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Genotype × Environment Interaction and Multi-environment Evaluation of Yield Stability in Groundnut (*Arachis hypogaea* L.)

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ABSTRACT

Background: Significant genotype × environment interactions (GEI) can mask true genetic potential and reduce selection efficiency. Therefore, multi-environment trials (METs), combined with robust analytical tools such as AMMI and GGE biplot analyses, are essential for dissecting GEI effects, identifying stable high-yielding genotypes and defining suitable mega-environments for targeted cultivation.

Methods: In this study, 14 groundnut genotypes were evaluated across seven locations in Andhra Pradesh, namely Kadiri, Ananthapuramu, Tirupati, Utukuru, Darsi, Yellamanchili and Peddapuram during *Kharif*, 2024 using a randomized complete block design with three replications. AMMI, GGE biplot and multi trait stability index (MTSI) analyses were worked-out to identify stable and high-yielding genotypes across environments.

Result: AMMI analysis showed that environments contributed the highest variation for pod yield (78.58%) and kernel yield (79.73%), followed by GEI and genotype. GGE biplot analysis identified Kadiri as an ideal test environment, owing to its high discriminating ability and representativeness. The which-won-where pattern revealed Kadiri Lepakshi, TCGS 2410 and TCGS 2306 as winning genotypes across most environments. Multi-trait stability index analysis identified TCGS 2438 as a balanced genotype for yield and quality traits. Overall, TCGS 2306 and TCGS 2410 exhibited stable and superior yield performance across diverse environments, highlighting their potential for commercial cultivation following multi-year validation.

Key words: AMMI, GEI, Groundnut, MTSI, Yield.

INTRODUCTION

Groundnut (*Arachis hypogaea* L.) is a major food and oilseed crop contributing significantly to global nutritional, economic and livelihood security. Its kernels are rich in protein (25-28%), edible oil (42-56%), vitamins, antioxidants, dietary fiber and essential minerals, making groundnut a vital component of human diet (Kamalasundari *et al.* 2025). Groundnut enhances soil fertility through biological nitrogen fixation, thereby supporting sustainable agriculture (Hariharan *et al.* 2026). Contempt these benefits, groundnut productivity remains low in several regions, particularly in India and Africa, with average yields of about 1 t ha^{-1}, compared to nearly 4 t ha^{-1} in countries like USA and China (Ding *et al.,* 2024). The yield gap is primarily attributed to limited availability of quality seed, inadequate agronomic management practices and vulnerability to biotic and abiotic stresses. Furthermore, climate change-induced drought, heat stress and erratic rainfall, which adversely affect pod development and kernel filling. Therefore, improving groundnut productivity through the development and adoption of sustainable breeding strategies is critical for reducing production costs and enhancing farmer's livelihood.

Enhancing groundnut productivity across diverse agro-ecological conditions is complicated by pronounced genotype × environment interactions (GEI), which often obscure true genetic potential and reduce selection

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efficiency based solely on mean performance. In this context, multi-environment trials (METs), combined with robust analytical tools such as AMMI and GGE biplot analyses, are effective for partitioning GEI, identify stable high-yielding genotypes and delineating mega-environments (Khan *et al.,* 2021; Kona *et al.,* 2024 and Choudhary *et al.,* 2026). The AMMI stability value (ASV) further aids in identifying genotypes with broad or specific adaptation. The integration of the Multi Trait Stability Index (MTSI) with AMMI and GGE Biplot analyses offers a comprehensive framework for genotype evaluation in METs. While AMMI and GGE biplot primary emphasis on yield and stability, MTSI enables simultaneous selection for multiple agronomic traits along with stability. This integrated approach has been successfully applied in soyabean (Zuffo *et al.,* 2020) and groundnut (Ntsoli *et al.,* 2026). Therefore, the combined use of these analytical tools enhances selection efficiency and facilitates identification of superior groundnut genotypes with high yield, stability and desirable trait combinations.

