685-9205
Suma S. Biradar
UNIVERSITY OF AGRICULTURAL SCIENCES, DHARWAD
Harisha K
UNIVERSITY OF AGRICULTURAL SCIENCES, DHARWAD
Jayateertha R Diwan
UNIVERSITY OF AGRICULTURAL SCIENCES, DHARWAD
Ratnakala B
UNIVERSITY OF AGRICULTURAL SCIENCES, DHARWAD
Harshitha Kumar
UNIVERSITY OF AGRICULTURAL SCIENCES, DHARWAD
Gangadhara Doggalli
UNIVERSITY OF AGRICULTURAL SCIENCES, DHARWAD
Muragesh M. Hiremath
UNIVERSITY OF AGRICULTURAL SCIENCES, DHARWAD https://orcid.org/0009-0006-4083-1900
Prajwal Khajuri
UNIVERSITY OF AGRICULTURAL SCIENCES, DHARWAD
Basavaraj Bagewadi
UNIVERSITY OF AGRICULTURAL SCIENCES, DHARWAD
Chitti Bharatkumar
UNIVERSITY OF AGRICULTURAL SCIENCES, DHARWAD
S. B. Patil
UNIVERSITY OF AGRICULTURAL SCIENCES, DHARWAD
Amaregouda Patil

UNIVERSITY OF AGRICULTURAL SCIENCES, RAICHUR
S. A. Desai
desaisa@uasd.in

UNIVERSITY OF AGRICULTURAL SCIENCES, DHARWAD
Mehdi Rahimi
mehdi83ra@gmail.com

Institute of Science and High Technology and Environmental Sciences, Graduate University of Advanced Technology, Kerman, Iran.

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Deciphering Yield Stability in Wheat Under Drought *via* Integrative Multi-Model Genotype × Environment Analysis

Shivashankaragouda Patil[1], Abhishek V. Karadagi[1,2*], Bobochand Singh Oinam[3], Suma S. Biradar[4], Harisha K[1], Jayateertha R Diwan[5], Ratnakala B[6], Harshitha Kumar[7], Gangadhara Doggalli[1], Muragesh M. Hiremath[8,15], Prajwal Khajuri[8], Basavaraj Bagewadi[9], Chitti Bharatkumar[10], S. B. Patil[11], Amaregouda Patil[12], S. A. Desai[13*], Mehdi Rahimi[14*]

[1]Ph.D. Scholar, Department of Genetics and Plant Breeding, UAS, Dharwad, Karnataka, India

[2]Research Scholar, Division of Vegetable Crops, ICAR- Indian Institute of Horticultural Research, Bengaluru, Karnataka, India

[3]Ph.D. Scholar, ICAR - Indian Agricultural Research Institute, New Delhi, India

[4]Principal Scientist and Head, AICRP on Wheat, MARS, UAS, Dharwad, Karnataka, India

[5]Principal Scientist and Head, ARS, Mugad, Dharwad, Karnataka, India

[6]Ph.D. Scholar, Department of Agricultural Entomology, UAS, Dharwad, Karnataka, India

[7]Ph.D. Scholar, Department of Genetics and Plant Breeding, UAS, Raichur, Karnataka, India

[8]M. Sc Scholar, Department of Genetics and Plant Breeding, UAS, Dharwad, Karnataka, India

[9]Assistant Professor, Department of Agricultural Biotechnology, UAS, Dharwad, Karnataka, India

[10]Assistant Professor, Department of Genetics and Plant Breeding, Vijayapura, UAS, Dharwad, Karnataka, India

[11]Assistant Professor, Department of Seed Science and Technology, UAS, Dharwad, Karnataka, India

[12]Director of Research, UAS, Raichur, Karnataka, India

[13]Professor and Head, Department of Genetics and Plant Breeding, UAS, Dharwad, Karnataka, India

[14]Department of Biotechnology, Institute of Science and High Technology and Environmental Sciences, Graduate University of Advanced Technology, Kerman, Iran.

[15] Ph.D. Scholar, Department of Agronomy, Horticulture and Plant Science, South Dakota State University, United States

*Correspondence should be addressed to Mehdi Rahimi: mehdi83ra@gmail.com; S. A. Desai: desaisa@uasd.in; Abhishek V. Karadagi: abhivk71@gmail.com

Abstract

Drought is a major constraint limiting wheat productivity in rainfed and semi-arid regions, necessitating the identification of stable and high-performing genotypes. This study evaluated 20 wheat genotypes across five drought-stressed environments using six parametric, nine non-parametric, ten AMMI-based, and four BLUP-based stability statistics, which were integrated through weighted rank aggregation (WRA). AMMI (Additive Main Effects and Multiplicative Interaction) analysis revealed significant genotype, environment, and genotype × environment (G×E) interaction effects for most traits, with IPCA1 contributing substantially to variation in grain yield and related traits. The AMMI2 biplot explained 66.54% of the total G×E interaction, with IPCA1 (Interaction Principal Component Axis 1) and IPCA2 accounting

for 37.19% and 29.35%, respectively. Correlation analysis indicated redundancy among several stability statistics due to shared mathematical structures. Stability assessment was model-dependent, reflecting trade-offs between yield performance and environmental responsiveness. Genotype G6 was consistently identified as stable, whereas G13, G14, G15, G16, and G17 were prioritized by the weighted rank aggregation of stability statistics and represent promising candidates for future varietal development. Multi-trait indices FAI-BLUP (Factor Analysis and Ideotype-Design Best Linear Unbiased Prediction), MTSI (Multi-Trait Stability Index) and MGIDI (Multi-Trait Genotype–Ideotype Distance Index), complemented stability analyses by integrating multiple agronomic traits and identifying genotypes closest to a predefined ideotype, prioritizing G15, G3, and G8 for their favorable multi-trait performance under drought-stressed environments. These candidate genotypes warrant further physiological validation before deployment in breeding programs. The findings demonstrate the value of integrating stability statistics and multi-trait selection indices to support wheat breeding under water-limited conditions.

Keywords: AMMI; BLUP; Multi-trait selection Models; Non-parametric; Parametric

Introduction

Common wheat (*Triticum aestivum* L.), or bread wheat, is a self-pollinating annual of the Poaceae family, accounting for more than 90% of global wheat production. It is a hexaploid species, while tetraploid durum wheat (*T. durum*) and emmer wheat (*T. dicoccum*) contribute the remaining share[1,2,3]. Bread wheat's extensive genetic diversity underpins its broad adaptability to diverse agroecological conditions, making it the most widely cultivated cereal and a vital source of nutrition[4,5]. To meet global food demand, wheat production must double by 2050[6].Among abiotic stresses, drought is a major constraint[7,8,9]. Since drought tolerance is complex and multigenic, breeding requires improved and stable genotypes across variable environments[10,11].

Genotype × environment interaction (GEI) influences phenotypic performance, as some genotypes exhibit broad adaptability while others are environment-specific[12,13]. Multi-environment trials (METs) are therefore critical to identify stable and high-yielding genotypes and delineate mega-environments[14]. Stability can be evaluated using different analytical models, each reflecting distinct concepts of genotype performance. Parametric stability statistics describe genotype performance based on variance components and regression behavior. These includes Wricke's ecovalence (Wi^2), which measures genotype contribution to GEI sum of squares[15], Shukla's stability variance (σ^2_i), which estimates stability after removing environmental effects[18], regression coefficient (bi) and deviation from regression (s^2di), which describe genotype responsiveness and predictability[16,17] and coefficient of variation (CVi), which reflects relative variability[19]. These statistics define stability in terms of minimum variance and predictable performance across environments.

Further, non-parametric stability statistics provide an alternative approach based on rank consistency rather than absolute values. These includes Huehn's and Nassar and Huehn's S(i) statistics[21,22] and Thennarasu's NP(i) indices[23] quantify rank variation and deviation across environments, while Kang's rank-sum (KR) integrates yield and stability rankings to identify genotypes combining high performance and stability[23]. These approaches are less sensitive to distributional assumptions and complement parametric methods. The Additive Main Effects and Multiplicative Interaction (AMMI) model is based on the primary analytical framework, combining analysis of variance (ANOVA) for additive effects with principal component analysis (PCA) for interaction effects[24,25]. Key AMMI statistics, including interaction principal component axes (IPCA1 and IPCA2), were used to explain GEI patterns, while AMMI-based stability parameters such as AMMI Stability Index (ASI), Modified AMMI Stability Value (MASV) and Modified AMMI Stability Index (MASI) quantify genotype stability based on IPCA scores[29,30,31]

In addition, mixed-model approaches based on best linear unbiased prediction (BLUP) estimate genotypic values under random environmental effects and incorporate shrinkage to improve prediction accuracy. Statistics such as arithmetic mean of genotypic values (AMGV), relative performance of genotypic values (RPGV), harmonic mean of genotypic values (HMGV) and harmonic mean of RPGV (HMRPGV) provide measures of yield performance and stability under heterogeneous environments[32].

In addition to single-trait stability analyses, multi-trait selection models have gained importance in modern breeding programs due to their biological relevance, as yield improvement must be achieved alongside multiple agronomic and adaptive traits. The Multi-Trait Stability Index (MTSI) integrates mean performance and stability across traits using factor analysis and distance-based selection, enabling simultaneous selection for productivity and resilience[14]. The Multi-Trait Genotype–Ideotype Distance Index (MGIDI) identifies superior genotypes by minimizing the distance between genotypes and an ideotype defined by desirable trait directions, offering an intuitive and efficient framework for multi-trait selection[36]. Similarly, the FAI-BLUP (Factor Analysis and Ideotype-Design Best Linear Unbiased Prediction) combines mixed-model BLUPs with factor analysis and ideotype planning, allowing robust genotype ranking under MET conditions while accounting for genetic correlations among traits[37]. These indices overcome limitations of traditional selection indices by avoiding multicollinearity, subjective economic weights and distributional assumptions and have proven effective in identifying high-performing and stable genotypes across environments and traits. Despite the availability of numerous stability models, most studies rely on a single analytical approach, which may lead to model-dependent or biased identification of superior genotypes. Furthermore, systematic comparisons of multiple stability models within the same dataset remain limited, particularly under drought conditions, restricting a comprehensive understanding of their complementarity. Given that different stability models are based on distinct assumptions and concepts of stability, we hypothesized that genotype rankings would vary across methods. From a breeding perspective, we further hypothesized that integrating parametric, non-parametric, AMMI, BLUP and multi-trait approaches may provide a more reliable and model-informed framework for selecting genotypes that combine high yield with appropriate stability, while helping distinguish between broadly adapted and location-specific genotypes and reducing the likelihood of model-dependent selection bias.

Materials and methods

Planting sites and plant materials

The study was carried out with twenty wheat genotypes (supplementary table 1). The study was conducted using twenty wheat genotypes (Supplementary Table 1), comprising a diverse set of genetic materials including durum wheat checks for rainfed conditions (UAS 446, Amruth, DWR-2006, AKDW-2997-16 and Bijaga Yellow), bread wheat checks (UAS 375, UAS 347 and HD 2888), susceptible or irrigated durum check (UAS 428), and susceptible bread wheat checks (UAS 334 and UAS 3020), along with a genetic stock (UASBW 13039/ UASD 22-5). In addition, advanced breeding lines evaluated under station trials included bread wheat lines (GDP 40, UASBW 11421, UASBW 12982 and UASBW 12380) and durum wheat lines (UASDW 30805, UASDW 31156 and UASDW 30820). In five environments of four location, these sites were chosen to represent three different agroclimatic zones of Karnataka state (Fig. 1). The longitude, latitude and environmental factors of those test ecological areas are presented in Table. 2. Drought stress environments were characterized using combined meteorological and soil moisture criteria across locations (Dharwad, Bijapur, Bagalkot, and Raichur) during 2023–2024 and Dharwad during 2024–2025. Seasonal rainfall during the crop growth period (November–March) was minimal (0–38.3 mm), with prolonged dry spells exceeding 20–30 days, particularly during the reproductive stage. Maximum temperatures frequently exceeded 33–38°C, intensifying evaporative demand (supplementary table 8 and 9).

