

Original Research Article

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Stability Analysis in Pigeonpea (*Cajanus cajan* (L.) Millspaugh) Genotypes for Yield and its Component Traits

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ABSTRACT

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The present study was conducted with seventeen advanced lines of pigeonpea along with three checks (Pusa 992, Paras and UPAS 120). The experiment at each location was laid out in a Randomized Block Design (RBD) with three replications. The result of pooled ANOVA revealed that G × E interaction was significant for most of the characters except number of primary branches/plant, number of secondary branches/plant, number of seeds/pod, main shoot length and seed yield per plot. The presence of significant G x E is must as further analysis is possible only if there is a reliable genotype x environment interaction and hence, for number of primary branches/plant, number of secondary branches/plant, number of seeds/pod, main shoot length and seed yield/plot no further analysis was carried out. The traits in which G x E interaction was found significant were analysed by using Eberhart and Russell's model and it was found that for days to 50% flowering, the check Paras was found as most stable across all environments however for days to maturity, plant height and 100-seed weight none of the genotype was found to be stable across all environments. The most stable genotypes exhibiting higher stability for number of pod/plant across all environments was PA 538 followed by PA 540.

Introduction

Among all the pulses cultivated in India, pigeonpea [*Cajanus cajan* (L.) Mill sp] holds most important status as it is a multipurpose legume and highly suitable for cultivation in *rainfed* areas under low input conditions or even under the condition of drought. It has tremendous potential to solve the challenge of global food production under the threat of climate change, soil degradation and

increasing production costs (Saxena *et al.*, 2016). Nearly all parts of pigeonpea are used for one or other purposes like grains and green pods as human food, leaves as animal fodder, woody stem as fuel and for making huts (Verma *et al.*, 2018). Pigeonpea can also play an important role in crop diversification by rotating the rice-wheat cropping system to pigeonpea-wheat cropping system. In India during 2017-18 cropping season, it was grown on 4.43 million hectare area with production

of 4.25 million tons, with a productivity level of about 960 kg/ha (Anonymous, 2018). Pigeonpea is grown almost all over the country, however, the major states in terms of area and production are Maharashtra, Karnataka, Tamil Nadu, Madhya Pradesh, Rajasthan, Gujarat, Bihar and Uttar Pradesh which together account for 86% of national area and 83.8% of national production.

Plant phenotype is a function of genotype, environment and genotype x environment interaction. Genotype x environment interaction always affects the genotypic performance of varieties in broad range of environments (Gauch and Zobel, 1996). Genotype x environment interaction is said to occur when different cultivars or genotypes respond differently to diverse environmental conditions. A significant genotype x environment interaction can seriously impair efforts in selecting superior genotypes for crop introductions and cultivar development programs (Yan and Racjan, 2002). The Genotype x environment interaction undermines the repeatability of experimental results and hence reduces efficiency of selection (Kearsey and Pooni, 1996). Therefore, understanding the structure and nature of genotype x environment interaction is of utmost usefulness to the plant breeders as it helps to determine whether to develop cultivars with wider adaptability or to develop cultivars for a specific targeted area.

The earliest attempt to analyse the stability of individual lines was made by Plaisted and Peterson (1959) but the method used was complex and not very effective in case of evaluation of large number of lines (Pabale and Pandya, 2010). After that several workers (Yates and Cochran, 1938; Mather and Jones, 1958 and Finlay and Wilkinson, 1963) proposed different statistical models for stability analysis but the model proposed by Eberhart and Russell (1966) was preferred

method of stability analysis because of its simplicity and reliability. In Eberhart and Russell (1966) model, the stable genotypes were identified based on high mean yield, regression coefficient (b_i) around unity and mean square deviations from regression (s^2_{di}) non significant from zero. The knowledge of $G \times E$ interaction and yield stability are important parameters for breeding new cultivars with improved adaptation to environmental constraints prevailing in the targeted environments (Meena *et al.*, 2017 and Rao and Prabhakaran, 2000). Therefore, the present investigation was undertaken with the objective to study $G \times E$ interaction for yield and yield contributing characters and to identify stable advance lines of pigeonpea.

