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Adaptability Studies in Advanced Breeding Lines of Groundnut (*Arachis hypogea* L.)

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ABSTRACT: Adaptability in different environments needs to be identified properly in order to discriminate between varieties in the targeted agro-ecologies. Furthermore, the presence of drought and biotic stresses continues to result in a yield penalty, which remains a major impediment to groundnut production. Hence, an experiment was conducted to identify specifically adaptable or widely adaptable TMV-2 type groundnut advanced breeding lines across the environments by Additive Main Effects and Multiplicative Interactions (AMMI), AMMI stability value (ASV), and Genotype plus GEI (GGE) bi-plot analysis. Eight advanced breeding lines derived from three crosses *viz.*, TMV-2 × ICGV-91114, TMV-2 × TG-69 and TMV-2 × ICGV-00350 along with two checks *viz.*, TMV-2 and K-6 following RCBD with three replications were sown at three locations. Based on GGE biplot for ranking of genotypes during *Kharif* 2021, ABLs *viz.*, T82 and T72 were found to be adaptable. "Which won where pattern" of GGE biplot showed that during *Kharif* 2021, ABLs T72 and T82 were winning genotype in GKVK, ABLs T77, T65 and T61 were winning genotypes in Mandya and ABLT89 was found to be winning genotype in Balajigapade for kernel yield plant^{-1}. Based on ASV and SI, for kernel yield plant^{-1}, during *Kharif* 2021 ABLs T65, T77, T81 and T82 were found to be adaptable whereas during *Rabi* 2021 ABLs T77, T81, T82 and T65 were found to be stable and recommended for mega environment production. ABLs T65, T77, T81 and T82were found to be stable across the seasons. The stable lines identified can be used as a parents in breeding programmes.

Keywords: Groundnut stability, AMMI, ASV, GGE bi-plot, GEI, Stability Analysis, "Which won where pattern".

INTRODUCTION

The peanut (*Arachis hypogaea* L.) and its wild relatives are self-pollinated, allotetraploid plants native to South America (Krapovickas and Rigoni 1960). Cultivated groundnut originated from hybridization event between *Arachis duranensis* (A genome) and *Arachis ipaensis* (B genome), followed by chromosome duplication (Halward *et al.,* 1991). Besides its scientific name, the peanut is known by various other names like Poor man's almond and King of oilseeds. It belongs to the family fabaceae family (Anamika *et al.,* 2021). The botanical name *Arachis hypogaea* L. refers to its development of pods below the ground. Groundnuts, rich in potassium, calcium, and phosphorus, offer a wide range of health benefits. Moreover, groundnut can be employed in crop rotation to enhance soil fertility through nitrogen fixation in root nodules, as it is a legume (Jasani, 2009).

According to Singh and Singh (1992), groundnut is commonly produced in semiarid countries with moist weather including Africa, America and Asia. Groundnut is cultivated worldwide on 27.9 million hectares, yielding 47 million tonnes with a productivity of 1685 kg/ha. India contributes 22% to global production, cultivating it on 6.014 million hectares, yielding 10.02 million tonnes (1703 kg/ha). Major groundnut-producing states in India include Gujarat, Andhra Pradesh, Rajasthan, Tamil Nadu, Karnataka, and Maharashtra, with a combined annual production of 100.96 lakh tonnes at a productivity rate of 2065 kg/ha. Among these, Karnataka ranks fourth with an area of 3,82,940 hectares (Anon., 2020).

Groundnut productivity in Karnataka is currently at 0.72 tonnes per hectare, which is less than half of the national average of 999 kg per ha (Anon., 2021). Despite high-yielding varieties available, TMV-2, developed 82 years ago, is still preferred. However, the government has denotified TMV-2, leading to its unavailability in official seed supply. Closing the productivity gap requires developing a new variety with higher yield potential while maintaining TMV-2's desirable pod and kernel characteristics. Slow adoption of improved varieties and their inconsistent performance in different conditions contribute to the low productivity of groundnuts nationwide.

Groundnut is affected by genotype by environment interactions (GEI) (Patil *et al.,* 2018). The complex interplay of various traits can have positive or negative connections with yield and other characteristics. To ensure stable crop production, genotypes need to adapt to environmental changes temporally and

geographically. Genotype-environment interactions (GEI) indicate that genotypes performing well in one environment may not perform similarly in another. Stability is influenced by GEI, with low GEI indicating higher stability. When developing high-yielding cultivars, it is crucial to consider both yield and stability, as high yield may be limited to specific climates. Studies on G × E interaction help assess genotype performance across different contexts. Techniques like AMMI analysis, joint regression analysis, linear regression analysis, and ANOVA provide insights into stability and the practical impact on crop varieties and genotypes.

Regression analysis helps to estimate phenotypic stability, aiding in the assessment of variety adaptability. Stability analysis identifies genotypes that can perform consistently across diverse environments (Comstock and Moll 1963). The interaction between genotype and environment is crucial for breeders to improve breeding programs and mitigate negative agro-climatic effects.

The dry pod yield of groundnut is strongly influenced by both genetic and environmental factors. Breeders have focused on enhancing plant characteristics to maximize genetic potential. However, the impact of environmental conditions on quantitative traits in groundnut genotypes has received limited attention. Stable genotypes adjust their phenotypic responses to maintain consistency despite environmental fluctuations (Patil *et al.,* 2014). The present study was conducted to evaluate TMV-2 type groundnut advanced breeding lines across different locations and to identify adaptable ABLs.

MATERIAL AND METHODS

The present investigation entitled "Adaptability of TMV-2 type Groundnut advanced breeding lines" was carried out with 10 groundnut genotypes. The description of the experimental material, its evaluation protocol and data collection on different growth as well as yield traits and also the statistical tools and analytical procedures used for the analysis of the obtained data are presented in this chapter under the following heads.

Experimental site

The present investigation was carried out in *Kharif* (2021) at three locations. They are

— National Seed Project (NSP), University of Agricultural Sciences, GKVK, Bengaluru, located at an altitude of 924m above MSL, 13008″ N latitude and 77034″ E longitude.

— Agriculture Research Station, Balajigapade located at an altitude of 915m aboveMSL,13043″N latitude and 77079"E longitude.

— Organic Farming Research Station, Mandya located at an altitude of 678m aboveMSL,12037″N latitude and 76066"E longitude.

Experimental materials

The material for the present investigation consisted of 8 genotypes derived from three connected crosses *viz.*, TMV-2 × ICGV-91114, TMV-2 × TG-69 and TMV-2 × ICGV-00350 along with two checks. The study was conducted during *Kharif* 2021. The details of genotypes and checks used in the present study are presented in Table 1.

Table 1: List of genotypes and checks.

Sr. No.	Genotypes	Pedigree
1.	T77	TMV-2×ICGV-91114
2.	T89	TMV-2×ICGV-91114
3.	T81	TMV-2×ICGV-91114
4.	T82	TMV-2×TG-69
5.	T79	TMV-2×TG-69
6.	T65	TMV-2×ICGV-00350
7.	T72	TMV-2×ICGV-00350
8.	T61	TMV-2×ICGV-00350

Sr. No.	Checks
1.	TMV-2
2.	Kadiri6

Table 2: Salient features of groundnut varieties used as parents in the crosses and checks.