Soil moisture content was monitored at regular intervals using the gravimetric method at 0–30 cm soil depth. A progressive decline in soil moisture was observed from 17–18% at early growth stages to 10–12% at later stages, indicating substantial soil moisture deficit. The lowest values were recorded in Bijapur (10.4%) and Raichur (11.4%), confirming severe drought stress conditions. Based on these criteria, environments were classified as moderate to severe drought stress, where soil moisture levels fell below 15% during critical growth stages, in conjunction with negligible rainfall and high temperature stress. These conditions ensured consistent and reproducible moisture stress across environments for evaluating genotype performance

Experimental design and data collection

A randomized block design with two replications was used to evaluate the test genotypes across five environments. Each plot consisted of six rows of 3 m length, with a spacing of 40 cm between rows and 10 cm between plants. Standard observations on five randomly selected plants from the middle rows of each plot were recorded as described by Mahajan et al.[61]. As the genotypes were genetically stabilized, observations from five representative plants sampled from the central rows were considered sufficient to obtain reliable estimates of genotype performance while minimizing border effects. Days to maturity (DM) was recorded as the number of days from sowing to physiological maturity. Plant height (PH) was measured in centimeters from ground level to the tip of the main spike (excluding awns) at maturity and averaged. The number of productive tillers per meter (NTM) was counted as ear-bearing tillers per meter at maturity. Peduncle length (PDL) was measured from the last node to the base of the spike, and spike length (SL) from the base to the tip of the main spike (excluding awns), both averaged over five plants. The number of grains per spike (NGP) was determined from the main spike of selected plants and averaged. Thousand-seed weight (TW) was estimated by weighing 200 seeds and converted to 1000-grain weight (g). Grain yield per plot (YLD) was recorded after drying and expressed in kg ha^{-1}. Stability analysis was subsequently performed using different models, and genotypes were ranked based on the respective indices.

Data analysis

Grain yield and associated traits were subjected to analysis of variance (ANOVA) across environments to partition the effects of genotype (G), environment (E), and genotype × environment interaction (G×E). Prior to combined ANOVA, homogeneity of error variances across environments was assessed using Bartlett's test. As the test indicated homogeneous residual variances, data from individual environments were pooled for combined analysis. Subsequently, the AMMI model was employed to further dissect G×E interaction by integrating ANOVA for additive effects with principal component analysis (PCA) for multiplicative interaction effects. The significance of interaction principal component axes (IPCAs) was used to interpret genotype stability and adaptability across environments. The formula of the AMMI model is[38,39,42]

$$Y_{ij}=\mu + g_i + e_j + \Sigma\lambda_k\alpha_{ik}\gamma_{ik} + \theta_{ij}$$

Where, Y_{ij} is observed mean performance of the i^{th} genotype in the j^{th} environment; μ is grand mean; g_i is fixed effect of the i^{th} genotype; e_j is fixed effect of the j^{th} environment, λ_k is singular value (eigenvalue) of the k^{th} Interaction Principal Component Axis (IPCA); α_{ik} is genotype eigenvector score for the k^{th} IPCA; γ_{ik} is environment eigenvector score for the k^{th} IPCA and n is number of significant IPCAs retained in the model.

Parametric and non-parametric based stability analysis

Genotype stability was assessed using both parametric and non-parametric approaches. Parametric statistics, including Wricke's ecovalence (Wi^2), Shukla's stability variance (σ^2_i), regression

coefficient (bi), deviation from regression (s^2di), and coefficient of variation (CVi), were used to evaluate genotype response and predictability across environments[42].

Non-parametric measures, including Huehn's S(i), Thennarasu's NP(i) and Kang's rank-sum (KR), were computed to assess stability based on rank consistency, independent of distributional assumptions. All parametric and non-parametric stability statistics were calculated using the web-based *STABILITYSOFT* application[42].

AMMI-based stability indices

AMMI-derived stability indices, including AMMI Stability Index (ASI), Modified ASV (MASV), and Modified ASI (MASI), were computed using IPCA scores[42]. These indices quantify genotype stability by integrating both the magnitude and structure of G×E interaction. All AMMI-based stability statistics were calculated using the R package "*metan*".

BLUP-based stability analysis

Genotypic effects were estimated using mixed linear models under the BLUP framework, considering environments as random effects. Stability and performance were assessed using AMGV, RPGV, HMGV, and HMRPGV, which jointly capture mean performance and adaptability across environments. A linear mixed-effects model was fitted using the lme4 package in R, where genotypes were treated as random effects, and environments and replications were considered fixed effects. The genotype × environment interaction was modeled as a random effect. Best Linear Unbiased Predictors (BLUPs) of genotypic values were obtained and used to compute stability indices, including HMGV, RPGV, and HMRPGV[42]. The model can be expressed as:

$$y_{ijk}=\mu + E_i + R_j(E_i) + G_k + (GE)_{ik} + \varepsilon_{ijk}$$

where, y_{ijk} is the observed value of the *k*th genotype in the *j*th replication within the *i*th environment; μ is the overall mean; E_i is the fixed effect of the *i*th environment; $R_j(E_i)$ is the fixed effect of the *j*th replication nested within the *i*th environment; G_k is the random effect of the *k*th genotype; $(GE)_{ik}$ is the random interaction effect between the *k*th genotype and the *i*th environment; and ε_{ijk} is the residual error term.

Multi-trait selection indices-based stability analysis

To identify superior genotypes based on multiple traits simultaneously, three multi-trait indices were employed. The Multi-Trait Stability Index (MTSI), Multi-Trait Genotype–Ideotype Distance Index (MGIDI), and FAI-BLUP were computed to integrate yield performance, stability, and trait relationships. These approaches enabled the selection of genotypes closer to the ideotype with desirable trait combinations. An ideotype was defined as a theoretical genotype with maximum values for desirable traits (PH, PDL, TW, NGP, NTM, SL, and YLD) and minimum value for days to maturity (DM), based on breeding objectives under drought conditions. To evaluate the agreement among these indices, a Venn diagram was constructed based on the top five genotypes selected by each index using the *Venny 2.1* tool.

Factor analytic best linear unbiased prediction (FAI-BLUP)

Multi-trait index based on factor analysis and ideotype design proposed by [37]. The formula used for calculating the FAI-BLUP index is as follows[60]:

$$P_{ij} = \frac{\frac{1}{dij}}{\sum_{i=1;j=1}^{i=n;j=m} \frac{1}{dij}}$$

Where: Pij is the probability the genotype (i = 1, 2,…, n) is similar to ideotype j (j = 1,2,…,m); dij is the genotype j distance, based on the standardized mean Euclidean distance.

Multi-trait selection index (MTSI)

Multi-Trait Selection Index (MTSI) is a quantitative method that facilitates the simultaneous selection of multiple traits by assigning appropriate weights to each trait, reflecting their relative economic or breeding importance [14,40]. This approach enables breeders to optimize overall genetic gain by considering the combined value of all targeted traits, rather than improving them individually[60]. The general formula for the selection index (I) is a linear combination of trait values:

$$I=b_1X_1+ b_2X_2 +...+ b_nX_n$$

Where, b_1 represents the weight assigned to trait X_1. By effectively balancing multiple traits, MTSI enhances the efficiency of breeding programs and accelerates the development of superior genotypes [41].

Multi-trait genotype–ideotype distance index (MGIDI)

The MGIDI is an effective index for evaluating and selecting genotypes relative to an ideal genotype[60]. It is computed by measuring the Euclidean distance between the scores of each treatment and those of the ideotype. The MGIDI index is computed as following formula [36].

$$MGIDI_i= \sqrt{\sum_{j=1}^{f}(Fij - Fj)(Fij - Fj)}$$

Where, MGIDIi is the multi-trait genotype-ideotype distance index for the ith genotype; Fij is the score of the ith genotype in the jth factor (i = 1, 2, …, g; j = 1, 2, …, f), being g and f the number of genotypes and factors, respectively, and Fj is the jth score of the ideotype.

Correlation Analysis and Visualization

Pairwise associations among different stability parameters were assessed using correlation analysis. The correlation matrix was computed in *R (version 4.4.0)* and visualized using the "corrplot" package to facilitate the interpretation of relationships among variables[60].

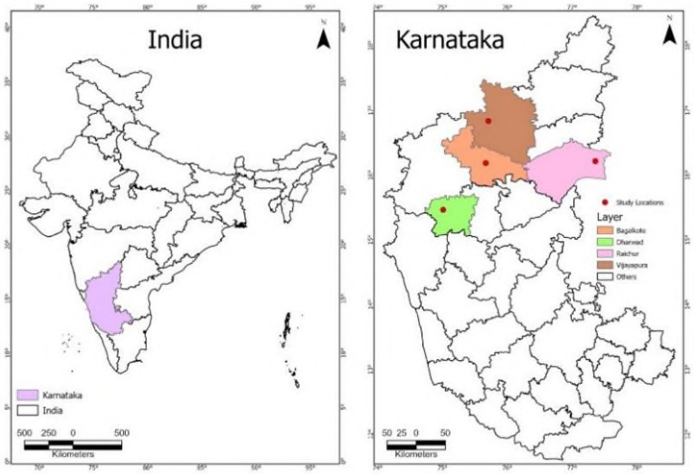


Figure 1. Map of Karnataka showing the locations of experimental study sites.

Weighted Rank Aggregation

Weighted Rank Aggregation (WRA), based on Ranker Accuracies (RA), is a statistical approach used to integrate multiple ranking methods into a single composite ranking by assigning weights according to their relative reliability[60].

The weight assigned to each index was computed as:

$$w_i = \frac{1-ri}{\sum_{i=1}^{n}(1-ri)}$$

where, ri represents the average absolute Spearman correlation of the i^{th} index with all other indices and w_i denotes the corresponding weight reflecting its ranker accuracy.

Results

AMMI ANOVA was employed to evaluate the yield performance of twenty wheat genotypes across five environments (Table 2). The model effectively partitioned genotype (G), environment (E) and genotype × environment (G×E) interaction effects, enabling interpretation of performance patterns. The yield heatmap (Figure 2A) indicated that genotypes G8, G6, G18 and G14 were superior performers, particularly in E4 and E5, whereas G1, G2 and G12 showed lower and unstable yields. Environment E5 consistently supported higher yields and was therefore considered a favorable testing environment, likely due to residual soil moisture from substantial pre-season rainfall in October 2024. In contrast, E3 recorded lower mean yields under negligible rainfall and higher temperatures, indicating greater drought stress and stronger discrimination among genotypes.

The AMMI analysis of variance revealed significant G, E and G×E effects for most traits, including days to maturity (DM), plant height (PH), number of tillers per meter (NTM), peduncle length (PDL), spike length (SL), number of grains per spike (NGP) thousand seed weight (TW) and grain yield per plot (kg/ha) (YLD) (Table 2). Significant genotypic effects reflected substantial genetic variability, while moderate environmental effects confirmed the distinctiveness of the test environments and their contribution to differential genotypic responses.