MATERIALS AND METHODS

The study was conducted during *Kharif*, 2024, at seven Agricultural Research Stations affiliated with Acharya N.G Ranga Agricultural University (ANGRAU) Andhra Pradesh *Viz*., Kadiri, Ananthapuramu, Tirupati, Utukuru, Darsi, Yellamanchili and Peddapuram. These locations were selected to represent diverse agro-ecological zones of major groundnut-growing regions. Variations in rainfall, soil types and temperature across locations provided diverse environmental conditions for genotype testing. A total of 14 groundnut genotypes were evaluated using a randomized complete block design with three replications. Each plot comprised of seven rows of 5 m length with a spacing of 30 cm × 10 cm. Standard agronomic and crop management practices were adopted throughout the crop growing period to ensure uniform crop establishment and optimum plant growth. Observations on days to 50% flowering, days to maturity, shelling percentage, pod yield, test weight, sound mature kernel and kernel yield, were recorded following standard groundnut descriptors and evaluation procedures.

Analysis of variance (ANOVA) using the AMMI mode land GGE biplot analysis (Soni *et al*., 2026) was carried out for pod and kernel yield, to investigate the impacts of environment, genotype and GEI. The AMMI stability value (ASV), genotype selection index (GSI) and yield stability index (YSI) were calculated to rank and select the groundnut genotypes based on their yield and stability over the environments (Reddy *et al.,* 2025). The multi-trait stability index (MTSI) is also worked out in R software (version 4.2.0) using the package *metan*.

RESULTS AND DISCUSSION

AMMI analysis of variance revealed highly significant effects of environment, genotype and genotype × environment interaction (GEI) on pod yield and kernel yield (Table 1).

Table 1: AMMI analysis of multi-environment yield performance of fourteen groundnut genotypes.

Source	Df	Pod yield				Kernel yield			
		Sum Sq.	Mean Sq.	Per cent contribution	Per cent contribution	Sum Sq.	Mean Sq.	Per cent contribution	Per cent contribution
ENV	6	143687602.3	23947933.70**	78.58		69597952.6	11599658.75**	79.73	
REP(ENV)	14	1073676.476	76691.17			571839.397	40845.671		
GEN	13	14048147.12	1080626.70**	7.68		5899514.91	453808.83**	6.75	
GEN: ENV	78	25108795.74	321907.63**	13.73		11789475.1	151147.11**	13.50	
PC1	18	10367168.63	575953.8127		41.3	5460725.51	303373.64		46.3
PC2	16	6497551.07	406096.9419		25.9	2496489.21	156030.58		21.2
PC3	14	5137702.175	366978.7268			2384961.05	170354.36		20.2

The environment accounted for the largest proportion of the total variation, contributing 78.58% for pod yield and 79.73% for kernel yield. In comparison, genotype effects explained only 7.68% and 6.75% of the variation for pod yield and kernel yield, respectively, while GEI contributed 13.73% and 13.50%. Similarly, Mahamane *et al.* (2026) reported the environment accounted up to 84.7% of the total yield variation. These results indicate that environmental and GEI effects had a much greater influence on yield performance than genotype alone, highlighting the strong sensitivity of groundnut productivity to agro-ecological variability. Consequently, genotype performance varied considerably across environments. Similar observations have been reported in earlier studies, highlighting the critical role of GEI in yield expression and adaptability (Agrawal *et al.,* 2025; Sharma *et al.,* 2025 and Choudhary *et al.,* 2026). Hence, multivariate analytical approaches such as AMMI and GGE biplot analysis are essential for partitioning interaction effects, understanding genotypes stability and identifying high-yielding, widely adaptable genotypes across diverse environments (Shilpa *et al.,* 2025).

Genotype performance and AMMI stability analysis

The mean performance, IPCA scores and stability parameters of all genotypes are presented in Table 2. Genotype stability for pod yield and kernel yield was assessed using the Eberhart and Russell model, which evaluates stability based on mean performance, regression coefficient (bi) and deviation from regression (S^2di) (Agrawal *et al.* 2025). For both pod and kernel yield, TCGS 2410 (2672.42, 1754.29), Kadiri Lepakshi (2587.52, 1741.27), TCGS 2306 (2399.19, 1588.38), TCGS 2409 (2306.81, 1547.10) and Visishta (2249.09, 1512.55) recorded comparatively higher mean performance. Among them, Visishta (bi = 1.14, 1.16), TCGS 2410 (bi = 1.34, 1.27) and Kadiri Lepakshi (bi = 1.55, 1.52) showed regression coefficients greater than unity coupled with non-significant deviations from regression, indicating responsiveness to favourable environments and predictable performance. In contrast, TCGS 2409 (bi=0.97, 0.91) and TCGS 2306 (bi=1.10, 1.08) showed significant deviations from regression, indicating instability despite relatively high mean yield.