Varieties	Year of release	Source	Parentage	Special features
TMV-2	1940	TNAU, Coimbatore	Selection from Gudiyatham bunch	Old variety, wider adaptability, desirable pod and kernel shape & size, kernels small with salmon colour testa, susceptible to drought and foliar diseases.
ICGV-91114	2007	ICRISAT, Hyderabad	ICGV-86055 ×ICGV-86353 Bulk pedigree method	Early maturing, moderate yielding, bold seeded, tolerant to drought & LLS, good seed size, better digestibility and palatability of haulms
ICGV-00350	2012	ICRISAT, Hyderabad	ICGV-87290× ICGV-87846 Bulk pedigree method	High yield and high oil content, resistant to LLS, rust and tolerant to drought and stem rot.
TG-69	2011	BARC, Trombay, Mumbai	Mutant variety	High harvesting index, shelling *per cent* and SMK *per cent.*
Kadiri 6	2003	ARS, Kadiri, Anantapur	JL-24 × AH-316	Early maturing and highyielding.

Experimental methods. The experimental material was evaluated in randomized block design with 3 replications under *Kharif* at three location. The sowing was carried out at the spacing of 30 cm and 10 cm between the rows and plants respectively. The method of sowing followed was dibbling. One plant per hill was maintained by thinning 15 days after sowing. All other cultural practices and plant protection measures were undertaken to maintain healthy crop. Intercultural operations like weeding were taken up to 45 DAS. Earthing-up operation was taken up after gypsum application at 30 DAS. Necessary plant protection measures were adopted except for the spray of fungicides during the crop growth period in all environments.

Data collection. The data on following yield and yield contributing traits were recorded on 5 randomly selected plants per replication per entry and mean was computed *viz.,* plant height (cm), primary branches plant^{-1}, days to 50% flowering, pods plant^{-1}, pod yield plant^{-1}(g), kernel yield plant^{-1} (g), shelling percentage, sound mature kernel (%) and 100 seed weight (g).

Statistical analysis. All statistical analyses were performed in R statistical software version 4.1.1. The replication-wise quantitative trait means of ABLs and their parents were used for all statistical analysis. Analysis of variance (ANOVA) (Panse and Sukhatme 1984) was performed to detect significant differences, if any, among the ABLs. Combined ANOVA was carried out to detect variation among the ABLs and to test the presence of GEI (Sundara Raj *et al*., 1972). Then, AMMI and GGE biplot methods were used to analyze multivariate stability and GEI. The AMMI and GGE biplots were computed using multi environment trial analysis (Olivoto and Lúcio 2020). Their methods are modeled on the AMMI and GGE concepts of Yan and Kang (2003); Yan and Manjit (2003); Yan *et al.* (2007). The GGE biplots and AMMI methods based on mega-environment assessment were used to plot the graphs of the following models: AMMI 1 and AMMI 2, which-won-where pattern of GGE, ranking of genotypes, mean performance vs. stability, discriminativeness and representativeness, ranking environments, and relationship among test environments. They were used to visualize the presence of G ×E interaction.

Detection and characterization of genotype × season interaction. To detect (ABLs + parents) × season interaction **(**GSI) effects, data recorded from three seasons was subjected to Additive main effects and multiplicative interaction (AMMI) model (Gauch and Zobel 1988). The additive main effects of ABLs + parents and seasons were fitted by univariate ANOVA (Table 5) followed by fitting (ABLs + parents) × season interaction by interaction principal component (IPC) analysis based on AMMI model (Gauch and Zobel,1988). The following model was used to estimate main effects of ABLs and seasons and (ABLs + parents) × season interaction effects.

$$Yij = \mu + gi + ej + \sum_{k=1}^{n} \lambda k \alpha ik \gamma jk + \varepsilon ij$$

Where, Yij is the quantitative trait mean of ith ABL in the jth season, μ is the experimental quantitative trait mean, gi and ej are the ith ABLs and jth seasons mean deviation from experimental quantitative trait mean values, respectively. λk is the square root of eigen value of the kth IPC axis, αik and γjk are the interaction principal components (IPC) scores for kth IPC of the ith ABL and jth season, respectively and εij is the residual. All the analyses were implemented using Genstat software v.18.

GGE bi-plot criteria to interpret ABL × season interaction. Genotype + Genotype × environment (GGE) bi-plot is a subjective/qualitative means of characterizing (ABLs+ parents) × season interaction patterns and assessment of stability which utilises combination of GGE concepts and AMMI bi-plot (Yan *et al*., 2000). GGE bi-plot was used for visual interpretation of patterns of GEI. The GGE biplot is based on the following model.

$$Yij - Yi = \lambda 1 \alpha i 1 \gamma i 1 + \lambda 2 \alpha i 2 \gamma j 2 + \varepsilon ij$$

Where, Yij is the trait mean of ith ABL in the jth season, Yi is trait mean of all the ABLs in the jth season, $\lambda 1$ and $\lambda 2$ are square root of eigen values of first and second IPC axes, 1 and 2, αi1 and αi2 are scores of the first and second IPC, respectively, for the ith ABL and γij and γij are first and second IPCs respectively for jth season. There are numerous ways to use and interpret GGE bi-plot. However, four views of the GGE bi-plot are most relevant (Segherloo *et al*., 2010). These are (1) average seasonal environment coordination (AEC) view of GGE bi-plot based on ABL-focused scaling for ranking of the test ABLs relative to ideal genotype; the ideal genotype is the one whose point is located in the centre of concentric circles in the GGE bi-plot (2) discriminating and representativeness of test seasonal environments view of GGE bi-plot, (3) polygon view of GGE biplot based on symmetrical scaling for determining "which won- where" pattern of ABLs with test seasonal environment, and (4) AEC view of biplot based on seasonal environment-focused scaling for interpreting mean performance of the ABLs *vs.* their stability patterns.

AMMI model-based parameters to identify stable genotypes

The relative stability of genotypes can be estimated quantitatively based on the estimates of AMMI stability value (ASV) (Purchase *et al*., 2000) and Stability Index (SI) (Farshadfar, 2011). The estimation of ASV and SI and criteria to assess relative stability of genotypes based on ASV and SI are described in the following sections.

AMMI stability value (ASV)

To facilitate an objective method of identifying genotypes with stable performance across different seasons of sowing, the ASV was estimated (Purchase *et al.*, 2000) as

ASV = √[$SSIPC1$ $SSIPC2$(IPC1 score)]2+(IPC2 score)2

Where, SSIPC 1 and SSIPC 2 are sum of squares (SS) attributable to first two IPCs. Conceptually, ASV is the distance from zero in a two-dimensional scatter

diagram of IPC 1 *vs.* IPC 2 scores (Purchase *et al*., 2000). Since the IPC 1 score generally contributes proportionately more to GSI, it is weighted by the proportional difference between IPC 1 and IPC 2 scores in order to compensate for the relative contribution of IPC 1 and IPC 2 scores to total GSI sum of squares. Lower magnitude of estimates of ASV indicates greater stability, while higher magnitude of ASV indicates lower stability of genotypes (Purchase *et al*., 2000).

