



Parametric and Non-parametric Statistical Approaches for Estimation of Genotype $\times$ Environment Interaction of Pigeon Pea [*Cajanus cajan* (L.) Millspaugh] Genotypes

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ABSTRACT

Background: The genotype-by-site interaction might be stronger than the genotype-by-year interaction, making it difficult to identify superior genotypes in multi-location trials. This is influenced by the Genotype $\times$ Environment interaction (GEI). The estimation of G, E and G $\times$ E interactions (or GEI) ensures valid recommendations of suitable varieties able to overcome the pressure due to variable occurring conditions. The determination of GEI factors helps geneticists in their breeding programs to shift the selection toward varieties suited for wide environments or specific to certain niches.

Methods: This requires genotype evaluation in multi-environment trials in the latter stages of selection. To evaluate genotype-environment interaction (GEI), fourteen pigeon pea genotypes were studied in four Gujarat sites. The additive main effects and multiplicative interaction (AMMI) analysis of variance (ANOVA) showed that genotype-environment interaction (GEI), IPCA 1 and IPCA 2 were significant across all genotypes.

Result: Pigeon pea genotype NPMK-15-05 (G9) yielded best. AMMI 1 and 2 plots showed stable ICPL-87119 (G12) and BP-12-31 (G5) genotypes. The genotypes with the strongest non-parametric stability were NPMK-15-05 (G9), ICPL-87119 (G12) and NPMK-15-03 (G8). GGE (Which-win-where) biplot analysis showed that NPMK-15-05 (G9) won.

Key words: AMMI, G $\times$ E interaction (GEI), GGE biplot, Non-parametric statistics, Parametric, Pigeon pea.

INTRODUCTION

Pulses, often referred to as “grain legumes,” serve as essential food sources for both humans and animals. India is the largest contributor to global pulse cultivation, accounting for 33% of the world’s land area and 22% of pulse production. Among these, pigeon pea [*Cajanus cajan* (L.) Millspaugh], known in India as redgram, arhar, tur, or thogari, is a versatile and climate-resilient legume that plays a crucial role in Indian rainfed agriculture. It ranks second in terms of acreage, production and productivity following chickpea.

In 2022, India produced 4.34 million tonnes of pigeon pea, cultivated over 5.05 million hectares, with a productivity of 859 kg per hectare (DES, MoA and FW, 2022). Notably, India is the primary importer of pigeon pea, making up 92.65% of global imports in 2021, with an import volume of 674.44 million kg. In 2020, India contributed 77.61% of global pigeon pea output (Tridge, 2023), while Gujarat cultivated the crop on 0.22 million hectares, yielding 0.24 million tonnes. Pigeon pea (*Cajanus cajan*) is generally considered the sixth most important edible legume globally, ranked after common bean, chickpea, field pea, cowpea, and lentil (Farooq *et al.*, 2025).

The per capita protein availability in the country is 37 g/day, although the WHO (2023) recommends 80 g/day, highlighting a significant malnutrition issue among impoverished populations, many of whom adhere to a vegetarian diet and eschew animal protein (Singh, 2020).

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It requires the fulfillment of demand by protein derived from pulses. Consequently, the pulse demand in the country is anticipated to reach 32 million tons by 2030 and 39 million tons by 2050. This requires an annual growth rate of 2.2% (Singh and Praharaj, 2020). Pigeon pea is regarded as a superior and economical source of plant-based protein, significantly exceeding that of main cereals (21.7 g/100 g compared to 6.0-15.0 g/100 g), along with additional

nutritious constituents. The development and identification of high-yielding and stable varieties are essential techniques to satisfy the increasing demand for pigeon pea.

Genotype-environment interactions are examined in terms of places and years. Plant breeding relies on genotype-by-environment interaction (GEI). Breeders face major challenges in developing enhanced varieties due to EI. Selective forces from the environment can influence a population's genetics, causing evolutionary changes (Dabholkar, 1992; Booker, 2024; Tom 2024). GEI obscures genotype, therefore quantifying this interaction variation is necessary to avoid overestimating or under estimating genotypic variance in breeding operations.