The AMMI Stability Value (ASV) identified genotypes with stable performance across environments, where lower ASV values indicate reduced GEI effects and greater stability (Reddy *et al.* 2025). For pod yield, TCGS 2306 (8.4), TCGS 2020 (9.0), TCGS 2347 (13.3), Kadiri Lepakshi (13.3), Kadiri 6 (14.4) and Visishta (15.8) exhibited relatively low ASV values. Similarly, for kernel yield, TCGS 2347 (3.6), TCGS 2020 (5.5), TCGS 2306 (13.0), Kadiri Lepakshi (14.2), K 1774 (14.6) and TCGS 2410 (14.6) recorded lower ASV values, suggesting consistent performance across environments. Interestingly, TCGS 2306 and Kadiri Lepakshi recorded pod and kernel yields above the overall mean, highlighting their superior and stable performance.

Table 2: Comparative evaluation of yield and stability indices of groundnut genotypes across seven environments.

Genotypes	Yield (kg/ha)		R yi		IPCA 1		IPCA 2		ASV		ASVR		GSI		YSI		bi		s^2di	
	PY	KY	PY	KY	PY	KY	PY	KY	PY	KY	PY	KY	PY	KY	PY	KY	PY	KY	PY	KY
TCGS 2347	2051.04	1385.66	10	9	-13.0	-13.5	-9.3	-6.5	13.3	3.6	3	1	23.3	12.6	13	10	0.93	0.92	85414.3**	54955.4**
TCGS 2435	2054.47	1367.18	9	10	5.4	5.3	-10.0	-8.0	27.3	34.0	13	14	36.3	44.0	22	24	0.96	0.92	56620.3**	19218.6
TCGS 2306	2399.19	1588.38	3	3	15.1	14.8	10.7	2.0	8.4	13.0	1	3	11.4	16.0	4	6	1.10	1.08	123862.1**	60393.7**
TCGS 2438	2155.19	1399.24	8	8	-13.5	-14.4	10.6	6.2	33.1	24.9	14	9	41.1	32.9	22	17	0.86	0.87	94935.1**	52287.0**
TCGS 2409	2306.81	1547.10	4	4	-0.7	-2.3	-18.1	13.6	26.4	30.3	11	11	30.4	34.3	15	15	0.97	0.91	98700.3**	30711.1**
TCGS 2020	2004.95	1360.02	12	11	-4.7	-0.6	-4.7	-5.3	9.0	5.5	2	2	20.9	16.5	14	13	0.75	0.78	-924.6	2927.1
TCGS 2019	2165.76	1461.47	6	6	-12.2	-11.8	17.8	15.6	26.5	32.5	12	13	32.5	38.5	18	19	0.94	0.99	181593.1**	86526.1**
K 2349	2042.61	1350.52	11	12	-16.2	-15.4	-8.5	-3.4	22.8	30.3	8	10	33.8	42.3	19	22	0.89	0.9	113191.0**	56722.5**
K 1774	1931.00	1275.17	14	14	-7.9	-0.3	-3.7	-3.5	18.2	14.6	7	5	32.2	28.6	21	19	0.70	0.74	18127.0	7558.8
TCGS 2410	2672.42	1754.29	1	1	14.5	6.5	-4.3	-3.4	23.5	14.6	9	6	24.5	15.6	10	7	1.34	1.27	30799.5	6949.0
Visishta	2249.09	1512.55	5	5	8.6	6.8	4.1	3.1	15.8	23.8	6	8	20.8	28.8	11	13	1.14	1.16	18265.1	7291.7
Kadiri Lepakshi	2587.52	1741.27	2	2	20.5	11.2	-5.2	-4.1	13.3	14.2	4	4	15.3	16.2	6	6	1.55	1.52	23378.0	8659.0
TCGS 2432	2156.71	1448.90	7	7	5.7	9.0	12.8	13.3	24.1	32.1	10	12	31.1	39.1	17	19	1.00	1.02	92524.9**	50399.3**
Kadiri 6	1957.47	1338.11	13	13	-1.5	4.8	8.0	7.6	14.4	15.3	5	7	27.4	28.3	18	20	0.86	0.91	19972.5	21509.5**
Overall mean	2195.30	1466.40																		

