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MULTI-ENVIRONMENT EVALUATION OF BREAD WHEAT GENOTYPES FOR YIELD STABILITY USING AMMI APPROACH

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ABSTRACT

Bread wheat is a vital staple crop worldwide, but its production is prone to various environmental constraints and yield reduction associated with adaptation. To identify stable and adaptable genotypes, a total of 30 wheat genotypes were evaluated for their genotype-environment interaction (GEI) and stability across three different seasons as season, late and very late sowing for two years using Additive Main Effect and Multiplicative Interaction (AMMI) and Eberhart and Russell Stability model. According to analysis of variance, all traits were significantly except spikelet per spike (SPS), indicating differential genotypic responses across environments. Using the Eberhart and Russell stability model, the highest number of stable genotypes was recorded for grain yield, while plant height and grain yield showed the greatest proportion of genotypes classified as adaptable. Overall, among all 30 genotypes including HD 2932, HD 3118, HD 3086, PBW 644, LOK1, PBW 804, DBW 46, and DBW 51 emerged as the most stable performers for grain yield, demonstrating consistent expression across environments. From, AMMI1 biplots showed that environment 2 displayed the lengthiest vector, indicating the sturdiest interaction, while environment 1 and environment 3 exhibited minimal interaction. Genotypes such as PBW 644, LOK 1, PBW 804, DBW173, and GK 307 had near-zero IPCA1 scores, marking them as highly stable, although only DBW 150, DBW 173, and HD 3118 achieved above-average yields. Conversely, PBW 723, HD3043, GW 366, and DBW14 were the most unstable based on their large IPCA scores. High-yielding genotypes with negative IPCA1 values—including HD3118, DBW 46, and HI 1563 demonstrated desirable performance. The AMMI2 biplot, which isolates G×E interaction, confirmed that genotypes near the origin (PBW 644, LOK 1, DBW 107, HD3118, DBW 46) were least influenced by environmental variability. Overall, DBW 107 and PBW 644 emerged as the most stable, high-yielding genotypes across environments.

KEYWORDS: Bread wheat, AMMI analysis, stability analysis.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the most important cereal crops belong to the family *Poaceae* and the genus *Triticum* and is a predominantly self-pollinated, allohexaploid species ($2n = 6x = 42$) with a genomic constitution of AABBDD. Bread wheat originated through two successive allopolyploidization events involving hybridization between *Triticum urartu* (A genome donor) and *Aegilops speltoides* (B genome donor) to form tetraploid emmer wheat (AABB), followed by introgression of the D genome from *Aegilops tauschii* to produce hexaploid wheat (Khalid et al., 2023). This complex genomic structure confers substantial genetic plasticity, enabling wheat to adapt to a wide range of agro-climatic conditions. Bread wheat constitutes more than 90% of the global wheat area and is widely regarded as the "King of Cereals" due to its dominant contribution to human nutrition. Wheat grain contributes nearly 20% of the global caloric and protein intake, while it's straw serves as an important source of fodder for livestock, supporting the rural economy (Kumar et al., 2021). During the 2022–23 rabi season, wheat was cultivated over 31.82 million hectares in India, producing 112.74 million tonnes with an average productivity of 3.54 tones pe hectare. Uttar Pradesh, Madhya Pradesh, Punjab, Haryana, Rajasthan, and Bihar together contribute more than 90% of the national wheat production, highlighting the dominance of the Indo-Gangetic Plains in wheat cultivation. Despite significant progress in varietal development and agronomic management, productivity gaps persist across regions, largely due to environmental variability and climate-induced stresses. Climatic variability, including fluctuations in temperature, variability in rainfall patterns, and differences in soil characteristics, exerts a strong influence on crop productivity and adaptability. To evaluate the performance and adaptability of genotypes under climatic conditions of the Moradabad region known for its both sub-humid and sub-tropical climates with warm and dry solstices & cool midwinter's. The monsoon season usually starts from the third or fourth week of June and extends up to the last week of September. Few showers are commonly received during winter. This create a critical information on genotype × environment interaction (GEI), which is essential for identifying genotypes that combine high yield potential with stable performance across diverse locations and seasons. Understanding the relationship between crop performance and environmental conditions has long been a central concern in plant breeding and genetics. The phenotypic expression of a genotype in a given environment represents the combined effects of genotype (G), environment (E), and their interaction (GEI). Genotype × environment interaction arises when genotypes respond differently to changes in environmental conditions. A range of statistical methodologies, collectively referred to as stability analyses, have been developed to assess genotype performance across environments, such as AMMI and the Eberhart and Russell Stability Model**.** Estimating G×E interaction is therefore essential for identifying stable and widely adapted genotypes. Yield and related traits were recorded using a randomized approach for observing stability, which refers to the ability of a genotype to perform consistently under a certain environment of Moradabad, which is a major objective of wheat breeding programmes under climate variability.

MATERIALS AND METHODS

Plant Material:

A collection of 30 diverse wheat genotypes, along with 2 checks comprising high-yielding, disease-resistant, water-logging-tolerant, and heat-tolerant varieties, constituted the investigational material for this study. These genotypes were selected based on their origin, malleability, miscellany, and morphological characteristics, viz., high yield potential, heat tolerance, and disease resistance.

The present experimentation was conducted at the Research farm of Institute of Foreign Trade & Management University, Moradabad, 28°49′52″N and 78°45′58″E, and the elevation is 271.230M (889.86Ft) during the two Rabi seasons 2023-2024 and 2024 -2025. The environments were created by three dates of sowing in two different seasons, which includes timely sowing, late sowing and very late sowing. All the 30 genetically diverse wheat genotypes were sown in Randomized block design (RBD) with three repetitions in three different atmospheres during Rabi 2023-2024 and 2024-2025. Each genotype was accommodated in two rows of 2 meters in length, along with a 25cm row-to-row distance. The experiment was conducted under irrigated conditions. Recommended crop production and protection practices were followed to raise a successful crop.

Data collection:

Yield and related traits were recorded. In separately plan, five competitive plants were haphazardly tagged for observations across the three environments. The mean values for each treatment were premeditated, and the traits studied along with the methods used for their measurement. The traits recorded included: (a) days to 50% flowering, (b) days to maturity, (c) plant height, (d) spike length, (e) spikelets per spike, (f) effective tillers, (g) grains per spike, (h) 1000-seed weight, (i) grain yield (kg/ha), (j) biological yield (kg/ha), and (k) harvest index. The collected data were averaged and subjected to analysis.

Statistical analysis:

The analysis of variance (ANOVA) was conducted using the "agricole" package, while other statistical analyses were performed in R Studio, running R version 4.5.2 by various packages, for graphical representation, Origin Pro 2026 (version10.3.0.180), and GEA-R version 4.1.

