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PHENOTYPIC STABILITY AND GGE BILOT ANALYSIS IN PIGEONPEA [*Cajanus cajan* (L.) Millsp.] GENOTYPES ACROSS THE ENVIRONMENTS

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Phenotypic stability

GGE Biplot and *Cajanus cajan* (L.) Millsp

ABSTRACT

Phenotypic stability was carried out by using Eberhart & Russell model, as well as recent GGE biplot approach for identification of the foremost genotypes across the different environments in pigeonpea [*Cajanus cajan* (L.) Millsp.] genotypes. Further, Pearson correlation was carried out to correlate the different yield contributing attributes with seed yield. Fifty six pigeonpea genotypes comprising fourteen parents, forty hybrids and two standard checks were evaluated at four environments during *kharif* season of 2013 and 2014, to study genotype × environment interaction for yield and related traits. A significant difference was obtained for yield and yield contributing characters among genotypes in individual as well as pooled environments except for pod length, 100 seed weight and seed protein content (%). For traits like days to maturity, plant height, pods per plant, pod clusters per plant, seeds per pod, 100 seed weight and seed yield per plant Genotypes × Environments (linear) values were significant when tested against pooled deviation. Some hybrids such as GT 610 A × GTR 84 (119.79 g), GT 603 A × GTR 81 (119.41 g), GT 610 A × GTR 82 (119.20 g), GT 607 A × GTR 82 (116.07 g), GT 601 A × GTR 82 (113.03 g) and GT 604 A × GTR 81 (110.92 g) depicted significant stability for the yield and yield components by Eberhart & Russell model. Similar results were observed by GGE biplot analysis for three hybrids viz., GT 610 A × GTR 84 (119.79 g), GT 603 A × GTR 81 (119.41 g) and GT 610 A × GTR 82 (119.20 g) which depicted significant stability for the yield and its components and could be promising for cultivation across different environments in Western India.

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1 Introduction

Pulses are climate smart and have been a nutritious part of the international diet for centuries. Nevertheless “slow runner” (Borlaug, 1972), pulses steadily rise in popularity among people and captured international attention due to their multi facet, nutrients and healthy diet appeal. The 2016 year has been declared as the “International Year of Pulses”/IYP-2016, on a global scale which would enhance productivity and awareness on pulses (Brick & Fisher, 2016). One of the fascinating legume crop pigeonpea [*Cajanus cajan* (L.) Millspaugh] belong to diploid genome ($2n = 2x = 22$) (Reddy et al., 1980) and have ~833.0 Mb of genome size (Varshney et al., 2012; Singh et al., 2012). It is the best versatile food legume, span over a wide area of the world with diversified uses and also benchmark with “sustainable agriculture” with enormous existing wild diversity, India is considered to be the “hot spot” and center of origin for pigeonpea (Van der Maesen, 1990). It is well known as finest nitrogen fixer and nutrient re-cycler (Graham & Vance, 2003; Srivastava et al., 2012). In India, the crop was grown under 3.90 million hectares with 3.17 million tonnes production having low productivity of 813 kg/ha during 2013-14 (Anonymous, 2017).

The lower productivity of the crop was the big concern that directly or indirectly affects the national food security hence reasons for lower productivity of the crop was the issue to be debated in numbers of forward thinking sessions in India. Some studies revealed that the yield plateau could be broken by identifying new and stable sources of male sterility or resistance for biotic-abiotic stresses from wild germplasm and also by adopting molecular tools for creating variability for use in future (Pagi et al., 2016).

To address this long standing yield stagnation in pigeonpea, Cytoplasmic Male Sterile (CMS) or Cytoplasmic Genetic Male Sterile (CGMS) based hybrids were used in breeding programme at the State Agricultural Universities (SAUs) having A_2 cytoplasm from *C. scarabaeoides* (Tikka et al., 1997; Saxena & Kumar, 2003) and at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) hybrids having A_4 type of cytoplasm from *Cajanus cajanifolius* (Saxena et al., 2005). Hence, the cytoplasmic genetic male sterility technology has flagged a way for heterosis breeding and set a stage for breaking the yield plateau.

