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Research Article

Genotype × Environment Interaction Studies in Rainfed Durum Wheat (*Triticum Durum* L.) using AMMI and Regression Models

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Abstract

A set of diverse 23 durum wheat (*Triticum durum* sp.) genotypes were evaluated for their stable performance and genotype × environment (GXE) interaction in wheat under rainfed environments of peninsular zone of Karnataka during rabi 2023-24 and 2024-25. Environmental variance was highly significant for grain yield and quality traits studied. The data were analysed by regression analysis, Additive Main Effects and Multiplicative Interaction (AMMI), and the Sites Regression (SREG) model. Results showed that 'UASDW30395' was the best yielder (3280 kg/ha) whereas, UASDW30615 had high sedimentation value (30.74 cm3) and yellow pigment (5.12 ppm). Genotypes UASDW30595, UAS DW-30377 and UAS DW-30508 performed stably in all the environments for grain protein (13.42%), grain iron (35.6 ppm) and grain zinc (35.06 ppm), respectively. AMMI considers the effects of G and G × E separately where, SREG model combines these sources of variation. This indicated that the AMMI and SREG/GGE Biplot Model are the most effective models to identify best ranked stable genotypes.

Key Words: *Triticum durum*, G×E, AMMI, SREG, Stable genotype

1. Introduction

Wheat (*Triticum aestivum* L.) is one of the most important rabi cereal crops globally and is regarded as the "king of cereals" due to its contribution to food and nutritional security (Amadou *et al.,* 2019; Shewry and Hey, 2015; FAO, 2023; Sharada *et al.,* 2025). Durum wheat (*Triticum durum* Desf. Synon. *Triticum turgidum* subsp. *durum*) is the hardest among cultivated wheat species and is primarily valued for its superior semolina and pasta quality (Sissons, 2008; Ficco *et al.,* 2014; De Vita *et al.,* 2020; Vijeth *et al.,* 2025). In India, wheat is predominantly consumed as chapati, whereas durum wheat is mainly utilized for processed products such as pasta, macaroni, semolina, couscous, bulgur and freekeh; hence it is often referred to as pasta or macaroni wheat (Morris and Rose, 1996; Pena *et al.,* 2002). Wheat grain yield is a complex quantitative trait governed by multiple genes and intricate physiological and biochemical processes (Trethowan *et al.,* 2007; Reynolds *et al.,* 2009; Sall *et al.,* 2019). Yield performance is influenced by genetic constitution and environmental variables such as soil properties, precipitation, nutrient management, and temperature regimes, along with genotype × environment (G × E) interaction (Peterson *et al.,* 1992; Johansson *et al.,* 2003; Tuberosa, 2012; Crespo-Herrera *et al.,* 2021). Crop output and observed phenotype are functions of genotype, environment and their interaction; GE interaction is the outcome of genotypes respond differential response of genotypes across environments (Shah *et al.,* 2009; Allard and Bradshaw, 1964; Snowdon *et al.,* 2021).

Genotype × environment interaction is therefore, a major factor affecting yield stability and varietal recommendation in wheat breeding programmes (Crossa *et al.,* 1997; Yan and Kang, 2003; Gauch, 2013; Manjappa *et al.*, 2014). The magnitude and complexity of GE interaction increases with the number of genotypes and testing environments involved (Crossa *et al.,* 1997; Bocianowski *et al.,* 2019; Olivoto *et al.,* 2019). Consequently, multi-environment trials (METs) combined with robust statistical approaches such as AMMI and GGE biplot analysis have become indispensable for dissecting GE patterns and identifying stable, high-yielding cultivars (Yan *et al.,* 2007; Olivoto *et al.,* 2019; Vaezi *et al.,* 2019). Durum wheat quality parameters including protein content, gluten strength and pigment concentration etc. are highly sensitive to environmental fluctuations, particularly heat and water stress during grain filling (Troccoli*et al.,* 2000; Sissons, 2008; Ficco *et al.,* 2014; Liu *et al.,* 2022). Climate variability further accentuates yield instability and quality fluctuations, necessitating stability-oriented breeding strategies (Asseng *et al.,* 2019; Snowdon *et al.,* 2021; Bellegowda *et al.,* 2022; Devate *et al.*, 2023). Therefore, understanding adaptability and stability across diverse agro climatic conditions is essential for sustainable durum wheat production. Hence, the present study was undertaken to analyze the adaptability, stability, and genotype × environment interaction effects on grain yield and to identify promising and stable durum wheat cultivars under varied locations through multi-environment evaluation.

