

Research Article

Interpretation of Genotype x Environment Interaction and Grain Yield Stability in Some Advance Lines of Pigeonpea [*Cajanus Cajan* (L.) Millsp.] Grown at Different Altitudes

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Abstract

Nineteen advance lines of pigeonpea with three checks were evaluated under three environments during *kharif* season of 2015 to obtain the knowledge of stability for yield and its component traits and used for identification of most stable genotypes of pigeonpea without effecting by altitudes. The experiment was carried out in randomized complete block design with three replications. Highly significant genotypic differences were observed for all the characters except number of secondary branches/plant. The variance due to Genotype x Environment found significant for all the characters like days to 50% flowering, number of seeds/pod and 100 seed weight. Environment (linear) interaction component was significant for all the characters except number of secondary branches/plant. The significant mean squares due to pooled deviation were observed for all traits except plant height, number of primary branches/plant and number of seeds/pod indicated that the deviation from linear regression also contributed substantially toward the difference in stability of genotypes. Three genotypes *viz.*, PA 337, PA 409 and PA 419 were identified as the most desirable and consistent for seed yield/plot across different environments.

Keywords: Pigeonpea, G x E interaction and stability analysis

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Introduction

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is an often cross pollinated crop reported and it was reported that cross pollination varied from 20% – 70%. Pigeonpea is a diploid crop ($2n = 2x = 22$) and genome size of 1C = 858 Mbp [1]. In India, pigeonpea is the second important pulse crop after chickpea and cultivated in 3.78 mha area with an annual production of 2.80 m tons [2]. In India, it is commonly known as redgram or arhar or tur or thogari. It is a hardy, widely adopted and drought tolerant crop with large temporal variation (97-299 days) for grain maturity. It is cultivated in wide range of environment and under different cropping systems [3]. India is considered as the native of pigeonpea [4] because of its natural genetic variability available in the local germplasm and the presence of its wild relatives in the country.

Genotype-environmental (G X E) interaction plays major role for stabilizing genotypes across the environments with high yield potential. Hence, it is essential to breed high yielding varieties, which may perform consistently well over years under different agro climatic regions as well as cropping systems. Development of high yielding varieties depends upon presence of genetic variability and diversity in breeding population, where selection of genetically diverse parents in hybridization programme is important to get wide array of recombinants. Pigeonpea breeders look forward for widely adapted genotypes responsive to input intensive as well as input deficient agriculture in order to enhance production and productivity of the crop. With this back ground the present study was conducted in three different locations to identify stable genotypes of pigeonpea for grain yield and its component traits.

Materials and Methods

Experimental material and cultivation

The experimental material used in present investigation was consisted of 19 advance lines of pigeonpea developed at G. B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand and three checks (**Table 1**). Each

genotype was sown in a single plot consisted of 6 rows of 4 m length with the 60 cm of inter-row and 15 cm of intra-row spacing. Recommended agronomic practices and plant protection measures were adopted for pigeonpea production for the locations to raise the uniform crop stand and to minimize environmental variations to a maximum possible extent.

Table 1 List of pigeonpea genotypes and checks along with their pedigree

S. No	Genotypes	Pedigree	S. No	Genotypes	Pedigree
1	PA 374	UPAS 120 X PA 291	13	PA 406	AL 201 X UPAS 120
2	PA 414a	UPAS 120 X PUSA 885	14	PA 409	UPAS 120 X AL 1483
3	PA 415	PUSA 992 X AL 201	15	PA 414b	UPAS 120 X PUSA 885
4	PA 429a	PUSA 992 X UPAS 120	16	PA 419	UPAS 120 X PUSA 971
5	PA 435	UPAS 120 X PUSA 855	17	PA 421	AL 201 X PUSA 992
6	PA 439	UPAS 120 X PUSA 971	18	PA 426	H 82-1 X UPAS 120
7	PA 441	UPAS 120 X H 82-1	19	PA 429b	PUSA 992 X UPAS 120
8	PA 443	UPAS 120 X ICPL 88039	Checks		
9	PA 444	UPAS 120 X H 82-1	1	PUSA 992	Selection of 90306
10	PA 300	H 82-1 X PUSA 992	2	PA 291	UPAS 120 X KPBR 80-2-1
11	PA 337	UPAS 120 X <i>C. acutifolius</i>	3	UPAS 120	Selection from germplasm P 4785
12	PA 402	UPAS 120 X H 82-1			

Experimental Site and Seasons

Breeding material was evaluated in randomized block design (RBD) with three replications during *kharif*, 2015. The experiment was conducted on three locations, one at Agricultural Research Station, Majhera (Almora) designated as EI (29.28° N latitude, 79.32° E longitude and at an altitude of 1000 meter above the mean sea level) and other two locations at the Norman E. Borlaug Crop Research Centre, Pantnagar (29.5° N latitude, 79.3° E longitude and at an altitude of 243.84 meter above the mean sea level) they were as EII= Pigeonpea Breeding Block and EIII= Pigeonpea Entomology Block of G. B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand.

Observed traits and sampling measurements

Observations were recorded on five randomly selected plants in each replication at each location with respect to the 9 metric traits, *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, 100 seed weight (g) and seed yield/plot (g). The mean values computed from the observations for each replications from every locations were used for statistical analysis.

Statistical analysis

The data recorded at all the locations were subjected to stability analysis according to Eberhart and Russell model using "INDOSTAT" software and three stability parameters mean (m), regression coefficient (b_i) and the deviation from linearity (S^2d_i) were estimated.