The AMMI1 biplot (Figure 2B) illustrated variation in mean yield and interaction effects, with yields ranging from 1058.5 kg/ha (G2 in E3) to 2977.5 kg/ha (G8 in E4). Genotypes G14, G6 and G15 exhibited consistently high mean yields, with G14 showing strong positive interaction in E1 and E5. In contrast, G2, G17 and G5 were low-yielding. Environments E1 and E5 were favorable for yield, while E2, E3 and E4 were relatively unfavorable. Genotypes G16, G20, G8, G3 and G9 clustered near the origin, indicating broad adaptability.

The AMMI2 biplot (Figure 2C and 2D), explaining 66.5% of total G×E interaction with the first principal component (PC1) explaining 37.19% of the variance and the second component (PC2) explaining 29.35%. Genotypes G1, G6, G16 and G17 showed high stability due to minimal interaction effects, whereas G12, G15, G4 and G20 displayed specific adaptation. Environments E1 and E5 were highly discriminating, while E3 and E4 exerted weaker interaction effects. Acute angles between genotype and environment vectors indicated positive interactions, notably for G14 and G10 with E1 and E5, whereas G3 and G4 performed better in E3 and E2, respectively. Overall, G6, G7 and G10 contributed substantially to G×E interaction and showed promise for targeted adaptation in high-yielding environments.

Parametric Stability Analysis

Parametric stability measures, including mean grain yield, variance components (θ_i and $\theta_i GE$), Wricke's ecovalence (Wi^2), Shukla's stability variance (σ^2_i), deviation from regression (s^2d_i) and coefficient of variation (CVi), are presented in supplementary table 3. Wricke's ecovalence and Shukla's stability variance consistently identified genotypes G1, G17 and G13 as the most stable across environments. Based on Pinthus's coefficient of determination (θ_i), genotypes G4, G11 and G2 showed superior performance. The GE interaction variance ($\theta_i GE$) further confirmed G1, G17 and G13 as genotypes with

minimal environment-specific interaction. The coefficient of variation identified G4 (15.42%), G15 (17.57%) and G14 (23.00%) as relatively stable, whereas G20 (42.09%) and G12 (41.00%) exhibited high variability and poor stability across environments. WRA of parametric indices further identified G6, G16, and G15 as the top-performing genotypes, reflecting their consistent performance across multiple stability measures (supplementary table 7).

Non-Parametric Stability Analysis

Non-parametric stability statistics, including Huhn's and Nassar and Huhn's indices ($Si^{(1)}$, $Si^{(2)}$, $Si^{(3)}$, $Si^{(6)}$), Thennarasu's indices ($NP^{(1)}$, $NP^{(2)}$, $NP^{(3)}$, $NP^{(4)}$) and Kang's Rank-Sum (KR), are summarized in supplementary table 2. Based on $Si^{(1)}$ and $Si^{(2)}$, genotypes G2, G6 and G1 were identified as the most stable, with G2 ranking first in both indices. Genotypes G6 and G1 also showed strong stability with consistently no rank variation.

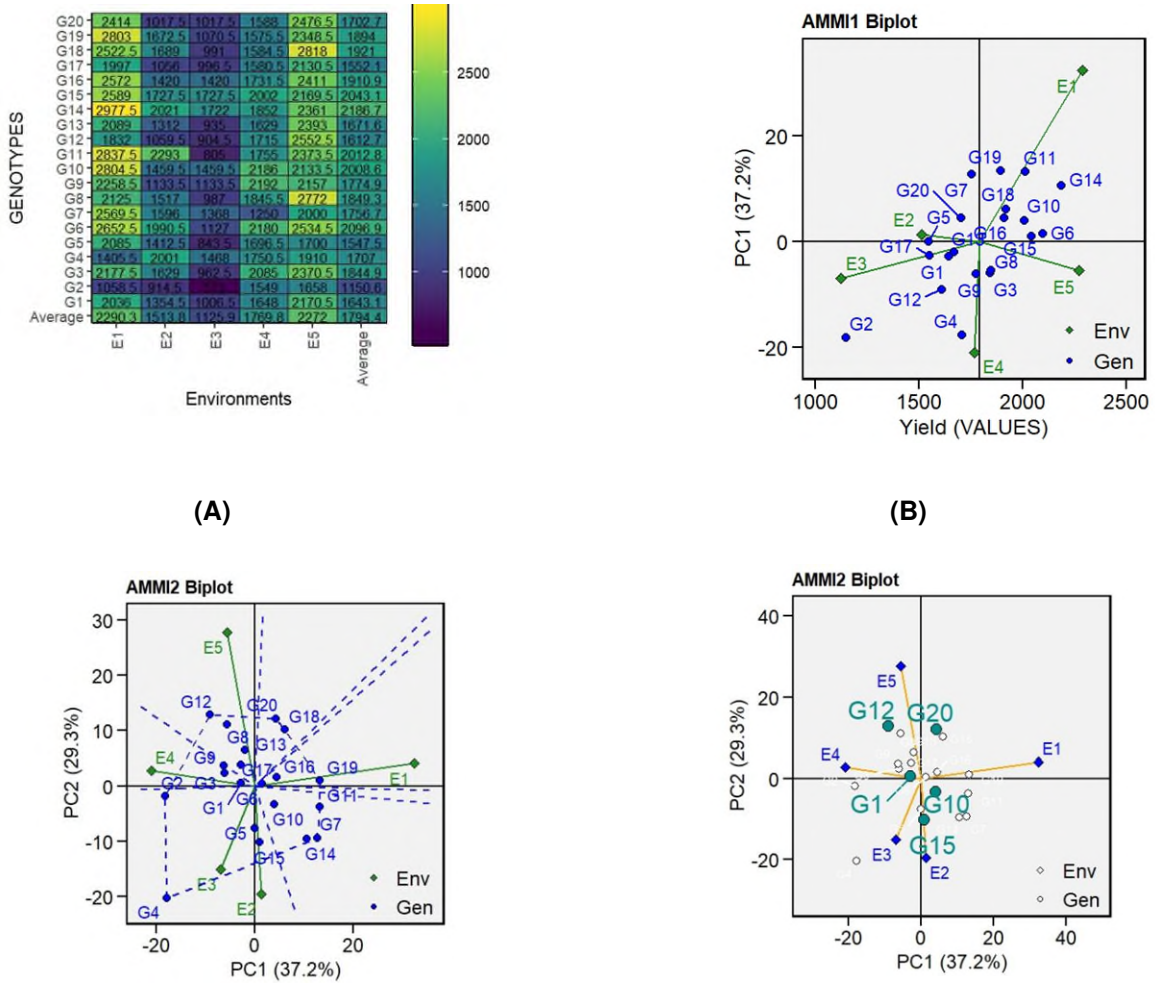


Figure 2. The seed yield variation of the studied twenty wheat genotypes across five environments **(A)**. The AMMI1 and AMMI2 biplot (yield vs. principal component 1 (PC1) for grain yield (kg/ha) of twenty wheat genotypes evaluated under five environments (**B, C and D**), respectively).

Table. 2 Characteristics of test environments and climatic conditions during wheat growing seasons 2023–2024.

Location	Location Code	Agro-climatic zone of Karnataka with number	Geographical Position		Altitude (m.a.s.l.)	Temperature (°C)	
			Latitude	Longitude		Max	Min
Dharwad- 24	E1	Northern Transition Zone (8)	15.46	75.01	750 m	32.76	18.29
Bijapur-24	E2	Northern Dry Zone (3)	16.83	75.71	606 m	33.57	18.84
Bagalkote-24	E3	Northern Dry Zone (3)	16.18	75.67	532 m	34.39	19.26
Raichur-24	E4	Northeastern Dry Zone (3)	16.21	77.36	407 m	33.39	32.06
Dharwad -25	E5	Northern Transition Zone (8)	15.46	75.01	750 m	39.45	17.77

Table. 3 ANOVA for AMMI model applied to yield and yield-related traits values of wheat genotypes tested in five environments under drought regime

Source of Variation	df	Mean Sum of Squares							
		DM	PH	NTM	PDL	SL	NGP	TW	YLD
Environments	4	133.05**	2305.31**	1125.88**	717.42**	12.32**	2079.69***	68.34	10002535.61***
Genotypes	19	29.62***	304.07***	115.36***	84.84***	13.91***	47.85***	58.32***	562581.35***
GXE interaction	76	6.07	74.28***	39.65	16.04***	0.92***	21.04***	21.00***	174832.84***
PC1	22	8.30	137.00***	94.64***	37.22***	1.93***	44.23***	29.58***	224630.86***
PC2	20	9.06	79.88**	29.82	9.65**	0.83***	18.82***	24.78***	194964.39***
PC3	18	3.36	40.98	12.34	7.54	0.37	10.68**	15.57***	157065.23**
PC4	16	2.29	18.49	7.041	4.45	0.28	3.57	10.57**	101184.70
Residuals	95	5.85	31.44	34.82	4.44	0.30	4.87	4.72	60073.57
Total	275	9.49	108.86	59.38	27.14	1.77	47.17	18.65	303505.51

Days to maturity (DM), Plant height (PH), Number of tillers per meter (NTM), Peduncle length (PDL), Spike length (SL), Number of grains per spike (NGP), Thousand seed weight (TW) and Yield per plot (kg/ha**)** (YLD)

According to $Si^{(3)}$ and $Si^{(6)}$, G6, G1, G2 and G14 were among the most stable genotypes. G6 exhibited minimal rank fluctuation, ranking second in $Si^{(3)}$ and first in $Si^{(6)}$, while G1 ranked third in both indices. In contrast, G2 and G14 showed greater rank variability, indicating relatively lower stability under these measures. Thennarasu's $NP^{(1)}$ identified G1, G13 and G17 as the most stable genotypes, whereas $NP^{(2)}$ highlighted G16, G6 and G14. Higher-order statistics $NP^{(3)}$ and $NP^{(4)}$ consistently identified G6, G16, G1 and G14 as stable genotypes. Genotypes G2, G4 and G12 ranked poorly in Kang's Rank-Sum (KR > 30), reflecting low yield and poor stability. WRA further identified G6, G16, and G15 as the top-performing genotypes, integrating both stability and yield-related non-parametric measures (supplementary table 7).

AMMI Stability Parameters

AMMI-based stability parameters, including AMMI Stability Index (ASI), Modified AMMI Stability Value (MASV), Modified AMMI Stability Index (MASI), Average Sum of the Absolute Value of GEI Modeled by AMMI (AVAMGE), Distance Between Genotype and Environment Means (DA), Distance Between Genotype and IPC Axes (DZ), Fitted AMMI Value (FA), AMMI-based Stability Parameter (ASTAB), Sum of the Absolute Value of IPC Scores (SIPC) and the Absolute Value of Relative Contribution of IPCAs (Za), are summarized in supplementary table 4. Indices incorporating the first two IPCAs (ASI, MASV and MASI) consistently identified genotypes G6, G1 and G17 as the most stable across environments, whereas G4 was ranked as the least stable (ASI rank: 20). Notably, MASV and MASI ranked G1, G6 and G17 within the top three positions, confirming their superior stability. The AVAMGE index further corroborated the high stability of G1, G6 and G17 (ranks: 1–3) and clearly identified G4 as the most unstable genotype. Similarly, FA, ASTAB, DA and DZ, which quantify AMMI model fit and GEI dispersion, consistently ranked G1, G6 and G17 among the most stable genotypes, while G4 and G11 showed pronounced instability. For example, FA values were lowest for G1 (13,121.99), G6 (62,052.22) and G17 (67,853.28), indicating minimal deviation from expected performance across environments.