Gauch and Zobel (1996) and Gauch (2006) suggest that understanding GEI can enhance selection and identify suitable genotypes for specific environments. Various methods exist for calculating G × E interactions, with parametric and non-parametric approaches being predominant (Huehn, 1996). Key parametric approaches include ecovalence (W^2_j), regression coefficient (b_i), deviation from regression (S^2_{di}) (Eberhart and Russell, 1966), stability variance (σ^2) (Shukla, 1972) and coefficient of variance (CV_i) (Francis and Kannenberg, 1978). The AMMI model-based stability parameters, including the ASV (AMMI stability value) and YSI (Yield stability index), were developed using a parametric model (Bajpai and Prabhakaran, 2000). Non-parametric measures include $S_{(i)}$ by Huehn (1990) and Nassar and Huehn (1987), $NP_{(i)}$ by Thennarasu (1995), and KR or rank-sum measures by Kang (1988). Both parametric and non-parametric GEI estimation methods, such as ANOVA and PCA, have their limitations. Two common biplots for G × E interactions are AMMI (Gauch, 2006) and GGE (Yan *et al.*, 2000), which effectively capture a significant portion of the interaction sum of squares while distinguishing between main and interaction effects, demonstrating genetic adaptation to specific environments (Jeberson *et al.*, 2017). The primary difference between these models is that the GGE biplot exclude the E component.

This study analyzes the genotype-environment interaction (GEI) of select elite pigeon pea genotypes in Gujarat. The determination of GEI factors helps geneticists in their breeding programs to shift the selection toward varieties suited for wide environments or specific to certain niches.

MATERIALS AND METHODS

The experimental material comprises 14 pigeon pea genotypes grown over four different locations of Gujarat i.e., Pulse and Castor Research Station, Navsari (E1:20.95°N 72.93°E, 9 m amsl), National Agricultural Research Project, Bharuch (E2:21.70°N 72.97°E, 15 m amsl), Agricultural Research Station, Achhalia (E3:21.97°N 73.18°E, 38 m amsl) and Agricultural Research Station, Mangrol (E4:21.12°N 70.12°E, 18 m amsl) (Fig 1) during

Kharif season. Table 1 represents Agro-climatic conditions of four different environments. The fourteen genotypes are evaluated under randomized block design (RBD) with three replications for the character grain yield. The various genotypes taken for the study are BP-08-06 (G1), BP-10-03 (G2), BP-11-11 (G3), BP-15-28 (G4), BP-12-31 (G5), NPMK-14-01 (G6), NPMK-15-02 (G7), NPMK-15-03 (G8), NPMK-15-05 (G9), NPMK-15-07 (G10), Vaishali (G11), ICPL-87119 (G12), GJP-1 (G13) and BDN-2 (G14). The performance of genotypes has been evaluated utilizing stability models such as AMMI (Gauch and Zobel, 1996) and the GGE Biplot or Site Regression Model (Yan and Kang, 2003). The AMMI ANOVA assesses the importance of Genotype-Environment Interaction (GEI). The GEI has been analyzed utilizing the AMMI model, which integrates ANOVA with IPC analysis (Zobel *et al.*, 1988).

$$Y_{ij} = \mu + g_i + e_j + \sum_k \lambda_k \alpha_{ik} \gamma_{jk} + R_{ij} \quad \dots(1)$$

Where,

Y_{ij} = Yield of i^{th} genotype in j^{th} environment.

μ = Grand mean.

g_i = Effect of i^{th} genotype.

e_j = Effect of j^{th} environment.

λ_k = Square root of the eigen value for the PCA of k^{th} axis.

α_{ik} and γ_{jk} = PC scores for PCA of k^{th} axis of the i^{th} genotype in j^{th} environment.

R_{ij} = Residual term.

The GGE biplots graphically represents G and GEI impacts in multi-location trial data using environment-centered data. This methodology uses a biplot to show the factors (G and GE) that are important in genotype evaluation and that are also sources of variation in GEI analysis of multilocation trial data (Yan *et al.*, 2007; Yan, 2001). The data was subjected to IRRIP.B. tools 1.4 version to get AMMI and GGE Biplots as well as the results of ANOVA. For ANOVA, normality was assessed using the Shapiro-Wilk test ($p > 0.05$ indicates normal distribution) while homoscedasticity was evaluated with Levene's test ($p > 0.05$ suggests equal variances).