The genotype stability index (GSI), which integrates yield and stability, identified TCGS 2306 (11.4) and Kadiri Lepakshi (15.3) as desirable genotypes for pod yield, while TCGS 2347 (12.6), TCGS 2410 (15.6), TCGS 2306 (16.0) and Kadiri Lepakshi (16.2) showed lower GSI values for kernel yield. Similarly, the Yield Stability Index (YSI) indicated superior stability and yield performance for TCGS 2306 (4), Kadiri Lepakshi (6), TCGS 2410 (10) and Visishta (11) for pod yield and for Kadiri Lepakshi (6), TCGS 2306 (6), TCGS 2410 (7) and TCGS 2347 (10) for kernel yield. Overall, the consistent performance of TCGS 2306 and Kadiri Lepakshi across GSI and YSI analyses highlights their potential as stable and high-yielding genotypes suitable for diverse agro-ecological conditions.

AMMI biplot analysis

The AMMI2 biplot, constructed using the first two interaction principal component (PC1 and PC2), provides an effective graphical depiction for interpreting GEI and identifying genotypes with wide or specific adaptability (Khan *et al.,* 2021). For both pod yield and kernel yield (Fig 1), the first two PCs explained a substantial proportion of the GEI variance. In pod yield, PC1 (41.3%) and PC2 (25.9%) together accounted for 67.2% of the total GEI, similarly for kernel yield, PC1 (46.3%) and PC2 (21.2%) jointly explained 67.5% of the interaction variance. These results indicates that the first two components sufficiently captured the major interaction patterns, enabling reliable interpretation of the AMMI model. Similar findings were reported by Khan *et al.* (2021) and Ntsoli *et al.* (2026). The biplot further revealed that environments located near the origin exhibited minimal interaction effects and greater stability, whereas those farther from the origin showed stronger interaction effects and greater discriminating ability (Esan *et al.,* 2023). Accordingly, Utukuru, Ananthapuramu and Yellamanchili had shorter vectors, indicating lower interaction effects for both traits. Conversely, Kadiri, Peddapuram and Darsi displayed longer vectors, reflecting greater discriminatory power and suitability for identifying specifically adapted genotypes. For pod yield, genotypes Kadiri 6, Visishta, K 1774 and TCGS 2020 were positioned near the origin, indicating wider adaptability and lower interaction effects. Conversely, TCGS 2019, TCGS 2438, TCGS 2349, TCGS 2409, Kadiri Lepakshi and TCGS 2306 were located farther from the origin, suggesting specific adaptation to particular environments. A similar trend was observed for kernel yield, where TCGS 2410, K 1774 and TCGS 2020 showed relatively stable performance across environments, while TCGS 2019, TCGS 2438, TCGS 2306 and TCGS 2409 exhibited stronger interaction effects and specific adaptation. Furthermore, Kadiri Lepakshi and TCGS 2410 were closely associated with the Kadiri environment, suggesting better performance under those conditions, whereas Kadiri 6 and TCGS 2432 appeared better adapted to the Peddapuram environment.

GGE biplot

The AMMI model, through biplot analysis, effectively identifies GEI across diverse environmental conditions. However, the GGE biplot provides a more comprehensive assessment by simultaneously considering genotype main effects and GEI effects, enables clearer and more intuitive interpretation of genotype behaviour in METs, particularly for evaluating newly developed varieties and hybrids (Khan *et al.,* 2021).