The SIPC index, reflecting cumulative GE interaction across all significant IPCAs, identified G1, G5 and G6 as the most stable genotypes, whereas G4, G11 and G7 exhibited the highest instability. Likewise, the Za index confirmed minimal GE contribution for G1 (0.03), G6 (0.06) and G5 (0.06), indicating static stability under drought conditions, while G4, G11 and G7 showed strong GE interaction. WRA further identified G6, G13, and G17 as the top-performing genotypes, reflecting their consistent stability across multiple AMMI-based parameters (supplementary table 7).

BLUP-Based Stability Analysis

BLUP-derived stability indices, including mean grain yield (Y/AMGV), harmonic mean of genotypic values (HMGV), relative performance of genotypic values (RPGV) and harmonic mean of RPGV (HMRPGV), are presented in supplementary table 5. Genotype G14 consistently ranked highest across all indices, indicating superior yield performance and stability across environments. WRA further identified G14, G15, and G6 as the top-performing genotypes, reflecting their consistent superiority across BLUP-based stability measures (supplementary table 7).

Multi-trait selection indices

Factor analytic best linear unbiased prediction (FAI-BLUP)

The ranking of twenty genotypes with score according to FAI BLUP is presented (supplementary table 6), whereas its visual representation is shown (Fig. 5B). FAI BLUP factor analysis grouped into four factor analyses: FA1, FA2, FA3 and FA4. cumulatively explaining 82.19% of the total variation. Trait communalities were high, ranging from 0.64 to 0.94, with values of PH (0.87), PDL (0.91), TW (0.84), DM (0.94), NGP (0.87), NTM (0.64), SL (0.77) and YLD (0.73), resulting in a mean communality of 0.82. The

selection differential analysis revealed a substantial improvement in several traits under the FAI-BLUP selection strategy. The highest positive gain was observed for SL with an increase of 17.34%, followed by PH (14.89%), YLD (9.55%), NTM (4.22%), TW (4.14%), NGP (2.27%) and PDL (0.33%). In contrast, DM showed a desirable reduction of 2.03%, consistent with the defined ideotype goal of earliness. Based on the FAI-BLUP scores, genotypes with higher index values were considered superior. Among the evaluated genotypes, G15 emerged as the best-performing genotype with the highest FAI-BLUP score (1.0678), followed by G5 (0.9142) and G14 (0.8695).

Multi - trait selection index (MTSI)

The ranking of twenty genotypes with score according to MTSI is presented supplementary table 6, whereas its visual representation is shown (Fig. 5A). Factor analysis grouped the eight traits into FA1, FA2, FA3 and FA4, with high communalities for all traits ranging from 0.605 (PH) to 0.848 (NTM) and an overall mean communality of 0.775. Based on the WAASBY index, the selection differential analysis showed substantial improvement in PDL (34.1%), followed by DM (21.0%), PH (20.8%), NGP (17.3%), SL (14.6%), YLD (14.4%), TW (11.6%) and NTM (3.98%). Similarly, selection differential for trait means indicated positive genetic gains for all traits except DM, which showed a desirable reduction (−0.61%) in line with the breeding objective. The genotypes having a low score are considered superior compared to lower score genotypes. Overall, the multi-trait stability and performance analysis identified G8 (4.425), G15 (4.623) and G3 (4.821) as the most desirable genotypes, combining superior mean performance with stability across environments.

Multi-trait genotype–ideotype distance index (MGIDI)

The ranking of twenty genotypes based on the MGIDI is presented in supplementary table 6, whereas its graphical representation is illustrated in Fig. 5C. Factor analysis grouped the eight traits into four latent factors (FA1, FA2, FA3 and FA4), cumulatively explaining 82.19% of the total variation. High communalities were observed for all traits, ranging from 0.64 (NTM) to 0.94 (DM), with an overall mean communality of 0.82, indicating an adequate representation of the original traits by the extracted factors. The selection differential analysis based on the MGIDI index revealed notable improvements in several traits. The highest positive gain was observed for PDL with an increase of 9.27%, followed by PH (11.00%), TW (4.10%), NGP (1.79%), NTM (0.76%) and YLD (0.67%). In contrast, days to maturity DM showed a desirable reduction of 0.55%, aligning with the breeding objective of earliness, while SL exhibited a slight negative response (−1.88%). In the MGIDI framework, genotypes with lower index values are considered superior, as they are closer to the ideotype. Accordingly, the most desirable genotypes identified were G3 (2.596), G15 (2.658) and G5 (2.733).

Correlation analysis and visualization

Correlation Analysis Among Parametric Stability Parameters

Correlation analysis among grain yield and parametric stability indices revealed that grain yield was weakly and negatively associated with most stability measures, including deviation from regression (s^2d_i; r = −0.09), Wricke's ecovalence (Wi^2; r = −0.08) and Shukla's stability variance (σ^2_i; r = −0.08) (Figure 3B). Strong and significant interrelationships were observed among the stability parameters. Pinthus's coefficient of determination (θ_i) was perfectly and negatively correlated (r = −1.00) with GE interaction variance (θ_iGE), Wi^2 and σ^2_i, indicating its inverse association with genotype instability. Conversely, θ_iGE, Wi^2 and σ^2_i were perfectly and positively correlated (r = 1.00), demonstrating their consistency in quantifying GEI effects. Deviation from regression (s^2d_i) showed strong positive correlations with θ_iGE, Wi^2 and σ^2_i (r = 0.91), confirming its sensitivity to GEI-driven instability. In contrast, the coefficient of variation (CVi) displayed weaker positive correlations with θ_iGE (r = 0.23), σ^2_i (r = 0.23)

and s^2d_i (r = 0.29), suggesting that it captures genotype variability partially but reflects a distinct stability dimension. These near-perfect correlations among several parametric indices indicate that they are mathematically related and capture similar components of genotype × environment interaction, reflecting redundancy rather than independent validation.

Correlation Analysis Among Non-Parametric Stability Parameters

Correlation analysis among grain yield and non-parametric stability indices revealed contrasting associations (Figure 3A). Grain yield showed negative correlations with $NP^{(4)}$ (r = −0.42) and $Si^{(3)}$ (r = −0.38) and weak negative associations with $Si^{(1)}$ (r = −0.22) and $NP^{(1)}$ (r = −0.20). In contrast, strong positive correlations were observed between grain yield and $NP^{(2)}$ (r = 0.86), $NP^{(3)}$ (r = 0.65) and Kang's rank-sum (KR) (r = 0.65), indicating their effectiveness in identifying high-yielding stable genotypes. Huhn's and Nassar and Huhn's statistics ($Si^{(1)}$–$Si^{(6)}$) were significantly and positively intercorrelated, confirming their consistency in assessing genotype stability, with $Si^{(1)}$ and $Si^{(2)}$ showing an almost perfect correlation (r = 0.99). Among Thennarasu's indices, $NP^{(1)}$ was positively correlated with $NP^{(3)}$ (r = 0.44) and $NP^{(4)}$ (r = 0.64), while $NP^{(3)}$ and $NP^{(4)}$ were also strongly correlated (r = 0.74). In contrast, $NP^{(2)}$ showed weak or negligible correlations with most indices, including $NP^{(1)}$ (r = 0.00) and $Si^{(1)}$ (r = −0.02), suggesting that it captures a distinct stability dimension. Kang's rank-sum (KR) exhibited strong positive correlations with $NP^{(3)}$ (r = 0.93), $NP^{(4)}$ (r = 0.78), $NP^{(2)}$ (r = 0.78), $Si^{(6)}$ (r = 0.80) and grain yield (r = 0.65), highlighting its robustness in integrating yield performance with stability. The strong intercorrelations among several non-parametric indices further suggest partial methodological overlap, although some indices (e.g., NP(2)) capture distinct aspects of stability.

Correlation Analysis Among AMMI Stability Parameters

Spearman's rank correlation analysis among grain yield and AMMI-derived stability indices revealed strong and statistically significant positive associations among most indices, confirming their internal consistency in characterizing genotype × environment interaction (GEI) (Fig. 3C). MASV showed exceptionally high correlations with Fitted AMMI value (FA; r = 0.99) and AVAMGE (r = 0.97), indicating close agreement with both model fit and GEI magnitude. Similarly, MASI was strongly correlated with FA (r = 0.98), reflecting concordance in AMMI-based genotype performance. The SIPC index was strongly correlated with Za (r = 0.96), suggesting that both indices effectively capture genotypic contributions to total GEI. Distance-based parameters also exhibited near-perfect associations: DA was correlated with FA (r = 1.00), AVAMGE (r = 0.98), MASI (r = 0.98) and MASV (r = 0.99), establishing it as a robust indicator of overall GEI magnitude. Likewise, DZ showed strong positive correlations with AVAMGE (r = 0.92), FA (r = 0.91), MASI (r = 0.87) and MASV (r = 0.89), confirming its effectiveness in identifying genotype sensitivity to interaction principal components. In contrast, grain yield exhibited weak and non-significant correlations with most AMMI stability indices, including SIPC (r = −0.23), DZ (r = −0.19) and AVAMGE (r = −0.10), reflecting the common trade-off between mean productivity and stability across heterogeneous environments. The high concordance among AMMI-based indices reflects their shared dependence on IPCA scores and eigenvalue structure, indicating that these measures are not independent but represent different transformations of the same underlying interaction patterns.

Correlation Analysis Among BLUP-Based Stability Indices

Spearman's rank correlation analysis among BLUP-based stability indices revealed a strong and significant positive association between all four indices—AMGV, HMGV, HMRPGV and RPGV (Figure 3D). The highest positive correlation was observed between HMRPGV and RPGV (r = 0.98), followed closely by AMGV and RPGV (r = 0.99) and HMRPGV and AMGV (r = 0.98). Notably, HMGV also showed significant positive correlations with AMGV (r = 0.93), HMRPGV (r = 0.96) and RPGV (r = 0.96). Such

strong associations indicate that BLUP-based indices largely represent the same underlying construct of genotypic performance with minor differences in scaling or penalization.

Correlation between Stability Statistics

Spearman's rank correlation coefficients were estimated among thirty stability parameters, encompassing parametric, non-parametric, AMMI-based and BLUP-based indices, to elucidate their interrelationships with yield performance. The relationships were visualized using schemaball and correlation plots (Figure 4A and 4B), providing an integrated view of clustering and connectivity among indices. Strong internal associations were observed among AMMI-based stability parameters, confirming their consistency in capturing genotype × environment interaction.

BLUP-based indices showed largely non-significant correlations with AMMI-based indices, except for AMGV, while RPGV, HMRPGV and HMGV were strongly and positively intercorrelated. BLUP-based indices also exhibited weak or non-significant correlations with parametric and most non-parametric stability measures. Among parametric indices, the coefficient of variation (CV) showed non-significant correlations with AMMI-based indices, whereas the mean variance component (θ_i) exhibited strong negative correlations with other parametric measures and AMMI-based indices, indicating its inverse relationship with genotype instability. Thennarasu's non-parametric statistic $NP^{(1)}$ also showed non-significant correlations with AMMI stability indices. Spearman's rank correlation revealed that mean grain yield was positively and significantly associated with $NP^{(1)}$, $NP^{(2)}$, Kang's rank-sum (KR), AMGV, RPGV, HMRPGV and HMGV. Overall, the schemaball analysis confirmed mean variance component (θ_i) exhibited strong negative correlations with other parametric measures and AMMI-based indices. Overall, the clustering of indices within methodological groups highlights the presence of redundancy due to shared computational frameworks, whereas weaker associations between groups indicate that different classes of stability statistics capture distinct dimensions of genotype performance.