2. Material and methodology

2.1 Plant material and environments

Twenty-three durum wheat (*Triticum turgidum* subsp. *durum*) genotypes (Table 1), comprising seventeen advanced breeding lines, two released checks and four locally adapted cultivars, were evaluated across six contrasting agro-ecological locations of Karnataka during the 2023–24 and 2024–25 cropping seasons. The trials generated six environments defined as year × location combinations: E1–Dharwad (2023-24), E2–Bagalkot (2023-24), E3–Vijayapur (2023-24), E4–Annigeri (2024–25), E5–Bagalkot (2024–25) and E6–Dharwad (2024–25).

The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications in each environment. Each genotype was sown with a spacing of 20 × 5 cm in a 5 m long plot consisting of six rows following recommended agronomic practices to ensure uniform crop management. Grain yield (GY; Kg ha^{-1}) was recorded by harvesting a net plot area of 5 m^2 and converting to hectare basis. Yield component traits including grains per spike (GS), number of spikelets per spike (NS/S) on the main spike, and thousand kernel weight (TKW; g) were recorded from randomly selected representative samples at physiological maturity. Grain protein content (GP %) was determined on a wet basis using a near-infrared transmittance (NIT) grain analyser (FOSS Infratech 1241), a rapid and reliable non-destructive method widely adopted in cereal quality assessment (Williams and Sobering, 1993; Osborne, 2020). Sedimentation value (SDV), an indicator of gluten strength, and yellow pigment content (YP) were estimated following the standard SDS sedimentation and pigment extraction procedures described by Mishra and Gupta (1995). Grain micronutrients, iron (Fe) and zinc (Zn), were quantified using near-infrared spectroscopy (NIRS), an efficient high-throughput approach for mineral estimation in breeding programs (Bouis and Saltzman, 2017; Suman *et al.,* 2021).

2.2 Statistical analysis

Data from each environment were initially subjected to analysis of variance (ANOVA). Homogeneity of error variances across environments was tested using Bartlett's chi-square test (Akcura *et al.,* 2009). Upon confirmation of homoscedasticity, pooled data were analyzed through combined ANOVA to partition total variation into genotype (G), environment (E), and genotype × environment interaction (G × E) components using R statistical software. Genotypic adaptability and stability were estimated using the regression model of Eberhart and Russell (1966), which employs regression coefficient (bi) and deviation from regression (S^{2}di) as stability parameters. The Additive Main Effects and Multiplicative Interaction (AMMI) model was applied to further

Table 1: Twenty three durum wheat genotypes used in study for estimation of G × E interaction.