Unlike the AMMI2 model, which applies principal component analysis (PCA) solely to the GEI component, the GGE biplot incorporates both genotype main effects and GEI effects. Consequently, it is considered more effective for identifying specifically adapted genotypes as well as those combining high yield and stability across environments (Khan *et al.*, 2021 and Ntsoli *et al.* 2026). In the GGE approach, PC1 represents the mean performance of genotypes, while PC2 reflects stability and the magnitude of interaction effects. In this study, PC1 accounted 56.54% of variation for pod yield and 52.37%

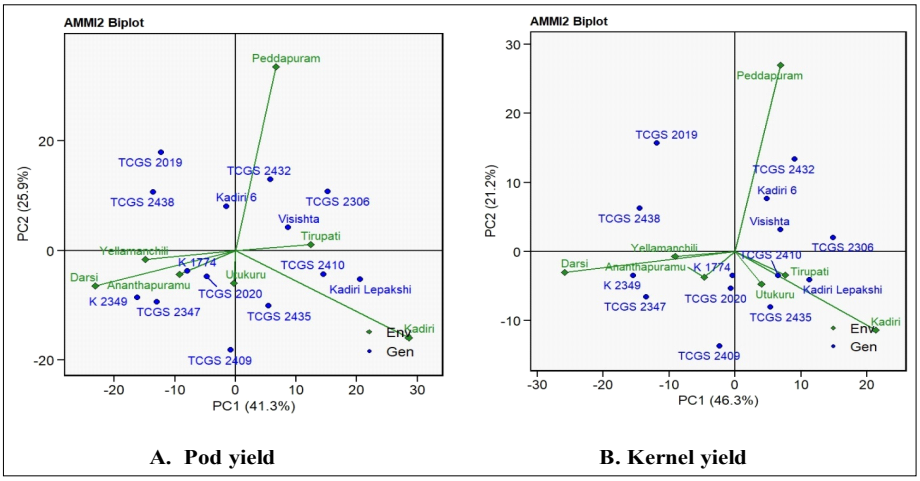


Fig 1: AMMI2 biplot for pod yield (PY) and kernel yield (KY) across seven test environments.

for kernel yield, whereas PC2 explained 17.11% and 23.91% of variation, respectively. Together, these components captured a substantial proportion of the total variation, enabling effective interpretation of genotype performance across environments.

Mean vs stability

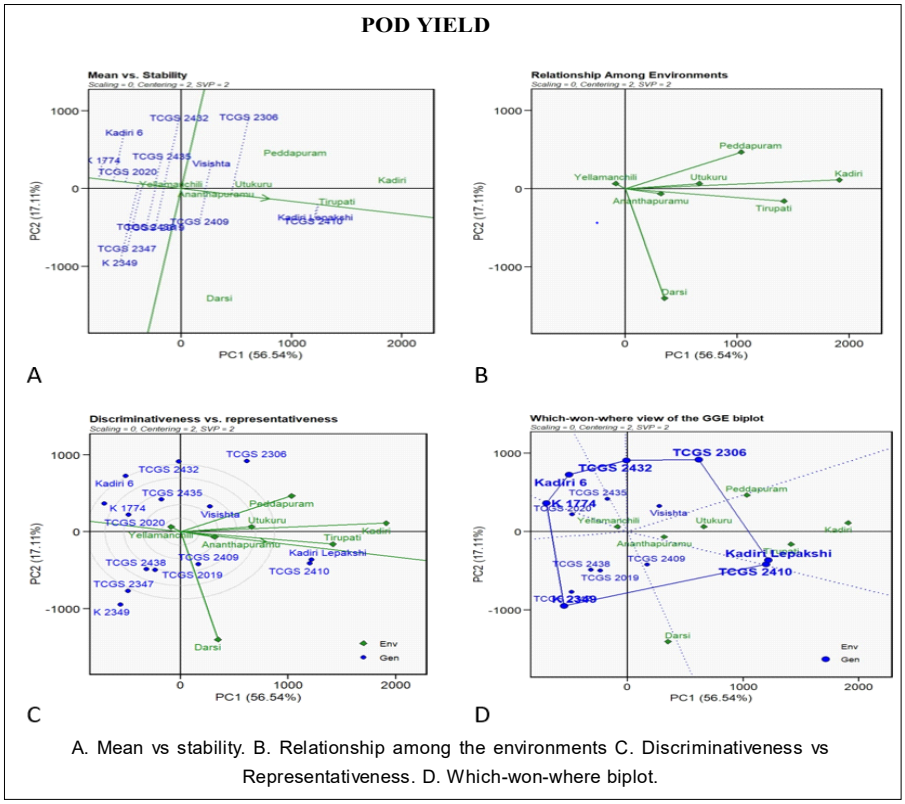
The mean versus stability GGE biplot, constructed using the first two principal components, was used to evaluate the average performance and stability of 14 groundnut genotypes for pod yield (Fig 2A) and kernel yield (Fig 3A). For pod yield, PC1 and PC2 together explained 73.65% of the total G + GE variation. In this approach, the Average Environment Coordination (AEC) abscissa represents the direction of increasing mean performance, with genotypes located toward the positive end exhibiting higher mean yield. Accordingly, Kadiri Lepakshi and TCGS 2410 were positioned on the positive side of the AEC abscissa, reflecting superior performance for both pod yield and kernel yield across environments. Genotype stability is determined by the projection onto the AEC ordinate, where shorter projections indicate greater stability and longer projections reflect higher instability (Esan *et al.,* 2023). In this context, Visishta, TCGS 2409 and TCGS 2020 exhibited better stability coupled with moderate to good kernel and pod yield. Furthermore, Kadiri Lepakshi and TCGS 2410 showed high mean performance with minimal deviation from the AEC axis, highlighting their desirable stability and wide adaptability. In contrast, TCGS 2347, TCGS 2349, TCGS 2306 and TCGS 2432 exhibited larger deviations from the AEC ordinate, suggesting lower stability and greater sensitivity to environmental variation, thereby indicating specific rather than broad adaptation.

