

Studies on $G \times E$ Interaction in Early Maturing Pigeonpea [*Cajanus cajan* (L.) Millsp.] Genotypes

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Abstract Present investigation was carried out with 21 pigeonpea genotypes during *kharif* 2014 to estimate $G \times E$ interaction and stability parameters. Genotype variance was significant for all traits, except number of pods plant⁻¹ and pod length. Non significant $G \times E$ interaction observed for number of pods plant⁻¹, pod length, number of seeds pod⁻¹ and 100 seed weight. Pooled deviation variance was significant for all traits, except days to first flower initiation, pod length and number of seeds pod⁻¹. MN-5 was found stable genotype for yield attributing traits.

Keywords $G \times E$ interaction, Pigeonpea, Stability.

Introduction

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is one of the major legume, cultivated in varied agro-climatic conditions. Yield is polygenically inherited and highly influenced by $G \times E$ interaction. Higher magnitude of $G \times E$ interaction among genotypes invali-

dates the fitness of genotypes across the environments. Hence, quantification $G \times E$ interaction and identification of stable genotypes across environments will enhance production and productivity of pigeonpea. Recently ICRISAT developed early maturing genotypes which are less photoperiod and temperature sensitive, hence these genotypes could be used for expansion of pigeonpea cultivation to non traditional niches and to provide alternative cropping system option. With this background the present study was undertaken in four dates of sowing to identify stable early maturing pigeonpea genotypes for yield and yield attributing traits.

Materials and Methods

The present investigation comprised of 21 pigeonpea genotypes. Sixteen were super early genotypes (<50 days to fifty percent flowering) from ICRISAT and rest five as checks. These genotypes were tested in four sowing environments (Environment-1 : 15th June sown, Environment-2 : 15th July sown, Environment-3 : 15th August sown and Environment-4 : 15th September sown). With RCBD design, genotype were sown in 4 rows of 4 meter length with a spacing of 60 × 20 cm. Stability parameters viz., mean, regression co-efficient (bi) and mean square deviation (S^2_{di}) were estimated as per the stability model proposed by Eberhart and Russel [1].

Results and Discussion

The pooled analysis of variance for $G \times E$ interaction revealed, genotype variances were significant

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Table 1. ANOVA for G × E interaction of 12 quantitative traits over four environments. ** =>Significant at $p=0.01$, * =Significant at $p=0.05$.

Source of variation	df	Days to first flowering	Days to 50% flowering	Days to maturity	Plant height (cm)	Braches/plant	Number of pods/plant
Rep within Env.	4	0.060	1.747	1.512	21.63	0.228	16.18
Genotypes	20	578.04**	728.76**	768.43**	1292.79**	7.661**	180.30
Env. + (G × E)	63	20.96**	51.63**	135.88**	952.49**	7.672**	403.41**
Environments	3	325.15**	664.21**	1443.09**	14460.3**	111.92**	6438.4**
G × E	60	5.75**	21.00**	70.52**	277.10**	2.460*	101.66
Environments (Lin.)	1	975.47**	1992.72**	4329.2**	43381.12**	335.76**	19315.3**
G × E (Lin.)	20	15.80**	57.66**	200.58**	701.6**	4.672**	95.55
Pooled deviation	42	0.699	2.544**	5.235**	61.73**	1.289**	99.73**
Pooled error	80	0.610	0.641	1.718	13.51	0.503	5.004
Total	83	154.64	214.79	288.30	1034.49	7.670	349.67

Table 1. Continued.