Stability Index (SI). As ASV considers only stability, regardless of grain yield potential of genotypes, SI was estimated to facilitate simultaneous selection of genotypes for desired performance for different quantitative traits and stability. SI was estimated as **SI= RASV + RY** where, RASV is rank of the ABLs based on ASV and RY is the rank of ABL based on quantitative trait mean (Farshadfar, 2011) across three different seasons of sowing. The ABLs with low SI were regarded as those with high trait expression and high stability.

RESULTS AND DISCUSSION

The kernel yield and its related features were assessed across three different locations in *Kharif* 2021 and the results are presented in Table 8. Sources attributable to ABLs, locations, and the interaction of ABLs and location, as well as pooled error, were divided into the overall variation.

AMMI model-based characterization of ABL × season interaction. The genotype (g) × environment (e) interaction (GEI) is only detected by additive ANOVA when the average of all (g-1) (e-1) contrasts is significant. Even when there is a large GEI for some of the contrasts, a classic additive ANOVA shows a lack of GEI. Therefore, detecting GEI cannot be done using standard additive ANOVA. To properly detect GEI, the AMMI model is frequently employed as a middle method between 1 and (g-1) (e-1) df (Gauch, 1988). The AMMI model utilizes additive ANOVA to identify the main effects of ABL and season, and multiplicative PCA to identify the effects of ABL and season interactions. As a result, ABLs frequently have a major impact on the testing environment (s).

For an ABL × location interaction to exist, different ABLs and/or location environments are required. In the proposed investigation, AMMI ANOVA found significant mean squares due to ABLs and ABL × location interaction for all the attributes (Table 11). With the exception of days to 50% flowering, mean squares related to locational contexts were significant for all traits, illustrating the potential of the temporal environments to distinguish the ABLs under study. Significant mean squares due to ABLs indicated that there was significant variation among the ABLs for each trait. Similarly, Souina *et al.* (2016) studied G × E interaction for kernel yield in groundnut genotypes using stability parameters and Additive Main effects and Multiplicative Interaction analysis (AMMI).

Combined analysis of variance showed significant differences between genotypes, locations and GEI, suggesting differential response of varieties across tested locations and the need for the stability analysis.

To identify widely adaptable TMV-2 type Groundnut Advanced Breeding Lines

GGE Biplot analysis of GEI patterns. The GGE bi-plot visual, which scatters ABLs according to their IPCs, can be used to qualitatively evaluate the stability and adaptation of ABLs over spatial settings. The conventional GGE bi-plot, often known as the SREG (sites regression) model, was proposed by Yan *et al.* (2000). It consists of genotype (G) + genotype × environment (GE) data. It is a multivariate analytical tool that clearly illustrates interactions among each ABL and each location environment.

It's a two-dimensional bi-plot that enables display of the relationships between various location environments as well as the relationships between ABLs and various location environments employing

1. Discriminating ability and representativeness
2. Ranking of genotypes relative to 'ideal genotype'
3. 'Mean vs Stability' GGE Biplot
4. "Which won where/what" pattern.

To detect and characterize genotype × spatial environments represented by location. The diagnostic procedure of analysis of variance (ANOVA) is used to identify various causes of variation pertinent to the outcomes of field experiments like those presented in the current study. Mean squares attributed to ABLs in all three locations were significant for all the characters, with the exception primary branches per plant in E1 and test weight in E2 (Table 3), in accordance with a location-based ANOVA. These findings showed that, with the exception of primary branches per plant and test weight, there were significant variations between the ABLs for all parameters examined.

Table 3: RCBD ANOVA of groundnut ABLs evaluated across the different locations for yield and its attributing traits during *Kharif* 2021-22.

Source of variation	Degrees of freedom	Plant height (cm)			Primary branches plant^{-1}			Days to 50% flowering		
		E1	E2	E3	E1	E2	E3	E1	E2	E3
ABLs	8	38.41**	38.72**	38.35**	1.53	2.09**	2.33**	11.67**	16**	18.17**
Replication	2	0.006	0.11	0.01	0.92	0.14	0.33	1.03	0.77	1.59
Error	16	0.056	0.11	0.005	0.75	0.52	0.29	0.28	0.44	0.25

Source of variation	Degrees of freedom	Pods plant^{-1}			Pod yield plant^{-1} (g)			Kernel yield plant^{-1} (g)		
		E1	E2	E3	E1	E2	E3	E1	E2	E3
ABLs	8	28.10**	28.88**	26.61**	6.78**	5.90**	6.06**	0.81**	1.04**	0.83**
Replication	2	0.03	0.01	0.02	0.02	0.01	0.005	0.01	0.0006	0.002
Error	16	0.009	0.03	0.005	0.01	0.009	0.006	0.0008	0.004	0.005

Source of variation	Degrees of freedom	Shelling percent			Sound mature kernel			Test weight(g)		
		E1	E2	E3	E1	E2	E3	E1	E2	E3
ABLs	8	61.26**	61.44**	62.23**	86.09**	86.96**	87.21**	139.75**	50.90	139.71**
Replication	2	0.23	0.22	0.21	0.0002	0.001	0.0081	0.026	5200.56	0.07
Error	16	0.14	0.18	0.19	0.003	0.006	0.004	0.008	35.85	0.036

*Significant at P=0.05; **Significant at P=0.01

Pooled ANOVA. The combined analysis of variance is a useful statistical model that helps express the main effect and estimate the interactions among and within the source of variations as shown in Table 4. Significance differences were observed for genotype-by-environment interactions, illustrating the differences in performances of accessions from one location to another, and the agro-pedology of the environments impacted the agronomic characteristics of accessions tested. The mean square of environment (location) for days to 50 % flowering indicated no significant difference ($p > 0.05$).

The entire variation is divided by the pooled ANOVA into sources attributed to the ABLs, the locations, the ABL × location interaction, and the pooled error. variance is a useful statistical model that helps express the main effect and estimate the interactions among and within the source of variations as shown in Table 4. From the perspective of plant breeding, only variations brought on by ABLs and ABLs × location interactions (GSI) are exploitable. In the current research, significant variances attributable to ABLs provide better scope for selecting ABLs with the desired combination of traits, whereas significant ABLs × locations interactions provide opportunities for maximising the productivity of selected ABLs by identifying those that are specifically suited to a specified location.

The kernel yield and its related features were assessed across three different locations in *Kharif* 2021. Significance differences were observed for genotype-by-environment interactions, illustrating the differences in performances of accessions from one location to another, and the agro-pedology of the environments impacted the agronomic characteristics of accessions tested. The mean square of environment (location) for days to 50 % flowering indicated no significant difference ($p > 0.05$).

Combined analysis of variance showed significant differences between genotypes, locations and GEI, suggesting differential response of varieties across tested locations and the need for the stability analysis.

Table 4: Pooled ANOVA of groundnut ABLs evaluated across three locations for yield and its attributing traits during *Kharif* 2021-22.