AMMI analysis

AMMI stability value (ASV) is not a quantitative stability metric, but it quantifies and ranks genotypes based on their yield stability. Genotypes with lower ASV values are considered more stable, while those with higher ASV values are deemed less stable. The stability and adaptability of genotypes across different environments were assessed using the AMMI model. This model integrates analysis of variance (ANOVA) for the additive effects of genotype and environment with principal component analysis (PCA) to capture the multiplicative effects of genotype × environment interaction, following the methodology of Gauch (1992).

$$Y_{ij} = \mu + g_i + e_j + \sum \lambda_n \alpha_{in} \gamma_{jn} + \theta_{ij}$$

Where,

Y_{ij}= Mean yield of the ith genotype in the jth environment

μ= General mean

g_i= i^{th} genotypic effect

e_j= j^{th} location (environment) effect

λ_n= Eigenvalue of the nth principal component axis

α_{in}= PCA score of the i^{th} genotype on the nth axis

γ_{jn}= PCA score of the j^{th} environment on the nth axis

θ_{ij}= Residual

n= Number of PCA axes retained in the model

Quantitative measure of stability derived from AMMI. While interpretation, lower the ASV value, greater the stability of the genotype.

$$ASV = \sqrt{\left(\frac{IPCA1}{SS_{IPCA1}}\right)^2 + \left(\frac{IPCA2}{SS_{IPCA2}}\right)^2}$$

Eberhart and Russell Stability Model

Genotype stability and adaptability across environments were evaluated using the regression model proposed by Eberhart and Russell (1966). This model assesses stability based on three parameters: mean performance, regression coefficient, and deviation from regression.

$$Y_{ij} = \mu_i + b_i I_j + \delta_{ij}$$

where,

Y_{ij}= Mean performance of the i^{th} genotype in the j^{th} environment

μ_i= Mean performance of the i^{th} genotype across environments

b_i= Regression coefficient of the i^{th} genotype

I_j= Environmental index of the j^{th} environment

δ_{ij}= Deviation from regression

RESULTS

Analysis of Variance:

To elucidate genotypic adaptability and differential environmental response, data were pooled across years and environments and between the years the adequate amount of variability was present but there was no significant difference for the genotype × environment, now onwards mentioned as G×E **(Table 2**). The pooled ANOVA revealed a significant GE interaction for all traits, except spikelets per spike (SPS), indicating differential genotypic responses across environments. These finding underscores the importance of stability analysis for identifying genotypes with wide and specific adaptability under diverse sowing conditions. **(Table 1)**

Table 1. Pooled analysis of variance for the 11 Agro-morphological traits for the various environments in two growing periods (2023-2024, 2024-2025)

	GEN	**ENV**	**GEN: ENV**	**ENV: REP**	**Residuals**
Df	29	2	58	6	174
DFF	186***	7605.3***	9.2**	44*	2.6
DTM	456.7**	9456.4**	23.5***	30	2.2
PH	189.6***	15510.7***	22.3***	45	3.4
SL	1.62**	332.92**	0.39**	22.91*	0.17
SPS	9.26***	1003.97**	1.01	27.64	0.77
ET	2.79***	437.91***	0.37**	30.47**	0.42
GS	108.9***	18979***	14***	40.5	3
TW	44.32***	653.47***	1.86**	29.89*	1.25
GY	10898442***	6303348727***	6506645***	8540794	2173978
BY	13261812***	765854374***	1341845***	8570577**	1088655
HI	19.56***	1690.9***	8.48***	21.11**	0.62

Where,**“***”**= Significant at p<0.001**,** **“***”**= Significant at p<0.01, **and “*”**= Significant at p<0.05, **GEN** Genotypes, **ENV** environments, **REP** Replication, **Df** degree of freedom, **DFF** Days to 50% flowering, **DTM** days to maturity, **PH** plant height, **SL** spike length, **SPS** spikelets per spike, **ET** effective tillers, **GS** grain per spike, **TW** 1000 seed weight**, GY** grain yield per hectare, **BY** biological yield per hectare, **HI** harvest index

Table 2. Analysis of variance of eleven Agro-morphological traits of thirty genotypes for various environmental condition of Eberhart and Russell model.

SV	**Df**	**DFF**	**DTM**	**PH**	**SL**	**SPS**	**ET**	**GS**	**TW**	**GY**	**BY**	**HI**
GEN	60	186.04**	456.70**	189.60***	1.62***	9.26***	2.78***	108.86***	44.31***	10898442.07***	13261811.92***	19.56*

SV	Df	DFF	DTM	PH	SL	SPS	ET	GS	TW	GY	BY	HI
ENV + (GEN × ENV)	1	262.4	337.90	538.62	11.47	34.44	14.96	646.14	23.58	216401380.97	26825596.20	64.56
ENV (linear)	29	15210.61	18912.71	31021.38	665.84	2007.93	875.83	37958.10	1306.95	12606697453.66**	1531708747.2	3381.8
GEN × ENV (linear)	30	11.61	30.82*	27.53	0.53***	1.26	0.39	20.52**	2.11	12659053.42**	892922.15**	8.36*
Pooled deviation	174	6.56	15.59	16.58	0.23	0.73	0.34	7.16	1.55	342428.52	1731076.06	8.31
Pooled error	89	460.76	2.20	3.39	0.17	0.77	0.42	2.96	1.25	2173977.91	1088655.40	0.62
Total	29	237.52	376.61	424.90	8.26	26.24	10.99	471.07	30.34	149439749.20	22405936.15	49.90

Where, **SV** source of variation, **D.f** degree of freedom , **ENV** environments, **GEN** genotypes, **DFF** Days to 50% flowering, **DTM** days to maturity , **PH** plant height, **SL** spike length, **SPS** spikelets per spike, **ET** effective tillers, **GS** grain per spike, **TW** 1000 seed weight**, GY** grain yield per hectare, **BY** biological yield per hectare, **HI** harvest index.

Stability analysis by the Eberhart and Russell model (1966)

Criteria for a Stable Genotype

A genotype is considered stable and widely adapted when it exhibits: High mean performance, Regression coefficient (b_i) close to unity, Deviation from regression (S^2_{di}) close to zero and non-significant. Stability analysis using the Eberhart and Russell method evaluates the performance of genotypes across different environments and their interactions. According to this approach, genotypes are considered stable if they show high mean performance with regression coefficients close to one, indicating minimal G×E interaction and consistent yield across environments. A pooled ANOVA was performed following the Eberhart and Russell model for eleven agro-morphological traits across three environments, named as E1, E2, and E3. Significant differences were observed among genotypes for all traits, including Days to 50% Flowering (DFF), Days to Maturity (DTM), Plant Height (PH), Spike Length (SL), Seeds per Spike (SPS), Effective Tillers (ET), Grain Size (GS), Test Weight (TW), Grain Yield (GY), Biological Yield (BY) and Harvest Index (HI) indicating substantial genetic variability. The G×E interaction in the pooled ANOVA was highly significant for DTM, SL, GS, GY, BY, and HI reflecting the impact of environmental conditions on these traits see **Table 1** and stable and adaptable genotypes were presented in **Table 3 (3a and 3b**).