Source of variation	df	Pod length (cm)	Number of seeds/pod	Pod bearing length (cm)	100 seed weight (g)	Seed yield /plant	Seed yield (kg/ha)
Rep within Env.	4	0.025	0.036	1.017	0.019	0.736	693.67
Genotypes	20	0.096	0.052*	181.33**	3.500**	13.31**	47305.27*
Env. + (G × E)	63	0.107*	0.059**	100.72**	0.240	9.280**	15334.6**
Environments	3	0.937**	0.644**	1002.57**	0.769	65.75**	2399375.0**
G × E	60	0.065	0.029	55.63**	0.214	6.456*	41032.6*
Environments (Lin.)	1	2.811**	1.933**	3007.72**	2.306**	197.25**	7198124.0**
G × E (Lin.)	20	0.075	0.036	144.96**	0.062	11.40**	77728.5**
Pooled deviation	42	0.057	0.025	10.44**	0.276**	3.793**	21604.4**
Pooled error	80	0.044	0.027	1.132	0.036	0.526	1099.3
Total	83	0.104	0.057	120.15	1.026	10.25	127785.4

for all traits, except for number of pods plant⁻¹ and pod length, indicates presence substantial variability (Table 1). Variability among the environments revealed by significant environmental variance for all the traits in agreement with Thanki et al. [2]. Highly significant G × E interaction suggesting that, genotypes behaved differently in different environments. The environment (linear) component was significant for all the traits except 100 seed weight, indicating the real genotypic difference for regression over environmental means. Further partitioning of G × E interaction into linear and non linear (pooled deviation) components with their significant variance for most of the traits indicates contribution of these in imparting the total G × E interaction. Reliable prediction of genotype performance over the environments indicated by the higher mag-

nitude of linear component than non linear component. The traits shown, significant Environmental + (Genotype × Environment) interaction were considered for stability analysis. Hence, a total of 11 characters were subjected for stability analysis (Table 1). The results are in accordance with, patel et al. [3], Sreelakshmi et al. [4], Chand et al. [5] and Arukumar et al. [6]. In contrast to this Mausumi et al. [7] observed significant G × E (linear) for number of pods per plant and 100 seed weight.

Once G × E interactions were found significant the next task was to identify the stable genotypes which interacts less with the environments giving a near consistent performance across environments. By considering the desirable mean, unit regression co-efficient and minimum deviation from regres-

Table 2. Stable genotypes for different quantitative traits under study, S^2di = Deviation from regression, bi = Regression co-efficient.

Sl. No.	Characters	Genotypes	Mean	S^2di	bi
1	Days to first flowering	PAU-881	44.25	-0.252	1.017
		ICPL-20341	42.25	-0.534	0.888
2	Days to fifty per cent flowering	ICPL-20330	50.00	1.222	1.020
		PAU-881	47.75	1.155	0.950
3	Days to maturity	PAU-881	89.37	-1.472	0.846
4	Plant height (cm)	ICPL-20337	63.03	-11.23	0.840
5	Branches per plant	MN-5	5.41	-0.310	0.947
		ICPL-20337	5.72	-0.252	0.888
6	Number of pods per plant	MN-5	37.95	5.40	1.237
7	Pod length (cm)	ICPL-2011253	4.64	0.024	1.103
		ICPL-20337	4.74	-0.024	1.116
8	Number of seeds per pod	ICPL-20330	3.84	-0.009	1.150
		ICPL-2011250	3.78	0.054	1.224
9	Pod bearing length (cm)	—	—	—	—
10	Seed yield per plant	ICPL-2011251	9.31	0.194	0.878
11	Seed yield (kg/ha)	MN-5	452.12	1945.69	1.178

sion, the genotype MN-5 was found stable for seed yield kg ha^{-1} ($X = 452.12$, $bi=1.178$, $S^2di = 1945.69$) and also for yield attributing traits like number of pods per plant and number of branches per plant. However, ICPL-20337 was also found stable for seed yield kg ha^{-1} . Except these two, none of the genotype found stable for either poorer or favorable environment, as they recorded significant deviation from regression. The genotypes which were found stable for each traits also investigated (Table 2). Similarly Sreelakshmi et al. [4], and Arunkumar et al. [6], found the stable genotypes for seed yield kg ha^{-1} .

Conclusion

Study reveals, there was significant influence of environment on genotypes. The genotypes MN-5 and ICPL-20337 found stable for seed yield kg ha^{-1} . The stable genotype identified could be used as parents in future breeding program for developing suitable genotype with wider adaptability.

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