The analysis provided insights into the genotype and environment interactions, allowing for a comprehensive understanding of the data. Following this, ranks of non-parametric statistics were calculated using Kang (1988), Nassar and Huehn (1987) and Thennarasu (1995) model, which facilitated the evaluation of the performance of different genotypes across various environments. This non-parametric approach complements the findings from the AMMI and GGE biplots, offering a robust framework for interpreting the results. The integration of these statistical methods enhances the reliability of the conclusions drawn from the data, ensuring that both parametric and non-parametric perspectives are considered in the analysis. Ranks of non-parametric statistics has been calculated using the following indices:

$$S^{(1)} = 2 \sum_j^{n-1} \frac{\sum_{j'=j+1}^n |r_{ij} - r'_{ij}|}{[n(n-1)]} \quad \dots(2)$$

$$S^{(2)} = \frac{\sum_{j=1}^n (r_{ij} - \bar{r}_i)^2}{(n-1)} \quad \dots(3)$$

$$S^{(3)} = \frac{\sum_{j=1}^n (r_{ij} - \bar{r}_i)^2}{\bar{r}_i} \quad \dots(4)$$

$$S^{(6)} = \frac{\sum_{j=1}^n |r_{ij} - \bar{r}_i|}{\bar{r}_i} \quad \dots(5)$$

Where,

r_{ij} = Rank of i^{th} genotype in j^{th} environment (Ranks are assigned from lowest to highest).

$\bar{r}'_{ij}$ = Mean of ranks across all environments.

$\bar{r}_i$ = Mean of ranks of i^{th} genotype across all environments.

The Thennarasu parametric models are as follows:

$$NP^1_i = \frac{1}{n} \times \sum_{j=1}^n |r^*_{ij} - M^*_{di}| \quad \dots(6)$$

$$NP^2_i = \frac{1}{n} \times \left[\sum_{j=1}^n \frac{|r^*_{ij} - M^*_{di}|}{M_{di}} \right] \quad \dots(7)$$

$$NP^3_i = \frac{\sqrt{\sum_{j=1}^n (r^*_{ij} - \bar{r}_i)^2 / n}}{\bar{r}_i} \quad \dots(8)$$

$$NP^4_i = \frac{2}{n(n-1)} \left[\sum_{j=1}^{n-1} \sum_{j'=j+1}^n |r^*_{ij} - r^*_{ij'}| / \bar{r}_i \right] \quad \dots(9)$$

Where,

M_{di} = Median ranks of i^{th} genotype.

M^*_{di} = Adjusted median ranks of i^{th} genotype.

r_{ij} = Rank of i^{th} genotype in j^{th} environment.

r^*_{ij} = Adjusted rank of i^{th} genotype in j^{th} environment.

Table 1: Agro-climatic conditions of four different environments.

Environments	Average annual rainfall (mm)	Temperature range ($^{\circ}\text{C}$)
E1: Navsari	1864.0	18.0-42.0
E2: Bharuch	962.0	10.0-43.0
E3: Achhalia	1150.0	11.0-45.8
E4: Mangrol	1192.5	19.5-38.5

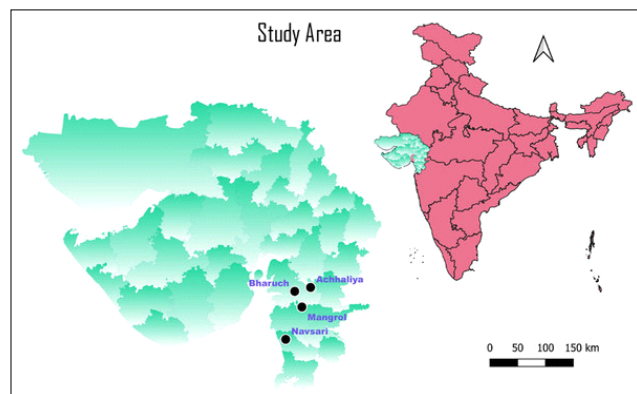


Fig 1: 14 pigeon pea genotypes grown over four different locations of Gujarat.

$\bar{r}_i$ = Mean rank of i^{th} genotype.

r^*_{ij} = Adjusted mean rank of i^{th} genotype.

The comparison between the parametric and non-parametric models has been done by using spearman rank correlation by SPSS v26.00.

