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ASSESSMENT OF MAIZE HYBRIDS PERFORMANCE ACROSS TWO ENVIRONMENTS USING CORRELATION AND GGE BIPLOT APPROACHES

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Abstract

Maize stands as one of the significant grain crops to meet the food demands of rapidly growing population amid diminishing natural resources. Therefore, developing high yielding maize hybrids, particularly in challenging climatic conditions, is crucial for ensuring food security. The present study assessed the performance of maize hybrids across variable environments. Thirty hybrids were sown in randomized complete block design (RCBD) with three replications in two environments (Faisalabad E1 and Sahiwal E2) during 2021. Analysis of variance revealed significant variation among hybrids for most traits except plant height (PH) and ear height (ErH). The G×E interaction was significant for grain yield GY (4.6×10^6 **), cob length CL (4.5*), cob girth CG (0.2**), No. of grains/row GR (17.8**) and 1000 grain weight GWt (15.7**). Correlation analysis revealed significant relationship of GY with CG (0.41*), CL (0.53**), PH (0.52**), ErH (0.37*) at E1, while only PH (0.49**) was positively correlated with GY at E2. Various GGE biplots, utilizing the first two principal components (PCs), were generated to elucidate the G×E interaction. The first two PCs for GY accounted for 74.63% and 25.37%. Based on PH, ErH, CL, CG, GR, GWt, DS and Shell, genotypes G11, G25, G3, G4, G7, G11, G16 and G8 were recognized as the most stable, respectively. Genotype G14 showed the highest stability in E1 and G11 in E2, whereas G16 consistently emerged as the most stable and high-yielding hybrid in both environments. Environment E1 was most representative; making it suitable for hybrid evaluation.

Key words: GGE biplots; Correlation; Stability analysis; G×E interaction; Grain yield

Introduction

Maize is a major grain crop in the Pakistan and worldwide. The cultivated maize species is diploid (2n = 20) and possessed broad adaption to wide range of agro-climatic environments, encouraging its cultivation at various parts of the world. It is preferably chosen by farmers due to its better grain yield/acre among cereal crops and existence of well-established industry (Shojaei *et al.*, 2022). It's a dual-purpose crop that can be used for fodder and grain. Moreover, maize is considered an industrial crop owing to its extensive usage (70-80%) in industry, while only 13% is a part of human consumption, globally (Yousaf *et al.*, 2021a). It was cultivated on 197 million hectare and produced 1200 million metric tons globally in 2021 (Anon., 2021). Maize has diverse utilization worldwide. Besides serving as food for humans and feed for animals, cob powder is used as an explosive fillers and in the production of glues, vinegar, plastics, resin, adhesives, artificial leather, paper, pulp and hardboard (Mallhi *et al.,* 2025). It is also used as carrier and diluents in pesticides and insecticides formulation. Corn grain is used for making flour, flakes, syrup, starch and oil extraction (Sah *et al.*, 2020).

Maize belongs to C4 group of plants that have ability to efficiently fix CO2 to produce comparatively higher grain yield (Shehzad *et al.*, 2019; Yousaf *et al.*, 2021b). Grain yield is a quantitative trait that is adversely affected by various biotic and abiotic stresses and ultimately exacerbating food shortage (Ghani *et al.*, 2020). Food security is a perpetual threat for agricultural progress as population of world is rapidly increasing, necessitating continuous research and development to breed food crops that can thrive in unpredictable environments and under the challenges of climate change (Khan *et al.*, 2023).

Enhancing national maize production can be achieved through the cultivation of hybrid types, well-adapted to specific environments. However, the sustained adoption of hybrids requires the development of improved hybrids with stable performance. Therefore, continuous efforts are required to develop and evaluate promising hybrids across diverse environments (Adham *et al.*, 2022). Yield selection in maize hybrids is challenging due to genotype × environment interaction (GEI). As a quantitative and polygenic trait, yield requires evaluation through multi-environment trials (METs) to assess GEI, identify specifically and widely adapted high-yielding genotypes and determine representative testing sites (Ruswandi *et al.*, 2021).

The stability and suitability of a crop are determined by its ability to thrive and yield reliably under local environmental conditions. External factors such as rainfall, soil chemistry, temperature, humidity and microbial activity are among the primary contributors to GEI effects,

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influencing plant growth throughout the growing cycle (Crevelari *et al.*, 2023). Thus, the importance of genotype × environment (G×E) interactions cannot be overlooked. Crop breeders typically prioritize agronomic traits particularly yield and its components, in relation to GEI to develop sustainable solutions for challenges affecting plant growth and development (Al-Naggar *et al.*, 2020). Consequently, various statistical methods and models have been developed to assess the impact of GEI in large-scale environmental experiments. One such approach is the GGE biplot model that integrates a which-won-where pattern, environment ranking, mean vs. stability, discriminativeness and representativeness of the environments, genotype rankings and the application of singular value decomposition (SVD) (Esan *et al.*, 2023; Lima *et al.*, 2023).

The present research aims to identify top-performing genotypes that consistently give higher yield across diverse environments, by employing various stability analysis techniques. Additionally, the impact of GEI on the agronomic characteristics of maize was to be quantified to better select high yielding and stable hybrids for commercial release.

Materials and Methods

Experimental sites: This experiment was carried out in 2021 (Feb-June) at two locations i.e., Maize Research Station (MRS), AARI Faisalabad (31.4504° N, 73.1350° E) with an altitude 186 m above the sea level (E1) and Maize & Millets Research Institute (MMRI), Yusafwala, Sahiwal (30.6682° N, 73.1114° E) with an altitude 152 m above sea level (E2)**.** Both soils were classified as clay loam texture. MRS soil plot exhibited greater EC, pH and organic content, but it had lesser available phosphorus, potash and saturation compared to the MMRI test plot soil (Table 3). But both plots at MRS and MMRI had well-aerated soil.

Plant materials and environmental conditions: In this study, out of thirty maize hybrids (Table 1), twenty-eight were taken from germplasm collection of MRS AARI Faisalabad, one from MMRI, Sahiwal and one from Corteva Seed (Pvt. Limited). The maize seeds were sown in the fields at both locations as part of multi-environment experiments during spring season.

Meteorological observations were recorded from both the locations on daily basis throughout the growing season. Observations pertaining to average daily maximum and minimum temperatures (°C) as well as rainfall (mm) were compiled on a monthly basis (Table 2).

Agronomic practices: This study was conducted using a randomized complete block design (RCBD) with three replications. A balanced dose of NPK fertilizer (247:113:62 kg/ha) was applied, with phosphorus and potash incorporated at sowing, while nitrogen was applied in four equal splits. Additionally, 3 kg of sulphur was applied at 40 days after sowing (DAS). Each genotype was allotted a plot size of 12 m², with a plant-to-plant spacing of 20 cm and row-to-row spacing of 75 cm. The first and last rows were considered non-experimental to minimize border effects. Two seeds were sown per hole to ensure optimum germination and surplus plants were thinned to one plant per hill after 20 DAS. Weed control was achieved by applying herbicide two weeks after germination. Fall armyworm (FAW) infestations, when observed, were managed with Tetraniliprole (200 g/L) applied at 100 mL/acre during the V3–V4 stage. At the V6–V7 stage, Fipronil + Emamectin Benzoate 0.35G granules were applied at 8 kg/acre. At 115 DAS, maize was harvested at an average grain moisture of 20–28%.

Table 1. List of tested 30 maize hybrids and their source.