Relationships among the environments

The relationship among test environments for the evaluated traits are illustrated in Fig 2B for pod yield and Fig 3B for kernel yield. For both pod yield and kernel yield Kadiri, Peddapuram, Utukuru, Ananthapuramu and Tirupati were positioned along the positive side of PC1, indicating similar environmental responses and positive correlations among these locations. Among them, Kadiri and Tirupathi were located farther from the origin, suggesting stronger discriminating ability and greater contribution to GEI. In contrast, Darsi was also positioned far from the origin but in a different direction, indicating pronounced interaction effects and a distinct environmental response compared to the other locations. Conversely, Ananthapuramu and Yellamanchili were situated close to the origin, reflecting lower discriminating ability and weaker interaction effects.

Discriminativeness and representativeness

The identification of an ideal test environment involves assessing both representativeness and discriminating ability, which can be effectively achieved using the GGE biplot approach (Khan *et al.,* 2021). In the present study,



A. Mean vs stability. B. Relationship among the environments C. Discriminativeness vs Representativeness. D. Which-won-where biplot.

Fig 2: GGE biplot for pod yield in groundnut.

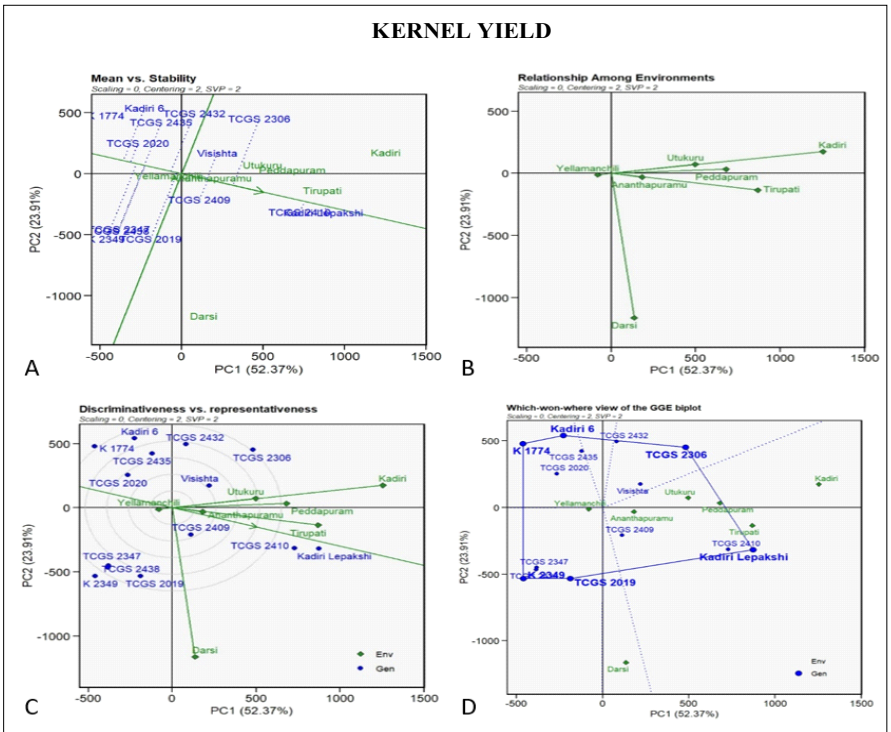
the environment vector view of the GGE biplot for pod yield (Fig 2C) and for kernel yield (Fig 3C) illustrates the Average Environment Axis (AEA), which passes through the biplot origin and the mean position of all environments. This visualization enables interpretation of relationships among test environments in terms of correlation, representativeness and discriminate ability.

The angle between the vectors of any two environments indicates their degree of correlation. Tirupati and Kadiri were oriented in a similar direction with relatively longer vectors, indicating strong positive association and high discriminating ability for genotypic performance. Peddapuram also exhibited a comparatively long vector, suggesting good discriminatory capacity. In contrast, Utukuru, Yellamanchili and Ananthapuramu were positioned closer to the origin, showed weaker GEI effects and reduced discriminating capacity.