RESULTS AND DISCUSSION

AMMI analysis

Table 2 displays the average yields of 14 pigeon pea genotypes across four different environments. The average grain production of genotypes across environments varied from 861.67 kg ha⁻¹ for G4 to 3776.67 kg ha⁻¹ for G4. The ANOVA results derived from the AMMI model for grain yield across 14 pigeon pea genotypes in four different environments are presented in Table 3. The table indicates that the major effects of the environment (E), genotypes (G) and their interactions (G $\times$ E) were highly significant ($p < 0.01$), accounting for 59.98%, 25.98% and 14.18% of the total variation, respectively. The interaction was divided among the first two principal component axes of interaction (IPCA) due to its significance in predictive evaluation. Two principal components analyses (PCAs) were notably significant, accounting for 80.50% of the overall variation in the genotype-by-environment (G $\times$ E) interaction sum of squares (54.70% and 25.80%, respectively) as presented in Table 3. Prior research indicated that in the majority of instances, the highest GEI may be elucidated by employing the initial two principal component analyses (Naresh *et al.*, 2025). The first and subsequent IPCA scores were determined to be very significant ($P < 0.01$), with mean sums of squares of 295803.6 and 160606.6, respectively.

AMMI 1 and AMMI 2 biplot analyses main effects and interactions across different environments. The AMMI 1 biplot shows genotype and environment's main effects on the abscissa and the first IPCA on the ordinate. A biplot implies that main effects with IPCA scores approaching zero have few interaction effects. When genotype and environment have the same IPCA axis sign, their interaction is positive; otherwise, it is negative (Rao *et al.*, 2020). The IPCA1 and IPCA2 scores for different genotypes and environments for AMMI and GGE analyses are presented in Table 4 and 5 respectively.

Mean performance and PCA1 scores for genotypes and environments used to build the AMMI 1 biplot (Fig 2a). Genotypes G4, G13, and G6 were unstable, although G12, G5, G7 and G11 were stable. The best yielding genotype is G9, followed by G8 and G12. Environment E1 produces the least, followed by E2 and E4. The IPCA 1 and IPCA 2 biplot shows genotype-environment interaction. Genotypes and environments furthest from the origin are more receptive and less compatible with the inferior genotype. Genotypes with limited interaction along both axes are near the origin (Anandan *et al.*, 2009). Genotypes and environments in opposing sectors have opposite impacts. IPCA2 and IPCA1 scores were used to create an AMMI 2 biplot for yield (Kg ha⁻¹) for 14 pigeon pea genotypes in four environments

(Fig 2b). Thus, genotypes G11, G12, G5, and G8 are most stable. Environment E1 favored genotype G6, while E2 favored G3. Genotypes G8 and G5 thrive in E3, while genotypes G11, G12 and G10 thrive in E4.

GGE biplot analysis

GGE biplot analysis used the average yield of 14 pigeon pea genotypes in four different environmental conditions.

The first two principal components in the GGE biplot explained 74.50% of GGE variation (PC1 = 50.90% and PC2 = 23.60%). In Fig 3a, a polygon view of the GGE biplot shows the “which-won-where” pattern based on the mean yield and stability of 14 pigeon pea genotypes in four different environments. The GGE biplot’s “which-won-where” perspective shows which genotypes perform best in different regions. All other genotypes are contained in

Table 2: Mean yield (kg ha^{-1}) of 14 pigeon pea genotypes in four environments.

Code	Genotypes	Navsari E1	Bharuch E2	Achhalia E3	Mangrol E4	Mean yield (Kg ha^{-1})
G1	BP-08-06	1555.00	1955.00	2006.00	2049.33	1891.33
G2	BP-10-03	1356.00	1646.67	1170.00	1845.67	1504.58
G3	BP-11-11	1478.33	2406.67	1427.33	1969.00	1820.33
G4	BP-15-28	1343.67	2541.67	861.67	1909.33	1664.08
G5	BP-12-31	1327.33	2045.00	1556.00	2185.00	1778.33
G6	NPMK-14-01	1814.67	1721.67	932.00	1808.33	1569.17
G7	NPMK-15-02	1259.67	1941.67	1312.00	1409.00	1480.58
G8	NPMK-15-03	1591.33	2135.00	1826.33	2202.33	1938.75
G9	NPMK-15-05	2066.33	2365.00	2160.33	2278.00	2217.42
G10	NPMK-15-07	1550.33	1936.67	1440.33	2083.33	1752.67
G11	Vaishali	1814.33	2195.00	1646.00	1621.67	1819.25
G12	ICPL-87119	1694.33	2125.00	1697.67	2081.67	1899.67
G13	GJP-1	1084.00	1943.33	1852.00	1518.33	1599.42
G14	BDN-2	1262.33	2020.00	2006.00	2134.67	1855.75
	Mean	1514.12	2069.88	1563.83	1935.40	

Table 3: AMMI variance analysis for grain yield of 14 pigeon pea genotypes in four environments.