Hybrid	Code	Origin	Hybrid	Code	Origin	Hybrid	Code	Origin
FH-1046	G1	MRS	FH-1865	G11	MRS	FH-1908	G21	MRS
P-1543	G2	Corteva Seed	FH-1866	G12	MRS	FH-1910	G22	MRS
FH-1847	G3	MRS	FH-1867	G13	MRS	FH-1911	G23	MRS
FH-1848	G4	MRS	FH-1868	G14	MRS	FH-1912	G24	MRS
FH-1849	G5	MRS	FH-1869	G15	MRS	FH-1913	G25	MRS
FH-1852	G6	MRS	FH-1870	G16	MRS	FH-1914	G26	MRS
FH-1855	G7	MRS	FH-1904	G17	MRS	FH-1915	G27	MRS
FH-1856	G8	MRS	FH-1905	G18	MRS	FH-1916	G28	MRS
FH-1858	G9	MRS	FH-1906	G19	MRS	FH-1918	G29	MRS
FH-1861	G10	MRS	FH-1907	G20	MRS	YH-5427	G30	MMRI

Note: MRS-Maize Research Station, AARI, Faisalabad, MMRI-Maize & Millets Research Institute, Sahiwal

Table 2. Climatic conditions of the two environments during the experiment (Year-2021).

Environments	Parameters	February	March	April	May	June
Faisalabad (E1)	Min Temp (°C)	9.8	15.3	18.4	24	25.6
	Max Temp (°C)	25.9	31	34.5	38.6	39
	Ave Temp (°C)	17.8	23.1	26.4	31.3	32.3
	Ave Humidity (%)	66	57	42.5	45	50
	Ave Rainfall (mm)	0	6.1	3.8	3.7	4.6
Sahiwal (E2)	Min Temp (°C)	10.5	15.4	18.5	22.5	29.1
	Max Temp (°C)	28.1	31.7	36.5	40	40.8
	Ave Temp (°C)	19.3	23.5	27.5	31.2	34.9
	Ave Humidity (%)	55.8	44.9	42.6	36.2	43.3
	Ave Rainfall (mm)	0	0	5.9	7.4	0

Table 3. Soil properties of Faisalabad (E1) and Sahiwal (E2) sites.

Properties	Faisalabad	Sahiwal
EC (dS/m)	1.7	1
Soil pH	8.6	8
Organic matter OM (%)	0.7	0.7
Available phosphorus P (PPM)	5.2	7.6
Available potassium K (PPM)	180	300
Saturation (%)	32	44
Texture	Clay loam	Clay loam

Data collection of yield associated agronomical traits: For data collection of agronomic traits, five mature, healthy and guarded plants were selected. Grain yield (GY) was recorded in kg/ha and calculated using the equation described by (Yousaf *et al.*, 2022).

Days to 50% silking (DS) were noted by calculating the sowing days to the completion of 50% ear silking. Plant height (PH) and ear height (ErH) were measured at 80 days using a measuring rod. Cob length (CL) was measured with a small-scale meter, number of grains per row (GR) was counted, cob girth (CG) was recorded using a digital vernier caliper and 1000 grain weight (GWt) was determined using a weighing balance. Shelling % (Shell) was calculated using the following formula at 11-12% grain moisture contents.

$$\text{Grain yield (kg/ha)} = \frac{\text{Fresh cob weight (kg/plot) x (100 – MC) x 0.8}}{\text{100 – 15 x Area harvested/plot x 1000}} \text{ x 1000}$$

Shelling % = Grain weight (g) / Ear weight (g) x 100

Statistical data analysis

Data pertaining to grain yield and yield related traits was analysed for combined analysis of variance (Steel *et al.*, 1997) with Statistix 8.1 (Analytical Software, Tallahassee, FL, USA). Correlation coefficient analysis and GGE biplots were generated using "*metan library*" in R. Adobe Illustrator (version 17.0.0) was used to collage the images in single frame.

Results

Metrological data: The metrological data (Table 2) reveals that Faisalabad's temperatures ranged from 9.8°C to 39°C, with humidity starting at 66% and decreasing to 50% by June, accompanied by minimal rainfall. In contrast, Sahiwal had temperatures between 10.5°C and 40.8°C, began with a humidity of 55.8% which dropped to 43.3% and experienced varied rainfall, peaking at 7.4mm before returning to a dry spell by mid-year.

Combined ANOVA: The combined ANOVA (Table 4) assessed the effects of different sources of variation (SOV) across environments (Env) for studied traits. For the environment effect, traits such as GY (4.7×10^7), PH (1380), CL (56.8) and GR (226) demonstrated significant variations ($p<0.05$). For the hybrid (Hyb) effect across both environments, traits including GY (1.1×10^7), CL (9.3), CG (0.21), GR (34.3), GWt (18.5), DS (0.01) and Shell (13.6) were significant ($p<0.01$ & 0.05). In the interaction effect (Env × Hyb), CL (4.5) and CG (0.1) were significant ($p<0.05$), while, GY (4.6×10^6),), GR (17.8) and GWt (15.7) exhibited highly significant results ($p<0.01$).

Correlation analysis: Both environments (E1 and E2) showed significant associations among most studied traits, though with varying patterns (Fig. 1). At MRS (E1), GY correlated significantly with CG (r = 0.40*), CL (r = 0.53**), PH (r = 0.52**) and ErH (r = 0.37*), whereas at MMRI (E2), GY showed a significant association only with PH (r = 0.49**) with weaker non-significant correlations to GR and GWt. Other trait relationships also differed between environments. In E1, PH correlated positively with CL (r = 0.40*), GWt (r = 0.37*) and strongly with ErH (r = 0.70***), while in E2, PH was primarily linked to GY. Ear height (ErH) was closely associated with PH in E1, but in E2 it correlated with CG (r = 0.41*), Shell (r = 0.42*) and DS (r = 0.68***). Similarly, CL was related to GR in E1 (r = 0.46*) but to both CG (r = 0.61***) and GR (r = 0.44*) in E2. CG correlated with GR in E1, whereas in E2 it aligned more with CL and ErH. Notably, GWt showed significant association with PH and CL in E1, but not in E2. Overall, correlations were stronger and more consistent in E1, while in E2, associations shifted toward reproductive traits such as DS, Shell and CL.

Table 4. Combined analysis of variance for yield related traits of 30 maize hybrids in two environments.

SOV/Trait	Env	Error Env* R	Hyb	Env* Hyb	Error Env* R* Hyb	CV% Env* R*Hyb	CV% (Env*R)	G. Mean	Range
DF	**1**	**2**	**29**	**29**	**58**	**-**	**-**	**-**	**-**
GY	4.7×10^7 *	1.30×10^6	1.1×10^7 **	4.6×10^6 **	1.41×10^6	11.8	11.5	10050	3364-13706
PH	1380.4**	60.3	351.8	333.5	323.9	9.7	4.2	185.6	150-270
ErH	6.1	787.4	309.1	235.6	261.2	14.5	25.2	111.2	70-145
CL	56.8**	1.1	9.3**	4.5*	0.3	3.0	5.7	18.5	14.3-22.1
CG	0.0	0.2	0.2**	0.1*	0.1	6.1	9.5	4.7	4.1-5.7
GR	226.8*	12.2	34.3**	17.8**	1.4	3.1	9.4	37.4	25-44
GWt	39.1	8.4	18.5**	15.7**	1	3.2	9.2	31.4	22-38
DS	0.5	15	0.0**	0.4	2.3	1.9	5.1	75.7	71-82
Shell	16.1	2.4	13.6**	1.8	1.4	1.4	1.8	85.5	77-90

* : Significant @ $p<0.05$, ** : Significant @ $p<0.01$

GY= Grain yield (kg/ha), PH= Plant height (cm), ErH= Ear height (cm), CL= Cob length (cm), CG= Cob girth (cm), GR= Grains/Row, GWt= Grain weight (g), DS= Days to 50% Silking, Shell= Shelling %