Environments forming smaller angles with the AEA are considered more representative of the target environments. An ideal test environment should therefore combine high discriminating ability with strong representativeness for effective selection of widely adapted genotypes. In this study, Kadiri and Darsi showed high discriminating ability, with Darsi exhibiting the longest vector. However, Kadiri, Tirupati, Peddapuram and Utukuru formed smaller angles with the AEA, indicating better representativeness across testing conditions. In contrast, Darsi showed a larger angle with the AEA, suggesting lower representativeness despite its strong discriminating capacity. Overall, Kadiri emerged as the most ideal test environment, combining high discriminating ability with strong representativeness for effective evaluation and selection of groundnut genotypes in METs.

Which-won-where

The "which-won-where" view of the GGE biplot is a powerful graphical tool for visualizing crossover GEI, identifying mega-environment differentiation and determining genotype-specific adaptation for pod yield (Fig 2D) and kernel yield (Fig 3D). In the polygon view, genotypes farthest from the origin form the convex hull, while perpendicular rays divide the biplot into sectors representing potential mega-environments (Kona *et al.* 2024). The vertex genotypes of each sector are considered the highest-performing genotypes within the respective environments. For pod yield, the polygon vertices included TCGS 2306, TCGS 2432, Kadiri 6, K 1774, K 2349, TCGS 2410 and Kadiri Lepakshi, representing the best performers in their respective environments. The biplot formed six sectors, of which two contained test environments, indicating two major mega-environments. The first mega-environment comprised Kadiri, Tirupati, Utukuru and Peddapuram, where Kadiri Lepakshi and TCGS 2410 were identified as the winning genotypes. The second mega-environment included Darsi and Yellamanchili, where TCGS 2019, TCGS



A. Mean vs stability. B. Relationship among the environments C. Discriminativeness vs Representativeness. D. Which-won-where biplot.

Fig 3: GGE biplot for kernel yield in groundnut.

Table 3: Selection differential for mean performance with stability.

Trait	Factor	Xo	Xs	SD (%)
Pod yield	FA 1	47.38	60.61	27.91
Kernel yield	FA 1	47.40	65.62	38.43
Test weight	FA 2	42.62	44.39	4.17
Sound mature kernels	FA 2	42.72	71.96	68.45
Days to 50% flowering	FA 3	54.91	51.31	-6.55
Days to maturity	FA 3	59.91	65.01	8.51
Shelling percentage	FA 4	56.96	69.72	22.39

Note: X_0= Population mean; X_s= Selected population mean; SD= Selection differential.