Sl No.	Entry No.	Genotype code	Pedigree details
1	UAS DW-30451	G1	CIRNO C 2008*2//KNIPA/TAGUA/Kiran
2	UAS DW-30374	G2	GUAYACANINIA/GUANAY//PORRON_4/BEJAH_7/Kiran
3	UAS DW-30377	G3	SNITAN/5/AJAIA_12/F3-LOCAL/Kiran
4	UAS DW-30395	G4	CBC 509 CHILE/SOMAT_3.1/Bijjaga Yellow
5	UAS DW-30508	G5	GUAYACAN INIA/GUANAY/Bijjaga Yellow
6	UAS DW-30613	G6	PLATA_7/ILBOR_1//SOMAT_3/Bijjaga Yellow
7	UAS DW-30601	G7	CIRNO C 2008*2/3/KNIPA/TAGUA/Bijjaga Yellow
8	UAS DW-30615	G8	CNDO/VEE//PLATA_8/3/6*PLATA_11/Bijjaga Yellow
9	UAS DW-30595	G9	ALTAR 84/STINT//SILVER_45/Bijjaga Yellow
10	UAS DW-30591	G10	PLATINUM/3/KNIPA/TAGUA/Bijjaga Yellow
11	UAS DW-30581	G11	CBC 509 CHILE/5/2*AJAIA_16/Amruth
12	UAS DW-30609	G12	ATIL/3/KNIPA/TAGUA/Amruth
13	UAS DW-30590	G13	CIRNO C 2008/HELLER /Amruth
14	UAS DW-30567	G14	CIRNO C 2008*2/3/KNIPA/TAGUA/Amruth
15	UAS DW-30460	G15	CIRNO C 2008*2/3/KNIPA/TAGUA/Amruth
16	UAS DW-30611	G16	CBC 514 CHILE/3/AUK/GUIL/Amruth
17	UAS DW-30597	G17	ARMENT//SRN_3/NIGRIS_4/3/Amruth
18	UAS 347©	G18	(TOB/ERA//TOB/CNO67/3/PLO/4/VEE#5/5/KAUZ/6/FRET2) /DWR-162
19	UAS 446 ©	G19	DWR-185/DWR-2006//UAS-419
20	Amruth	G20	ANLC/GAZA
21	Bijjaga yellow	G22	Selection-Bijaga Red Sibling
22	Kiran	G23	HB(M)65-50 (Mexican line)
23	Bansi white	G24	GULAB

elucidate G × E interaction by integrating ANOVA with principal component analysis (PCA) of interaction effects (Crossa *et al.,* 1991; Gauch and Zobel, 1996).

Additionally, Site Regression (SREG) or GGE biplot analysis was performed following Yan and Tinker (2006) to visualize genotype performance across environments and identify stable and specifically adapted genotypes. Statistical analysis for the AMMI model was done using *window stat 9.2. The* GGE methodology, which focuses on genotype main effects and G × E interaction, is widely recommended for multi-environment trial analysis in crop breeding (Olivoto *et al.,* 2019).

3. Results and discussion

The pooled ANOVA revealed highly significant mean squares for genotypes across the yield and quality attributes (Table 2), demonstrating the presence of substantial exploitable genetic variability. Highly significant environmental effects further indicated strong environmental influence on trait expression, reflecting the contrasting agro-climatic conditions of the test locations. Bartlett's chi-square test confirmed the homogeneity of error variances across the six environments (Table 3), as the test was statistically non-significant, thereby validating the appropriateness of pooled analysis (Akcura *et al.,* 2009; Olivoto *et al.,* 2019). The absence of heteroscedasticity indicated that environmental residual variances were comparable, permitting reliable estimation of genotype (G), environment (E), and genotype × environment (G × E) interaction effects through combined analysis. The G × E interaction effects were significant for grain yield and for most quality parameters, suggesting differential genotypic responses across environments. Moreover, the non-significant Bartlett's test indicated that error variances were homogeneous across environments, supporting the validity of pooled analysis. In contrast, the significant genotype × environment interaction demonstrated that genotypes responded differently under varying environmental conditions. This suggests that, despite comparable experimental precision across environments, the performance of genotypes varied significantly, indicating the presence of differences in adaptability and stability among the evaluated lines. Such interaction patterns were indicative of crossover interactions and reinforce the necessity of multi-environment testing for precise varietal recommendation (Yan and Tinker, 2006; Gauch, 2013; Vaezi *et al.,* 2019). Significant variation among replications within environments for several traits confirmed experimental sensitivity to micro-environmental fluctuations, although pooled error remained relatively low, indicating acceptable experimental precision.