Materials and Methods

The experimental material used in present investigation consisted of seventeen early maturing advanced breeding lines of pigeonpea along with three checks viz. Pusa 992, Paras and UPAS120. The experiment was conducted at three different locations, two at the Norman E. Borlaug Crop Research Centre, Pantnagar (Pigeonpea Breeding Block) and Pigeonpea Entomology Block of G. B. Pant University of Agriculture and Technology, Pantnagar and the third at Agricultural Research Station, Majhera (Almora), G. B. Pant University of Agriculture and Technology, Pantnagar. Each genotype was grown in a 6 row plot of 4 m length with three replications. A row to row distance of 60 cm and plant to plant distance of 15 cm was maintained. All the recommended agronomic practices and plant protection measures were adopted to raise the uniform and normal healthy crop. At each location, observations were recorded on five randomly selected competitive plants from each genotype from each replication on 10 different morphological characters viz., days to 50% flowering, days to maturity, plant

height (cm), number of primary branches/plant, number of secondary branches/plant, number of pods/plant, number of seeds/pod, main shoot length (cm), 100 seed weight (g) and seed yield/plot (g). The stability parameters were calculated as per the procedure given by Eberhart and Russell (1966) and three stability parameters mean (m), regression coefficient (bi) and the deviation from linearity (S^2_{di}) were estimated.

Results and Discussion

Pooled Analysis of variance

The results of pooled analysis of variance for ten characters over three different environments revealed that mean squares due to genotypes were significant for all the characters except number of primary branches/plant, number of seed/pod and main shoot length indicating the presence of enough genetic variability among the genotypes for these characters (Table 1). It is also evident from the table 1 that mean sum of square due to environment were significant for all the characters except days to maturity and number of primary branches/plant indicating that these traits were greatly influenced by environments. Similar findings for different characters were also reported earlier by Sawargaonkar *et al.*, (2011), Pawar *et al.*, (2013), Patel and Tikka (2014), Singh *et al.*, (2015) Meena *et al.*, (2017) and Gaur *et al.*, (2020). Mean squares for G x E interaction was found to be significant for days to 50% flowering, days to maturity, plant height, number of pods/plant and 100 seed weight. However, for other traits such as number of primary branches/plant, number of secondary branches/plant, number of seeds/pod, main shoot length and seed yield/plot non- significant G x E is obtained indicating that these traits remained unaffected across environments. The presence

of significant G x E is must as further analysis is possible only if there is a reliable genotype x environment interaction and hence, for number of primary branches/plant, number of secondary branches/plant, number of seeds/pod, main shoot length and seed yield/plot no further analysis was carried out. These findings are in agreement with the earlier findings of Verma and Bajpai (2002), Muthiah *et al.*, (2005) and Gaur *et al.*, (2020). The partitioning of mean squares (environment + genotypes × environments) showed that environment (linear) differed significantly and were quite diverse with respect to their effects on the performance of genotypes for all the traits except days to maturity and number of primary branches/plant. Further, higher value of mean squares due to environment (linear) as compared to genotype x environment (linear) displayed that linear response of environments accounted for the most of total variation for most of the traits under study. Similar findings in this regard were also obtained by Kumara *et al.*, (2015). The significance of mean squares due to genotypes x environment (linear) component against pooled deviation were observed for days to 50% flowering, plant height, number of secondary branches/plant, number of pods/plant, main shoot length and seed yield/plot indicated that genotypes were diverse for their regression response to change with environment. Similar results for these characters were also observed by Meena *et al.*, (2017). The significant mean squares due to pooled deviation were observed for all traits except plant height, number of pods/plant, number of seed/pod, main shoot length and seed yield/plot indicated that the deviation from linear regression also contributed substantially toward the differences in stability of genotypes. These findings are in agreement with the earlier findings of Sawargaonkar *et al.*, (2011) and Kumara *et al.*, (2015).