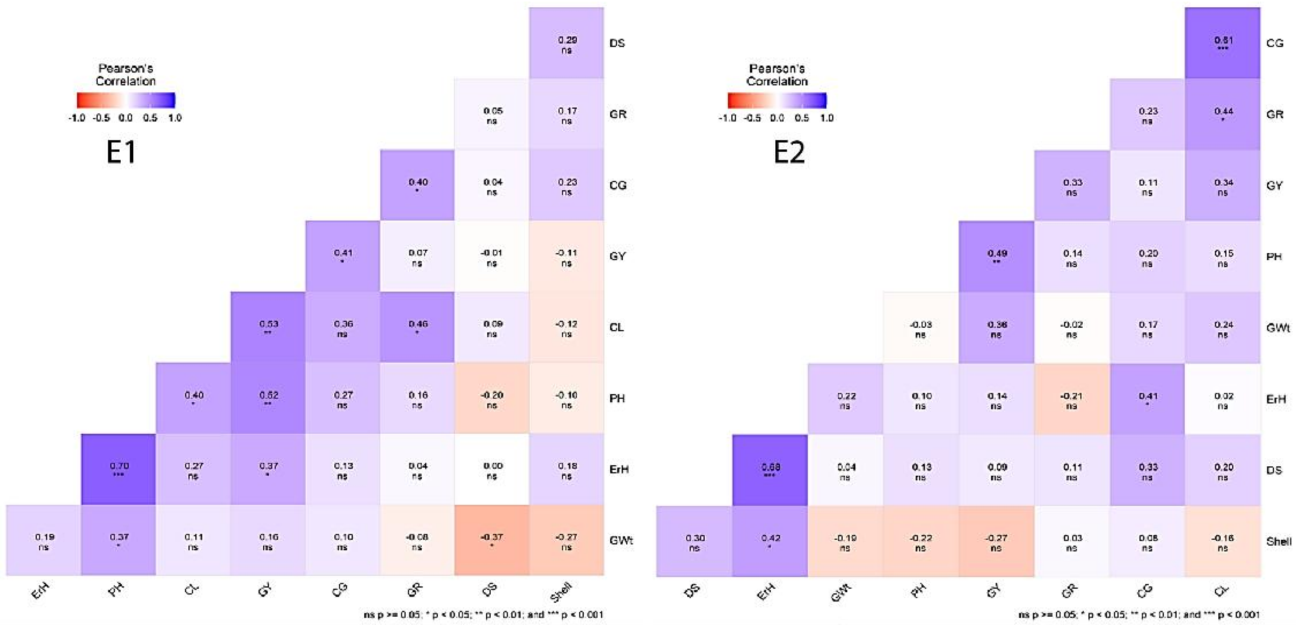

Fig. 1. Pearson correlation analysis under two environments E1 (Faisalabad) and E2 (Sahiwal) for nine traits.

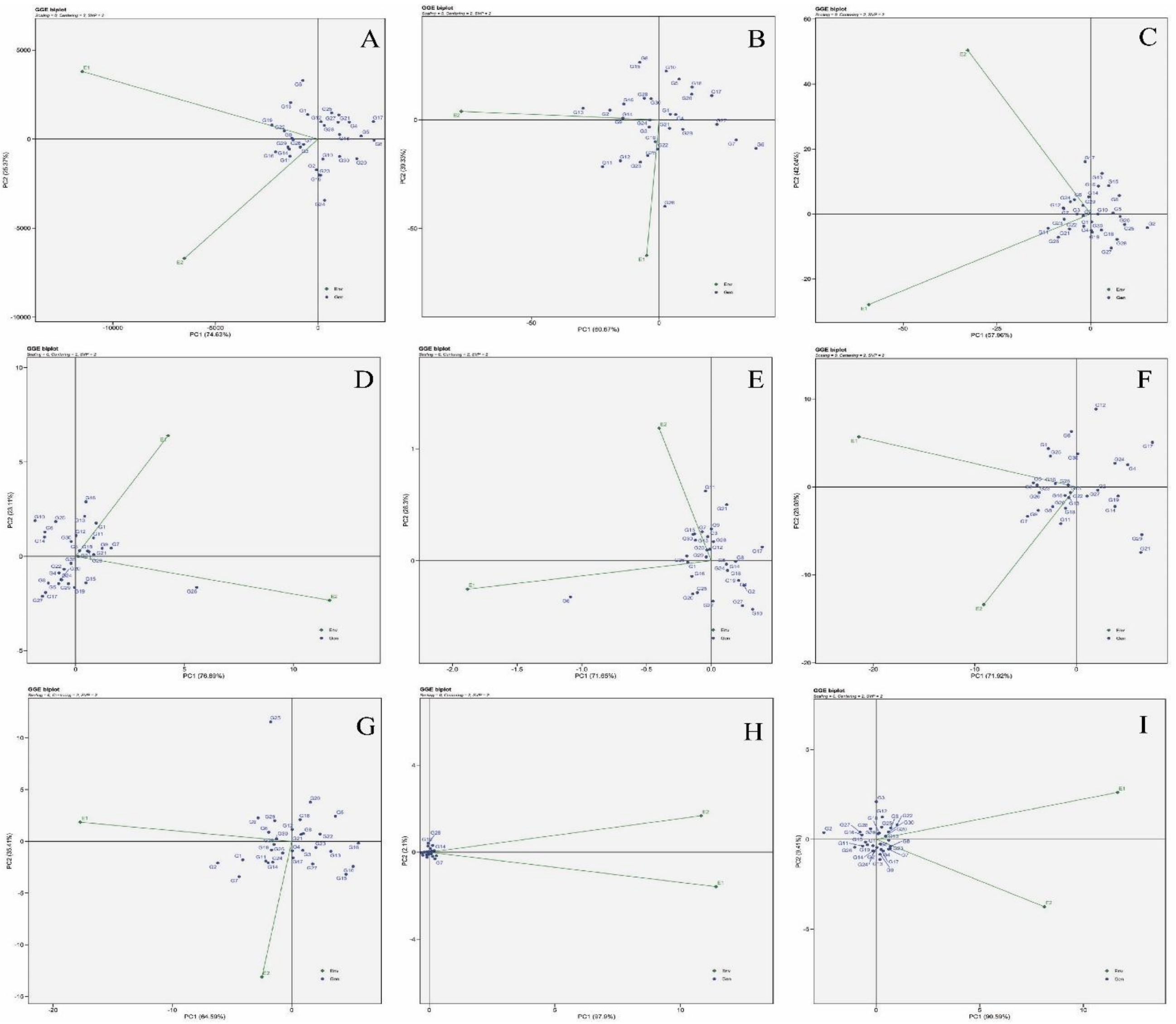

Fig. 2. Patterns (A-1) GGE biplots (PC1+ PC2) showing GEI of 30 maize hybrids under two environment for nine traits A-GY, B-PH, C- ErH, D- CL, E- CG, F- GR, G- GWt, H-DS, I-Shell. The GGE biplots were generated on scaling = 0, cenering = 2 and SVM = 2.