Table 2: Pooled ANOVA for various grain yield and quality related traits.

Source of variation	**df**	**Mean sum of square**								
		NS/S	**GS**	**TGW**	**GY**	**SDV**	**YP**	**GP**	**Fe**	**Zn**
Replication within Environment	12	0.0098	0.2616	0.0402	0.01509**	0.0035**	0.1053**	0.0381**	0.1213**	0.0226**
Genotypes (G)	22	0.0959**	0.5809**	0.2994**	0.0102**	0.7703**	0.5868**	0.1156**	0.3999**	0.4343**
Environments (E)	5	0.5317**	4.1683**	1.73537**	0.54868**	0.2523**	0.1492**	0.0414**	0.3610**	0.4283*
Genotypes.* Environments.	110	0.018*	0.0530	0.0570	0.00254*	0.021*	0.0025*	0.0014*	0.0018*	0.008*
Pooled error	264	0.0019	0.0185	0.0214	0.0011	0.0007	0.0036	0.0010	0.0027	0.0045

*-Significant at 5% level **-Significant at 1% level

Table 3: Test for homogeneity of variance for six environments

Sl No.	**Bartlett's test of Significance**		
	Traits	**Factor**	**Significance**
1	Plant height	6.87	NS
2	Tillers per meter	5.87	NS
3	Days to flowering	6.06	NS
4	Days to maturity	4.40	NS
5	Spike length	3.10	NS
6	Number of spikelets per spike	7.49	NS
7	Grains per spike	7.62	NS
8	Thousand grain weight	9.71	NS
9	Grain yield	9.79	NS
10	Sedimentation value	8.67	NS
11	Yellow pigments	15.04*	S
12	Grain protein	3.27	NS
13	Grain iron	3.44	NS
14	Grain zinc	1.79	NS

*-Significant at 5% level **-Significant at 1% level

3.1 Genotype environment interactions and stability analysis for yield and quality parameters using Eberhart and Russell's model:

Genotypic variance was highly significant for all the test traits, indicating substantial exploitable genetic variability among the durum wheat genotypes. Environmental variance was also highly significant, confirming the pronounced influence of location and season on phenotypic expression. The genotype × environment (G × E) interaction effects were significant for all characters, demonstrating differential genotypic responses across environments and reflecting the complexity of quantitative trait regulation under variable agro-ecologies as has been reported earlier (Gauch, 2013; Olivoto *et al.,* 2019; Crespo-Herrera *et al.,* 2021). Partitioning of G×E interaction into linear and non-linear components revealed statistical significance for both the components across different traits (Table 4). The non-linear component predominated for most of the morphological traits and remained significant for grain yield and its components except for days to maturity, suggesting the presence of unpredictable environmental responses. A comparatively greater magnitude of non-linear variance for grains per spike and thousand grain weight indicated sensitivity of sink-related traits to environmental fluctuations as has been observed by (Yan and Tinker, 2006; Vaezi *et al.,* 2019; Bocianowski *et al.,* 2019). As has been observed in the present studies, such responses are frequently associated with crossover interactions and environmental heterogeneity (Crossa *et al.,* 1997; Hussain *et al.,* 2021; Sharada *et al.,* 2021).

Table 4: ANOVA of Eberhart and Russel model for various grain yield and quality related traits.

Source of variation	**df**	**Mean sum of squares**								
		NS/S	**GS**	**TGW**	**GY**	**SDV**	**YP**	**GP**	**Fe**	**Zn**
Genotypes(G)	22	0.0959**	0.5809**	0.2995**	0.0102**	0.7702**	0.5869**	0.1156**	0.3999**	0.4343**
Env. + (G×Env.)	115	0.0408**	0.3348**	0.1307**	0.0263**	0.0114**	0.0084**	0.0032**	0.0174**	0.0194**
Environments (Lin.)	1	2.6589**	20.84**	8.67**	2.743**	1.26**	0.7462**	0.2069**	1.80**	2.14**
G×Env.(Lin.)	22	0.0304*	0.1120	0.0292	0.0064**	0.0006	0.0018	0.0012	0.0013	0.0005
Pooled Deviation	92	0.0148**	0.1652**	0.0622**	0.0015*	0.0005	0.0020	0.0014*	0.0019	0.0008
Pooled error	264	0.0019	0.0185	0.0214	0.0011	0.0007	0.0036	0.0010	0.0027	0.0045