Table 3: list of stable and adaptable genotypes by Eberhart and Russell model for 30 genotypes of various environmental conditions:

Trait	Adaptable Genotypes	Stable Genotypes	Adaptable and Stable
Days to 50% Flowering	HD 3118 (G19)	HI 1563 (G14)	
	PBW 804 (G3)	DBW 107 (G10)	
Days to Maturity	RAJ 3765 (G11)	HD 3043 (G20)	DBW 39 (G5)
	PBW 780 (G2)	PBW 644 (G24)	
	K 1006 (G23)		
	PBW 804 (G3)		
	DBW 14 (G4)		
	DBW 39 (G5)		

	DBW 46 (G6)		
Plant Height	DBW 107 (G10)	HD 3118 (G19)	HD 3118 (G19)
	HI 1612 (G15)	HD 3043 (G20)	HD 3043 (G20)
	HD 3118 (G19)		
	HD 3043 (G20)		
	PBW 644 (G24)		
	PBW 725 (G28)		
	PBW 765 (G29)		
	WB 2 (G30)		
Spike Length	RAJ 3765 (G11)	PBW 723 (G1)	–
	HD 2932 (G18)	DBW 173 (G9)	
	K 1006 (G23)		
	DBW 46 (G6)		
	DBW 51 (G7)		
Seeds per Spike	K 1006 (G23)	HD 2733 (G17)	–
	PBW 725 (G28)	NW 5054 (G26)	
	DBW 51 (G7)		
Effective Tillers	PBW 804 (G3)	WB 2 (G30)	–
		DBW 14 (G4)	
		DBW 150 (G8)	
Grain Size	LOK 1 (G25)	PBW 780 (G2)	PBW 804 (G3)
	PBW 765 (G29)	DBW 150 (G8)	
	PBW 725 (G28)	PBW 804 (G3)	
	PBW 804 (G3)	PBW 644 (G24)	
	DBW 14 (G4)		
	DBW 51 (G7)		
Test Weight	DBW 107 (G10)	HI 1612 (G15)	–
	LOK 1 (G25)	LOK 1 (G25)	
	HD 2932 (G18)	PBW 677 (G27)	
	DBW 14 (G4)	K 1006 (G23)	
	NW 5054 (G26)	PBW 804 (G3)	
		PBW 644 (G24)	
Grain Yield	RAJ 3765 (G11)	HD 2932 (G18)	–
	GW 322 (G12)	HD 3118 (G19)	
	HUW 234 (G16)	HD 3086 (G21)	
	HD 2733 (G17)	PBW 644 (G24)	
	HD 2932 (G18)	LOK 1 (G25)	
	PBW 780 (G2)	PBW 804 (G3)	
	PBW 725 (G28)	DBW 46 (G6)	
	DBW 150 (G8)	DBW 51 (G7)	
Biological Yield	HD 2932 (G18)	PBW 723 (G1)	–
	LOK 1 (G25)	DBW 107 (G10)	

Harvest Index	HD 3043 (G20)	HD 2932 (G18)	–
	NW 5054 (G26)	HD 3118 (G19)	
	DBW 14 (G4)		
	DBW 51 (G7)		

Table 3(a). Stability parameters regression coefficient (bi) and deviation from regression (S2di), of 30 genotypes for 11 Agro-morphological traits over the three environments viz, timely sown, late sown, very late sown.

	DFF			**DTM**			**PH**			**SL**			**SPS**		
GEN	**Mean**	**b1**	**s2di**	**Mean**	**b1**	**s2di**	**Mean**	**b1**	**s2di**	**Mean**	**b1**	**s2di**	**Mean**	**b1**	**s2di**
G1	69.06	0.93	9.41***	130.39	1.0584	-0.232	74.17	0.809**	10.952**	7.97	0.81*	-0.057	16.32	0.964	-0.226
G2	73.17	1.01	3.55**	132.61	1.172**	0.148	77.36	0.986	2.380	8.31	1.024	0.124	18.02	0.986	0.092
G3	71.00	1.11	-0.412	133.28	1.130*	-0.616	81.49	1.102	1.096	8.15	0.873	0.205*	18.46	1.035	-0.170
G4	67.50	1.04	-0.644	128.17	1.147*	-0.364	75.61	0.839**	3.473*	8.08	0.940	-0.027	17.37	1.003	-0.258
G5	68.94	1.13	-0.721	131.06	1.17**	-0.729	81.92	1.032	12.667***	8.31	0.919	-0.010	17.30	0.950	0.238
G6	67.17	1.14*	0.056	129.78	1.227***	-0.471	76.58	1.019	0.958	7.91	1.149	0.010	16.55	1.113	-0.084
G7	64.61	1.06	-0.552	123.61	1.092	1.161	78.11	0.995	9.846**	8.61	1.173*	-0.004	16.78	1.273*	0.155
G8	68.39	1.06	3.40*	125.00	1.155**	25.240***	73.12	0.781***	-1.126	8.14	0.818*	-0.051	17.22	0.934	0.091
G9	68.89	1.05	-0.882	129.83	0.920	-0.257	75.26	0.83**	-1.111	8.20	1.102	-0.056	16.11	1.056	0.272
G10	67.94	1.15*	4.09*	132.00	0.996	4.095*	80.71	1.111	-0.749	8.24	1.175*	-0.044	17.43	1.030	0.904*
G11	74.83	1.07	-0.377	139.89	1.121*	-0.44	83.02	0.765***	8.217**	8.97	1.181*	-0.004	18.97	1.137	-0.118
G12	74.61	1.11	-0.846	138.28	1.104	0.432	84.56	0.775***	3.447*	8.90	0.997	0.042	19.00	1.075	-0.038
G13	72.22	1.04	-0.230	130.39	1.036	8.029***	87.36	0.935	4.021*	8.58	1.069	-0.053	16.98	0.946	0.180
G14	71.44	1.03	-0.862	134.00	1.050	15.704***	86.03	0.998	18.453***	8.61	0.970	-0.049	17.32	1.049	-0.189
G15	68.83	1.01	-0.667	131.56	1.013	2.996*	83.19	1.110	-0.163	8.11	0.872	-0.003	17.64	1.090	0.130

G16	65.78	0.95	5.57**	130.78	1.016	-0.543	80.69	0.878*	-1.057	8.19	0.867	0.041	17.02	0.722*	0.083
G17	64.94	1.18*	6.39**	129.39	0.849*	4.468**	81.85	0.981	6.975**	8.01	1.037	-0.055	17.13	0.930	-0.252
G18	65.39	0.90	-0.648	132.11	1.036	6.493**	85.44	1.253***	21.898***	8.66	1.34***	-0.012	17.16	0.690**	-0.093
G19	66.17	1.05	-0.014	132.28	0.910	27.323***	85.77	1.239***	-1.125	8.11	0.819*	-0.054	16.30	0.854	-0.204
G20	67.67	0.91	-0.719	129.00	1.041	-0.73	85.12	1.220***	-1.121	8.46	1.164	-0.049	17.89	0.961	-0.210
G21	57.00	0.36***	-0.146	108.78	0.270***	0.39	72.14	0.741***	-0.359	7.57	0.866	0.080	14.94	0.954	-0.158
G22	65.94	1.02	8.918	129.67	0.934	0.17	87.72	0.924	7.943**	8.67	1.146	-0.050	17.60	0.795	-0.101
G23	73.78	1.06	-0.67986	136.44	1.128*	0.05	85.38	0.938	10.719**	9.15	1.090	0.009	18.71	1.255*	-0.219
G24	65.72	1.05	4.08*	130.67	1.041	-0.73	87.17	1.120	-0.889	8.82	1.066	-0.037	18.17	1.027	-0.096
G25	63.44	0.88	0.075	124.00	0.879*	0.09	82.35	0.964	7.009**	9.16	1.103	0.125	18.00	1.037	-0.049
G26	60.50	0.84*	-0.672	116.06	1.16**	21.861***	75.84	1.045	-0.204	7.63	0.716**	0.094	15.09	0.899	-0.258
G27	59.61	0.78**	-0.175	114.89	1.166**	3.667*	75.92	0.942	-0.920	7.52	0.662***	0.023	15.41	1.063	0.141
G28	60.39	0.96	0.715	116.72	0.278***	1.219	82.80	1.110	-0.410	8.36	1.056	-0.053	17.58	1.259*	-0.246
G29	61.17	1.02	-0.326	118.56	0.876*	11.015***	81.99	1.426***	10.80**	8.16	1.024	0.528**	17.36	1.023	0.130
G30	63.83	0.96	2.385	124.50	1.0042	4.522**	84.35	1.115*	0.256	8.25	0.965	-0.053	17.37	0.889	0.101

Where, **DFF** Days to 50% flowering, **DTM** days to maturity , **PH** plant height, **SL** spike length, **SPS** spikelets per spike, **ET** effective tillers, **GS** grain per spike, **TW** 1000 seed weight**,** **GY** grain yield per hectare, **BY** biological yield per hectare, **HI** harvest index.