For heterogeneous varieties in terms of their domain of time and space, assessing their Genotype x Environment interaction is indispensable and worthy for predicting their stability across environment. The success of variety of any crop depends upon its stable performance over varied environments (Wanjari et al., 1988). Hence, identifying the stable genotypes across the environments for yield and its attributing traits is the prime

requisite for any breeding programmes. The GGE (Genotype and Genotype×Environment interaction) biplot methodology of analyzing Multi-Environment Trial (MET) data has emerged as a powerful tool for G×E analysis with smart and immaculate visual outputs for plant breeders, quantitative geneticist and agronomists (Yan et al., 2000; Yan & Kang, 2003; Yan & Tinker, 2006). This approach puts G and GE interaction together called GGE (Yan et al., 2000), on a graphic biplot imagining tool based on methodology endorsed by Gabriel (1971). Hence, the present investigation was planned and executed to understand the $G \times E$ interaction of A_2 cytoplasm based pigeonpea hybrids and varieties over the geographical locations for yield and its attributes conferring their stability by using Eberhart & Russell model as well as GGE biplot analysis.

2 Materials and Methods

The field trials were conducted during *kharif* 2012 to 2014. During *kharif* 2012, the genotypes were developed by crossing ten CMS lines viz., GT 601 A, GT 602 A, GT 603 A, GT 604 A, GT 605 A, GT 606 A, GT 607 A, GT 608 A, GT 609 A and GT 610 A containing A_2 cytoplasm (Tikka et al., 1997; Saxena & Kumar, 2003) with four different fertility restorers i.e., GTR 81, GTR 82, GTR 83 and GTR 84. The crosses were attempted in line × tester mating design. The resultant F_1 s along with their parents and two standard checks (GT 101 and GTH-1) were evaluated at two different location i.e., Pulses Research Station ($24^{\circ}12' N$, $72^{\circ}12' E$ and 154.5 m), Sardarkrushinagar Dantiwada Agricultural University (SDAU), Sardarkrushinagar and Main Maize Research Station ($23^{\circ}76' N$, $73^{\circ}24' E$ and 204 m), SDAU, Bhiloda during the *kharif* seasons of the year 2013 and 2014, using a Randomized Block Design (RBD) with three replications. The observations for eleven characters viz., days to flowering (DF), days to maturity (DM), plant height (PH) in cm, number of branches per plant (NBP), pod clusters per plant (PCP), pods per plant (PP), seeds per pod (SP), pod length (PL) (cm), 100 seed weight (SW) in g, seed yield per plant (SYP) in g and protein content (PC) (%) were recorded after random selection of five plants from the each plots. All the cultural practices were adopted to raise a normal healthy crop (Mula et al., 2010).

Statistical analysis was carried out using INDOSTAT software. Analysis of variance was partitioned into variation due to genotypes, environments and genotype by environment interaction. The stability analysis was done as per suggested by Eberhart & Russell model (1966). The stable genotypes were further studied to estimate the main and genotype-environment interaction effect for seed yield, using GGE (G = genotype effect and GE = genotype-by-environment) biplot approach proposed by Yan (1999) and Yan et al., (2000). The GGE biplot analysis was done using PBTtools software version 1.4 (PBTtools, 2014). The asset of the association

between yield and its components were verified using Pearson correlation analysis computed by XLSTAT version 2015.6.03.

3 Results and Discussion

The genotypes which are phenotypically stable are of immense important for viable production of crop plants. According to Eberhart & Russell (1966) model of stability analysis, three kinds of linear responses of regression coefficient (b_i) have been considered and interpreted as $b_i=1$, average stability and widely adaptable to different environments; $b_i>1$, below average stability, increasing sensitivity to environmental changes and well adapted to favorable environment and $b_i<1$, above average stability, greater tolerance to environmental changes; thereby genotypes would have specific adaptability to poor yielding environment.

The current study was conducted to have the information about the performance of newly developed cross combinations and controls across diverse environments. All the fifty six genotypes were significantly differed from each other signifying presence of variation among them to carry out study (Table 1). Therefore, the mean performance of hybrids for phenotypic stability and $G \times E$ interaction was deduced. The genotypes $\times$ environment interaction was found significant for days to maturity, plant height, pod clusters per plant, pods per plant, seeds per pod, 100-seed weight and seed yield per plant which indicates that genotypes interacted differently with environmental variations for above characters. Those characters which observed significant for $G \times E$ interaction were also reported significant for $G \times E$ (linear) and possessed higher value than the non linear components i.e. pooled deviation. Phad et al (2005) also found significant $G \times E$ interaction for yield and its related traits of pigeonpea. This reflected greater importance of linear portion in building up total $G \times E$ interactions

and the possibility of prediction across the environments for these characters.