Table.1 Pooled analysis of variance for different character in pigeonpea genotypes over three environment

Source of variation	d.f.	Mean sum of square									
		Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/plant	No. of secondary branches/plant	Number of pods/plant	Number of seed/pod	Main shoot length(cm)	100 seed weight(g)	Seed yield/plot
Genotype	19	26.05***	58.56***	469.07*	5.25	37.52*	2582.07**	0.15	103.75	1.46***	129057.53***
Environment	2	101.78***	36.85	43829.89***	7.62	135.21**	59416.31***	0.80**	6732.05***	0.69**	6920868.50***
G ×E	38	9.24***	22.55***	262.56***	3.97	19.00	1189.36*	0.12	99.90	0.13***	46077.33
E+(G×E)	40	13.87	23.26	2440.93	4.15	24.81	4100.70	0.15	431.51	0.16	389816.89
E(Linear)	1	203.57***	73.70	87659.78***	15.24	270.43***	118832.62***	1.60***	13464.10***	1.39**	13841737.0***
G ×E (Linear)	19	15.03***	15.11	466.87***	1.24	28.78***	2289.56***	0.12	162.59***	0.10	84833.98***
Pooled deviation	20	3.29***	28.48***	55.33	6.31***	8.76*	84.70	0.11	35.35	0.15***	6954.65
Pooled error	114	1.113	1.79	229.56	3.34	15.13	83613.63	0.24	118.52	1.79	104999.32

*, ** refers to significance at 5 and 1 % respectively

Table.2 Stability parameters for different traits in pigeonpea genotypes

S. No.	Genotypes	Days to 50% flowering			Days to maturity			Plant height (cm)			Number of pod per plant			100- Seed weight		
		Mean	b _i	S ² d _i	Mean	b _i	S ² d _i	Mean	b _i	S ² d _i	Mean	b _i	S ² d _i	Mean	b _i	S ² d _i
1	PA 535	78.44	2.42	4.32	138.77	2.32	15.08**	196.55	1.12	6.13*	163.55	1.39	-171.01	7.23	0.31	0.04
2	PA 536	81.00	2.58	6.79*	142.33	1.97	-0.08	196.00	1.25	-75.54	188.00	1.62	-174.42	7.47	2.36	0.32
3	PA 537	77.22	2.73	9.77**	132.44	2.35	19.00**	194.66	1.27	-70.56	150.66	1.30	-232.72	7.25	0.31	-0.00
4	PA 538	83.55	0.50	0.26	143.44	1.54	1.81	234.88	1.52	-15.84	228.00	0.94	-244.06	8.45	2.35	0.16
5	PA 539	82.77	0.11	1.56	141.22	-0.14	-0.59	212.66	1.33	-75.17	137.11	0.38	-199.25	6.59	0.50	0.04
6	PA 540	82.66	-0.13	7.65*	143.55	1.03	2.19	198.66	1.07	134.66**	200.55	1.02	-232.25	7.56	1.24	0.24
7	PA 541	79.22	2.4	1.07	141.66	4.04	89.47**	210.55	1.33	-74.49	201.33	1.68	-228.21	7.18	2.54	0.20
8	PA 542	77.66	1.53	0.21	131.00	0.81	-0.15	220.55	1.39	-36.96	184.55	1.76	31.61**	6.65	0.64	0.08
9	PA 543	79.55	0.25	3.50	132.33	-1.77	57.96**	211.44	1.13	70.96**	181.00	0.10	-79.18	7.48	0.43	-0.01
10	PA 544	79.22	-0.99	1.24	140.00	-1.68	38.45**	204.11	0.56	-1.59	189.00	0.09	-155.75	7.79	1.42	0.07
11	PA 545	81.66	2.58	6.79*	138.88	3.56	18.56**	225.44	1.31	-75.55	194.77	2.11	-220.83	7.51	-0.22	-0.01
12	PA 546	78.33	2.11	3.48	136.55	2.46	14.82**	202.88	0.73	183.79**	190.66	0.92	-222.79	6.32	0.67	-0.01
13	PA 547	79.88	-0.46	0.59	135.00	-4.08	182.11**	209.22	0.46	-70.67	159.00	-0.36	-63.12	7.53	-0.70	0.12
14	PA 548	79.33	1.36	1.37	137.00	1.44	5.68*	212.77	1.10	29.99**	119.00	0.67	-240.66	7.54	-1.14	0.28
15	PA 549	82.11	0.89	-0.36	141.66	-0.57	4.41*	209.22	0.77	-75.70	199.22	0.75	-224.64	8.40	0.80	0.18
16	PA 550	85.00	-0.49	5.10*	144.66	-0.58	33.01**	221.88	0.83	-64.37	226.77	0.76	282.65**	7.71	4.48	1.05
17	PA 551	82.33	-0.64	4.94*	140.77	-0.10	13.66**	195.00	0.65	-76.52	204.22	1.39	-217.57	6.43	0.98	0.02
18	PUSA 992	78.33	0.80	-0.01	138.22	2.75	24.86**	192.22	0.58	-75.40	140.33	1.04	-221.92	8.83	0.83	0.01
19	PARAS	72.00	0.94	0.02	130.44	2.29	11.59**	184.66	0.59	-76.50	153.00	1.35	-149.53	6.37	0.82	0.00
20	UPAS 120	83.55	1.42	0.02	142.88	2.33	25.88**	207.00	0.93	15.65**	189.66	1.02	-231.97	7.98	1.33	-0.01
	General mean	80.19	1.00		138.64	1.00		207.04	1.00		180.02	1.00		7.42	1.00	