*-Significant at 5% level **-Significant at 1% level

Stability analysis using the Eberhart and Russell (1966) regression framework revealed significant genotypic main effects and G × E components. The environmental mean squares exceeded genotypic mean squares, emphasizing the dominant contribution of environmental factors in determining yield and micronutrient accumulation. Similar findings have also been reported in recent multi-environment wheat trials under climate variability (Asseng *et al.,* 2019; Pujer *et al.,* 2020; Snowdon *et al.,* 2021; Liu *et al.,* 2022). These results underscore the necessity of identifying genotypes with either broad adaptability or specific adaptation to defined agro-ecological zones. Joint regression analysis considering grain yield and grain zinc concentration as primary dependent traits facilitated identification of stable genotypes based on regression coefficient (bi ≈ 1), minimal deviation from regression (S^2di ≈ 0), and superior mean performance. Genotypes UAS DW-30395, UAS DW-30615 and UAS DW-30601 exhibited desirable stability parameters for grain yield, whereas UAS DW-30601, UAS DW-30451 and UAS DW-30615 consistently ranked superior across environments for grain zinc content (Table 5). These findings corroborate the effectiveness of regression-based stability models in discriminating broadly adapted and nutritionally enhanced genotypes under heterogeneous production systems (Olivoto *et al.,* 2019; Farshadfar *et al.,* 2020).

3.2 Comparative analysis of AMMI and SREG model for identifying stable genotypes across environments for grain yield and grain zinc content.

Comparative evaluation of Additive Main effects and Multiplicative Interaction and Site Regression models was undertaken to identify high-yielding and stable genotypes across six diverse environments for grain yield and grain zinc concentration. The AMMI biplot (Fig 1) revealed that

Table 5: Stability parameters for grain yield and grain zinc content.

Sl No.	Genotypes	Grain yield				Grain Zinc			
		Mean	b_i	S^2di	Rank	Mean	b_i	S^2di	Rank
1	UAS DW-30451	3280	0.780*	-0.001	4	31.75	0.999	-0.0053	2
2	UAS DW-30374	3120	0.948	-0.0012	7	29.97	1.204	-0.0034	23
3	UAS DW-30377	3240	1.189	-0.006	10	29.70	0.985	-0.0051	8
4	UAS DW-30395	3280	0.968	-0.001	1	34.76	1.173	-0.0006	22
5	UAS DW-30508	2920	1.310*	-0.0009	19	35.06	0.967	-0.0053	12
6	UAS DW-30613	3440	1.108	-0.001	5	25.17	1.009	-0.0022	5
7	UAS DW-30601	3400	0.823	-0.001	3	35.75	1	-0.0052	1
8	UAS DW-30615	3360	1.09	-0.0013	2	31.90	0.996	-0.005	3
9	UAS DW-30595	3400	0.731	0.001	21	34.71	1.014	-0.0052	7
10	UAS DW-30591	3080	1.044	-0.0001	11	31.51	0.972	-0.0045	11
11	UAS DW-30581	3440	0.628*	-0.0005	13	35.64	0.943	-0.0053	15
12	UAS DW-30609	3080	1.078	-0.0011	12	36.32	1.070*	-0.0045	16
13	UAS DW-30590	3440	0.843*	-0.0014	22	35.33	0.909	-0.0052	20
14	UAS DW-30567	3200	1.033	-0.0015	8	31.23	0.966	-0.0027	13
15	UAS DW-30460	3080	0.71	-0.0001	20	38.33	0.928*	-0.0053	19
16	UAS DW-30611	3040	1.224	0.0026*	18	35.67	1.071	-0.0023	18
17	UAS DW-30597	3240	1.079	-0.0013	9	37.77	0.977	-0.0052	9
18	UAS 347©	4160	0.759*	-0.0009	6	31.72	0.929	-0.0048	17
19	UAS 446 ©	3040	1.077	-0.0014	13	34.78	1.013	-0.0052	6
20	Amruth	2760	0.973	0.0036*	14	34.94	1.024	-0.005	10
21	Bijjaga yellow	2640	0.896	0.0034*	16	35.13	0.951	-0.0053	14
22	Kiran	2720	1.693*	0.0019	17	35.26	1.008	-0.0052	4
23	Bansi white local	2760	1.029	-0.0004	15	36.54	0.892*	-0.0052	21