The analysis of variance for stability analysis revealed that genotype $\times$ environments interaction was significant (Table 1). The linear components were found to be more significant for both linear and pooled deviation of $G \times E$ study. The significance of linear component of $G \times E$ interaction suggested that the genotypes responded in linear fashion to environments and performance could be predicted.

Eighteen hybrids had higher mean than average mean (94.18 g) among these hybrids four and three hybrids were exhibiting significant b_i and S^2d_i , which indicating more contribution from linear components of $G \times E$ interactions (Table 2). The six stable hybrids over environments were GT 610 A $\times$ GTR 84 (119.79 g), GT 603 A $\times$ GTR 81 (119.41 g), GT 610 A $\times$ GTR 82 (119.20 g), GT 607 A $\times$ GTR 82 (116.07 g), GT 601 A $\times$ GTR 82 (113.03 g) and GT 604 A $\times$ GTR 81 (110.92 g) had higher mean than average mean, non-significant regression unity and least deviation from regression revealed that stable hybrids for varied environments for seed yield per plant (higher mean $>$ cross mean, $b_i = 1$ NS, $S^2d_i = 0$ NS). Hybrids GT 609 A $\times$ GTR 83 (110.56 g) and GT 606 A $\times$ GTR 81 (104.63 g) had higher mean than average mean, significant regression above the unity and least deviation from regression revealed that stable hybrids for favourable environments for seed yield per plant (higher mean $>$ cross mean, $b_i > 1$ significant, $S^2d_i = 0$ NS).

The mean yield of each genotype depends on the particular set of environmental conditions. It is, therefore, suggested that in order to identify stable genotype, actual testing over a wide range of environments. Hence, while selection, more emphasis should be

Table 1 Analysis of variance (mean squares) for phenotypic stability pertaining to various characters in pigeonpea

Source of variation	d.f.	Characters										
		Days to flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Pod clusters per plant	Pods per plant	Seeds per pod	Pod length (cm)	100-seed weight (g)	Seed yield per plant (g)	Protein content (%)
Genotypes (G)	55	288.15**	119.43**	12852.35**	1.32**	269.52**	7268.51**	0.14**	0.20	1.95**	1355.61**	36.85**
Environments (E)	3	155.67**	132.27**	806.27**	3.64**	2267.72**	1867.17**	0.48**	0.27	0.01	194.44**	2.22
$G \times E$	165	2.59	9.46*	24.53**	0.15	26.81**	352.52**	0.07**	0.17	0.08**	25.62**	4.42
Environments (linear)	1	467.00**	396.82**	2418.80**	10.91**	6803.15**	5601.51**	1.43**	0.81*	0.02	583.33**	6.65
$G \times E$ (linear)	55	3.70**	15.61**	62.74**	0.14	72.96**	382.49**	0.12**	0.15	0.16**	26.58**	1.54
Pooled deviation	112	1.99	6.27	5.33	0.15	3.67	331.51**	0.04	0.18**	0.04**	22.74**	5.76**
Pooled error	440	6.15	9.21	80.83	0.14	13.04	128.84	0.03	0.06	0.06	27.36	0.32

*, ** Significant at 5 and 1 per cent probability levels, respectively.

Table 2 Stability analysis of hybrids for average, favorable and poor environments

S. No.	Environments	Hybrids	Seed yield per plant (g)	Bi	S ² di	Stability for component characters
1.	Average Env.	GT 610 A × GTR 84	119.79	2.80	24.35	DM, PP, SP, SW
		GT 603 A × GTR 81	119.41	2.71	65.59	DM, PCP, PP, SP, SW
		GT 610 A × GTR 82	119.20	3.83	30.54	DM, PP, SP, SW
		GT 607 A × GTR 82	116.07	4.28	31.67	DM, PCP, PP, SP, SW
		GT 601 A × GTR 82	113.03	4.80	-8.66	DM, NBP, SP
2.	Favorable Env.	GT 604 A × GTR 81	110.92	-0.34	18.98	DM, PCP, PP, SP, SW
		GT 609 A × GTR 83	110.56	3.53*	-31.34	PH, SP
3.	Poor Env.	GT 606 A × GTR 81	104.63	3.29*	-33.36	-
		-	-	-	-	-