Table 3(b) Stability parameters regression coefficient (bi) and deviation from regression (S2di), of 30 genotypes for 11 Agro-morphological traits over the three environments viz, timely sown, late sown, very late sown.

	ET			**GS**			**TW**			**GY**			**BY**			**HI**		
GEN	**Mean**	**b1**	**s2di**	**Mean**	**b1**	**s2di**	**Mean**	**b1**	**s2di**	**Mean**	**b1**	**s2di**	**Mean**	**b1**	**s2di**	**Mean**	**b1**	**s2di**

G1	7.22	1.034	0.029	51.89	0.860**	-0.698	26.79	0.925	-0.238	6998.591	0.60***	-267211.15	12102.814	0.978	390522.880	31.438	0.613	-0.011
G2	7.17	1.140	-0.068	54.61	0.995	-0.986	22.94	0.694	2.711**	10347.460	1.23**	-551936.17	11985.677	0.920	-209276.449	34.319	1.338	12.810
G3	7.67	1.259*	-0.090	58.67	1.155**	-0.988	22.83	0.438**	0.386	9500.601	1.061	-724608.32	11381.890	0.963	-360035.012	35.707	1.188	6.111
G4	7.50	0.891	-0.141	59.50	1.094	-0.543	25.97	1.303	-0.206	7786.267	0.78**	-462712.62	10075.108	1.158	242545.556	36.454	1.354	-0.074
G5	7.50	1.043	0.157	51.67	0.855**	12.160***	25.31	0.806	-0.277	7936.213	0.80**	-608520.13	11509.123	0.751	171461.966	35.405	1.365***	3.777
G6	7.22	1.034	0.029	58.78	1.138**	2.161	27.30	0.916	-0.245	9049.008	0.973	-713127.41	11848.611	0.941	-312790.742	36.383	1.257***	5.377***
G7	7.61	1.025	-0.063	56.72	1.2005***	-0.864	28.11	1.315	-0.366	8821.193	1.01224	-707677.20	10695.077	1.007	-250616.638	35.947	1.444***	-0.182
G8	6.44	0.849	-0.141	57.22	0.989	-0.974	26.53	0.739	-0.148	10031.977	1.24***	-188178.91	11046.260	0.892	-295564.957	33.602	0.820***	2.562
G9	6.67	1.084	0.135	52.33	0.86**	-0.074	28.39	0.960	2.788**	9261.148	1.046788	-636681.95	11751.590	0.972	60505.358	33.173	0.798*	-0.018
G10	7.00	0.942	-0.103	54.78	1.083	-0.690	26.37	1.437*	0.426	8831.030	0.94	-720232.25	10411.114	0.927	3063488.721**	35.212	1.371***	8.155
G11	8.28	0.951	-0.032	61.78	1.098*	2.728	29.95	0.975	-0.344	10837.248	1.219**	-654096.72	13648.603	0.943	-340979.504	35.830	0.918***	2.742***
G12	7.89	0.756*	-0.087	61.89	1.008	0.296	29.59	0.851	-0.301	10482.298	1.172*	-645353.09	13061.654	0.915	-340640.579	36.163	0.745	0.399***
G13	6.94	1.043	0.181	52.33	0.833***	2.303	26.74	1.200	-0.221	7707.099	0.78**	-639962.89	10548.260	0.830	-66350.603	35.447	1.141***	0.863

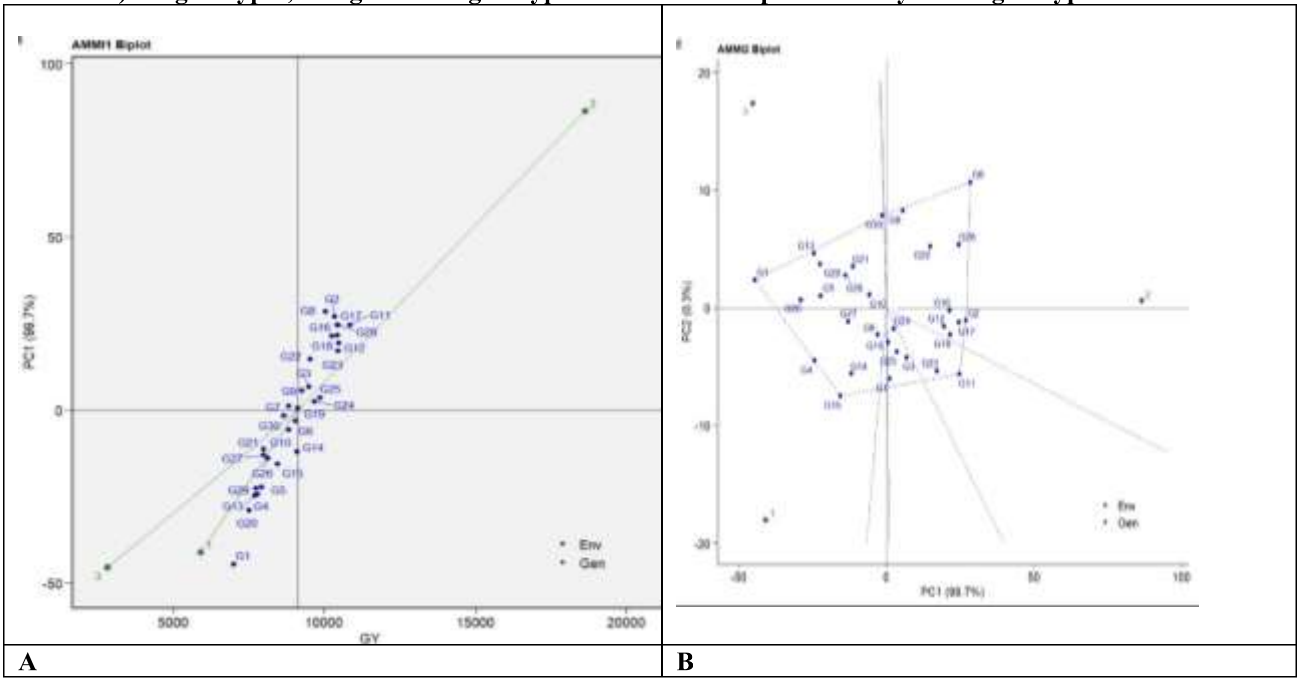
G14	7.33	1.015	-0.120	57.72	0.966	2.963*	28.45	1.158	-0.399	9105.722	0.896	-612167.71	13163.293	0.898	-323676.521	35.330	1.237	1.005*
G15	7.06	1.103	-0.074	56.50	0.841**	-0.655	27.60	1.201	-0.412	8453.348	0.86	-529557.15	11619.374	1.168	-286863.184	36.408	0.97**	9.752*
G16	7.22	0.983	-0.084	56.22	0.888*	0.142	27.83	1.125	-0.094	10252.303	1.189**	-604467.66	13453.963	1.142	-241242.350	33.089	0.576	4.285***
G17	7.06	0.785	-0.114	56.33	0.859**	0.182	27.28	1.118	0.444	10435.203	1.21**	-585185.47	13575.807	1.217	-288334.815	32.525	0.644***	0.497***
G18	7.56	0.909	-0.058	56.17	0.938	1.540	27.34	0.953	0.394	10432.608	1.19**	-634807.99	12941.602	1.280	-35283.427	34.275	0.485***	-0.205
G19	7.06	1.154	-0.134	54.11	1.035	3.224	27.85	0.919	0.238	9132.150	1.005	-720652.61	12497.048	0.977	563391.022	33.564	1.073***	-0.206
G20	7.17	1.038	-0.136	58.28	1.061	6.29**	26.91	0.971	0.015	7510.277	0.743***	-512810.65	10967.794	0.739	1970390.44*	35.812	1.264***	0.151***
G21	6.11	1.145	-0.094	49.28	0.867**	1.685	21.73	0.808	-0.375	8006.145	0.89	-714631.28	10161.440	1.111	-225491.219	33.414	0.985***	0.239
G22	7.33	1.158	0.190	55.56	0.931	-0.941	23.48	0.722	0.571	9546.446	1.12	-585416.73	12552.415	1.023	-63942.015	32.411	0.800	4.760
G23	8.11	0.900	-0.117	61.89	1.144**	1.949	30.14	0.686	-0.071	10457.587	1.152*	-702563.28	13269.460	0.891	-362645.167	37.016	1.057**	0.200***
G24	6.78	0.992	0.409	54.61	0.977	-0.969	27.71	0.976	-0.407	9685.032	1.022	-724647.21	13359.359	1.068	231892.408	34.986	0.677	0.608
G25	7.06	0.978	0.006	60.33	1.202***	1.305	25.90	1.115	-0.414	9863.191	1.03	-723494.84	13901.524	1.094	2936.753	34.109	0.846***	4.617*
G26	6.11	0.997	-0.1	50.	0.817***	-0.876	23.	1.149	-0.	8137.389	0.875	-698	10404.343	0.9	-3118	34.259	1.305*	-0.161