Correlation and venn diagram among multi-trait selection methods

Relationships among the three multi-trait selection indices (MTSI, MGIDI and FAI-BLUP) were evaluated using Spearman's rank correlation analysis and visualized in a correlation plot (Fig. 5D). A strong and significant positive correlation was observed between MGIDI and FAI-BLUP ($r = 0.85$), indicating close agreement in genotype ranking. In contrast, correlations of MTSI with MGIDI ($r = 0.37$) and with FAI-BLUP ($r = 0.31$) were positive but non-significant.

To examine agreement among methods, a Venn diagram based on the top five genotypes selected by each index was constructed (Fig. 5E). Two genotypes (G3 and G15) were consistently identified across all three indices, indicating agreement across selection approaches. G11 and G5 were jointly selected by MGIDI and FAI-BLUP, reflecting partial overlap between these methods. In contrast, MTSI uniquely identified G1, G8 and G6, while MGIDI and FAI-BLUP each selected specific genotypes (e.g., G19 and G14), suggesting that different indices capture distinct aspects of genotype performance. Overall, both shared and unique selections indicate that these indices provide complementary rather than identical information. Accordingly, overlap among indices should be viewed as supportive evidence, whereas unique selections may reflect method-specific sensitivity to particular trait combinations. WRA further identified G15, G3, and G8 as the top-ranked genotypes, integrating information across indices into a single composite ranking. (supplementary table 6 and 7).

Discussion

Wheat is central to global food and nutritional security, particularly in Asia and drought-prone regions. In this study, twenty wheat genotypes were evaluated under drought stress across four contrasting environments that differed markedly in rainfall and temperature regimes. These environmental contrasts significantly influenced soil moisture availability and crop water use efficiency, resulting in pronounced genotype × environment (G×E) interactions for grain yield. ANOVA analyses confirmed that temperature extremes and reduced precipitation during critical growth stages intensified drought stress, leading to variable genotype performance across locations. These findings highlight the necessity of multi-environment testing to reliably identify genotypes with wide or specific adaptation under drought conditions. ANOVA revealed highly significant differences among environments, genotypes and GEI for grain yield, indicating substantial environmental heterogeneity and genetic diversity. Similar results have been reported for agronomic traits in mungbean[46], maize[47–49], rice[50–52] and okra[53]. AMMI analysis detected significant genotype, environment and GEI effects for most traits, except days to maturity and number of tillers per meter, where GEI was nonsignificant. Environments E5 and E4 supported higher mean yields, whereas E3 exhibited lower productivity. Residual soil moisture from substantial October 2024 rainfall likely contributed to the favorable performance of E5, while minimal rainfall and higher temperatures in E3 increased drought stress, making it suitable for genotype discrimination under moisture-limited conditions.

Stability analysis in multi-environment trials is inherently model-dependent, as different methods embody distinct concepts of stability[42]. Stability may be defined as biological stability (consistency across environments), agronomic stability (high yield with moderate responsiveness) and statistical stability (minimum deviation or variance)[54], explaining shifts in genotype ranking across AMMI, parametric, non-parametric, BLUP-and multi trait-based approaches.

AMMI1 biplot interpretation showed that genotypes with high mean yield and PC1 scores near zero combine productivity with stability[55,56]. Although G14 had the highest yield, its large PC1 score indicated specific adaptation. In contrast, G6 combined high yield with moderate PC1, indicating wide adaptation. AMMI2 further revealed that genotypes near the origin (G1, G6, G16) exhibited minimal interaction effects, whereas G14 and G20 showed environment-specific responsiveness[57].

Parametric indices (W_i^2, σ^2_i, S^2d_i, CV_i, θ_i) emphasized uniformity and low interaction variance, favoring genotypes such as G1 and G17 while penalizing genotypes with high genotype × environment interaction[30]. For instance, genotype G11, despite its high mean yield (ranked 4th), exhibited high values of W_i^2, σ^2_i, and S^2d_i, indicating substantial environmental sensitivity and resulting in lower stability rankings. Similarly, genotypes such as G4 showed poor stability due to large interaction variance, although without corresponding high yield advantage. This demonstrates that parametric stability measures prioritize predictability and uniform performance across environments, often penalizing genotypes with high responsiveness even if they possess superior yield potential. Consequently, such genotypes may be more suitable for specific environments rather than broad adaptation, highlighting a trade-off between yield performance and stability.

Non-parametric indices, based on yield ranks rather than absolute values[30], these include $Si^{(1)}$ and $Si^{(2)}$, which measure rank variance and mean rank deviation; $NP^{(1)}$ – $NP^{(4)}$, which assess absolute deviation from environment mean ranks; and KR (Kang's rank-sum), which integrates yield and stability

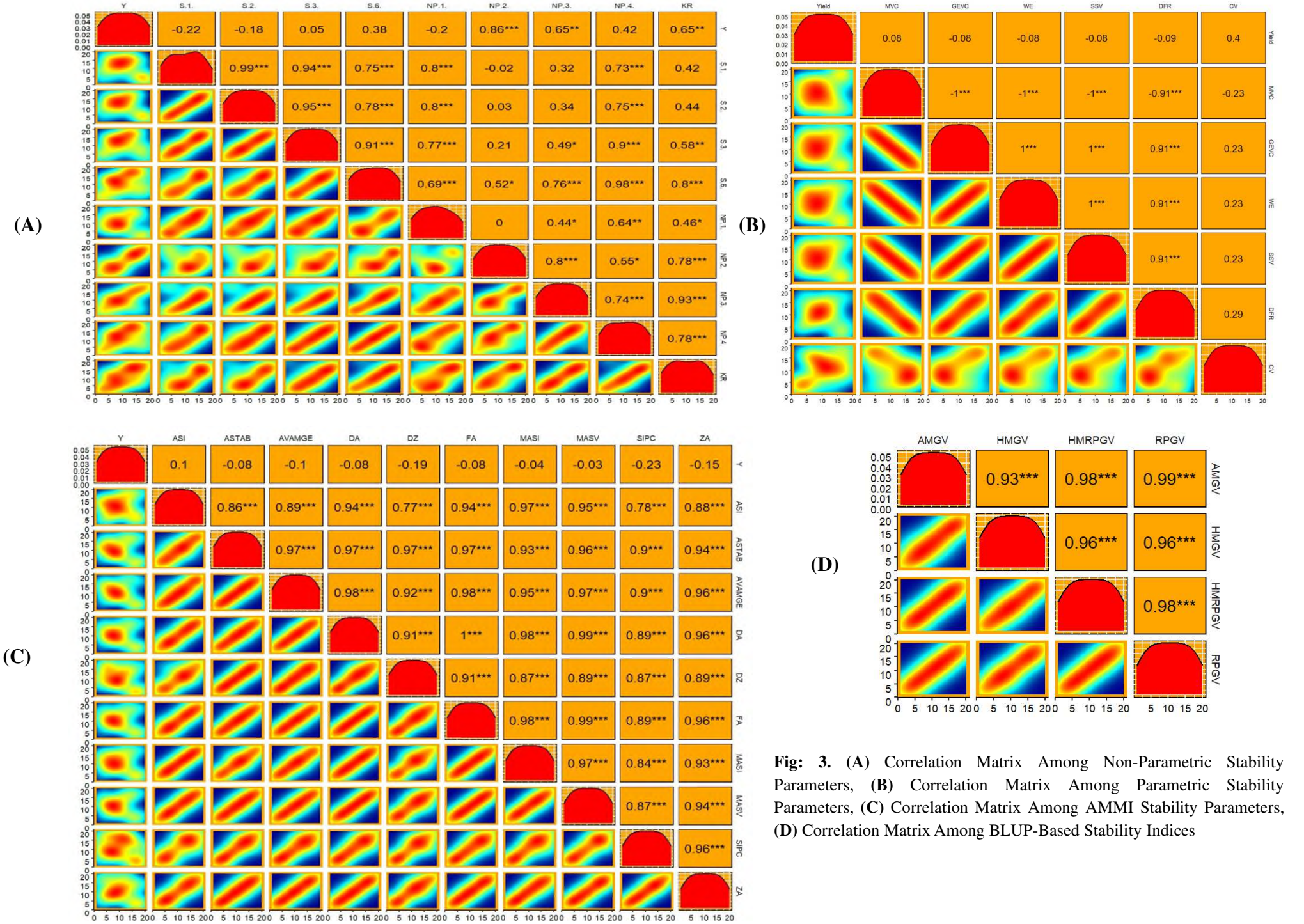
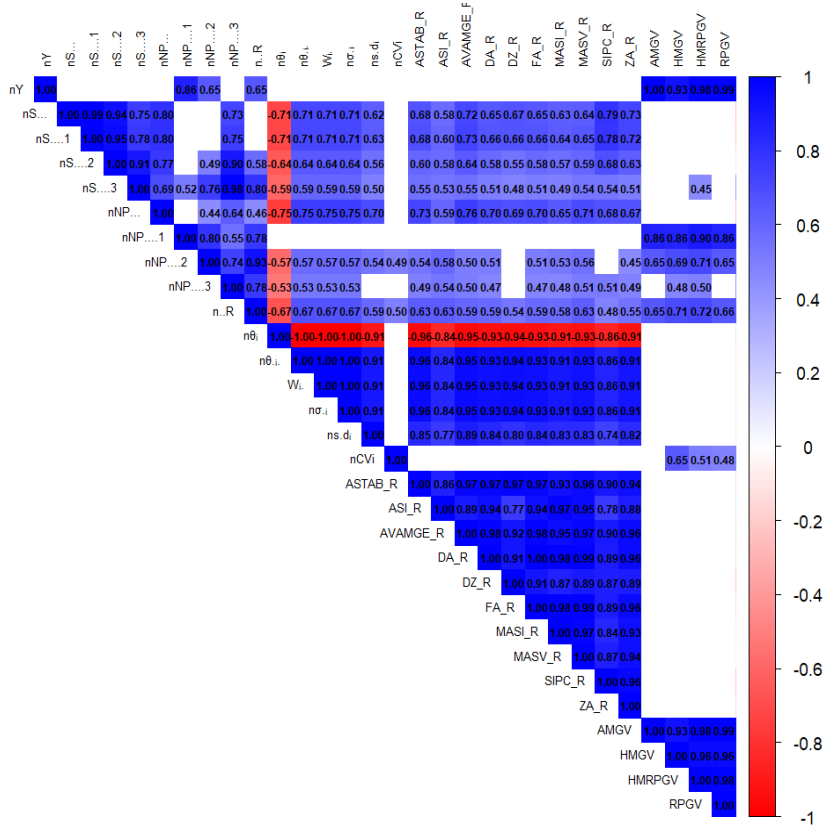
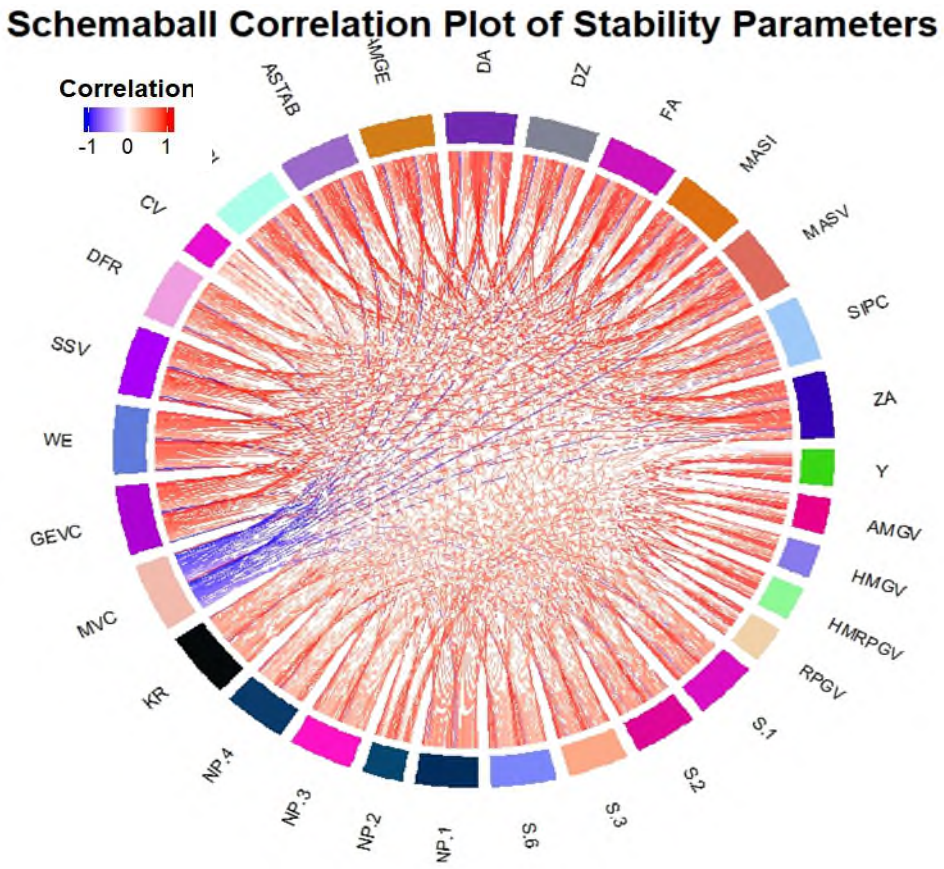