Source of variation	DF	PH (cm)	PBP	DFF	PP	PYP	KYP(g)	SP	SMK	TW(g)
Replication	6	0.28	0.46	1.13	0.02	0.013	0.006	0.22	0.0031	0.03
ABLs	8	114.77**	5.22**	45.22*	83.44*	18.67**	2.64**	182.76**	0.005**	420.74**
Location	2	4.22**	0.38**	3.04	9.19*	8.64**	2.18**	9.32**	3.038**	1.11**
ABLs × Location	16	0.35**	0.36**	0.31*	0.07*	0.04**	0.02**	1.10**	4.72**	0.02**
Pooled error	48	0.05	0.52	0.33	0.016	0.009	0.003	0.17	0.004	0.016

*Significant at P=0.05; **Significant at P=0.01; DF: Degrees of freedom; PH: Plant height; PBP: Primary branches per plant; DFF: days to fifty percent flowering; PP: Pods per plant; PYP: Pod yield per plant; KYP: Kernel yield per plant; SP: Shelling per cent; SMK: Sound mature kernel; TW: Test weight

The genotype (g) × environment (e) interaction (GEI) is only detected by additive ANOVA when the average of all (g-1) (e-1) contrasts is significant. Even when there is a large GEI for some of the contrasts, a classic additive ANOVA shows a lack of GEI. Therefore, detecting GEI cannot be done using standard additive ANOVA. Researchers should only claim a lack of GEI if the GEI sum of squares for one degree of freedom (df) is not statistically significant (Gauch, 1988). To properly detect GEI, the AMMI model is frequently employed as a middle method between 1 and (g-1) (e-1) df (Gauch, 1988). The AMMI model utilizes additive ANOVA to identify the main effects of ABL and season, and multiplicative PCA to identify the effects of ABL and season interactions. According to the AMMI model's justification, the performance of ABLs as viewed in a given context is not the best indicator of how well they actually operate in that environment. As a result, ABLs frequently have a major impact on the testing environment (s).

For an ABL × location interaction to exist, different ABLs and/or location environments are required. In the proposed investigation, AMMI ANOVA found significant mean squares due to ABLs and ABL × location interaction for all the attributes (Table 5). Mean squares related to locational contexts were significant for all traits, illustrating the potential of the temporal environments to distinguish the ABLs under study. Significant mean squares due to ABLs indicated that there was significant variation among the ABLs for each trait. Similarly, Souina *et al.* (2016) studied G × E interaction for kernel yield in groundnut genotypes using stability parameters and Additive Main effects and Multiplicative Interaction analysis (AMMI).

This study revealed very highly significant differences in genotypes and significant differences in environments, which could be credited to environmental conditions, the genetic diversity of the genotypes, and the effects of the interaction between the genotypes and environments. The highly significant GEI for some agronomic traits could be explained by the heterogeneity of the nature of the multi-environments tested with the different genetic makeup of the genotypes planted, and similar results were reported by many researchers (Yan and Kang, 2003; Andrade *et al.,* 2016; Olanrewaju *et al.,* 2021; Khan *et al,* 2021). Nevertheless, the variance component analysis is insufficient to elucidate all the attributes of the genotype-by-environment interaction.

Subsequently, more statistical tools and models could be more beneficial and prolific in describing and comprehending the more the GEI (Oladosu *et al.,* 2017). The genotype-by-environment interaction effect primarily highlights the fact that genotypes responded inversely to various locations, emphasizing the need for genotype assessment in diverse environments. Similarly, the GEI study is a means through which plant breeders select the ideal and best genotypes for commercial purposes, which is not without challenges. The partitioning of the environment indicates that the sources of variation could be due to experimental sites, climatic conditions of the sites, or growing season of the crops (Oladosu *et al.,* 2017; Khan *et al.,* 2021; Azrai *et al.,* 2022).

Discriminating ability and representativeness. The discriminativeness vs. representativeness pattern of the GGE biplot pinpoints how the best environment can be informative and representative. The two concepts focus on environments in terms of their ability to detect the best genotypes (discriminativeness) and to adequately represent the test environments (representativeness) (Yan and Tinker, 2006; Oladosu *et al.,* 2017; Khan *et al.,* 2021). The use of multi-environmental trials is very beneficial because it helps to avoid overestimation of heritability and genetic variance, which are always observed with one location experiment (Azrai *et al.,* 2022).

Table 5: AMMI ANOVA of groundnut ABLs evaluated across three locations for yield and its attributing traits.

Source of variation	Degrees of freedom	Plant height (cm)		Primary branches plant^{-1}		Days to 50% flowering		Pods plant^{-1}		Pod yield plant^{-1} (g)		Kernel yield plant^{-1} (g)	
		Mean sum of squares	% variation	Mean sum of squares	% variation	Mean sum of squares	% variation	Mean sum of squares	% variation	Mean sum of squares	% variation	Mean sum of squares	% variation
Total	80	11.69		0.95		4.94		8.60		2.09		0.32	
Treatments	26	35.86**	99.67	1.86**	63.38	14.34**	94.26	26.43**	99.85	6.43**	99.68	0.99**	99.23
ABLs	8	114.77**	98.16	5.22**	54.66	45.22**	91.45	83.45**	97.00	18.67**	88.99	2.64**	81.87
Environments	2	4.23**	0.90	0.38**	1.00	3.04**	1.54	9.20**	2.67	8.64**	10.29	2.18**	16.44
ABLs× Location	16	0.36**	0.60	0.36**	7.71	0.30**	1.26	0.08**	0.17	0.042**	0.39	0.02**	1.68
IPCA1	9	0.61**	96.49	0.44**	67.79	0.45**	82	0.08**	66.66	0.0070**	94.02	0.03**	72.72
IPCA2	7	0.03**	3.50	0.27**	32.20	0.12**	18	0.06**	41.66	0.006**	5.97	0.01**	25
Error	48	0.06	0.29	0.52	32.94	0.33	4.00	0.02	0.116	0.007	0.26	0.003	0.61

Source of variation	Degrees of freedom	Shelling percent		Sound mature kernel		Test weight(g)	
		Mean sum of squares	% variation	Mean sum of squares	% variation	Mean sum of squares	% variation
Total	80	18.85		26.07		42.12	
Treatments	26	57.62**	99.35	80.20**	99.99	129.56**	99.97
ABLs	8	182.75**	96.94	260.18**	99.80	420.74**	99.88
Environments	2	9.33**	1.24	1.47**	0.13	1.11**	0.06
ABLs× Location	16	1.10**	1.16	0.05**	0.03	0.02**	0.16
IPCA1	9	1.61**	82.38	0.06**	75	0.02**	96.49
IPCA2	7	0.43**	20.68	0.03**	25	0.02**	3.50
Error	48	0.18	0.55	0.01	25	0.02	0.08

*Significant at P=0.05; **Significant at P=0.01

Seasonal vector is a dotted line that connects the test seasonal environment and points to the origin. The capacity to distinguish and recognise the representativeness of the temporal environments is aided by the length of seasonal vectors and the angle at which each seasonal vector intersects with the AEC. Whereas a representational seasonal environment should represent the average of all three test seasonal environments, a discriminative seasonal environment can distinguish between ABLs. Lower and stronger seasonal environment discriminative abilities are shown by short and long seasonal 43 Adaptability of TMV-2 Type Groundnut Advanced Breeding Lines environment vectors, respectively. The most and least representational capabilities of seasonal environments are indicated, respectively, by small and large angles between seasonal environment vectors and AEC. The seasonal environment vectors' acute show how similar the test seasonal settings are and obtuse angles show how distinct the test seasonal settings are.