Where, DM = Days to maturity, PP = Pods per plant, PH = Plant height (cm), SW = 100-seed weight (g), PCP = Pod clusters per plant, SP = Seeds per pod,

Table 3 Pearson correlation between different yield and yield contributing traits at four locations

Variables	Environments	DF	DM	PH	NBP	PCP	PP	SPP	PL	SW	SYP
DF	Sardarkrushinagar 2013	1	0.467**	0.372**	-0.207	0.151	0.395**	-0.057	-0.001	-0.17	0.286
	Bhiloda 2013	1	0.517**	0.445**	0.080	0.204	0.455**	-0.192	-0.095	-0.149	0.268
	Sardarkrushinagar 2014	1	0.611**	0.430**	-0.021	0.118	0.386**	0.033	0.176	-0.138	0.267
	Bhiloda 2014	1	0.443**	0.407**	0.136	0.228	0.472**	0.020	-0.134	-0.107	0.288
DM	Sardarkrushinagar 2013	1	0.345**	0.04	0.253	0.359**	-0.044	-0.029	0.085	0.381**	
	Bhiloda 2013	1	0.364**	0.290	0.395**	0.442**	-0.202	-0.037	0.058	0.422**	
	Sardarkrushinagar 2014	1	0.301	0.128	0.286	0.379**	0.173	-0.087	0.175	0.359	
	Bhiloda 2014	1	0.107	0.131	0.182	0.254	0.113	0.074	0.017	0.253	
PH	Sardarkrushinagar 2013	1	-0.129	0.384**	0.747**	-0.101	-0.043	0.117	0.424**		
	Bhiloda 2013	1	0.014	0.481**	0.744**	-0.292	-0.016	0.038	0.395**		
	Sardarkrushinagar 2014	1	-0.040	0.202	0.828**	0.044	0.105	-0.063	0.496**		
	Bhiloda 2014	1	-0.024	0.416**	0.707**	0.100	-0.243	0.052	0.448**		
NBP	Sardarkrushinagar 2013	1	-0.067	-0.1	-0.104	-0.083	0.256	0.075			
	Bhiloda 2013	1	0.128	0.224	-0.068	0.201	0.331	0.250			
	Sardarkrushinagar 2014	1	0.203	0.015	0.058	0.037	0.479**	0.075			
	Bhiloda 2014	1	0.121	0.074	-0.099	0.042	0.178	0.273			
PCP	Sardarkrushinagar 2013	1	0.258	-0.001	0.164	0.252	0.334				
	Bhiloda 2013	1	0.389**	-0.127	0.081	0.179	0.459**				
	Sardarkrushinagar 2014	1	0.112	0.024	-0.027	0.283	-0.031				
	Bhiloda 2014	1	0.410**	0.150	-0.062	0.140	0.371**				
PP	Sardarkrushinagar 2013	1	-0.175	-0.093	0.077	0.640**					
	Bhiloda 2013	1	-0.160	-0.070	0.124	0.724**					
	Sardarkrushinagar 2014	1	0.022	0.172	0.048	0.670**					
	Bhiloda 2014	1	-0.087	-0.213	0.064	0.678**					
SPP	Sardarkrushinagar 2013	1	0.256	0.074	0.12						
	Bhiloda 2013	1	0.070	0.015	0.174						
	Sardarkrushinagar 2014	1	-0.103	0.090	0.290						
	Bhiloda 2014	1	-0.208	-0.059	0.032						
PL	Sardarkrushinagar 2013	1	0.103	0.133							
	Bhiloda 2013	1	0.242	-0.029							
	Sardarkrushinagar 2014	1	-0.010	0.081							
	Bhiloda 2014	1	-0.047	-0.195							
SW	Sardarkrushinagar 2013	1	0.347**								
	Bhiloda 2013	1	0.246								
	Sardarkrushinagar 2014	1	0.252								
	Bhiloda 2014	1	0.239								
SYP	Sardarkrushinagar 2013	1									
	Bhiloda 2013	1									
	Sardarkrushinagar 2014	1									
	Bhiloda 2014	1									

Values in bold with ** marks are different from 0 with a significance level alpha of 0.01 and significant at $p < 0.0001$; DF = Days to flowering, PP = Pods per plant, DM = Days to maturity, SP = Seeds per pod, PH = Plant height (cm), PL = Pod length (cm), NBP = Number of branches per plant, SW = 100-seed weight (g), PCP = Pod clusters per plant, SYP = Seed yield per plant (g).

paid to the phenotypic stability of traits which were directly related to seed yield per plant to achieve maximum stability for the end product *i.e.*, seed yield in pigeonpea.