** Significantly different from unity (bi) and from zero for (S^2di) at the 0.005 and 0.001 probability levels, respectively.

the first two interaction principal component axes (IPCA1 and IPCA2) collectively explained 99.52% of the G × E interaction variance (PC1 = 71.38%; PC2 = 28.14%), indicating robust capture of multiplicative interaction effects and enhanced interpretability of stability patterns, as widely demonstrated in recent multi-environment trials (Olivoto *et al.,* 2019; Bocianowski *et al.,* 2019; Ajay *et al.,* 2020). Likewise, the SREG biplot accounted for 99.78% of the total phenotypic variability, confirming its strong discriminative ability and graphical efficiency for mega-environment delineation (Yan *et al.,* 2021; Kendal, 2019).

Graphical interpretation indicated that genotype UAS DW-30601 was positioned proximal to the origin within the stability circle, reflecting wide adaptability, superior mean grain yield and minimal interaction deviation. Genotypes UAS DW-30395 and UAS DW-30567 exhibited positive PC1 scores with near-zero PC2 values, signifying high productivity coupled with dynamic stability across environments. The convergence of AMMI and SREG outputs substantiates the reliability of these genotypes under heterogeneous agro-ecological conditions, aligning with contemporary stability concepts integrating mean performance and interaction variance (Olivoto and Lucio, 2020; Vaezi *et al.,* 2018). The magnitude and orientation of environmental vectors further underscore the decisive influence of climatic variability and edaphic heterogeneity in modulating genotypic responsiveness and yield stability (Nowosad *et al.,* 2020; Kumar *et al.,* 2022).

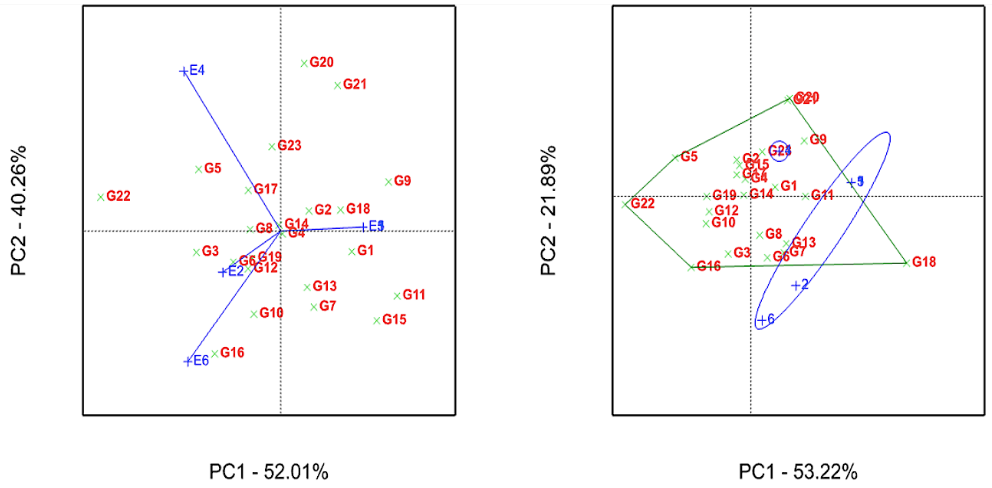

Fig 1: Comparative Graph of AMMI and GGE biplots of twenty three durum wheat genotypes for grain yield