			27	06			04		055			722.82		71	02.049			
G27	5.72	1.029	-0.097	51.39	0.945	0.594	22.70	1.145	-0.413	7987.266	0.88	-665622.15	10167.678	1.106	-272649.283	32.839	1.096***	4.922
G28	7.44	0.826	-0.099	58.28	1.242***	-0.870	26.83	1.196	0.889	10445.691	1.21**	-437296.92	13019.257	0.970	2022557.031*	32.468	0.838	1.706***
G29	7.11	0.928	0.166	53.72	1.157**	-0.717	27.27	1.104	-0.386	7747.890	0.799**	-646930.21	11105.659	0.940	1606369.46*	35.621	0.89*	-0.128
G30	7.22	1.006	-0.141	53.11	0.948	13.318***	28.14	1.095	-0.393	8658.970	0.983	-696220.47	11197.986	1.208	686329.593	34.030	0.88*	2.365***

Where, **DFF** Days to 50% flowering, **DTM** days to maturity , **PH** plant height, **SL** spike length, **SPS** spikelets per spike, **ET** effective tillers, **GS** grain per spike, **TW** 1000 seed weight**, GY** grain yield per hectare, **BY** biological yield per hectare, **HI** harvest index.

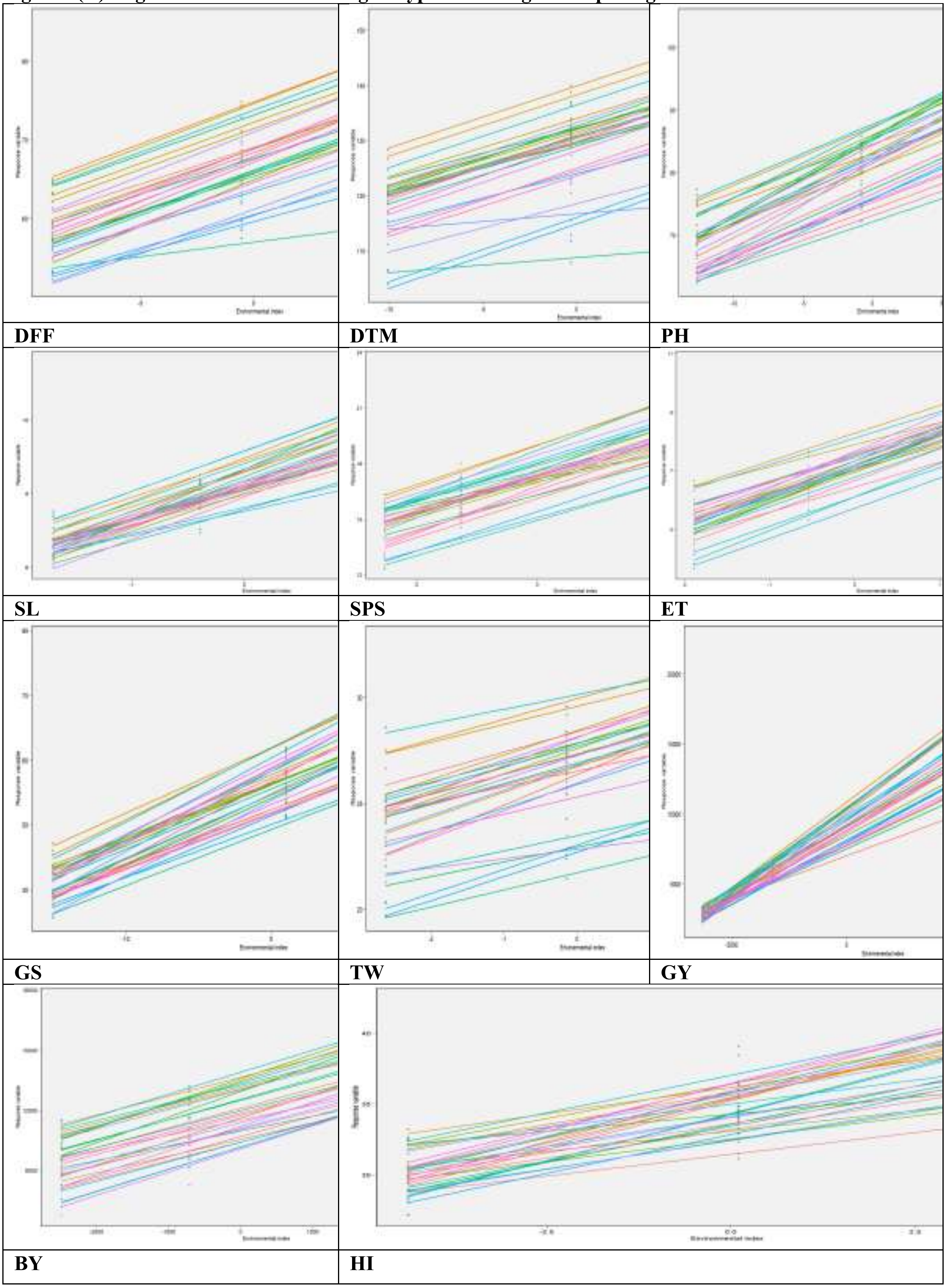
The average grain yield of the thirty wheat genotypes across the tested environments ranged from 8,699.59 kg/ha to 10,837.25 kg/ha, with the highest yields recorded for genotypes K 1006, PBW 725, RAJ 3765, and G 322, while the lowest yields were observed in PBW 723, GW 322, HD 3043, and PBW 765. According to Eberhart and Russell (1966), both bi and S²di components of G×E interactions are essential for evaluating wheat stability. A bi close to 1, along with a deviation from S²di of 0, indicates average stability. Genotypes with bi > 1 are more responsive to environmental changes, showing above-average adaptability to high-yielding conditions, whereas genotypes with bi < 1 are less responsive, indicating stability in low-yielding environments. The observed variation in regression coefficients reflects the differing responses of genotypes to environmental fluctuations. Stability parameters, including regression coefficient (bi) and deviation from regression (S²di), were calculated for 11 agro-morphological traits to determine genotype stability and adaptability across environments. The regression coefficient measures responsiveness, while S²di indicates stability, with a stable genotype characterized by a high mean, bi ≈ 1 and S²di ≈ 0**) (figure 1 and 2).**

Figure 1: AMMI bi-plots visualizations, the combined effect of the two principal components (PC1 and PC2) for genotypes, along with the genotype-environment impact of thirty wheat genotypes.