*, ** refers to significance at 5 and 1 % respectively

Phenotypic stability analysis based on Eberhart and Russell (1966) model

The study of G x E interactions is essential for identification of phenotypically stable genotypes and it includes the three parameters i.e. mean performance (\bar{X}), regression coefficient (b_i) and deviation from regression ($S^2 d_i$). A genotype is said to be stable, if it had high mean performance above average of all genotypes, regression coefficient does not differ from unity and minimum deviation from regression. Genotypes with b_i lesser than unity ($b_i < 1$), do not respond favourably to improved environmental conditions and hence could be regarded as specifically adapted to poor environments when their mean performance is more than average. On the other hand, a genotype is said to be specially adapted to a favourable environment, when its regression is more than unity ($b_i > 1$), higher mean performance and have minimum deviation from regression. Such genotypes tend to respond favourably to better environment but perform poor in unfavourable environments.

The stability parameters viz., mean, linear regression coefficient (b_i) and deviation from regression ($S^2 d_i$) for each character have been presented in (Table 2). Earliness is one of the most desirable traits in the pigeonpea breeding programmes. Farmers requires early maturing genotypes of pigeonpea which can be harvested before the sowing of the preceding wheat crop keeping this point in view investigation was done to identify early maturing and stable genotypes that can be grown under different zones of Uttarakhand. For days to 50% flowering, check Paras (\bar{X} = 72.00, b_i = 0.94 and $S^2 d_i$ = 0.02) exhibited low mean (< 80.19), $b_i \approx 1$ and minimum deviation from regression and hence considered stable across all environments. The genotypes viz., PA 535 (\bar{X} = 78.44, b_i = 2.42 and $S^2 d_i$ = 4.32),

PA 542 (\bar{X} = 77.66, b_i = 1.53 and $S^2 d_i$ = 0.21) and PA 546 (\bar{X} = 78.33, b_i = 2.11 and $S^2 d_i$ = 3.48) recorded low mean for flowering (< 80.19) along with ($b_i > 1$), and minimum deviation from regression and hence suitable for favourable environment while the check Pusa 992 (\bar{X} = 78.33, b_i = 0.80 and $S^2 d_i$ = -0.01) had low mean for flowering (< 80.19) along with ($b_i < 1$), and minimum deviation from regression and hence suitable for poor environment. Similar results were also reported by Sawargaonkar *et al.*, (2011) and Meena *et al.*, (2017). Similarly for days to maturity none of the genotype was found to be stable across environments as well as under favourable environment. However for days to maturity, PA 542 (\bar{X} = 131.00, b_i = 0.81 and $S^2 d_i$ = -0.15) was found suitable for suitable for poor environment because of low mean (< 138.64) along with ($b_i < 1$), and minimum deviation from regression.