For grain zinc concentration, AMMI partitioned 91.07% and 8.93% of the G × E interaction sum of squares into PC1 and PC2, respectively whereas, the SREG biplot explained 99.92% of the total variability (PC1 = 99.06%; PC2 = 0.86%). Genotypes Kiran, UAS DW-30508 and UAS DW-30460 were identified as stable micronutrient-dense performers across environments (Fig 2). The comparative evaluation of stability models revealed a consistent identification of stable genotypes across traits, Grain yield stability was consistently attributed to UAS DW-30395 and UAS DW-30595 across AMMI and SREG models, while Eberhart and Russell's model additionally identified UAS DW-30601, highlighting slight methodological differences in genotype ranking. For quality traits, particularly protein content and micronutrients (iron and zinc), certain genotypes such as UAS DW-30615 and UAS DW-30508 demonstrated stable performance across multiple models, suggesting their potential for simultaneous improvement of yield and nutritional quality (Table 6). Overall, the SREG model exhibited superior discriminatory power by integrating both genotype main effects and G×E interaction, thereby providing a more comprehensive assessment of genotype stability compared to AMMI and Eberhart and Russell's approaches. The strong concordance between AMMI and GGE/SREG frameworks reinforces their complementary utility in biofortification-driven breeding programs aimed at nutritional security and climate resilience (Ajay *et al.,* 2020; Kumar *et al.,* 2022).

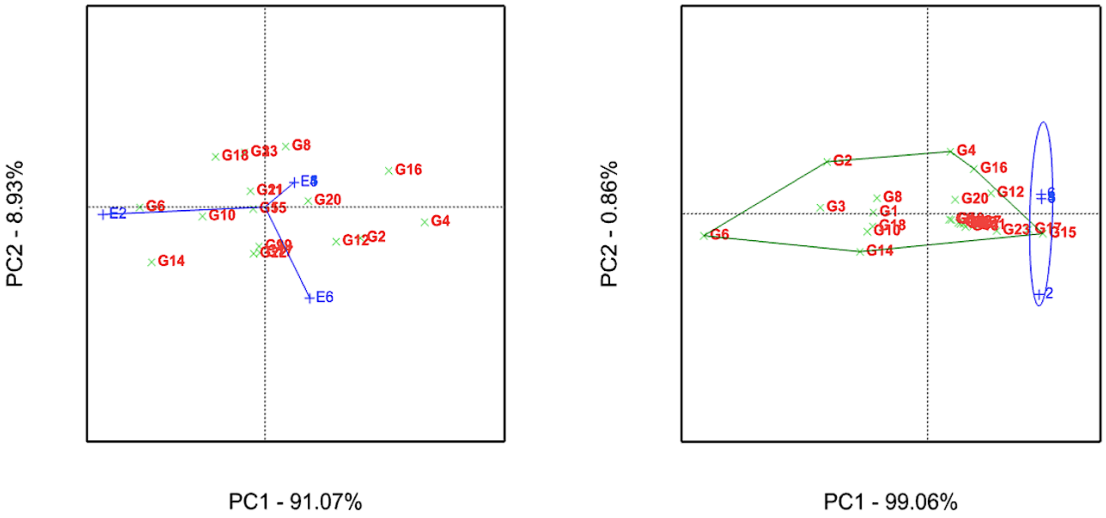

Fig 2: Comparative Graph of AMMI and GGE biplots of twenty three durum wheat genotypes for grain zinc

Table 6: Stably performing genotypes across all the 6 environments by three stability models