A B

Figure 1(A) Regression coefficient of 30 genotypes for 11 Agro-morphological traits:



DFF DTM PH

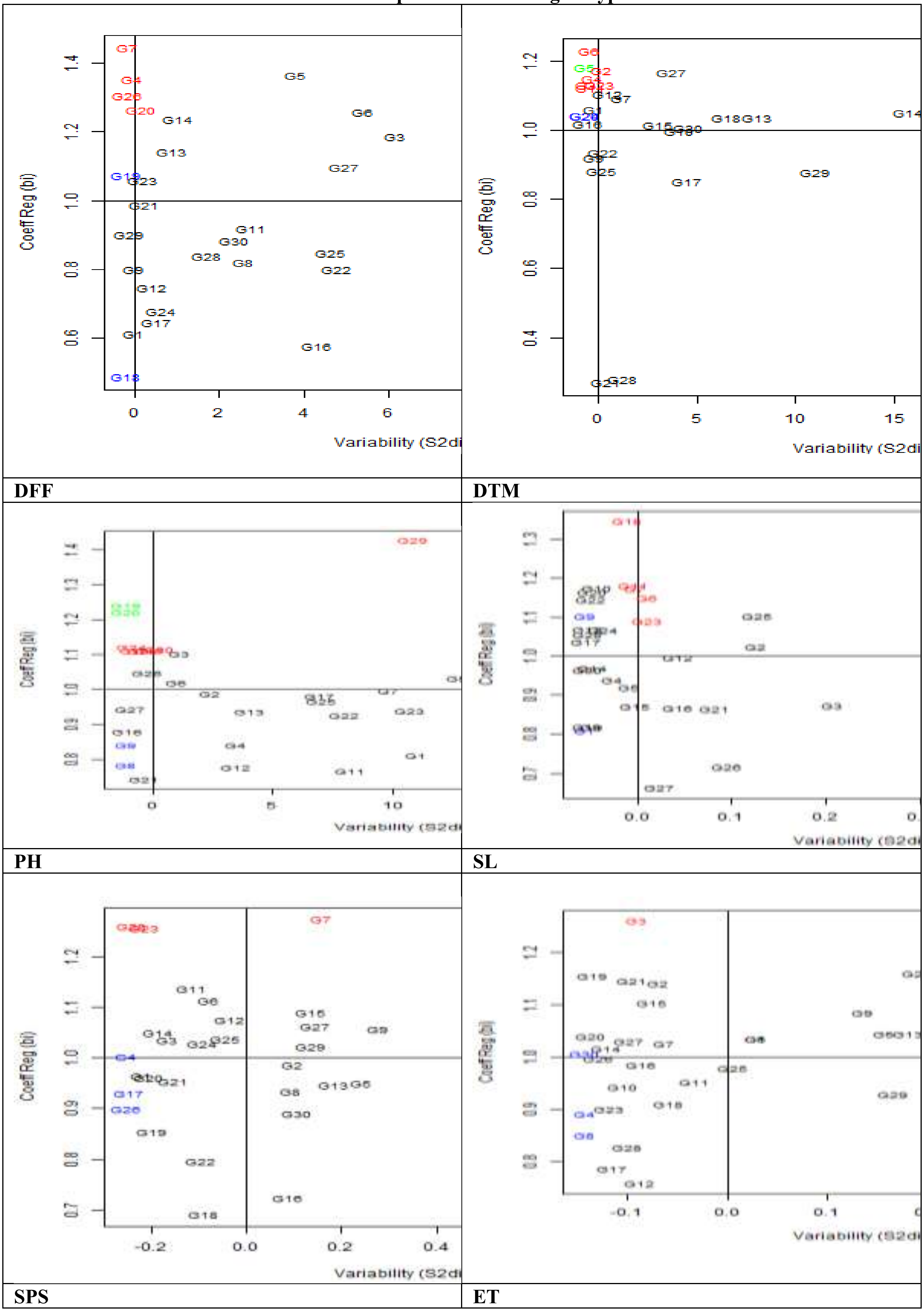
SL SPS ET

GS TW GY

BY HI

Where, **DFF** Days to 50% flowering, **DTM** days to maturity , **PH** plant height, **SL** spike length, **SPS** spikelets per spike, **ET** effective tillers, **GS** grain per spike, **TW** 1000 seed weight**,** **GY** grain yield per hectare, **BY** biological yield per hectare, **HI** harvest index.

Figure 1(B) Plotting of Stable and Adaptable genotypes based on regression coefficient and variability identified by Eberhart and Russell model 1966. RED: adaptable genotypes, BLUE: stable genotypes, GREEN: adaptable and stable genotypes:



DFF

DTM

PH

SL

SPS

ET

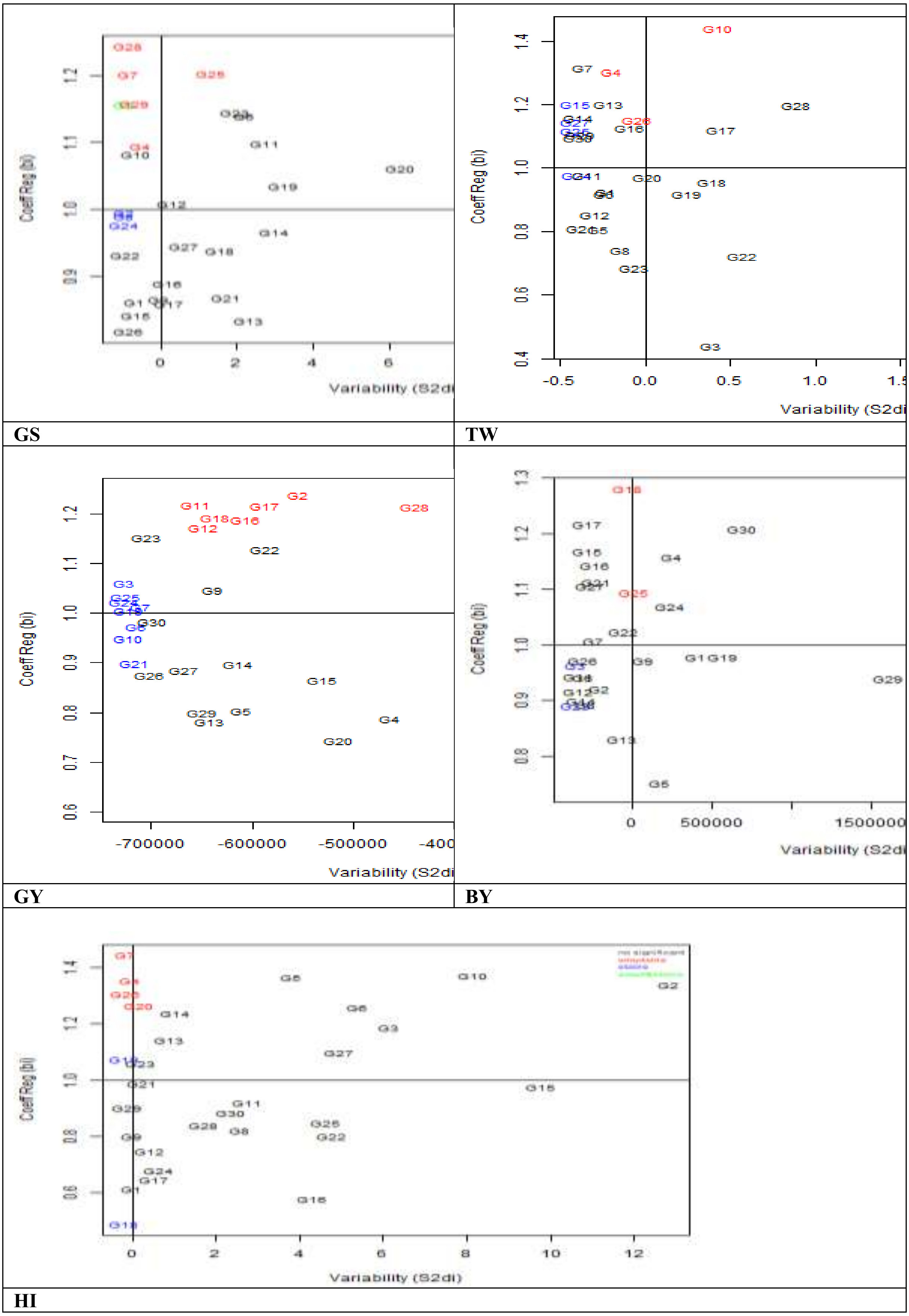
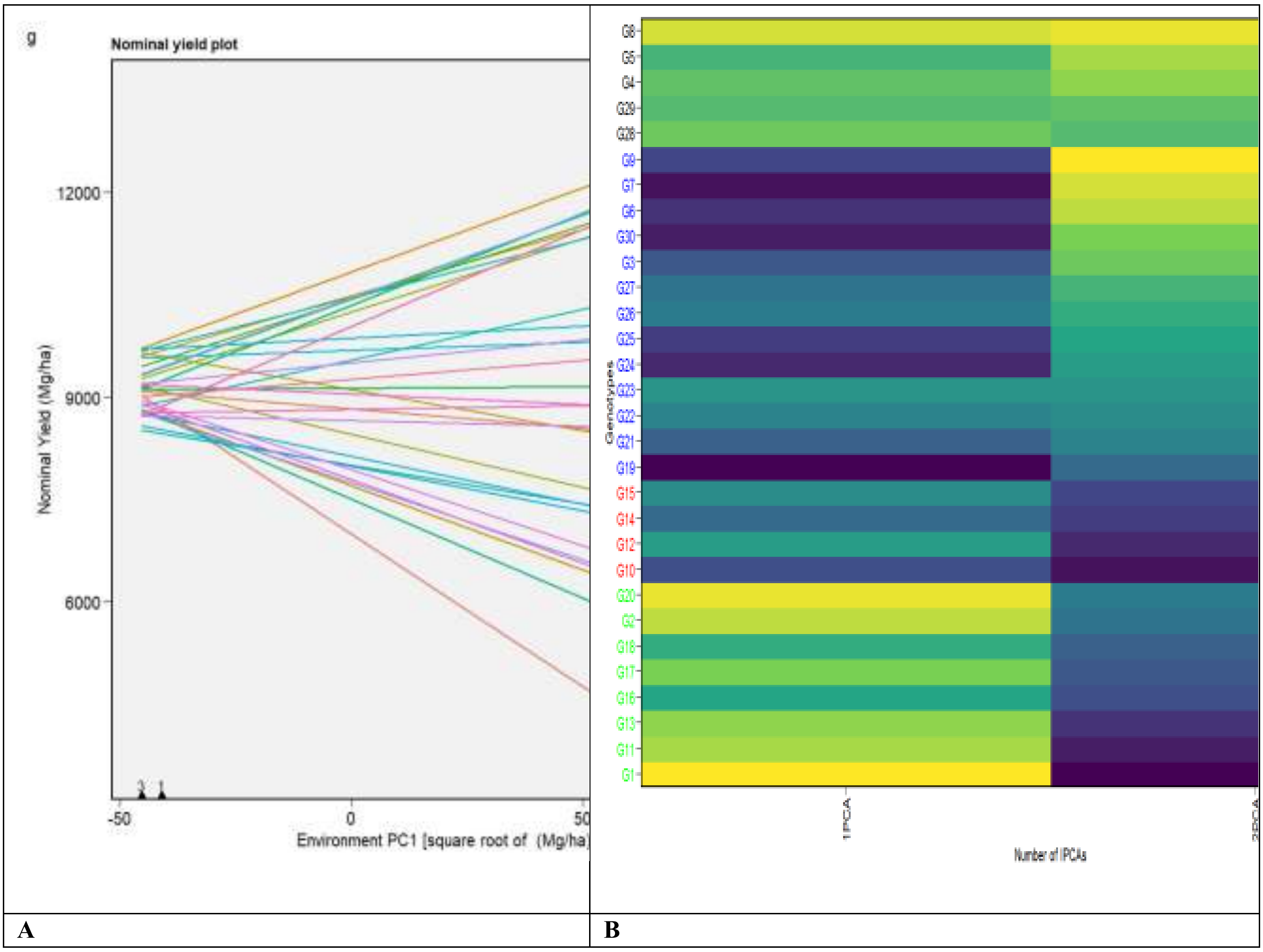


Figure 2 Nominal analysis and genotype ranking on the IPCA score for grain yield for 30 wheat genotypes as a function of the IPCA 1 score of three tested environments.



A **B**

Grouping of genotypes in various categories based on Eberhart and Russell model:
The stable genotypes were classified based on stability parameters derived from the Eberhart and Russell (1966) model, which evaluates genotypic performance across environments using mean trait performance, the linear regression coefficient (b_i), and the deviation from regression (S^2d_i). Genotypes exhibiting non-significant deviations for both b_i and S^2d_i were considered stable. The highest number of genotypes classified as stable was recorded for grain yield (kg ha^{-1}), whereas the greatest number of genotypes categorized as adaptable was observed for plant height and grain yield (kg ha^{-1}). For plant height, the maximum number of genotypes fell under the adaptable and stable category. In contrast, for days to 50% flowering, spike length, spikelets per spike, effective tillers, 1000-seed weight, grain yield (kg ha^{-1}), biological yield (kg ha^{-1}), and harvest index, no genotype was identified as both adaptable and stable. Notably, HD 2932, HD 3118, HD 3086, PBW 644, LOK 1, PBW 804, DBW 46 and DBW 150 were identified as the most stable genotypes for grain yield (kg ha^{-1}). Further categorized as, stable, adaptable and stable and adaptable genotypes see table 3.