Source	df	SS	MS	%SS _T	%SS _{G×E}
Environment	3	9461107	3153702***	59.98	
Genotype	13	6092704	468670***	25.98	
G $\times$ E	39	8108185	207902***	14.18	
IPCA 1	15	4437054	295803.6**		54.70
IPCA 2	13	2087886	160606.6**		25.80
Total	83				

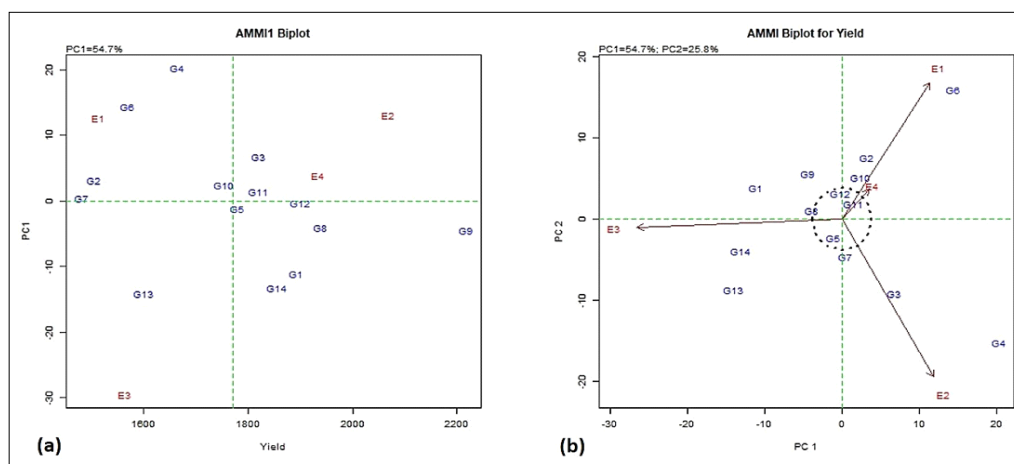


Fig 2: (a) AMMI 1 biplot (IPCA 1 vs. mean); (b) AMMI 2 biplot (IPCA 2 vs. IPCA 1) for grain yield.

the polygon made by joining extreme genotypes. Light rays orthogonal to the biplot borders divided it into sectors. The top genotype in each region yields the most. This study addressed vertex genotypes G4, G6, G7, G9, G13, and G14. All environments are in one of the five sectors the ray divided the biplot into (Fig 3a). G9 dominates this area, making it the best genotype in all situations. Fig 3b ranks 14 pigeon pea genotypes by average yield and stability in four situations. The average environmental coordinate (AEC) axis starts at the biplot's origin. Right and left AEC ordinates indicate high- and low-performing genotypes. The genotypic stability line is perpendicular to the AEC from the biplot's origin.

Thus, the yield ranking allowing order $G9 > G8 > G12 > G1 > G14 > G3 > G11 > G5 > G10 > G4 > G13 > G6 > G2 > G7$. The genotypes G9, G12, G11, G5, G7 and G5 were found highly stable owing to their closeness to AEC axis. The genotype G9 was found to be the ideal genotype. The genotypes G4, G6 and G13 were least in stability.

Environmental patterns were assessed using the environment-centered GGE biplot (Fig 4a). Vectors are drawn from test environments to the biplot origin to investigate environment links. Connection between environments is measured by the cosine of their angle (Dehghani *et al.*, 2010). Acute angles (positive correlation) exist between E1 and E2. Environments with a broad obtuse angle indicate a large genotype-environment crossover (Yan and Tinker, 2006). Present study shows a negative connection with E3 environment. The genotype-focused scaling GGE biplot vector additionally compares genotype distinction. Fig 4b shows equal group location for genotypes G5, G8 and G9. G11 and G12 were divided into groups, however G7 had low grain yield and was unsuited for any environment. Genotypes can also be distinguished by dissimilarity.