Plant height is another important trait in pigeonpea breeding programmes as the plant height has positive correlation with yield (Gaur *et al.*, 2018). For plant height the most desirable and stable genotypes for rich environment were PA 538 (\bar{X} = 234.88, b_i = 1.52 and $S^2 d_i$ = -15.84), PA 539 (\bar{X} = 212.66, b_i = 1.33 and $S^2 d_i$ = -75.17), PA 541 (\bar{X} = 210.55, b_i = 1.33 and $S^2 d_i$ = -74.49) and PA 542 (\bar{X} = 220.55, b_i = 1.39 and $S^2 d_i$ = -36.96) due to high mean (> 207.04), $b_i > 1$ and minimum deviation from regression while for poor environment PA 547 (\bar{X} = 209.22, b_i = 0.46 and $S^2 d_i$ = -70.67), PA 549 (\bar{X} = 209.22, b_i = 0.77 and $S^2 d_i$ = -75.70), PA 550 (\bar{X} = 221.88, b_i = 0.83 and $S^2 d_i$ = -64.37) were found suitable due to high mean (> 207.04), $b_i < 1$ and minimum deviation from regression. None of the genotype as well as check was found stable under all environments. Stability of genotypes for plant height was also

observed by Sawargaonkar *et al.*, (2011) and Meena *et al.*, (2017).

The most desirable and suitable genotypes exhibiting higher stability for number of pod/plant were PA 538 (\bar{X} =228.00, b_i =0.94 and S^2d_i =-244.06), PA 540 (\bar{X} =200.55, b_i =1.02 and S^2d_i =-232.25), PA 546 (\bar{X} =190.66, b_i =0.92 and S^2d_i =-222.79) and UPAS 120 (\bar{X} = 189.66, b_i = 1.02 and S^2d_i =-231.97) due to high mean (>180.02), $b_i \approx 1$ and minimum deviation from regression. The most desirable and stable genotypes for number of pods/plant under rich environment were PA 536 (\bar{X} =188.00, b_i =1.62 and S^2d_i =-174.42), PA 541 (\bar{X} =201.33, b_i =1.68 and S^2d_i =-228.21) and PA 545 (\bar{X} =194.77, b_i =2.11 and S^2d_i =-220.83) due to high mean (>180.02), $b_i > 1$ and minimum deviation from regression while for poor environment PA 544 (\bar{X} =189.00, b_i =0.09 and S^2d_i =-155.75) and PA 549 (\bar{X} =199.22, b_i =0.75 and S^2d_i =-224.64) were found suitable due to high mean (>180.02), $b_i < 1$ and minimum deviation from regression. Stability of genotypes for number of pods/plant was also observed by Sawargaonkar *et al.*, (2011), Patel and Tikka (2014) and Meena *et al.*, (2017). For 100 seed weight genotypes PA 538 (\bar{X} =8.45, b_i =2.35 and S^2d_i =0.16), PA 540 (\bar{X} =7.56, b_i =1.24 and S^2d_i =0.24), PA 544 (\bar{X} =7.79, b_i =1.42 and S^2d_i =0.07), PA 548 (\bar{X} =7.54, b_i =-1.14 and S^2d_i =0.28), PA 550 (\bar{X} = 7.71, b_i =4.48 and S^2d_i =1.05) and UPAS 120 (\bar{X} =7.98, b_i =1.33 and S^2d_i =-0.01) were suitable for rich environment because of high mean (>7.42), $b_i > 1$ and minimum S^2d_i nearly zero. The genotypes PA 545 (\bar{X} =7.51, b_i =-0.22 and S^2d_i =-0.01), PA 547 (\bar{X} =7.53, b_i =-0.70 and S^2d_i =0.12) and PA 549 (\bar{X} =8.40, b_i =0.80 and S^2d_i

=0.18) found suitable for poor environment. None of the genotype was found stable for 100-seed weight across all environments Vanniarajan (2007), Reddy *et al.*, (2011) and Patel and Tikka (2014) also observed stability of genotypes for 100 seed weight.

The results of above findings provides information that for the trait days to 50% flowering, the check Paras was found as most stable across all environments however for days to maturity, plant height and 100-seed weight none of the genotype was found to be stable across all environments. The most desirable and suitable genotypes exhibiting higher stability for number of pod/plant across all environment was PA 538 followed by PA 540.

Declaration

The authors are declaring that there is no conflict of interest and manuscript is not sent anywhere for publication.

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