Additive main effect and multiplication interaction (AMMI) analysis
The AMMI analysis clarified the relative contributions of the first two interaction principal component axes (IPCA1 and IPCA2) to the genotype × environment interaction (GEI) by projecting genotype and environment means onto biplots with systematically coded environments (E1–E3) and various enlisted genotypes as (G1–G30) (**Figure 2).** The AMMI1 biplot (**Figure 1a**), where X axis indicates that environment E2 had the longest vector length, signifying the strongest interaction effect, whereas E1 and E3 were positioned closer to the origin, reflecting weaker GEI influence. The AMMI2 biplot showed that IPCA1 and IPCA2 together explained 100% of the interaction variance, with the horizontal axis representing the main effects and the vertical axis denoting the interaction component, and reference lines indicating zero interaction and the grand mean. Genotypes located near the IPCA origin, including PBW 644, LOK 1, PBW 804, DBW 173, and K 307, exhibited minimal interaction and were therefore considered stable; however, only DBW 150, DBW 173, and HD 3118 among these produced above-average yields. In contrast, PBW 723, HD 3043, GW 366, and DBW 14 displayed large interaction effects, indicating high sensitivity and instability across environments. In the AMMI2 biplot, **(Figure 1b)** genotypes positioned close to the origin on both axes were identified as stable, while those farther from the origin were highly responsive to environmental variation; accordingly, PBW 644,, LOK 1, DBW 107, ,DBW 173, , HD 3118,

and DBW 46 showed low GEI and greater stability, whereas DBW 150, , PBW 780, RAJ 3765, HI 1612, , DBW 14, PBW 723, , GW 366, WB 2, DBW 173, , K 1006, and DBW 51 were highly interactive. Notably, DBW 107 and PBW 644combined high mean yield with minimal GEI, while HD 3118, DBW 46, and HI 1563were distinguished by high productivity coupled with favourable IPCA1 scores, indicating wide adaptability and stable performance across environments.

DISCUSSION

In present study a total of 30 bread wheat genotypes were studied across different environment for yield and yield contributing characters. A highly noteworthy difference was found among the genetic constitution for all the traits over the various environments over the two years that was more considerable amount of genetic variability among themselves and same conditions has been observed by Kumar *et al*. 2025, Reddy *et al*. 2021. The G×E interaction for timely late and very late sown conditions was showed a significant difference by DFF, SL, ET, TW, BY, GY, and HI and SPS did not show any significant difference for the G×E interaction. The same conditions have been testified through Wani *et al.* (2018), Mishra *et al.* (2024). Rathod *et al.* (2019), Saxena *et al.* (2016), Irfan *et al.* (2018) and Mamrutha *et al.* (2020).

Eberhart and Russell stability model

The stability analysis based on the Eberhart and Russell model revealed significant genetic variability among the 30 wheat genotypes across three sowing environments. The presence of highly significant G×E interactions for key traits such as DTM, SL, GS, GY, BY, and HI highlights the differential responses of genotypes to environmental changes, underscoring the need for stability assessment. Mean performance, bi, and S^2di were used to determine genotype stable performance. A wide variation in regression coefficients across traits indicated differing adaptability, with some genotypes performing better under favourable conditions while others maintained stable performance even in stressful environments. For grain yield, the most critical trait genotypes RAJ 3765, GW 322, K 1006, and PBW 725recorded the highest mean performance. However, based on stability parameters, genotypes HD 2932, HD 3118, HD 3086, PBW 644, LOK 1, PBW 804, DBW 46, and DBW 51 showed more stability, combining consistent performance with predictable environmental responses. Trait-specific stability varied, with plant height showing the highest number of genotypes categorized as adaptable and stable, whereas traits such as SL, SPS, ET, and TW exhibited fewer stable genotypes, indicating stronger environmental influence. Overall, the study demonstrates that while many genotypes show high mean performance, only a few possess true stability across environments. These stable genotypes represent valuable candidates for breeding programs aimed at enhancing wheat productivity under varying climatic and management conditions. These observations are backed by Castillo *et al.* (2012), Sabaghnia *et al.* (2014), Khaki *et al.* (2019), and Patidar *et al*. 2023. The genotypes were categorised for eleven quantitative characters under study in well-adapted and poorly-adapted environments.

AMMI model:

AMMI effectively clarified G × E interaction patterns among the 30 wheat genotypes evaluated across three contrasting environments. The AMMI1 biplot showed that environment E2 exhibited the strongest interaction, as indicated by its longer vector, whereas E1 and E3 had relatively smaller interactions. Such variability across environments aligns with earlier findings that longer environmental vectors reflect greater discriminative ability and instability. Genotypes located near the origin of the IPCA1 axis in the AMMI1 biplot, including PBW 644, LOK 1, PBW 804, BDW 173, and K 307 contributed minimally to GEI, indicating strong stability across environments. Despite this, only a few genotypes, such as DBW 150, DBW 173, and HD 3118, combined stability with above-average yield, meeting the criteria for desirable performance under variable conditions (Eberhart & Russell, 1966). The AMMI2 biplot, which captured 100% of the GEI variation through IPCA1 and IPCA2, reinforced these observations by distinguishing genotypes with low interaction effects. Genotypes such as PBW 644, LOK 1, DBW 107, DBW 173, HD 3118, and DBW 46 were positioned closest to the origin, confirming their stability and reduced environmental sensitivity. In contrast, genotypes like DBW 150, PBW 780, RAJ 3765, HI 1612, DBW 14, PBW 723, and GW 366, which lie farther from the origin, exhibited stronger interaction and greater responsiveness to environmental changes. Overall, AMMI analysis identified DBW 107 and PBW 644 as the most looked-for genotypes by their high yield, low GEI scores. These genotypes demonstrated wide malleability and stability across environments, confirming the value of AMMI models for selecting reliable and high-performing wheat genotypes under variable production conditions. These findings are consistent with patterns previously Omarani *et al.* (2022), Ali *et al.* (2017), and Teharian *et al.* (2024).

CONCLUSION

The present investigation, carried out across three contrasting sowing environments, timely, late, and very late, offers an inclusive understanding of the genetic behaviour, trait dynamics, and malleability patterns of 30 genotypes. The highly significant variability revealed through ANOVA across all agro-morphological traits establishes that the evaluated germplasm possesses sufficient genetic breadth to support future breeding interventions. Stability analyses, engaging the Eberhart and Russell model, reinforced status of evaluating genotypes under multi-environment trials. The significant G×E interactions for several yield-associated traits highlight the complexity of genotype expression under environmental fluctuations. Among the tested genotypes, HD 2932, HD 3118, HD 3043, PBW 644, LOK 1, PBW 804, DBW 46, and DBW 51 emerged as superior stable performers for GY, exhibiting regression coefficients close to unity and minimal deviation from relapse. These genotypes show potential for broad adaptation, key candidates for environments characterized by inconsistent climatic patterns. Notably, plant height was the only trait exhibiting simultaneous stability and adaptability among several genotypes, underscoring its reliability under varied conditions. The AMMI model provided a more nuanced perspective of stability by decomposing interaction effects. The identification of E2 as the environment exerting the strongest interaction, along with genotypes such as PBW 644, LOK 1, DBW 107, HD 3118, and DBW 46 clustering near the origin in AMMI2 biplots, confirms their resilience to environmental fluctuations. High-yielding genotypes with favourable interaction patterns, such as HD 3118, DBW 46, and HI 1563**,** exhibit both stability and productivity an essential combination for breeding under climate uncertainty.

Author's contribution: AK and YS designed and performed the experiment; AK, SG and AT have done analysis and compiled result. AB, AS, HK, SV, AG and AT drafted and reviewed the manuscript.

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