In the current study, the GGE biplot graph shows the discriminating ability and representativeness of the test environment related to podsplant^{-1}across three environments. Balajigapade's position is distinctive with regard to pods plant^{-1}because its location environment vector is longer than other location vectors, and Mandya's location is distinctive due to its acute angle with AEC (Fig 1a). Regarding pod yield plant^{-1}, Balajigapade location is representative as its location environment vector is having small angle than the other location environment vectors and forms an acute angle with AEC, while GKVK location is discriminative as its location environment vector is longer than other location vectors (Fig 1b). On the other

hand, in the kernel yield plant^{-1}, GKVK location is discriminative due to the longer length of location environment vectors. However, the Mandya site is more representative due to its small angle with the AEC (Fig 1c). As a result, GKVK location is thought to be the best one to assess kernel yield plant^{-1}since it is similarly discriminative with other locations. The use of multi-environmental trials is very beneficial because it helps to avoid overestimation of heritability and genetic variance, which are always observed with one location experiment (Azrai *et al.*, 2022). Present study revealed the environments closely related, demonstrating the discriminativeness ability and the representativeness of the test environments. The longer the vector of an environment, the higher its capability to discriminate among genotypes, while the shorter the angle formed with the abscissa, the more it is representative.

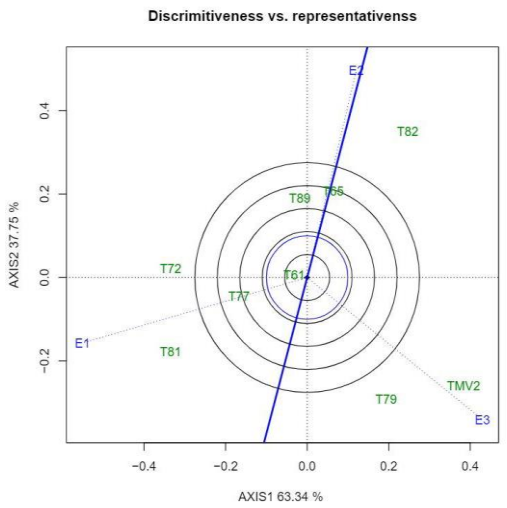

Fig. 1a. Discriminative *vs*. representativeness view of GGE bi-plot for pods plant^{-1}.

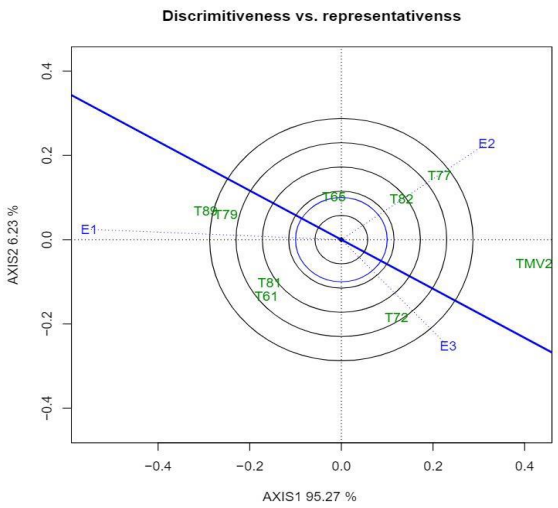

Fig. 1b. Discriminative *vs*. representativeness view of GGE bi-plot for pod yield plant^{-1}(g)

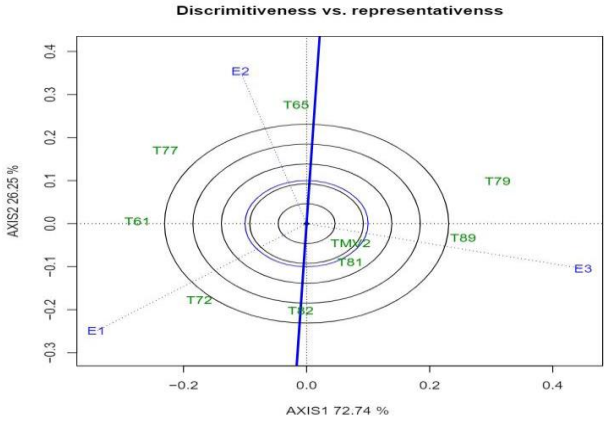

Fig. 1c. Discriminative *vs*. representativeness view of GGE bi-plot for kernel yield plant^{-1}(g).

Ranking of genotypes relative to ideal genotype. A genotype that has high mean performance and good environmental stability is ideal. The ideal genotype is represented by the little circle on the axis for the average environment in the GGE Biplot graph "Ranking genotypes" (AEA). The average performance of genotypes diminishes as we move away from the origin and away from the location where the ideal genotype is found on the average environment axis (AEA). Location on the average environment coordinate axis (AEC) can be used to estimate the position of the relevant genotype's mean performance.

The test environments were further assessed using the GGE model to define the relationship among the components of mega environments, to better discriminate the best and most stable genotypes important in a breeding program. The adaptability of the genotypes enhances as we go closer to the site of origin, whereas it decreases as we move farther away from the point of origin. Due to its close proximity to the place of origin T79, T77 and T81 has a high mean performance and adaptable performance when compared to other locations for pods plant^{-1} (Fig. 2a). T89 and T79 is situated very close to the site of origin for pod yield plant^{-1} (Fig. 2b) and for kernel yield plant^{-1} T82 and T72 are adaptable (Fig. 2c). To locate the concerned ABLs and assess variety, one uses the average environment coordinate axis (AEC). Similar results were obtained by Oladosu *et al.* (2017); Khan *et al.* (2021), who reported that the GGE biplot vividly

explained the existing relationships among tested locations in a genotype-by-environment analysis.

'Mean vs Stability' GGE Biplot. Based on the genotype's distance from the origin and the length of the projection line from the average environment axis, one might understand the stability of the genotype versus the mean performance in the "Mean vs. Stability" GGE Biplot graph (AEA). Stability diminishes as genotypes migrate farther from the origin and rises as genotypes move closer to the origin.

Stability reduces as the projection line's length from the AEA axis increase, and stability increases as the projection line's length from the AEA axis decreases. Knowing the precise location of the genotype from the AEA axis is done using the AEC axis (average environment coordinate axis).

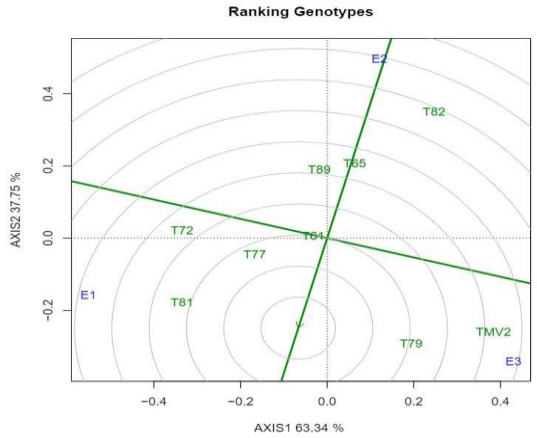

Fig. 2a. Average environment coordinate axis (AEC) view of GGE bi-plot for ranking genotypes relative to ideal genotype across different environment pods plant^{-1}.