Sl. no	**Trait**	**Genotypes**		
		Additive Main Effect and Multiplicative Interaction model (AMMI)	**Site Regression Model (GGE/SREG)**	**Eberhart and Russels model**
1	Plant height	UAS DW-30597	UAS DW-30597	UAS DW-30597
2	Tillers per meter	UAS DW-30567, UAS DW-30613	UAS DW-30567	UAS466©, UAS DW-30613, UAS DW-30591
3	Days to flowering	UAS DW-30613, UAS DW-30601, UAS DW-30605	UAS DW-30613, UAS DW-30601, UAS DW-30605	Amruth , Kiran
4	Days to maturity	UAS DW-30613, UAS DW-30601, UAS DW- 30605	UAS DW-30613, UAS DW-30601, UAS DW-30605, Bansi white	Amruth , Kiran
5	Spike length	UAS DW-30609, Bansi white	UAS DW-30609, Bansi white	UAS 347, Kiran
6	Number of spikelet's per spike	UAS DW-30590, UAS DW-30609	UAS DW-30590, UAS DW-30609	UAS DW-30567, UAS DW-30613
7	Grains per spike	UAS DW-30615, UAS DW-30567	UAS DW-30615, UAS DW-30567	UAS DW-30615, UAS DW-30374, UAS DW-30567
8	Test weight	UAS DW-30597, UAS DW-30508. UAS 347	UAS DW-30597, UAS DW- 30508.UAS 347©	UAS DW-30597, UAS DW-30508.
9	Grain yield	UAS DW-30395, UAS DW-30567	UAS DW-30395, UAS DW- 30595, UAS DW-30615	UAS DW-30 601, UAS DW-30395, UAS DW-30615
10	Sedimentation value	UAS DW-30590, UAS DW-30609, UAS DW- 30615	UAS DW-30590, UAS DW-30609, UAS DW-30615	Kiran, UAS446©, UAS DW-30590, UAS DW-30609, UAS DW-30615,
11	Yellow pigment	UAS 347©	UAS DW-30 415, UAS DW-30615	UAS DW-30 415, UAS DW-30615
12	Grain protein	UAS DW-30615, UAS446©, UAS DW-30595	UAS DW-30615, UAS DW-30595,UASDW-30460	UAS DW-30615, UAS DW-30415
13	Grain iron	UAS446©, UAS DW-30377	UAS DW-30581, UAS DW-30377	UAS DW-30581, UAS DW-30415
14	Grain zinc	Kiran, UAS DW-30508, UAS DW-30460	UAS DW-30508, UAS DW-30597, UAS DW-30460	UAS DW-30508, UAS DW-30597

4. Conclusion

Identification of stable donors with high trait value across the major wheat growing regions is of paramount importance to develop wheat varieties with wide adaptability. Based on the experiment, Eberhart and Russell's model considers three parameters as mean value, regression coefficient and deviation from regression coefficient and the stable genotypes over environments were identified based on GE interactions. But the AMMI considered the effects of G and G×E separately. While, SREG model combined these sources of variation. This suggested SREG analysis as a viable tool with high discriminatory power because it integrates G+G×E effectively for evaluating the response of distinct cultivars in multiple environments which was not possible with AMMI analysis. So SREG analysis is the most efficient and perfect methodology to analyze the G × E interaction and allowed determining the variety with the best response in all the environments and groups the genotype for target environments. Cultivars UASDW30395, UASDW30567 and UAS DW-30597 were found promising for grain yield, grains per spike and number of spikelets per spike, and test weight, respectively and can further utilized for rainfed breeding programme.

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Authors' contributions

VGM, UGR, CGB and SJ- compiled and edited the manuscript; UGR helped in the statistical analysis of the findings and in editing of the manuscript.

Conflict of interest

The authors declare that they have no conflict of interest.

Ethical Approval

The article doesn't contain any study involving ethical approval.

Use of Generative AI or AI assisted technologies

Authors declare that no Generative AI or AI assisted technologies have been used in preparation of this manuscript.

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