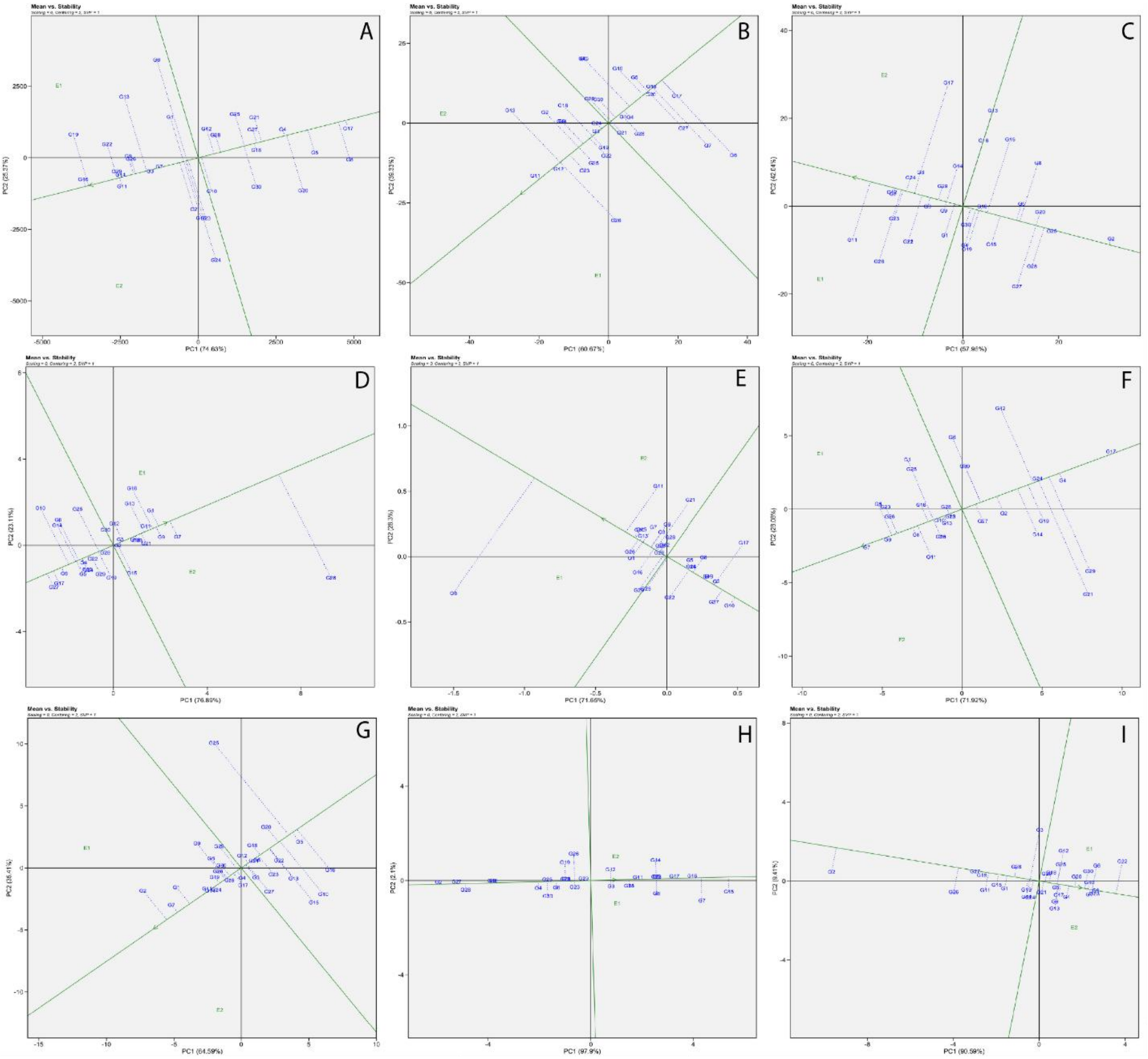

Fig. 3. Patterns (A-1) Mean vs Stability biplots (PC1+PC2) showing GEI of 30 maize hybrids under two environment for nine traits A-GY, B-PH, C- ErH, D- CL, E- CG, F- GR, G- GWt, H-DS, I-Shell. The Mean vs Stability biplots were generated on scaling = 0, cenering = 2 and SVM = 1.

GGE biplots analysis of various traits

GGE biplot: The GGE biplots (Fig. 2) A, B, C, D, E, F, G, H and I illustrated patterns of variation for GY, PH, ErH, CL, CG, GR, GWt, DS and Shell traits respectively. PC-1 contributed 74.63%, 60.67%, 57.96%, 76.89%, 71.65%, 71.92%, 64.59%, 97.9% and 90.59% to the total variation. While, PC-2 accounted for 25.37%, 39.33%, 42.04%, 23.11%, 28.3%, 28.08%, 35.41%, 2.1% and 9.41% for each trait. The genotypes clustered together and aligned with environments vectors exhibited higher trait value, whereas those positioned behind the origin and lacking environmental orientation showed lower performance. For example, The genotypes clustered alongside the environments and positioned ahead of the origin were as follows: in GY (Fig. 2A), G16, G19, G22, G29, G11, G14, G9, G26, G13 and G3; in PH (Fig. 2B), G11, G12, G23, G25, G14, G13, G9, G19, G3 and G24; in ErH (Fig. 2C), G11, G12, G7, G26, G6, G24, G3, G1, G4, G22, G21 and G23; in CL (Fig. 2D); G26, G7, G1, G9, G16, G11, G13, G21, G23, G18, G12 and G3; in CG (Fig. 2E), G6, G11, G30, G15, G26, G13, G7, G1, G16, G23 and G12; in GR (Fig. 2F), G7, G9, G3, G5, G26, G23, G8, G11, G16, G20, G18, G10, G13 and G15; in GWt (Fig. 2G), G2, G7, G1, G11, G14, G24, G19, G28, G9, G6, G26 and G30; in DS (Fig. 2H), G15, G7, G16, G17; in Shell (Fig. 2I), G22, G8, G23, G6, G7, G10, G30, G20 and G4.

Mean vs. Stability: Patterns 3A–3I (Fig. 3) showed the mean vs. stability analysis. The abscissa indicated the main effect and closeness to the ideal genotype, while the ordinate represented GEI magnitude, with higher values representing lower stability. Genotypes above the mean and closer to the arrow included: G16, G19, G22, G11, G29, G14, G26, G9, G13, G3, G2, G1, G6 and G24 for GY (Fig. 3A); G11, G12, G26, G13, G23, G2, G25, G14, G9, G22, G16, G19, G3 and G24 for PH (Fig. 3B); G11, G12, G7, G26, G23, G24, G6, G17, G22, G3, G29, G9, G14 and

G1 for ErH (Fig. 3C); G26, G7, G1, G9, G16, G11, G13, G21, G23, G18, G12 and G3 for CL (Fig. 3D); G6, G11, G30, G15, G26, G13, G7, G9, G1, G3, G16, G21 and G23 for CG (Fig. 3E); G7, G9, G3, G5, G26, G23, G8, G11, G16, G1, G20, G25, G18, G10, G13, G15 and G28 for GR (Fig. 3F); G2, G7, G1, G11, G14, G24, G19, G28, G9, G6, G26, G30, G17, G4 and G29 for GWt (Fig. 3G); G15, G7, G16, G17, G14, G8, G13, G22, G5, G11, G21, G18 and G3 for DS (Fig. 3H); and G22, G8, G23, G6, G7, G10, G30, G20, G4, G17, G13, G9, G25, G12, G5, G18, G29 and G21 for Shell (Fig. 3I).

The abscissa indicated cultivar performance whereas the ordinate reflected stability. For GY, PH, ErH, CL, CG, GR, GWt, DS and Shell, the top genotypes were G16, G11, G11, G26, G6, G7, G2, G15 and G22, whereas G17, G17, G2, G27, G10, G17, G16, G2 and G2 ranked lowest. Stability assessment showed G3, G11, G12, G3, G29, G7, G11, G16 and G8 as stable, while G24, G6, G17, G26, G6, G21, G25, G26 and G3 were unstable.

Which won where: The GGE biplots for "which-won-where" having patterns (Fig. 4) 4A, 4B, 4C, 4D, 4E, 4F, 4G, 4H and 4I, described distribution of test environments across different sectors in polygon view i.e. two of six sectors for GY, PH, ErH, GR, GWt, two of five for CG and Shell traits and, two of the four for CL and one of seven for DS traits. Thus, mega environments were revealed for each parameter, with two mega-environments for all traits except DS (Fig. 4H), which had only one. The top-performing genotypes were identified i.e. G19 in the first mega-environment (E1) and G24 in the second mega-environment (E2) for GY (Fig. 4A) and PH (Fig. 4B); G11 and G26 in the E1 while G17 and G13 in the E2 for ErH; G16 in E1 and G26 in E2 for CL (Fig. 4D); G6 in E1 and G11, G21 in E2 for CG (Fig. 4E); No genotypes in E1 and G7 in E2 for GR (Fig. 4F); G2 and G7 in E1 and none in E2 for GWt (Fig. 4G); G7 and G15 in E1 and E2 for DS and G22 and G23 in E1 and G7 in E2 for Shell (Fig. 4I).