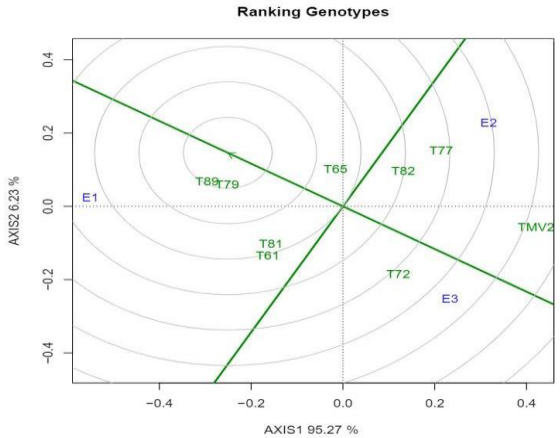

Fig. 2b. Average environment coordinate axis (AEC) view of GGE bi-plot for ranking genotypes relative to ideal genotype across different environment pod yield plant^{-1} (g).

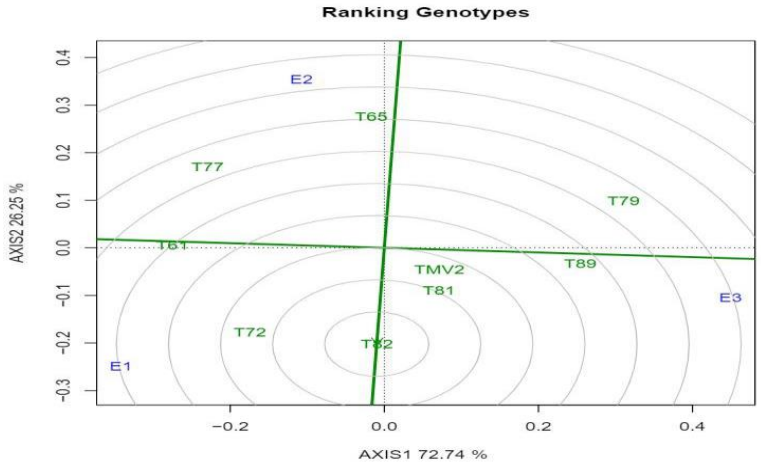

Fig. 2c. Average environment coordinate axis (AEC) view of GGE bi-plot for ranking genotypes relative to ideal genotype across different environment kernel yield plant^{-1}(g).

According to the current study, the adaptability of the ABLs across three locations could be determined based on the ABL's distance from its origin, which can be determined by the length of projections from the average environment axis (AEA). T89 and T82 which are placed relatively close to the origin for pods plant^{-1} (Fig. 3a), indicates good adaptability.

As they move farther away from the AEA axis and remain on it, their stability declines. Of all the ABLs, T79, T89 and T72 had the highest stability for pod yield plant^{-1} (Fig. 3b). For kernel yield plant^{-1} T65, T81 and T82 has a high yield, is situated close to the origin, indicating strong adaptability (Fig. 3c).

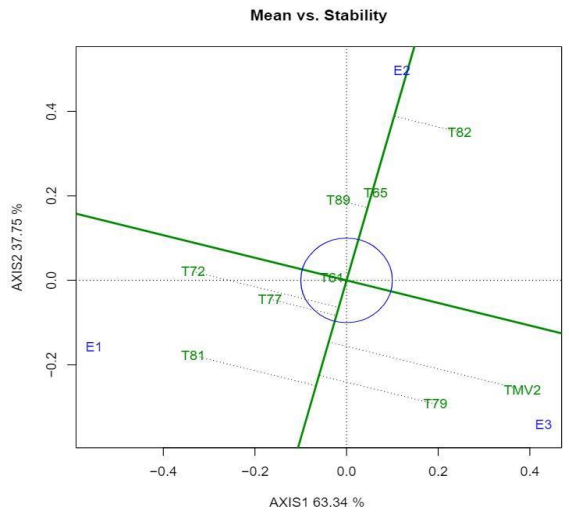

Fig. 3a. Average seasonal environment coordination (AEC) view of GGE bi-plot based on locational environment-focused scaling for the mean performance vs. stability for pods plant^{-1}.

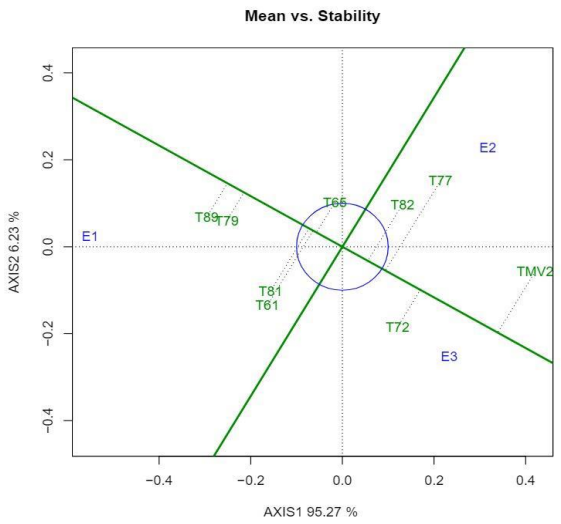

Fig. 3b. Average seasonal environment coordination (AEC) view of GGE bi-plot based on locational environment-focused scaling for the mean performance vs. stability for pod yield plant^{-1} (g).

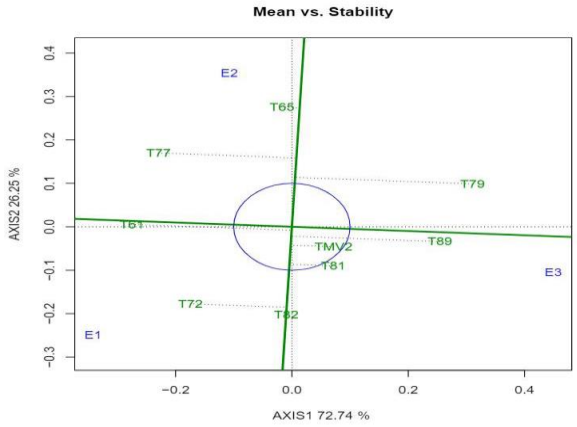

Fig. 3c. Average seasonal environment coordination (AEC) view of GGE bi-plot based on locational environment-focused scaling for the mean performance vs. stability for kernel yield plant^{-1} (g).

"Which won where/what" patterns. The "which-won-where" is also one of the important components of the GGE biplot for the GEI analysis. The "which-won-where" biplot identifies mega-environment disparity for an environment suitable for the genotypes' adaptability, the best genotypes in each mega environment, and the ideal genotype with high agronomic performance and stability (Gauch and Zobel 1997; Yan, 2001). From the GGE biplot, it was shown that accessions were well adapted in each environment and confirmed the presence of interaction differentiation between genotypes and environments. The detected mega-environment for each agronomic trait allows us to select the outstanding accessions for that very trait in that environment, especially the accessions at the corners of the polygons in the biplot. Thus, the vertex genotypes were identified, indicating their performance and adaptability in the mega environment. This infers that the vertex genotypes were most favoured by the environments, and therefore, they were the most responsive and exceptional genotypes when considering their potential yield in their respective mega-environments (Hashim *et al.*, 2021). However, vertex genotypes with no environment in the sector are not desirable because of their poor performance across the environments (Khan *et al.*, 2021).

The ability to show the genotypes "which-won-where/what" patterns is one of the characteristics of a "GGE bi-plot graph". The polygon view of the GGE biplot illustrates this feature. The polygon is constructed by placing either the superior or winning genotype in the farthest position on the vertices in a way that it contains all genotypes. In one or even more locations, the genotype positioned at the polygon's vertex exhibits the best or worst performance.