Phenotypic stability of various component traits deciphering their seed yield stability was also reported by various workers *viz.*, Vanniarajan et al., 2000; Patel, 2004; Vanniarajan et al., 2007; Patel et al., 2009; Sreelakshmi et al., 2010; Sawargaonkar et al., 2011; Pawar et al., 2013 and Chand et al., 2014.

3.1 Correlation among the traits

The correlation coefficients were estimated among all the pairs of variables (Table 3). The traits, days to maturity, plant height and pods per plant had a positive and significant association with days to flowering for Sardarkrushinagar and Bhiloda in *kharif* 2013 and 2014. The plant height was a significant and exhibited positive correlation with days to maturity at Sardarkrushinagar and Bhiloda during *kharif* 2013. The significant and positive correlation was exhibited by pod clusters per plant with days to maturity (at Bhiloda, during *kharif* 2013) and plant height among locations. The number of pods per plant showed significant and positive association with days to flowering and plant height at all the environments, while it was significantly correlated in desired direction with pod clusters per plant at Bhiloda during *kharif* 2013 and *kharif* 2014. Hundred seed weight found significant and positively correlated with the number of branches per plant at Sardarkrushinagar during *kharif* 2013 and *kharif* 2014 while, plant height and pods per plant depicted positive correlation with seed yield across the environments. Seed yield also exhibited a significant and positive relationship with days to maturity during *kharif* 2013 at both the locations and pod clusters per plant during *kharif* 2013 and 2014 at Bhiloda. It indicated that these characters may be used in selection indices for amelioration of seed yield in pigeonpea for high yield. Similar findings were also reported by Sawargaonkar et al. (2011) in pigeonpea.

3.2 GGE Biplot analysis for parents and hybrids

Asserting phenotypic stability of genotypes over MET is prerequisite for checking variety performance and for such objective in past research has been focused on mean performance and further modified it to incorporating with the interaction component as AMMI (Additive Main Effects and Multiplicative Environments). From, long with introduction of AMMI (Williams, 1952) and GGE biplot (Yan, 1999; Yan et al., 2000), it has been always remain contrasting to choice one for better analysis.

Nevertheless, various modifications of the AMMI model were carried out; GGE biplots are thought to be a lucrative where biplot deliberates the relative magnitude of the G, environment main effect, and IPC1. GGE biplot explains an intercession proportion

of the sum of squares of both genotypes + genotypes by environments ($G + GE$), compared AMMI1 and AMMI2 mega-environment graphs. To more details, GGE model emphasizes the fact that the so-called G not only has a genotypic basis, but also is dependent on the environmental conditions so G is influenced by GEI. Therefore, viewing G in terms of GEI has one potential advantage: an examination of PC1 scores not only identifies genotypes with better overall performance but also suggests environmental conditions that facilitate identification of these genotypes hence; it is believed that GGE biplots are more accurate than AMMI1 and more pragmatic than AMMI2 mega-environment (Yan et al., 2007). Hence, if purpose is to find which cultivar won in which environments, AMMI biplot could be misleading and GGE biplot could be more effective and practical as it displays the relative magnitude of the G, environment main effect and IPC1.

3.3 What-won-where biplot for vertex genotype

In polygon “What-won-where” biplot genotype positioned as vertex showing longest detachment from biplot origin was considered to be most $G \times E$ interactive with stability. From our analysis biplot generated based on standard singular value decomposition model of untransformed mean seed yield data exhibited 98.6% ($PC\ 1 = 95.9\%$, $PC\ 2 = 2.7\%$) of total GGE variation, that strongly explained environment centered data and power of model to ascertain the stability of genotype across environment.

In the present study, the genotypes *viz.*, G_{54} (119.79 g), G_{23} (119.41 g), G_{52} (119.20 g), G_{37} (113.37 g) and G_{40} (116.07 g) were the vertex genotype which had a higher seed yield (Figure 1). The three environments *viz.*, E_1 , E_3 and E_4 were placed in the same plane on the graph, suggesting no significant difference among them. The individual environment, E_2 was positioned in separate plane. For environment E_2 , G_{48} (107.58 g) was the only vertex genotype. No single environment and the genotypes G_{11} , G_{12} , G_{13} , G_{14} and G_{59} were placed in a same sector of the graph specifying that the said genotypes were not suitable for cultivation in these studied environments.