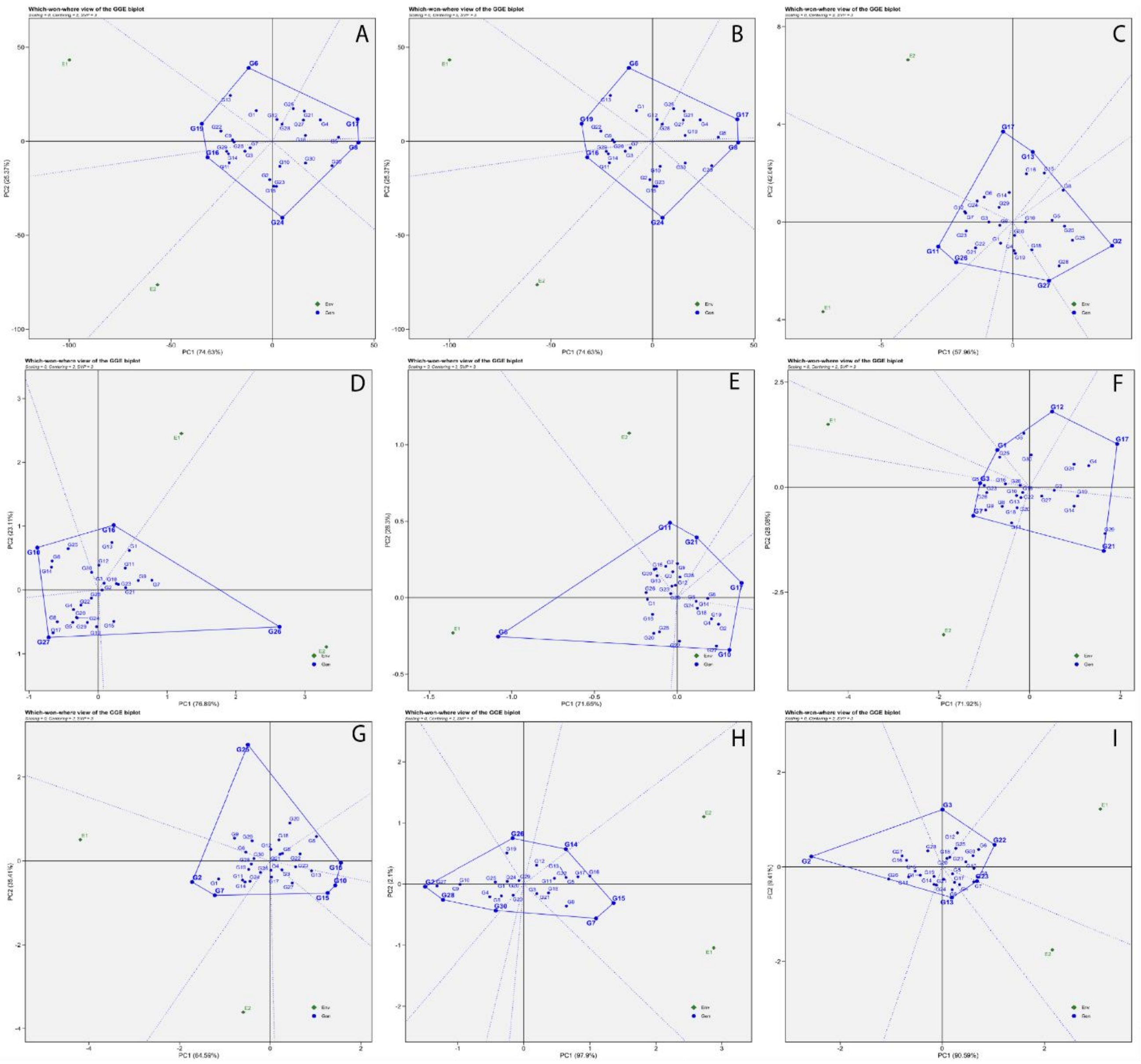

Fig. 4. Patterns (A-1) Which-Won-Where biplots (PC1+PC2) showing GEI of 30 maize hybrids under two environment for nine traits A-GY, B-PH, C- ErH, D- CL, E- CG, F- GR, G- GWt, H-DS, I-Shell. The GGE biplot polygons were created on scaling = 0, cenering = 2 and SVM = 3.

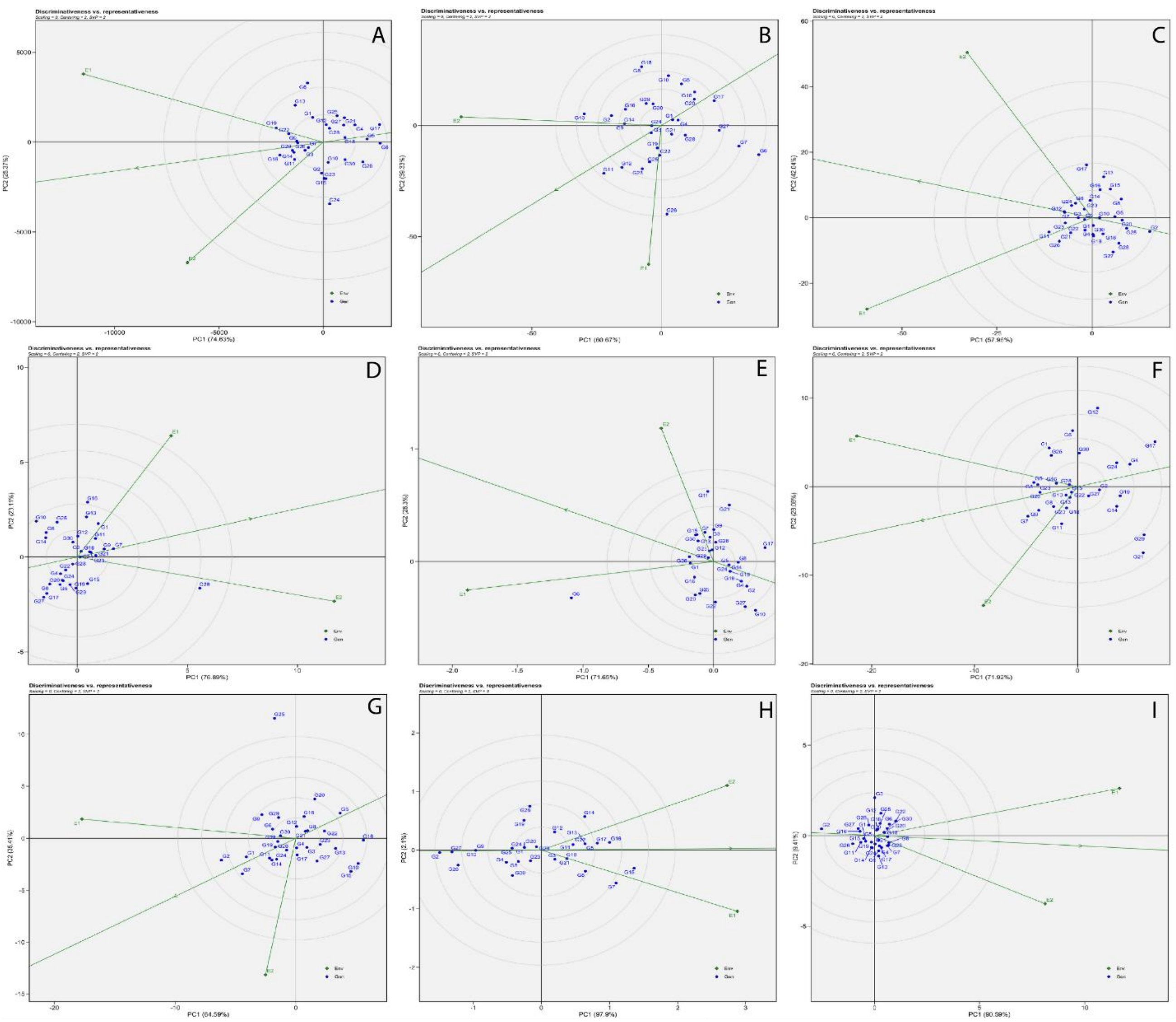

Fig. 5: Patterns (A-1) Discriminativeness vs Respresnetativeness biplots (PC1+ PC2) showing GEI of 30 maize hybrids under two environment for nine traits A-GY, B-PH, C- ErH, D- CL, E- CG, F- GR, G- GWt, H-DS, I-Shell. The GGE biplots were generated on scaling = 0, cenering = 2 and SVM = 2.