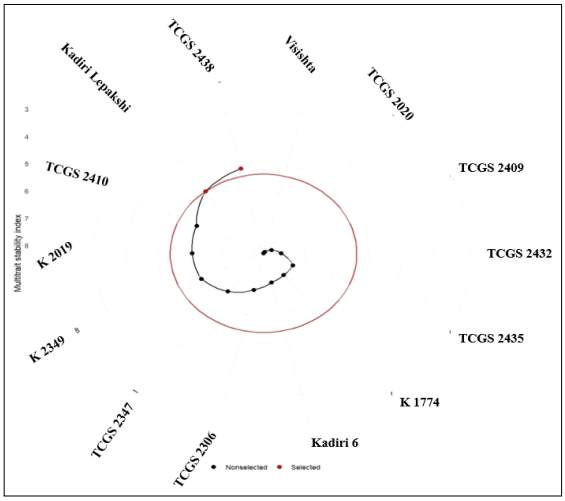


Fig 4: Genotype ranking and selected genotypes for the multi-trait stability index (MTSI) of 14 genotypes based on seven traits.

2349, K 1774 and Kadiri 6 showed superior performance. Genotypes positioned near the origin exhibited greater stability but lower responsiveness to specific environments. While for kernel yield, the winning genotypes were TCGS 2306, Kadiri 6, K 1774, K 2349, TCGS 2019 and Kadiri Lepakshi and the biplot was divided into 4 sectors. Peddapuram, Utukuru, Kadiri, Tirupati and Ananthapuramu constituted the first mega-environment where Kadiri Lepakshi showed superior performance, while Darsi and Yellamanchili formed the second mega-environment, where TCGS 2019, TCGS 2349, K 1774 and Kadiri 6 performance best. Similar results were reported by Rao *et al.* (2023); Soni *et al.* (2026) and Mahamane *et al.* (2026), highlighting the effectiveness of the GGE biplot analysis in identifying mega-environments and specifically adapted high-performing genotypes.

Multi trait stability index

The multi-trait stability index (MTSI) analysis identified superior genotypes among the 14 evaluated groundnut entries, as presented in Fig 4. The selected genotypes exhibited higher mean performance (Xs) compared with the overall population mean (Xo), along with predominantly positive selection differentials for most traits, indicating considerable scope for genetic improvement through MTSI-based selection. The negative selection differential for days to 50% flowering reflects a desirable shift toward early-maturing genotypes. Factor analysis showed that pod yield and kernel yield (Factor 1) were the primary contributors to overall productivity, while test weight and sound mature kernels (Factor 2) were associated with kernel quality attributes (Table 3). Additionally, days to 50% flowering and maturity (Factor 3) captured variation related to phenological adaptation. Based on the lowest MTSI scores, TCGS 2438 and Kadiri Lepakshi were identified as superior genotypes, combining high yield potential with stable performance across environments, thereby demonstrating their suitability for broad adaptation and multi-trait improvement (Zuffo *et al.,* 2020 and Ntsoli *et al.,* 2026).

CONCLUSION

The present study emphasizes the importance of stability-oriented selection in groundnut breeding due to significant genetic variability and GEI for all evaluated traits. The marked environmental influence on yield performance underscores the necessity of multi-environment testing for reliable genotype assessment. Among the test locations, Kadiri emerged as an ideal environment because of its high discriminating ability and representativeness. Genotypes TCGS 2306 and TCGS 2410 exhibited high yield and stability across environments, suggesting their suitability for wider adaption and commercial cultivation. Additionally, the multi-trait stability index identified TCGS 2438 as an ideal genotype with superior sound mature kernels and optimal performance for multiple traits, making it a valuable candidate for simultaneous enhancement of yield and quality attributes. Overall, the stable performance of TCGS 2410 and TCGS 2306 across diverse environments suggests their potential for commercial release or nomination to All India Coordinated Trials for future groundnut improvement programs.

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Conflict of interest

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