Non-parametric stability measures

Table 6 shows the non-parametric stability statistics values along with mean yield for various genotypes.

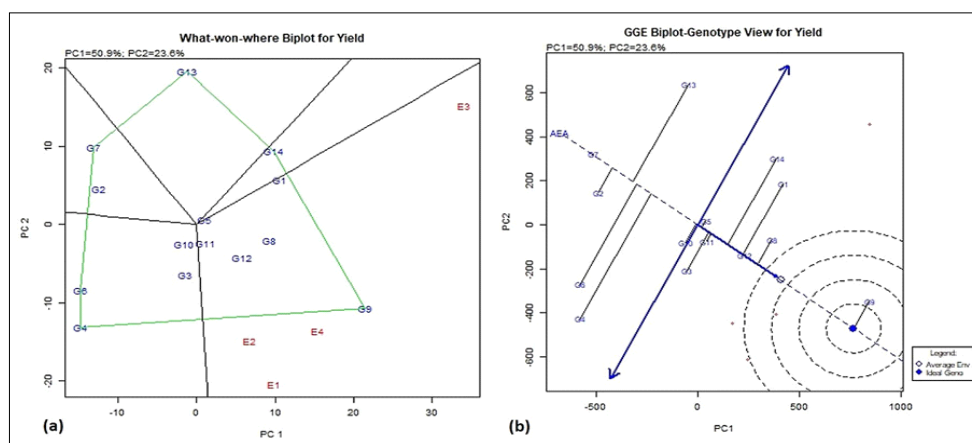


Fig 3: (a) Polygon view of the GGE biplot showing the “which-won-where” pattern; (b) Average environment coordination (AEC) view of the ranking GGE biplot.

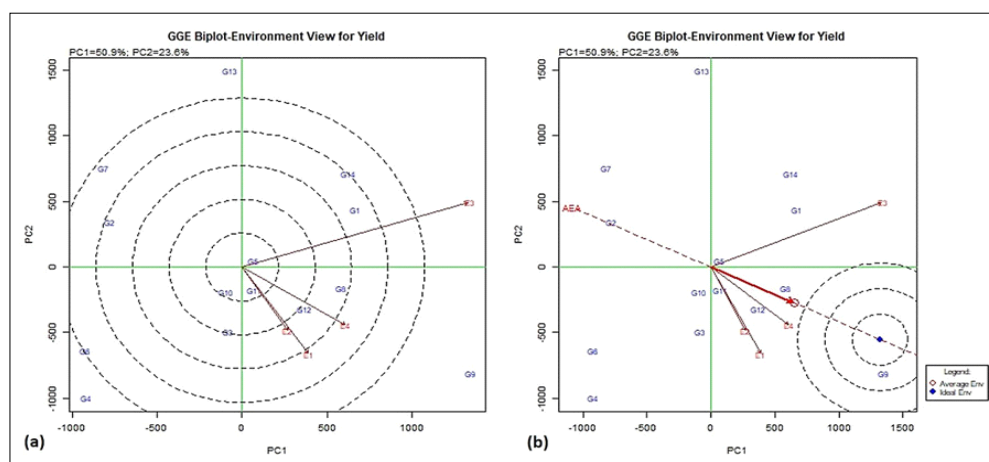


Fig 4: (a) Vector view of GGE biplot of environment-focuses scaling; (b) comparison of environments with ideal environment.

The mean values across the environment shows that the genotypes G9 is the highest in yield followed by G8 and G12. The Huen's stability statistics $S^{(1)}$, $S^{(2)}$, $S^{(3)}$ and $S^{(4)}$ showed that the genotype G9 is the most stable followed by G12. According Thennarasu's stability statistics $NP^{(1)}$, the genotype G12 is the stable followed by G8 and G7. Similarly according to $NP^{(2)}$, the genotypes G12, G8 and G5 are stable. As per $NP^{(3)}$, the genotypes G12, G8 and G9 are stable and as per $NP^{(4)}$, the genotypes G9, G12 and G8 are stable in their decreasing orders of stability. Fig 5 shows the rankings of all the non-parametric stability statistics along with ranking for mean yield for all the genotypes. It is very well depicted by Fig 5 that G9 genotype came 6 times on rank 1 among all the measures.