Discriminativeness vs. Representativeness: The discriminativeness vs. representativeness analysis of GGE biplots (Fig. 5) expressed the ability of each environment to differentiate genotypes and represent overall performance. The length of each vector indicated the discriminatory ability of an environment with shorter vectors indicating lower discrimination and longer vectors showing higher discrimination. In this study, the least discriminatory environments were E2 for GY, ErH, CG, GR, GWt, DS and Shell, while E1 was the least discriminatory for PH and CL. Conversely, the most discriminatory environments were E1 for GY, ErH, CG, GR, GWt, DS and Shell, whereas E2 exhibited the highest discrimination for PH and CL. The angle between each vector and the abscissa assesses how well an environment representing the overall genotype performance. MRS environment (E1) formed shortest angle for GY, CG, GR, GWt and Shell indicating its strong representativeness for these traits, while MMRI environment (E2) formed shortest angle for PH, ErH, CL and DS making it a more suitable environment for evaluating these traits.

Ranking environments: Patterns 6A, 6B, 6C, 6D, 6E, 6F, 6G, 6H and 6I (Fig. 6) illustrated the ranking biplots for comparing environments with the best environment, assessing the most suitable and least favorable environments. The optimal environment is the one closest to the best environment (concentric circles), while the least desirable is the environment farthest from it. For GY, CG, GR, GWt and Shell, E1 was nearer to the putative ideal environment than E2 (Fig. 6A, 6E, 6F, 6G, 6I). For PH and CL, E2 was the ideal environment in comparison to E1 due to its proximity to the putative ideal environment in the innermost circle (Fig. 6B, 6D). Regarding ErH, both environments were equidistant from the putative ideal environment (Fig. 6C). For DS, both environments were situated far behind all the circles, indicating they were the least favorable (Fig. 6H).

Ranking genotypes: The genotype ranking (Fig. 7) identified superior genotypes across traits. The biplots recognized superior and optimal genotypes. An exemplary genotype is consistently located within the innermost circle, positioned closest to the arrowhead representing the ideal genotype at the center of the concentric rings. For GY, G16 was ideal, with G29, G14, G11, G26, G9, G3, G7, G22 and G19 nearby (Fig. 7A). For PH, G11 was in the innermost circle, followed by G12 and G23 (Fig. 7B). For

ErH, G12 was ideal, with G7, G24, G6, G23, G3, G1, G22, G21, G11 and G26 close (Fig. 7C). No genotype reached the innermost circles for CL and CG (Fig. 7D–7E). For GR, G26 was ideal, followed by G23, G9, G5, G3, G8 and G7 (Fig. 7F). For GWt, G2 was closest to the center, followed by G7 (Fig. 7G). Most genotypes were near the center for DS (Fig. 7H). For Shelling %, all genotypes were ideal except G2, with G10 closest, followed by G20, G8, G30, G23, G7 and G6 (Fig. 7I).

Discussion

Combined analysis of variance expressed the effects of environments (Env), hybrids (Hyb) and their interaction extended from non-significant to highly significant across all traits (Table 4). The environments impact was significantly influencing the agronomic traits of hybrids (GY, PH, CL, GR) indicating variability between E1 and E2. Conversely, the lack of significance for some traits suggested insufficient variation for effective selection of breeding material. The Env × Hyb interaction's significance ($p<0.01$ & 0.05) for GY, CL, CG, GR and GWt demonstrated genotype-specific responses across environments. The study unveiled highly significant hybrids differences and significant environmental differences, driven by genetic diversity and genotype-environment interactions. Esan *et al*., (2023) found statistically significant to highly significant effects of location, genotype and interaction on six studied traits. Notably, genotype alone had significant or highly significant effects on all traits. Interestingly, the genotype × location interaction, which indicates how well a genotype performs across different environments, was only highly significant for two traits (HSW, LOS). The pronounced genotype-by-environment interaction was attributed to the diverse nature of tested multi environments and the distinct genetic backgrounds of the varieties used (Rafique *et al*., 2020). This study underscored genotype-environment interaction as a key tool for breeding superior maize hybrids (Shehzad *et al*., 2019).

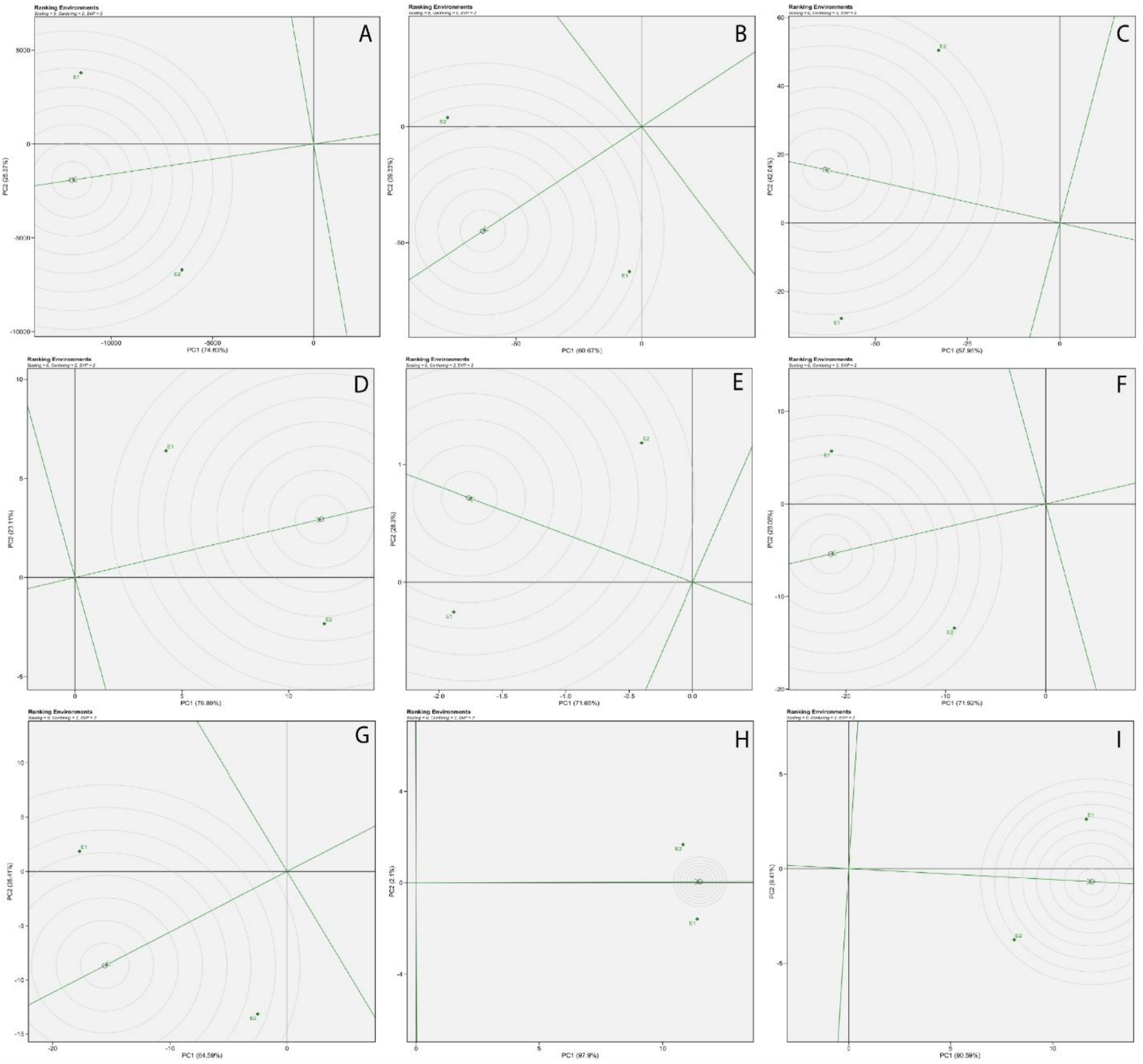

Fig. 6. Patterns (A-1) Ranking environments biplots (PC1+PC2) showing GEI of 30 maize hybrids under two environment for nine traits A-GY, B-PH, C- ErH, D- CL, E- CG, F- GR, G- GWt, H-DS, I-Shell. The GGE biplots were generated on scaling = 0, cenering = 2 and SVM = 2.