Fig: 3. (A) Correlation Matrix Among Non-Parametric Stability Parameters, **(B)** Correlation Matrix Among Parametric Stability Parameters, **(C)** Correlation Matrix Among AMMI Stability Parameters, **(D)** Correlation Matrix Among BLUP-Based Stability Indices

Y- Yield (kg/ha), **S.1, S.2, S.3, S.6 -** Huhn's and Nassar and Huhn's non-parametric statistics, **NP.1, NP.2, NP.3, NP.4 -** Thennarasu's non-parametric statistics, ***K*R**- Kang's rank-sum, **MVC-** Mean variance component, **GEVC-** GE variance component, **WE -** Wricke's ecovalence, **SSV**. Shukla's stability variance, **DFR-** Deviation from regression, **CV-** Coefficient of variation, **ASI** -AMMI Stability Index, **AVAMGE** -Average Sum of the Absolute Value of the GEI Modeled by AMMI, **DA**-Distances Between Genotype and Environment Means, **DZ** -Distances Between Genotype and Interaction Principal Component Axes, **FA** -Fitted AMMI Model Value, **ASTAB** -AMMI-Based Stability Parameter, **MASV** -Modified AMMI Stability Value, **MASI**-Modified AMMI Stability Index, **SIPC**-Sum of the Absolute Value of IPC Scores, **ZA-** Absolute Value of the Relative Contribution of IPCAs to the Interaction, **AMGV**-Arithmetic Mean of Genotypes Values, **RPGV**-Relative performance of genotypes values, **HMRPGV-**Harmonic mean of RPGV



(A)



(B)

Fig: 4A Correlation Matrix Among Stability Parameters (only significant associations), **4B** Schemaball correlation plot Among Stability Parameters

Y- Yield (kg/ha), **S.1, S.2, S.3, S.6 -** Huhn's and Nassar and Huhn's non-parametric statistics, **NP.1, NP.2, NP.3, NP.4 -** Thennarasu's non-parametric statistics, ***K*R**- Kang's rank-sum, **MVC-** Mean variance component, **GEVC-** GE variance component, **WE -** Wricke's ecovalence, **SSV**- Shukla's stability variance, **DFR-** Deviation from regression, **CV-** Coefficient of variation, **ASI** -AMMI Stability Index, **AVAMGE** -Average Sum of the Absolute Value of the GEI Modeled by AMMI, **DA**-Distances Between Genotype and Environment Means, **DZ** -Distances Between Genotype and Interaction Principal Component Axes, **FA** -Fitted AMMI Model Value, **ASTAB** -AMMI-Based Stability Parameter, **MASV** -Modified AMMI Stability Value, **MASI**-Modified AMMI Stability Index, **SIPC**-Sum of the Absolute Value of IPC Scores, **ZA-**Absolute Value of the Relative Contribution of IPCAs to the Interaction, **AMGV**-Arithmetic Mean of Genotypes Values, **RPGV**-Relative performance of genotypes values, **HMRPGV-**Harmonic mean of RPGV

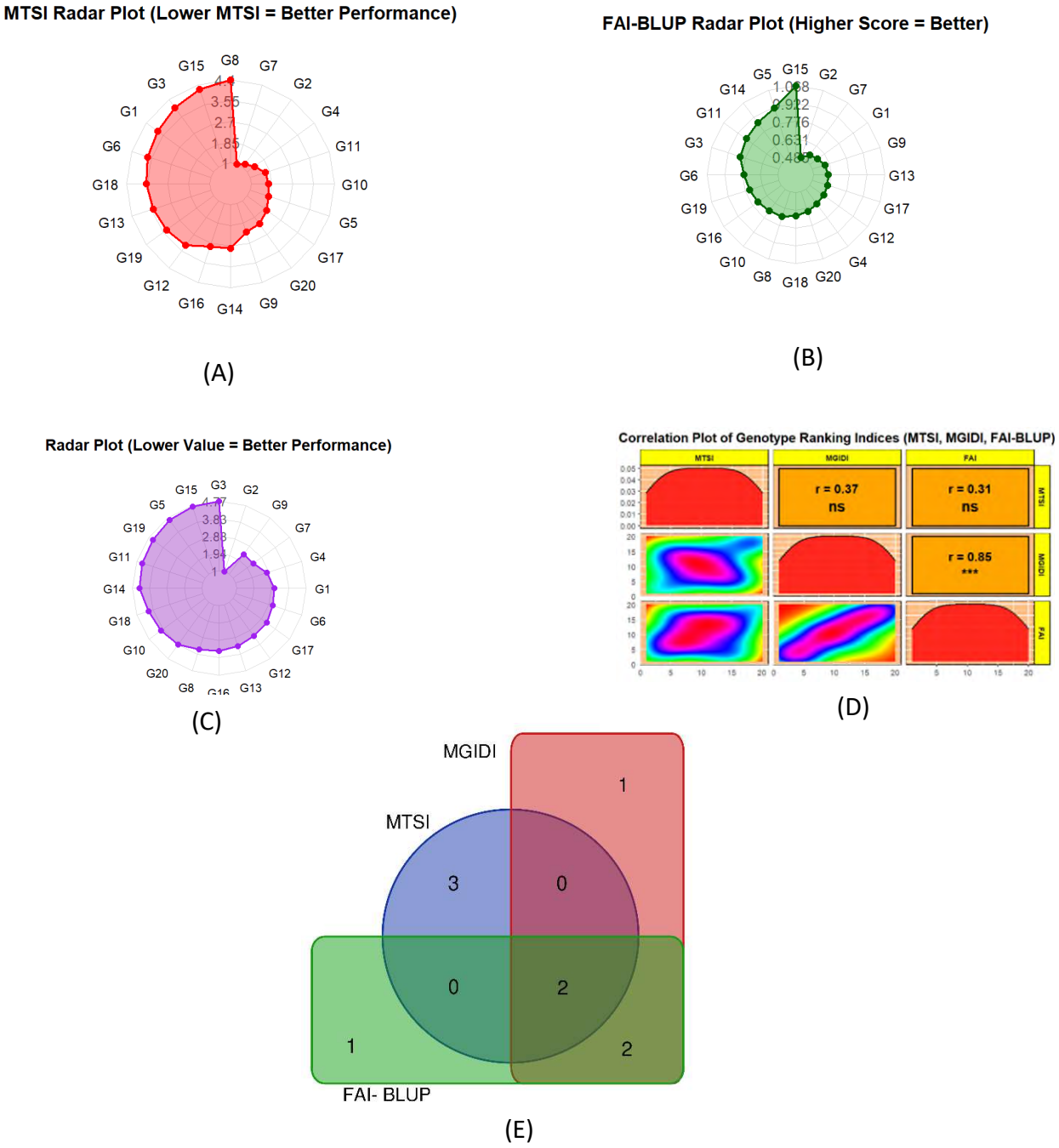


Figure 5.(A) Radar plot of multi-trait stability index (MTSI) scores for wheat genotypes under drought stress, (B) Radar plot of Factor analytic best linear unbiased prediction (FAI-BLUP) scores for wheat genotypes under drought stress, (C) Radar plot of multi-trait genotype–ideotype distance index (MGIDI) scores for wheat genotypes under drought stress, (D) Correlation plot among multi-trait selection indices, (E) Venn analysis among multi-trait selection indices for stable genotypes.

ranks. These methods penalize rank fluctuation rather than yield magnitude. G6 was classified as stable by non-parametric indices due to its consistently low rank across environments, a pattern that reflects rank constancy rather than superior performance. In contrast, G14 was penalized because of large rank shifts across environments despite high yield. Therefore, non-parametric methods primarily capture consistency of ranking, not yield superiority.

Advanced AMMI-based indices such as ASTAB, MASV and SIPC assign weights based on eigenvalues and account for the variance explained by each IPCA, while integrating stability across multiple axes [58,59] and consistently ranked G6, G13 and G17 as stable and G14, G7 and G12 as unstable, confirming their robustness in quantifying interaction magnitude.

BLUP models redefine stability as the expected performance of a genotype under random environmental sampling [58]. AMGV, HMGV, RPGV and HMRPGV are based on average genetic value, penalized dispersion, relative advantage and resilience index, respectively. BLUP stabilizes estimates by applying variance shrinkage, pulling unstable genotypes toward the overall mean. Hence, G14 dominated due to its consistently high genotypic value, not necessarily low interaction. This distinction is critical, as it illustrates that BLUP-based selection is more aligned with modern breeding strategies aimed at maximizing genetic gain, even at the cost of increased interaction. BLUP therefore defines stability as yield reliability rather than GEI minimization.

Across all models, the consistent identification of advanced breeding line G6 highlights its potential as a valuable donor for stability and drought adaptation. In addition, lines G13, G14, G15 (genetic stock), G16 and G17 emerged as promising candidates for varietal development, allowing breeders to select genotypes tailored either for specific adaptation or for broad stability depending on the breeding objective based as represented by WRA results. These results confirm that stability is model-dependent, varying with whether the breeding objective emphasizes consistency (non-parametric), interaction minimization (AMMI), statistical predictability (parametric), or genetic merit (BLUP).