In a given season, the winning genotype or the inferior genotype occupy the polygon's vertices. "which won where/what" graph illustrates which genotype gives the largest kernel yield plant^{-1} in each habitat. The genotype that is present in the vertices of polygon is said to be winning genotype.

Since the lines from the origin have an acute angle between them and divide this graph into several sectors, genotype at the vertex exhibits a positive correlation

with the specific environment. In a polygon, vertical lines perpendicularly divide each side. The winning genotype is shared among environments in the same sector, whereas it varies among environments in other sectors. As a result, the polygon view of a GGE biplot shows whether or not GEI crosses over.

The "which won where/what" graph in the present research demonstrates which ABL (winning genotype) produces higher yield in which environment. The polygon's vertices contain the winning Groundnut ABLs. In a polygon, a vertical line separates each side perpendicularly. ABLs at the vertices indicate a positive association with that of the environment between the lines because of this the graph is segmented into different sectors by lines with acute angles between them. The polygon is created by placing the farthest position of either the superior or winning ABL on the vertices in such a way that the polygon contains all groundnut ABLs.

The trait pods plant^{-1}T81 has prevailed in environment 1 (GKVK), T82 was the genotype that prevailed in environment 2 (Mandya), and TMV-2 and T79 were the genotypes that prevailed in environment 3 (Balajigapade) (Fig. 4a). For pod yield plant^{-1}, T89 and T79 were the winning genotypes in environment 1 (GKVK), T77 was the winner in environments 2 (Mandya) and T72 and TMV-2 were winners in Balajigapade (Fig. 4b). For Kernel yield plant^{-1} was shown to T72 and T82 were the winning genotype in environment 1 (GKVK), T77, T65 and T61 in environment 2 (Mandya) and T89 found to be the winning genotype in environment 3 (Balajigapade) (Fig. 4c). Similar results were obtained by many researchers including Nehe *et al.* (2019); Kendal (2019). The environmental adaptation of varieties is very paramount in comprehending their genetic basis, which is only achieved through genotype-by-environment interactions (Hudson *et al.*, 2022).

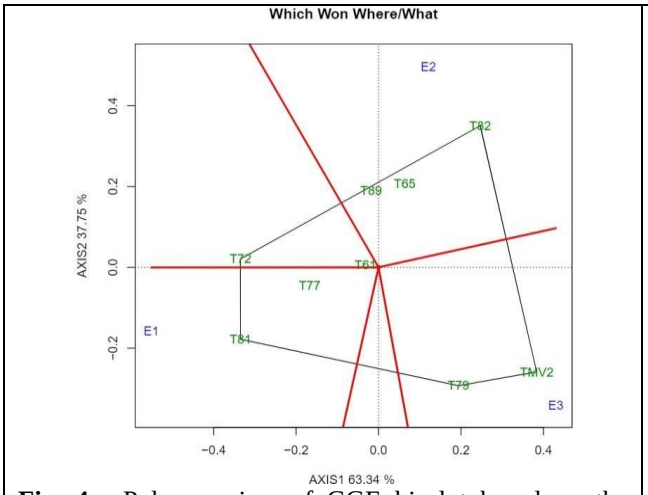

Fig. 4a. Polygon view of GGE bi-plot based on the symmetrical scaling for "which won-where" pattern of ABLs and locational environments for pods plant^{-1} (g) during *Kharif* 2021.

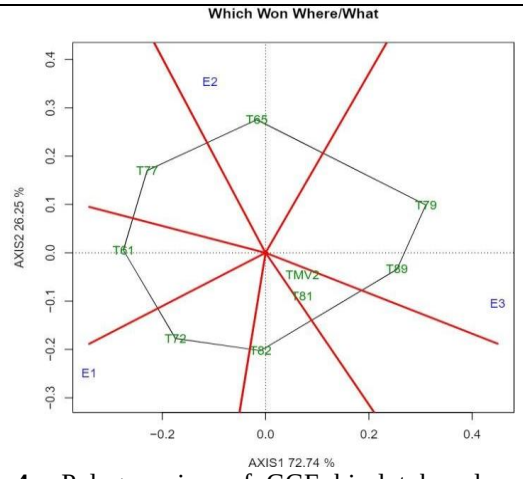

Fig. 4c. Polygon view of GGE bi-plot based on the symmetrical scaling for "which won-where" pattern of ABLs and locational environments for kernel yield plant^{-1} (g) during *Kharif* 2021.

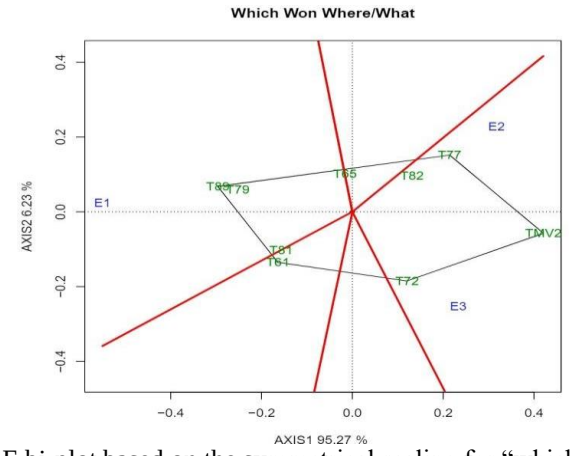

Fig. 4b. Polygon view of GGE bi-plot based on the symmetrical scaling for "which won-where" pattern of ABLs and locational environments for pod yieldplant^{-1} (g) during *Kharif* 2021.

AMMI model-based stability parameters

AMMI Stability value (ASV). ASV offers an unbiased evaluation of stability, which aids in identification of ABLs that are consistent across the three seasonal conditions. ASV is the distance from zero in a two-dimensional scatter-gram of IPCA 1 (Interaction Principal Component Analysis Axis 1) scores against IPCA 2 (Interaction Principal Component Analysis Axis 2) scores. The IPC scores and ASV values is shown in Table 6. The adaptable genotypes are presented in (Table 7). Similarly AMMI and GGE biplot analysis was carried out by Esan *et al.* (2023) for stability analysis in bambara groundnut under three environmental conditions. Similarly, AMMI model stability analysis was carried out by Ajay *et al.* (2020) in fifty two peanut genotypes for two years under two phosphorous levels.

Genotype × environment interaction (GEI).

Table 6: Estimates of ASV and SI to assess stability of groundnut ABLs across three locations.