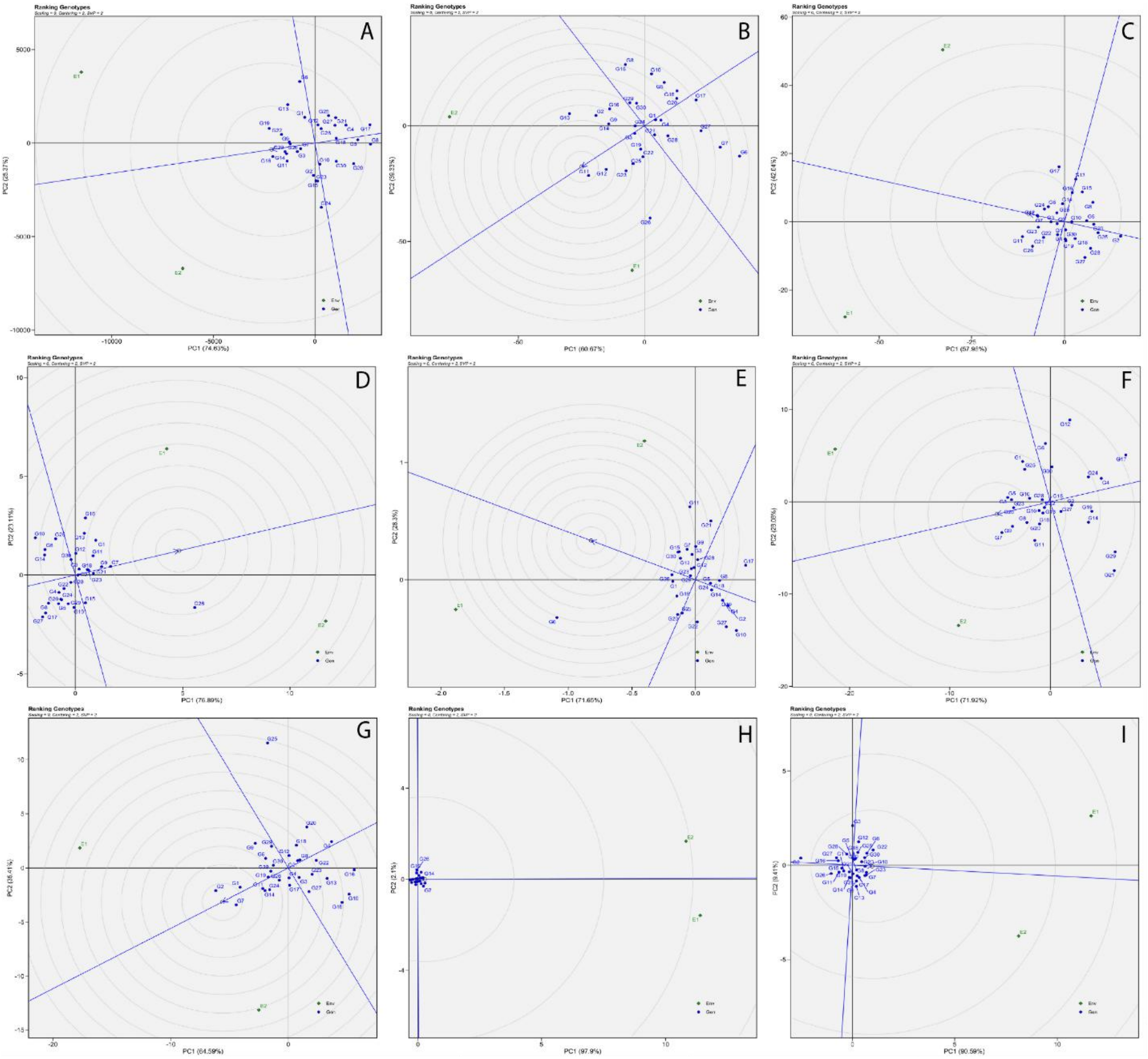

Fig. 7. Patterns (A-1) Ranking genotypes biplots (PC1+PC2) showing GEI of 30 maize hybrids under two environment for nine traits A-GY, B-PH, C- ErH, D- CL, E- CG, F- GR, G- GWt, H-DS, I-Shell. The GGE biplots were generated on scaling = 0, cenering = 2 and singular value partitioning SVM = 2.

Pearson correlation analysis was conducted separately for both environments (Fig. 1) to assess relationships among traits. At MRS (Fig. 1-E1), GY showed significant positive associations with CG, CL, PH and ErH, whereas in MMRI (Fig. 1-E2), GY correlated significantly only with PH and exhibited weaker, non-significant links with GR and GWt. These results are partly consistent with Yahaya *et al*., (2021), who reported positive correlations of GY with PH (0.77), GWt (0.79) and CL (0.78) across multiple locations.

Plant height (PH) was positively correlated with CL, GWt and ErH in E1, but in E2 it was mainly associated with GY. This shift can be attributed to environmental differences between the two sites; favorable conditions in E1 supported stronger associations with vegetative traits, while stress factors in E2 likely redirected plant resources toward reproductive development, thereby altering trait relationships. Cob length (CL) correlated strongly with GR in E1 and with both CG and GR in E2. Similarly, ErH was strongly linked with PH in E1 but with CG, Shell and DS in E2. GWt displayed positive associations with PH and CL in E1 but no meaningful correlations in E2. Overall, correlations were stronger and more consistent in E1, while in E2 associations shifted toward reproductive traits such as DS, Shell and CL. These findings align with Yousaf *et al*., (2023), who observed positive correlations of GY with ear length (0.77), ear width (0.44), kernels/ear (0.45) and starch % (0.62), but a negative correlation with PH (-0.79). Likewise, Yousaf *et al*., (2022) reported strong positive associations of GY with ear width (0.64), rows/cob (0.49), kernels/ear (0.95) and starch % (0.51), but negative links with PH (-0.81) and oil % (-0.63). Similar patterns were highlighted by Rafique *et al*., (2020) and AL-Asadi & Muhamed (2023).

Overall, the present study confirms that grain yield in maize is influenced by multiple agronomic traits, emphasizing the need for a well-planned selection strategy. Improving traits with strong positive associations, particularly CL and CG identified here, is crucial for enhancing maize productivity due to their consistent genetic relationship with yield.

The GGE biplot approach is widely recognized for analyzing genotype-by-environment interaction (GEI) and evaluating genotypic performance across diverse environments (Esan *et al*., 2023). In this study, thirty maize hybrids were tested in two environments (E1 and E2) and their performance was assessed through multiple GGE biplot techniques, including mean vs. stability, which-won-where, discriminativeness vs. representativeness and ranking of environments and genotypes. These analyses facilitated the identification of both ideal genotypes with stable yield and environments with strong discriminating power (Yue *et al*., 2019).