Comparison with the check cultivars further supports the performance of the selected genotypes under drought stress. The advanced breeding line GDP 40 (G6), which was consistently identified as stable across analytical approaches, produced substantially higher grain yield than the rainfed durum wheat check Amruth (G2). Likewise, the susceptible bread wheat checks UAS-334 (G11) and UAS-3020 (G12) showed inferior overall stability rankings, while UAS-3020 also exhibited relatively low grain yield under drought stress. Several advanced breeding lines, including G13, G14, G15, G16 and G17, also compared favorably with the check cultivars in terms of yield and/or stability. These results suggest that the identified genotypes represent promising candidates for future varietal development and breeding programs targeting drought-prone environments, subject to further multi-location and physiological validation.

Integrating results across models provides a more balanced and reliable assessment of genotype performance and stability, which is valuable for identifying candidates suited to diverse and unpredictable environments. However, these findings are based on phenotypic responses rather than direct physiological measurements. The superior performance of above identified genotypes under drought may be associated with traits such as improved water-use efficiency or deeper rooting, but these were not directly assessed. Therefore, these genotypes should be considered as promising candidates for drought-prone environments, with further physiological and molecular studies needed to validate the underlying mechanisms.

Multi-trait selection indices (FAI-BLUP, MTSI and MGIDI) offered a rigorous and biologically coherent framework for identifying superior genotypes by integrating GEI, mixed-model genetic prediction and ideotype-based selection. FAI-BLUP, based on factor analysis of BLUP values, efficiently reduced trait dimensionality while preserving genetic covariance, as indicated by high explained variance (>80%)

and communalities. Its favorable selection differentials for yield, associated traits and reduced maturity demonstrate effective translation of statistical optimization into drought-adaptive responses, identifying G15, G5 and G14 as high-merit genotypes. MTSI, which ranks genotypes by ideotype distance weighted by WAASBY, emphasizes stability over absolute performance, explaining its weaker correlation with other indices and its effectiveness in selecting consistently performing genotypes such as G8, G15 and G3, in agreement with[60]. MGIDI, an ideotype-distance approach without explicit stability penalization, favored balanced trait improvement and showed close concordance with FAI-BLUP, jointly selecting G3, G15 and G5. The strong agreement between FAI-BLUP and MGIDI reflects their shared reliance on factor analysis and BLUP-derived values, whereas partial divergence of MTSI reflects its stability-centered philosophy. These multi trait selection indices identified G15 (genetic stock), G3 and G8 genotypes as best performing as indicated by WRA, effectively bridge the gap between statistical optimization and biological relevance by capturing multiple trait interactions and translating them into practical breeding decisions.

The study was conducted with a limited number of replications and without well-watered (non-stressed) control environments, which restricted direct comparison of genotype responses under contrasting moisture regimes. Although the genotypes were evaluated across multiple drought-stressed environments, the selected genotypes were not validated in an independent set of environments or years. Furthermore, the study focused primarily on yield-based stability analyses and did not include physiological measurements; therefore, the mechanisms underlying genotype performance under drought remain to be confirmed.

Correlation analysis clarified whether different stability metrics capture the same biological phenomenon or distinct aspects of genotype performance. Clear clustering among parametric and AMMI-based indices indicated strong conceptual overlap. Perfect positive correlations among θ_i', Wi^2 and σ^2_i, together with their perfect negative association with θ_i, confirm that these parameters are mathematically equivalent expressions of GEI magnitude. Wricke's ecovalence and Shukla's stability variance both arise from GE sum of squares partitioning, while θ_i' represents genotype-specific variance contribution within the same framework, resulting in identical genotype rankings. The inverse behavior of θ_i reflects its formulation as a complement of GE variance, favoring interaction-neutral genotypes. Strong correlations between S^2d_i and interaction variance parameters further indicate that regression residual variance is a proxy for GEI magnitude, whereas CV_i showed weak associations because it depends on both mean yield and variance and therefore reflects dispersion rather than pure interaction. These results clearly indicate that strong agreement among several parametric stability measures arises from shared mathematical formulation rather than independent validation, highlighting redundancy within this class of indices.

The weak negative correlation between grain yield and parametric stability indices highlights the common MET trade-off whereby high productivity is often associated with increased environmental sensitivity, causing parametric measures to favor conservative, uniformly performing genotypes. Strong intercorrelations among AMMI-based indices result from their shared geometric foundation, as MASV, MASI, AVAMGE, FA, DA and DZ are all derived from IPCA scores and differ mainly in eigenvalue weighting. Near-perfect correlations among DA, FA and MASV indicate that distance-based indices closely approximate total GEI magnitude, while the strong association between SIPC and Za reflects their common aim of quantifying genotype contribution to GEI sum of squares. The weak and nonsignificant correlations between yield and AMMI parameters confirm that AMMI stability is orthogonal to productivity, favoring interaction-neutral genotypes (e.g., G1 and G6) over high-yield but environment-sensitive ones (e.g., G14). Similarly, the high concordance among AMMI-derived indices reflects their common dependence on IPCA structure, indicating that these indices represent alternative formulations of the same interaction patterns rather than independent evidence of stability.

BLUP-derived indices (AMGV, HMGV, RPGV, HMRPGV) showed exceptionally high mutual correlations, indicating that they represent variations of a single construct genotypic performance under random environmental realization consistent with earlier reports[42]. Because BLUP indices do not quantify

instability, they showed little association with interaction-based metrics. Instead, shrinkage stabilizes genotype predictions without eliminating GEI, allowing high-value but interaction-sensitive genotypes such as G14 to rank superior. Consequently, BLUP defines stability as predictability of superiority rather than interaction neutrality. The lack of correlation between BLUP- and AMMI-based indices confirms that these approaches capture different biological dimensions of genotype performance[59,42]. AMMI and parametric indices quantify interaction magnitude, whereas BLUP evaluates performance robustness despite interaction. This distinction explains limited rank concordance across methods and reinforces that stability assessment should be guided by breeding objectives rather than statistical convenience, as also reported previously[59,42]. Thus, agreement within BLUP-based indices also reflects shared computational structure, whereas lack of agreement with AMMI and parametric approaches underscores their conceptual independence. Robustness in this study is therefore inferred from agreement across conceptually distinct analytical frameworks rather than within-method consistency. These complementary approaches provide practical guidance for breeders by enabling the identification of genotypes suited for either broad adaptation or specific environments, thereby supporting more targeted and efficient selection decisions.

Conclusion

This study demonstrates the value of integrating multiple analytical frameworks, including parametric, non-parametric, AMMI and BLUP models, together with multi-trait selection indices (FAI-BLUP, MTSI and MGIDI) and weighted rank aggregation, for genotype evaluation under drought-stressed environments. The results highlight that genotype rankings and stability assessments are inherently model-dependent, reflecting different concepts of performance, adaptability and stability. Nevertheless, G6, G13, G14, G15, G16 and G17 were frequently prioritized across multiple analytical approaches and therefore represent promising candidates for further evaluation under drought-stressed environments in Karnataka. Likewise, multi-trait indices frequently prioritized G15, G3 and G8 because of their favorable multi-trait profiles. These findings provide a useful framework for selecting candidate genotypes for breeding and testing programs; however, their broader adaptation and underlying physiological mechanisms require further validation across additional environments and years.

Declarations

Ethics approval and Consent to participate

This study adhered to all relevant institutional, national, and international guidelines and legislation in India. Plant materials were collected from Department of Genetics and Plant Breeding, UAS, Dharwad, Karnataka, India. No special permissions were required for sample collection. All plant materials used in the study were in compliance with Indian regulations and legislation.

Consent to publish

Not applicable.

Clinical trial

Not applicable.

Clinical Trial Number

Not applicable.

Conflicts of interest

The authors declare that they have no conflict of interest.

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Declaration of generative AI

The author(s) declare that generative AI tools were used for language refinement and editing in the preparation of this paper.

Data Availability

Data used during the preparation of this manuscript is available within the article.

Authors' contributions

SAD, SSB and AVK: conceived and designed the project; SP, AVK, BSO, SSB, HK, JRD, RB, HK, GD, MMH, PK, BB, CB, SBP, AP, SAD and MR: analyzed, wrote, revised and proofread the manuscript. All authors contributed to the article and read and approved the final manuscript.

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References

1. Shewry, P. R. and Hey, S. Do "ancient" wheat species differ from modern bread wheat in their contents of bioactive components. *Journal of Cereal Science.* 65, 236–243 (2015). https://doi.org/10.1016/j.jcs.2015.07.014
2. Peng, J., Sun, D. and Nevo, E. Wild emmer wheat: genetic resources for tolerance. *Australian Journal of Crop Science.* 5, 1127–1133 (2011).
3. Upadhyay, K., Adhikari, N. and Sharma, S. Genetic variability and cluster analysis of wheat (*Triticum aestivum* L.) genotypes in the foothill of Nepal. *Archives of Agriculture and Environmental Science.* 4(3), 350–355 (2019). https://doi.org/10.26832/24566632.2019.0403013
4. Gupta, P. K. and Vasistha, N. K. Wheat cytogenetics: present status and future prospects. *Nucleus.* 61, 195–212 (2018). https://doi.org/10.1007/s13237-018-0243-x
5. Arzani, A. and Ashraf, M. Cultivated ancient wheats (*Triticum* spp.): A potential source of health-beneficial food products. *Comprehensive Reviews in Food Science and Food Safety.* 16, 477–488 (2017). https://doi.org/10.1111/1541-4337.12262
6. Food and Agriculture Organization. *Crop prospects and food situation*. FAO, Rome (2021).
7. Wang, W., Vinocur, B. and Altman, A. Plant responses to drought, salinity and extreme temperatures: towards genetic engineering for stress tolerance. *Planta.* 218, 1–14 (2003). https://doi.org/10.1007/s00425-003-1105-5
8. Bayoumi, T. Y., Eid, M. H. and Metwali, E. M. Physiological and biochemical screening for drought tolerance in wheat. *African Journal of Biotechnology.* 7, 2341–2352 (2008).
9. Fang, Y. and Xiong, L. General mechanisms of drought response in plants. *Cellular and Molecular Life Sciences.* 72, 673–689 (2015). https://doi.org/10.1007/s00018-014-1767-0
10. Ahmed, H. G. M.-D., Naeem, M., Zeng, Y., Rashid, M. A. R., Ullah, A., Saeed, A., Wu, J., Gao, F. and Zhang, G. Genome-wide association mapping for high temperature tolerance in wheat through a 90K SNP array using physiological and yield traits. *PLoS ONE.* 17, e0262569 (2022). https://doi.org/10.1371/journal.pone.0262569
11. Xiong, W., Reynolds, M. and Xu, Y. Climate change challenges plant breeding. *Current Opinion in Plant Biology.* 70, 102308 (2022). https://doi.org/10.1016/j.pbi.2022.102308
12. Nyquist, W. E. and Baker, R. J. Estimation of heritability and prediction of selection response. *Critical Reviews in Plant Sciences.* 10, 235–322 (1991). https://doi.org/10.1080/07352689109382313
13. Malosetti, M., Ribaut, J.-M. and van Eeuwijk, F. A. Statistical analysis of multi-environment data. *Frontiers in Physiology.* 4, 44 (2013). https://doi.org/10.3389/fphys.2013.00044
14. Olivoto, T., Lúcio, A. D., Silva, J. A. G., Marchioro, V. S., de Souza, V. Q. and Jost, E. Mean performance and stability in multi-environment trials: combining AMMI and BLUP. *Agronomy Journal.* 111, 2949–2960 (2019). https://doi.org/10.2134/agronj2019.03.0220
15. Wricke, G. Über eine Methode zur Erfassung der ökologischen Streubreite in Feldversuchen. *Zeitschrift für Pflanzenzüchtung.* 47, 92–96 (1962).
16. Finlay, K. W. and Wilkinson, G. N. The analysis of adaptation in a plant-breeding programme. *Australian Journal of Agricultural Research.* 14, 742–754 (1963). https://doi.org/10.1071/AR9630742
17. Eberhart, S. A. and Russell, W. A. Stability parameters for comparing varieties. *Crop Science.* 6, 36–40 (1966). https://doi.org/10.2135/cropsci1966.0011183X000600010011x
18. Shukla, G. K. Some statistical aspects of partitioning genotype–environmental components of variability. *Heredity.* 29, 237–245 (1972).
19. Francis, T. R. and Kannenberg, L. W. Yield stability studies in short-season maize. I. A descriptive method for grouping genotypes. *Canadian Journal of Plant Science.* 58, 1029–1034 (1978). https://doi.org/10.4141/cjps78-157
20. Purchase, J. L. *Parametric analysis to describe genotype × environment interaction and yield stability in winter wheat*. PhD thesis, University of the Free State, Bloemfontein, South Africa (1997).
21. Huehn, M. Nonparametric measures of phenotypic stability. *EDV in Medizin und Biologie.* 10, 112–117 (1979).