Spearman rank correlation among various stability statistics

A heat map based on Spearman rank correlation coefficients was plotted to show the relationships of yield with parametric and nonparametric stability statistics (Fig 6). The mean yield was found to be significant and positively correlated with $S^{(3)}$, $S^{(6)}$, $NP^{(2)}$, $NP^{(3)}$ and $NP^{(4)}$. The AMMI IPCA1 shows significant and positive correlation with GGE IPCA1 and GGE IPCA2, whereas the GGE IPCA1 shows significant and positive correlation with mean yield, AMMI IPCA1, $S^{(3)}$, $S^{(6)}$, $NP^{(2)}$, $NP^{(3)}$ and $NP^{(4)}$. GGE IPCA2 shows significant and positive correlation with AMMI IPCA1. $S^{(1)}$ was found to be significant and positively correlated with $S^{(2)}$, $S^{(3)}$, $S^{(6)}$, $NP^{(1)}$, $NP^{(3)}$ and $NP^{(4)}$. $S^{(2)}$ was found significant and positively correlated with $S^{(1)}$, $S^{(3)}$, $S^{(6)}$, $NP^{(1)}$ and $NP^{(4)}$. $S^{(3)}$ was found

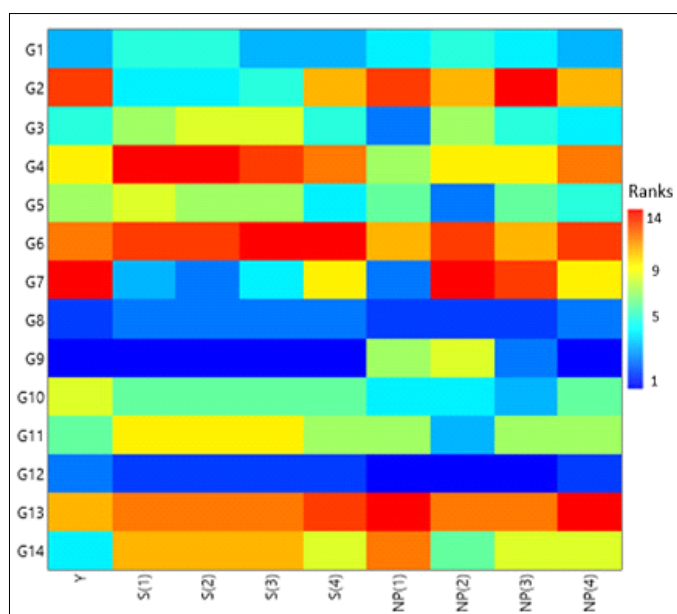


Fig 5: Rankings of mean yield and non-parametric stability statistics for various genotypes of pigeon pea.

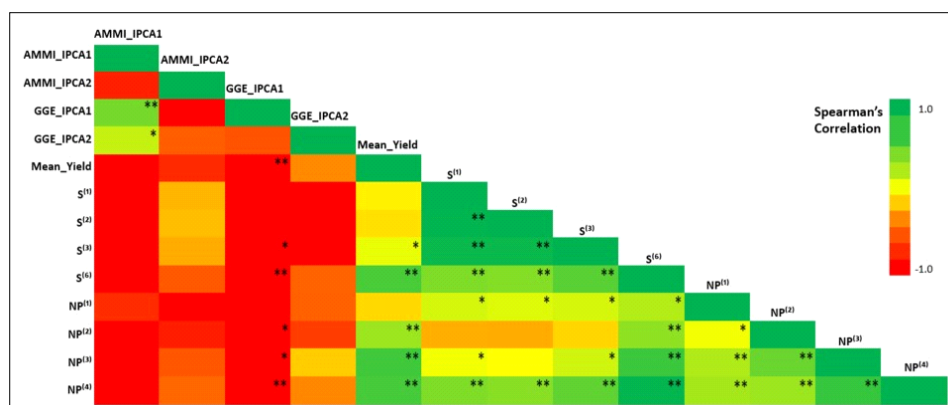


Fig 6: Comparison among the stability models (Parametric and non-parametric) using spearman rank correlation coefficients for the character yield of pigeon pea.

Table 4: AMMI scores for genotypes and environments.