ABLs	Plant height (cm)							Primary branches plant^{-1}						
	MEAN	RY	IPCA1	IPCA2	ASV	RASV	SI	MEAN	RY	IPCA1	IPCA2	ASV	RASV	SI
T61	35.04	2	-0.42	-0.36	2.21	8	10	4.78	9	-0.47	0.05	0.69	8	17
T65	29.11	8	-0.31	0.02	1.61	7	15	5.33	6	-0.40	0.34	0.67	6	12
T72	30.1	6	-0.29	0.12	1.51	5	11	5.44	5	0.37	-0.26	0.59	5	10
T77	31.79	3	0.21	-0.02	1.10	3	6	5.78	4	-0.47	0.05	0.69	7	11
T79	24.41	9	-0.12	0.14	0.66	2	11	5.33	7	0.12	-0.33	0.37	4	11
T81	30.79	4	0.10	-0.14	0.52	1	5	6.44	2	-0.05	-0.10	0.13	1	3
T82	36.86	1	0.24	0.21	1.28	4	5	7.33	1	0.12	-0.33	0.37	3	4
T89	29.44	7	0.89	-0.10	4.66	9	16	5.78	3	0.59	0.61	1.05	9	12
TMV2	30.24	5	-0.30	0.11	1.59	6	11	5.22	8	0.19	-0.04	0.28	2	10

ABLs	Days to 50% flowering							Pods plant^{-1}						
	MEAN	RY	IPCA1	IPCA2	ASV	RASV	SI	MEAN	RY	IPCA1	IPCA2	ASV	RASV	SI
T61	39.67	5	0.01	-0.08	0.08	1	6	29.98	4	-0.03	-0.01	0.04	1	5
T65	38.56	8	-0.46	0.16	1.00	7	15	35.72	1	0.06	-0.21	0.22	3	4
T72	42.56	1	0.39	0.40	0.93	6	7	32.94	2	-0.34	-0.02	0.42	6	8
T77	35.11	9	-0.66	-0.07	1.40	9	18	28.72	6	-0.17	0.04	0.22	4	10
T79	42.44	2	0.48	-0.32	1.08	8	10	29.33	5	0.19	0.29	0.38	5	10
T81	41.11	3	0.06	-0.44	0.46	2	5	27.77	8	-0.33	0.18	0.46	7	15
T82	39.44	6	0.20	0.16	0.46	4	10	30.71	3	0.25	-0.35	0.47	8	11
T89	40.11	4	-0.23	0.04	0.49	5	9	28.44	7	-0.02	-0.19	0.19	2	9
TMV2	39.44	7	0.20	0.16	0.46	3	10	25.21	9	0.38	0.26	0.55	9	18

ABLs	Pod yield plant^{-1} (g)							Kernel yield plant^{-1} (g)						
	MEAN	RY	IPCA1	IPCA2	ASV	RASV	SI	MEAN	RY	IPCA1	IPCA2	ASV	RASV	SI
T61	23.67	5	-0.16	-0.14	0.67	5	10	16.57	4	0.28	-0.01	0.47	8	12
T65	24.83	4	-0.02	0.10	0.12	1	5	17.89	1	0.02	-0.28	0.28	4	5
T72	24.91	3	0.12	-0.18	0.51	2	5	16.51	5	0.17	0.18	0.35	5	10
T77	21.88	8	0.21	0.15	0.86	6	14	16.89	3	0.23	-0.17	0.43	6	9
T79	23.58	6	-0.25	0.06	1.00	7	13	17.08	2	-0.31	-0.10	0.54	9	11
T81	24.67	2	-0.16	-0.10	0.63	4	6	16.33	7	-0.07	0.09	0.15	2	9
T82	24.85	1	0.13	0.10	0.53	3	4	16.43	6	0.01	0.20	0.20	3	9
T89	23.11	7	-0.30	0.07	1.18	8	15	16.14	9	-0.25	0.03	0.43	7	16
TMV2	20.87	9	0.42	-0.06	1.67	9	18	16.29	8	-0.07	0.05	0.13	1	9

ABLs	Shelling percent							Sound mature kernel						
	MEAN	RY	IPCA1	IPCA2	ASV	RASV	SI	MEAN	RY	IPCA1	IPCA2	ASV	RASV	SI
T61	70	5	-0.25	-0.58	0.79	4	9	77.23	5	0.23	-0.05	0.40	7	12
T65	72.07	4	0.17	-0.37	0.53	2	6	70.38	8	-0.13	0.03	0.24	4	12
T72	66.27	7	-0.63	0.00	1.39	7	14	80.07	3	0.29	0.07	0.50	8	11
T77	77.19	2	-0.33	-0.22	0.76	3	5	80.13	2	0.01	0.22	0.22	3	5
T79	72.47	3	0.89	0.05	1.96	9	12	74.89	7	0.08	-0.25	0.29	5	12
T81	66.21	8	0.09	0.00	0.19	1	9	76.38	6	-0.52	0.04	0.90	9	15
T82	66.11	9	-0.36	0.46	0.92	6	15	66.13	9	0.05	0.07	0.11	1	10
T89	69.89	6	0.75	0.17	1.65	8	14	83.23	1	0.06	0.17	0.21	2	3
TMV2	78.03	1	-0.33	0.49	0.88	5	6	79.94	4	-0.07	-0.30	0.32	6	10

ABLs	Test weight (g)						
	MEAN	RY	IPCA1	IPCA2	ASV	RASV	SI
T61	26.55	9	0.19	-0.19	1.01	8	17
T65	36.13	5	-0.08	0.04	0.40	3	8
T72	38.01	3	0.00	0.37	0.37	2	5
T77	29.41	7	-0.42	-0.17	2.21	9	16
T79	36.54	4	0.11	-0.13	0.59	6	10
T81	48.51	1	0.15	-0.06	0.79	7	8
T82	39.08	2	0.03	-0.01	0.16	1	3
T89	29	8	0.08	0.01	0.42	5	13
TMV2	30.15	6	-0.06	0.13	0.34	4	10

Table 7: Stable and adaptable groundnut ABLs across three locations identified based on Stability Index for different traits.

Traits	Adaptable ABLs
Plant height (cm)	T81, T82, T77
Primary branches plant^{-1}	T81, T82, T72
Days to 50% flowering	T81, T72, T61
Pods plant^{-1}	T65, T61, T72
Pod yield plant^{-1}(g)	T82, T72, T65
Kernel yield plant^{-1}(g)	T65, T77, T81, T82
Shelling percent	T77, T65, TMV-2, T61
Sound mature kernel	T89, T77, T82, TMV-2
Test weight(g)	T82, T72, T65

CONCLUSIONS

TMV-2, the variety developed and released in 1940 (82 years back) is still ruling despite other varieties better than TMV-2 with good pod and kernel features. On the other hand, it has been denotified, thus it is no longer available in the official seed supply chain. There is a pressing need to develop a variety with higher yield potential than TMV-2 but with similar pod and kernel type. One of the reasons for the low productivity of groundnut in the nation is the slow adoption of improved varieties and their variable performance in various conditions. Due to genotype environment interactions (GEI), it is generally known that genotypes that perform well in one environment may or may not perform well in another. A genotype with low GEI will have high stability and vice versa. Therefore, if care is not taken to select for both yield and stability of performance when developing a high yielding cultivar, one may end up with a high yielding genotype that is only suitable for a specific climate.

Pooled analysis of variance indicated significant variability attributable to ABLs and their interaction with spatial environments for all the traits considered for the study. For kernel yield plant^{-1}, ABLs T65, T77, T81 and T82 were found to be adaptable. Four ABLs *viz.*, T65, T77, T81 and T82 were found to be stable across the seasons for kernel yield plant^{-1}. Based on which won where pattern for the trait kernel yield plant^{-1} T72 and T82 were the winning genotypes in environment 1 (GKVK), T77, T65 and T61 in environment 2 (Mandya) and T89 found to be the winning genotype in environment 3 (Balajigapade). Found adaptable lines will be checked for kernel yield potential in future years and after their validation the stable lines can be released as a variety or these stable lines can be used as parents breeding programs.

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Conflict of Interest. None.

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