22. Nassar, R. and Huehn, M. Nonparametric measures of phenotypic stability in plant breeding. *Biometrics.* 43, 45–53 (1987). https://doi.org/10.2307/2531947
23. Vaezi, B., Pour-Aboughadareh, A., Mohammadi, R., Mehraban, A., Hossein-Pour, T., Koohkan, E., Ghasemi, S., Moradkhani, H. and Siddique, K. H. M. Integrating different stability models to investigate genotype × environment interactions and identify stable and high-yielding barley genotypes. *Euphytica.* 215, 63 (2019). https://doi.org/10.1007/s10681-019-2386-5
24. Mukherjee, A. K., Mohapatra, N. K., Bose, L. K., Jambhulkar, N. N. and Nayak, P. Additive main effects and multiplicative interaction analysis of G × E interactions in rice–blast pathosystem. *African Journal of Agricultural Research.* 8, 5492–5507 (2013).
25. Tekalign, A., Sibiya, J., Derera, J. and Fikre, A. Analysis of genotype × environment interaction and stability for grain yield and chocolate spot disease resistance in faba bean. *Australian Journal of Crop Science.* 11, 1228–1235 (2017).
26. Crossa, J. Statistical analyses of multilocation trials. *Advances in Agronomy.* 44, 55–85 (1990). https://doi.org/10.1016/S0065-2113(08)60818-4
27. Yan, W., Hunt, L. A., Sheng, Q. and Szlavnics, Z. Cultivar evaluation and mega-environment investigation based on the GGE biplot. *Crop Science.* 40, 597–605 (2000). https://doi.org/10.2135/cropsci2000.403597x
28. Yan, W. and Kang, M. S. *GGE biplot analysis: a graphical tool for breeders*. CRC Press, Boca Raton (2002).
29. Rao, A. R. and Prabhakaran, V. T. Use of AMMI in simultaneous selection of genotypes for yield and stability. *Journal of the Indian Society of Agricultural Statistics.* 59, 76–82 (2005).
30. Farshadfar, E. AMMI stability value and grain yield index in wheat. *Pakistan Journal of Biological Sciences.* 11, 1791–1796 (2008).
31. Verardi, S., Dahourou, D., Ah-Kion, J., Bhowon, U., Tseung, C. N., Amoussou-Yeye, D., Adjahouisso, M., Bouatta, C., Dougoumalé Cissé, D. and Mbodji, M. Psychometric properties of the Marlowe–Crowne social desirability scale in eight African countries and Switzerland. *Journal of Cross-Cultural Psychology.* 41, 19–34 (2010). https://doi.org/10.1177/0022022109348918
32. De Resende, M. D. V. *Selegen-REML/BLUP statistical system*. Embrapa Florestas (2007).
33. Gauch, H. G., Piepho, H. P. and Annicchiarico, P. Statistical analysis of yield trials by AMMI and GGE. *Crop Science.* 48, 866–889 (2008). https://doi.org/10.2135/cropsci2005.07-0193
34. Yan, W. Mega-environment analysis and test location evaluation based on unbalanced multiyear data. *Crop Science.* 55, 113–122 (2015). https://doi.org/10.2135/cropsci2014.03.0203
35. Da Cruz, D. P., Gonçalves, L. S. A., Rodrigues, E. V., Ferreira, R. P., Lima, R. O. and Barros, W. S. Phenotypic adaptability and stability in cowpea using GGE biplot. *Euphytica.* 216, 160 (2020). https://doi.org/10.1007/s10681-020-02693-9
36. Olivoto, T. and Nardino, M. MGIDI: toward an effective multivariate selection in biological experiments. *Bioinformatics.* 37, 1383–1389 (2021). https://doi.org/10.1093/bioinformatics/btaa981
37. Rocha, J. R. A. S. C., Machado, J. C. and Carneiro, C. S. Multitrait index based on factor analysis and ideotype design. *GCB Bioenergy.* 10, 52–60 (2018). https://doi.org/10.1111/gcbb.12443
38. Bradu, D. and Gabriel, K. R. The biplot as a diagnostic tool for models of two-way tables. *Technometrics.* 20, 47–68 (1978). https://doi.org/10.1080/00401706.1978.10489617
39. Gauch, H. G. and Zobel, R. W. Predictive and postdictive success of statistical analyses of yield trials. *Theoretical and Applied Genetics*.76, 1–10 (1988). https://doi.org/10.1007/BF00288824
40. Beavis, W., Lamkey, K. and Mahama, A. A. Multiple trait selection. In *Quantitative Genetics for Plant Breeding* (eds. Suza, W. and Lamkey, K.), 155–171. Iowa State University Digital Press (2023). https://doi.org/10.1038/s41598-025-07721-z
41. Van der Werf, J. H. J. Potential benefits of genomic selection in sheep. *Proceedings of the Association for the Advancement of Animal Breeding and Genetics.* 18, 38–41 (2009).
42. Hossain, M. A., Azam, M. G., Roychowdhury, R., Sarker, U., Nair, R. M. and Golokhvast, K. S. Integrating BLUP, AMMI and GGE models for lentil yield stability. *Plants.* 12, 2079 (2023). https://doi.org/10.3390/plants12112079
43. R Core Team. *R: A language and environment for statistical computing*. R Foundation for Statistical Computing, Vienna (2024).
44. Pour-Aboughadareh, A., Yousefian, M., Moradkhani, H., Poczai, P. and Siddique, K. H. M. STABILITYSOFT: a new online program to calculate parametric and non-parametric stability statistics for crop traits. *Applications in Plant Sciences.* 7, e01211 (2019). https://doi.org/10.1002/aps3.1211
45. Zobel, R. W., Wright, M. J. and Gauch, H. G. Statistical analysis of a yield trial. *Agronomy Journal.* 80, 388–393 (1988). https://doi.org/10.2134/agronj1988.00021962008000030002x

46. Azam, M. G., Hossain, M. A., Sarker, U., Alam, A. K. M. M., Nair, R. M., Roychowdhury, R., Ercisli, S. and Golokhvast, K. S. Genetic analyses of mungbean breeding traits using multivariate and multi-trait approaches. *Plants.* 12, 1984 (2023). https://doi.org/10.3390/plants12101984
47. Azam, M. D. G., Sarker, U. and Uddin, M. D. S. Screening maize genotypes for phosphorus deficiency at the seedling stage. *Turkish Journal of Agriculture and Forestry.* 46, 802–821 (2022).
48. Biswas, A., Sarker, U., Banik, B. R., Rohman, M. M. and Mian, M. A. K. Genetic divergence study in maize for salinity tolerance. *Bangladesh Journal of Agricultural Research.* 39, 621–630 (2014). https://doi.org/10.3329/bjar.v39i4.22540
49. Azam, M. G. A., Sarker, U., Mian, M. A. K., Banik, B. R. and Talukder, M. Z. A. Genetic divergence of maize inbreds. *Bangladesh Journal of Plant Breeding and Genetics.* 26, 9–14 (2013).
50. Faysal, A. S. M., Ali, L., Azam, M. G., Sarker, U., Ercisli, S., Golokhvast, K. S. and Marc, R. A. Genetic variability, character association and path coefficient analysis in transplant Aman rice genotypes. *Plants.* 11, 2952 (2022). https://doi.org/10.3390/plants11212952
51. Kulsum, U., Sarker, U. and Rasul, M. Genetic variability, heritability and interrelationship in salt-tolerant lines of *T. aman* rice. *Genetika.* 54, 761–776 (2022). https://doi.org/10.2298/GENSR2202761K
52. Ali, M. A., Sarker, U., Mian, M. A. K., Islam, M. A. and Johora, F. T. Estimation of genetic divergence in Boro rice (*Oryza sativa* L.). *International Journal of BioResearch.* 16, 28–36 (2014).
53. Ashraf, A. T. M., Rahman, M. M., Hossain, M. M. and Sarker, U. Correlation and path analysis in selected okra genotypes. *Asian Research Journal of Agriculture.* 12, 1–11 (2020).
54. Lin, C. S., Binns, M. R. and Lefkovitch, L. P. Stability analysis: where do we stand. *Crop Science.* 26, 894–900 (1986). https://doi.org/10.2135/cropsci1986.0011183X002600050012x
55. Zali, H., Farshadfar, E., Sabaghpour, S. H. and Karimizadeh, R. Evaluation of genotype × environment interaction in chickpea using measures of stability from AMMI model. *Annals of Biological Research.* 3, 3126–3136 (2012).
56. Azam, M. G., Iqbal, M. S. and Hossain, M. A. Stability investigation and genotype–environment interaction in chickpea. *Genetics and Molecular Research.* 19, gmr16039980 (2020).
57. Derbew, S., Mekbib, F., Lakew, B., Bekele, A. and Bishaw, Z. AMMI and GGE biplot analysis for barley yield stability. *Agrosystems, Geosciences & Environment.* 7, e20565 (2024). https://doi.org/10.1002/agg2.20565
58. Anuradha, N., Patro, T. S. S. K., Singamsetti, A., Rani, Y. S., Triveni, U., Kumari, A. N., Govanakoppa, N., Pathy, T. L. and Tonapi, V. A. Comparative study of AMMI- and BLUP-based simultaneous selection for grain yield and stability in finger millet. *Frontiers in Plant Science*. 12, 786839 (2022). https://doi.org/10.3389/fpls.2021.786839
59. John, B. A., Saraswathi, R., Manonmani, S., Kumaresan, D., Gunasekaran, M., Pushpa, R. and Ramalingam, J. Comparative analysis of stability models for identifying rice inter-subspecific breeding lines adapted to different temperature regimes. *BMC Plant Biology.* 25, 563 (2025). https://doi.org/10.1186/s12870-025-06484-z
60. Kumar, R., Kumar, M., Gangwar, L. K., Kumar, V., Singh, S., Edhigalla, P. and Rahimi, M. Association and reliability analysis of multi-trait selection methods and selection of superior genotypes across traits in Indian mustard. *Scientific Reports.* 15, 23405 (2025). https://doi.org/10.1038/s41598-025-07721-z
61. Mahajan, R. K., Sapra, R. L., Srivastava, U., Singh, M. & Sharma, G. D. *Minimal Descriptiors for Characterization and Evaluation of Agri Horticultural Crops-Part 1* 230 (National Bureau of Plant Genetic Resources, 2000).

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