The results showed that genotypes G16, G19, G22, G29, G11, G14, G9, G26, G13 and G3 exhibited superior adaptability and higher grain yields across environments. The GGE biplot is an effective model for understanding GEI effects and identifying genotypes adapted to specific environments, as no genotype consistently excels in all conditions (Ruswandi *et al.*, 2021). Environmental vectors were used to predict divergence among the nine agronomic traits. The genotypes that clustered together and oriented toward specific environments exhibited higher grain yields. For example, those positioned ahead of the origin performed better for their associated traits. By effectively illustrating GEI effects, the GGE biplot approach is a valuable tool for identifying stable and well-adapted genotypes, thereby improving breeding strategies and cultivar selection (Esan *et al.*, 2023).

Genotype stability was assessed through the projection on the ordinate (Fig. 3), where longer projections reflect greater instability and inconsistency (Adham *et al.*, 2022) such as G24, while shorter projections indicate higher stability as seen in G3. In maize breeding, broadly adapted hybrids must combine superior mean performance with minimal interaction effects, thereby ensuring both productivity and stability (Boreddy *et al.*, 2020). Across PH, ErH, CL, CG, GR, GWt, DS and Shell traits, genotypes G11, G12, G3, G29, G7, G11, G16 and G8 exhibited higher stability. Stability analysis thus complements genotype ranking by identifying hybrids that consistently perform across environments (Azrai *et al.*, 2022). Hybrids located near the arrow on the abscissa achieved the highest mean grain yield in both environments, with G16 emerging as the top performer, followed by G19. In contrast, G17, positioned opposite to the arrowhead, recorded the lowest yield. These findings highlight that selection should not rely on mean performance alone, as unstable genotypes may cause yield fluctuations and economic losses. The integration of stability and adaptability with yield potential remains critical for hybrid evaluation and site targeting (Yue *et al.*, 2019). According to Ruswandi *et al.* (2021), the ideal genotype combines high yield with stability across environments. In this study, G16 proved the most consistent and productive genotype, confirming its suitability across both environments.

The "which-won-where" analysis is a key component of GEI studies, identifying suitable mega-environments for genotype adaptability (Adham *et al*., 2022). The GGE biplots (Fig. 4) revealed clear genotype–environment interactions, with polygon vertices marking the best-performing genotypes in each sector, thereby guiding breeders in selecting superior accessions (Boreddy *et al.*, 2020). When environments are grouped into distinct sectors, it indicates that different cultivars perform best in different conditions. In this study, two mega-environments were detected for all traits except DS. Genotype G19 was the best performer in E1, while G24 excelled in E2 for grain yield and PH, reflecting their strong responsiveness to specific environments. Positive interactions occurred when genotypes and environments clustered within the same sector (Özata, 2020), such as G19, G22 and G9 with E1 and G24, G15 and G23 with E2. Similarly, Esan *et al.*, (2023) identified G8, G3, G2, G11, G6 and G4 performed better in each environment and were also identified as the vertex genotypes for each respective environment.

The discriminativeness vs. representativeness identifies the most suitable environment and best performing genotype by measuring vector length and angle formed with abscissa. A longer environmental vector improves genotype discrimination, while a shorter angle with the abscissa enhances representativeness (Ozata, 2020). The current study revealed the representativeness of environments as; E1 formed shortest angle for GY, CG, GR, GWt and Shell, whereas E2 had shortest angle for PH, ErH, CL and DS (Fig. 5). (Ruswandi *et al.*, (2021) emphasized that environments with large vectors and lesser angles along with the AEC abscissa are the most valuable for genotype evaluation. In the current study, the longest vector was observed for E1 in Fig. 5A (GY), Fig. 5C (ErH), Fig. 5E (CG), Fig. 5F (GR), Fig. 5G (GWt), Fig. 5H (DS) and Fig. 5I (Shell), while E2 had the longest vector in Fig. 5B (PH) and Fig. 5D (CL). Conversely, the shortest vector was recorded for E2 in Fig. 5A, 5C, 5E, 5F, 5G, 5H and 5I and for E1 in Fig. 5B and Fig. 5D. Similarly, Adham *et al.*, (2022) reported that E9 exhibited the highest discrimination ability, while E7 was the most representative environment.

Ranking environments: Ranking environments identifies the most suitable and least favorable environments for genotype performance (Al-Naggar *et al.*, 2020). The optimal environment is defined as the one located closest to the ideal environment within the concentric circles, whereas the least desirable is farthest from it (Esan *et al.*, 2023). In the present study, E1 was most suitable environment for GY, CG, GR, GWt and Shell, (Fig. 6A, 6E, 6F, 6G, 6I) while E2 was less favorable (Fig. 6), leading to ranking as E1 > E2. Further, E2 was best for PH and CL traits (Fig. 6B, 6D) and revealed E2 > E1 environmental ranking. Regarding ErH (Fig. 6C), both environments were equidistant from the ideal, suggesting similar adaptability. Overall, the variation in genotype performance across E1 and E2 may be attributed to environmental factors such as soil type, temperature, relative humidity and rainfall, which differently influence maize hybrids. Similar findings by Esan *et al.*, (2023) showed that GGE biplots explained the relationship among various locations in GEI analysis and concluded that Bowen was the superior environment.

Ideal genotypes were identified for multiple traits of maize hybrids using genotype ranking method (Fig. 7). This approach placed most ideal genotypes closest to the centre of concentric circles, where proximity to the arrowhead indicates superior performance, particularly for yield (Esan *et al.*, 2023). Genotypes within the inner circle are deemed ideal, while those in the outer circle are less desirable. If no genotype is within inner circle, then closest ones are considered optimal (Esan *et al.*, 2023). The arrangement of concentric circles thus provides a clear visual framework for evaluating agronomic traits and their influence on genotype ranking (Li *et al.*, 2023).

In this study, Genotype G16 was positioned within the inner circle and identified most stable for GY (Fig. 7A). The ranking of top-yielding genotypes was **G16 > G29 > G14 > G11 > G26 > G9 > G3 > G7 > G22 > G19**. Plant breeders employ mean performance and stability data to pick genotypes bred for specific environments within multi-environment trials (Li *et al.*, 2023). Here, ideal hybrids for PH (Fig. 7B) are G11, G12, G23; for ErH (Fig. 7C) includes G12, G7, G24, G6, G23; for GR (Fig. 7F) are G26, G23, G9, G5, G3, G8; for GWt (Fig. 7G) are G2, G7. For CL and CG, no genotypes were found in innermost circle, suggested lack of ideal genotypes. Similarly, Adham *et al.*, (2022) evaluated 11 maize genotypes across 10 environments and reported V14, V4 and V2 as superior in grain yield and stability, consistent with the findings of this study.

In conclusion, among the tested genotypes, G16 consistently demonstrated superior grain yield across environments, followed by G19, G22, G11, G29 and G14. Several hybrids, including G19, G22, G13, G8 and G24, exhibited above-average yields but lacked yield stability. Considering multiple agronomic traits (GY, PH, ErH, CL, CG, GR, GWt, DS and Shell), hybrids such as G3, G4, G7, G14, G11, G16 and G25 were identified as stable performers across environments. MRS (E1) was identified as the most representative and favorable environment for evaluating grain yield, confirming its suitability for multi-environment testing. At MRS, hybrids G19 (13,309 kg/ha), G13 (12,538 kg/ha), G6 (12,270 kg/ha), G16 (12,258 kg/ha) and G22 (12,198 kg/ha) achieved the highest yields. In contrast, MMRI (E2) favored different genotypes, with G24 (13,508 kg/ha), G16 (13,150 kg/ha), G11 (12,755 kg/ha), G15 (12,465 kg/ha) and G14 (12,420 kg/ha) identified as top performers. Overall, this study highlighted the importance of breeding environment-specific maize hybrids to maximize yield potential and ensure stability across diverse and changing climatic conditions.

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