“Ideal genotypes” exhibits stable performance over wide range of environment with higher yield (Yan & Kang, 2003). Among all the genotype, as per “ideal” view as shown in figure 2, G_{54} (119.79 g) found to be nearest to the “ideal genotype” followed by G_{52} (119.20 g) and G_{40} (116.07 g).

3.4 Average yield and stability of genotypes based biplot

Deciphering average mean performance with their phenotypic stability, a ranking or performing is achieved by drawing performance line (*i.e.* AEC) over GGE biplot. Here based on mean performance, ideal genotype is shown with an open blue the circle with arrows indicating absolute stable genotype, located on AEC abscissa as shown in figure 2. Hence, genotypes closer to circle are consistently stable while cultivar (genotype) farthest from point

Figure 1 Polygon view of the GGE biplot, showing which genotype yielded best in which environments

Figure 2 Comparison of genotypes with the ideal genotype showing the environmental axis (AEA) the GGE biplot. Environments and genotypes are denoted by 'E' and 'numeric value', respectively.

Figure 3 Comparison of all the environments with an ideal environment. The genotypes and environments are indicated by E and numeric value, respectively.

indicating poor stability. Therefore, it become apparent that in the current study, genotype G_{54} (119.79 g) was highest average seed yielder with consistent stability followed by G_{23} (119.41 g), G_{52} (119.20 g) and G_{40} (116.07 g) which were located very close to the genotype G_{54} (Figure 2). Our result were similar to the analyzed results of Eberhart & Russell model (1966) of the present study and can be recommended for cultivation across different environments in Western India

3.5 Evaluation of an environment based on GGE biplots

Nevertheless, potential of genotype to deliver maximum performance is locked into the genome. Yet is a cumulative function of genotype to environment. Therefore, ascertaining unbiased and whole representative environment that is suitable for genotype under testing is a complex yet prerequisite job. For MET with the question of phenotypic stability study, screening of genotype over “ideal” and discriminating environment is major emphasize job.

In current study, “ideal environment” (Figure 3) is represented by a small circle with an arrow pointing to it and further other environment are ranked based on distance from ideal environment. The pattern of environment in the biplots (Figure 3) on the basis

suggested that all the environments were clustered in one group. In the present study, as the angle between any two environments was less than 90° , $G \times E$ was moderately small and these environments tend to discriminate among genotypes in a similar manner. The environment, E_3 found to be far away from the origin of the plot and had the shortest projection onto AEA Y-axis signifying most discriminating environment. Both E_3 and E_4 depicted the longer vectors indicating the best environments for genetic discrimination of the genotypes, while, the environments, E_1 and E_2 were observed to be least representative environments in current study. A strong relationship was present between E_3 and E_4 based on the minimum angles between the vectors of them. The environments E_4 and E_2 were positioned close to E_1 , respectively. This showed that stable production of pigeonpea is possible in this environment. As per Tonk et al. (2011), these were the best environments for genotypes differentiation, while, the environment which showed large projection onto the AEA Y-axis suggesting them to be unfavorable and didn't have ability to discriminate the genotypes (Figure 3).

Conclusion

Understanding of decoding phenotypic stability of genotype is a major concern and it emphasize that $G \times E$ interaction benchmark

tremendous potential for deciphering stability of genotype. The present study clearly partitioned the effect of $G \times E$ interaction for seed yield and other related component traits associated with building up total $G \times E$ interaction. The traits, plant height and pods per plant illustrated positive correlation with seed yield across the four environments. Seed yield also exhibited a significant and positive relationship with days to maturity in *kharif* 2013 at both the locations and pod clusters per plant in *kharif* 2013 and 2014 at Bhiloda. It indicated that these characters may be used in selection indices for amelioration of seed yield in pigeonpea. From the GGE biplot analysis, it was also concluded that in “ideal” view, the genotype G₅₄/ GT 610 A $\times$ GTR-84 (119.79 g) was the closest to the ideal genotype, followed by G₅₂/ GT 610 A $\times$ GTR-82 (119.20 g) and G₄₀/ GT 607 A $\times$ GTR-82 (116.07 g).

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