AMMI	G1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12	G13	G14	E1	E2	E3	E4
IPCA1	-11.19	3.09	6.68	20.29	-1.21	14.29	0.43	-4.02	-4.51	2.41	1.45	-0.33	-14.13	-13.24	12.56	13.09	-29.53	3.88
IPCA2	3.86	7.53	-9.19	-15.23	-2.29	15.98	-4.62	1.00	5.58	5.16	1.81	3.14	-8.78	-3.95	18.65	-21.64	-1.12	4.11

Table 5: GGE IPCA1 and IPCA2 scores of various environment and genotypes of pigeon pea.

GGE	G1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12	G13	G14	E1	E2	E3	E4
IPCA1	-418.11	490.29	55.28	579.18	-39.96	581.63	512.63	-363.52	-843.17	62.6	-45.35	-228.91	46.25	-388.85	-0.25	-0.17	-0.87	-0.39
IPCA2	-186.02	-146.87	209.96	426.87	-20.23	271.24	-321.88	67.67	347.00	81.54	75.73	137.28	-638.13	-304.16	0.63	0.46	-0.47	0.42

Table 6: Non-parametric stability statistics values for various genotypes of pigeon pea.

Genotype	Y	S ⁽¹⁾	S ⁽²⁾	S ⁽³⁾	S ⁽⁶⁾	NP ⁽¹⁾	NP ⁽²⁾	NP ⁽³⁾	NP ⁽⁴⁾
G1	1891.33	3.17	6.25	2.14	0.80	2.75	0.32	0.45	0.36
G2	1504.59	2.83	4.92	3.93	1.87	4.75	1.06	1.28	0.76
G3	1820.33	4.00	12.00	4.50	1.25	2.50	0.43	0.48	0.50
G4	1664.09	6.67	29.67	13.69	2.31	3.75	0.82	0.72	1.03
G5	1778.33	4.17	10.92	4.23	1.16	3.50	0.30	0.52	0.54
G6	1569.17	5.83	27.58	15.76	2.95	4.00	1.42	0.87	1.11
G7	1480.59	1.83	2.25	2.45	1.82	2.50	1.92	1.18	0.67
G8	1938.75	1.50	2.25	0.63	0.42	2.25	0.23	0.23	0.14
G9	2217.42	1.00	1.00	0.22	0.22	3.75	0.43	0.28	0.07
G10	1752.67	3.83	8.92	3.96	1.33	2.75	0.32	0.42	0.57
G11	1819.25	5.00	16.33	5.76	1.41	3.75	0.32	0.54	0.59
G12	1899.67	1.00	1.00	0.32	0.32	0.75	0.22	0.09	0.11
G13	1599.42	5.50	20.25	12.79	2.74	5.00	1.07	1.09	1.16

significant and positively correlated with $S^{(1)}$, $S^{(2)}$, $S^{(6)}$, $NP^{(1)}$, $NP^{(3)}$ and $NP^{(4)}$. $S^{(6)}$ was found significant and positively correlated with all the Thennarasu's non-parametric statistics. $NP^{(1)}$ was found significant and positively correlated with all Thennarasu's non-parametric statistics $NP^{(2)}$, $NP^{(1)}$ and $NP^{(1)}$. $NP^{(2)}$ was found significant and positively correlated with $NP^{(3)}$ and $NP^{(4)}$.

CONCLUSION

Some plant breeders use dynamic stability to select genotypes with good yield and stability in different environments. G9, one of 14 pigeon pea genotypes tested, was stable and productive in four conditions, indicating GEI. G12, G5, and G8 were the most stable genotypes in parametric and non-parametric stability models. AMMI analysis improved understanding of the Genotype-Environment Interaction (GEI) through variance analysis and genotypic fitness sensitivity to environments. The AMMI study found that environment E2 yields the most, followed by E4 and E1. Environment E1 favored genotype G6, but E2 favored genotype G3. G11, G12 and G10 yield well in E4, while G8 and G5 thrive in E3. The comparison between parametric and non-parametric stability models showed that AMMI IPCA1 has a significant and positive correlation with GGE IPCA1 and GGE IPCA2, while GGE IPCA1 has a significant and positive correlation with mean yield, AMMI IPCA1, $S^{(3)}$, $S^{(6)}$, $NP^{(2)}$, $NP^{(3)}$ and $NP^{(4)}$. The non-parametric stability statistics are positively correlated.

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Conflict of interest

The authors declare no potential conflict of financial or non-financial interest relevant to this article.

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