Results and Discussion

Pooled analysis of variance for stability performance of genotypes (Table 2) revealed that mean square due to genotypes were significant for all characters except number of secondary branches/plant, indicating that genotypes possessed significant variation for these traits. Similar findings for these characters were also reported by [5], [6], [7] and [8]. Mean square due to environment were significant for all the characters except number of secondary branches/plant and 100 seed weight indicates considerable difference between environment for days to 50% flowering, days to maturity, plant height, number of primary branches/plant, number of pods/plant, number of seeds/pod and seed yield/plot and these traits were greatly influenced by environments. Similar results for these characters were also reported by [7], [9] and [10]. G x E interaction mean squares was significant for days to maturity, plant height, number of primary branches/plant, number of secondary branches/plant, number of pods/plant and seed yield/plot, indicating differential response of genotypes in different environments for these traits. However, other

traits such as days to 50% flowering, number of seeds/pod and 100 seed weight were unaffected by the changing environments. Similar results were observed by [11], [12] and [13].

Table 2 Pooled analysis of stability for seed yield and its component traits in pigeon pea

Source of variation	d. f.	Mean Sum of Squares								
		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	100 seed weight (g)	Seed yield/plot (g)
Genotype (G)	21	15.96 ^c	78.03 ^c	1073.34 ^c	10.63 ^c	1.13	1587.83 ^c	0.21 ^a	1.57 ^c	313250.91 ^c
Environment (E)	2	290.62 ^c	910.67 ^c	7716.20 ^c	391.44 ^c	16.25	15010.03 ^c	1.00 ^c	0.51	3827083.00 ^c
GXE	42	3.50	27.85 ^c	60.29 ^b	2.32 ^c	0.82 ^c	348.23 ^b	0.15	0.25	59605.40 ^c
E+(GXE)	44	16.55 ^c	67.98 ^c	408.28 ^c	20.00 ^c	1.52 ^c	1014.68 ^c	0.19 ^a	0.26	230854.38 ^c
E(Linear)	1	581.24 ^c	1821.34 ^c	15432.39 ^c	782.88 ^c	32.49	30020.07 ^c	1.99 ^c	1.02 ^a	7654166.00 ^c
GXE (Linear)	21	5.02 ^a	49.92 ^c	97.80 ^c	4.12 ^c	0.74	578.67 ^c	0.22	0.32	108200.92 ^c
Pooled deviation	22	1.90 ^c	5.51 ^c	21.75	0.49	0.85 ^c	112.43 ^c	0.08	0.17 ^c	10509.43 ^c
Pooled error	126	0.07	0.19	19.44	0.72	0.13	33.50	0.08	0.00	3656.87

a, b, c = Significance at 5%, 1% and 0.1% probability levels, respectively

Component analysis of environment + (Genotype x environment) was significant for all the traits except 100 seed weight under study. The partitioning of mean squares (environment + genotypes x environments) showed that environment (linear) differed significantly and were quite diverse with respect to their effects on the performance of genotypes for all traits except number of secondary branches/plant. It has been suggesting that environments were random and different and they reflected the expression of these traits and this variation could have arisen due to the linear response of the regression of the cultivars to the environments. The significance of mean squares due to genotypes x environment (linear) component against pooled deviation were observed for days to 50% flowering, days to maturity, plant height, number of primary branches/plant, number of pods/plant 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 [14], [15] and [16].

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 major of total variation for most of the traits studied. Similar kind of observations for days to 50% flowering, days to maturity, plant height, number of primary branches/plant, number of secondary branches/plant, number of pods/plant, number of seeds/pod, 100 seed weight and seed yield/plot were also reported by [13],[17] and [18]. The non-linear component arising due to the heterogeneity measured as mean square due to pooled deviation was significant for all traits except plant height, number of primary branches/plant and number of seeds/pod revealing presence of non-linear response of the genotypes to the changing environments. In the traits where non-linear component was non-significant, the G x E interaction of these traits was greatly influenced by environmental factors and there exists either relationship or complex relationship between genotype and environment effect making its prediction more difficult for that trait. These results clearly indicate that there is sufficient variability for each of the character except number of secondary branches/plant among the twenty two genotypes studied. Also, all the characters except number of secondary branches and 100 seed weight showed highly significant differences across the environments which indicated the presence of G x E interactions and thus validates the need for stability analysis so that the stable genotypes could be identified.

Phenotypic stability was estimated on the basis of three parameters namely; mean performance over environments, regression coefficient (b_i) and deviation from regression (S^2d_i) as suggested by [19]. The stability parameters for yield and its contributing characters are presented in **Table 3**. According to Eberhart and Russell (1966) [19] a genotype is likely to be stable if it had high mean performance above the average of all genotypes, regression coefficient (b_i) *i.e.* does not differ from unity and deviation from regression approaching zero ($S^2d_i = 0$) (non-significant). High value of regression ($b_i > 1$) indicates that the genotype is more responsive to the favorable environment, whereas low value of regression coefficient ($b_i < 1$) indicates that the genotype may be suitable in poor environment. Based on stability parameters the genotypes *viz.*, PA 435 and PA 444 were found to be stable for days

to 50% flowering as indicated by non-significant deviation from regression and regression coefficient ($b_i \approx 1$). Stability of genotypes for days to 50% flowering was also observed by [16] and [20].

Table 3 Mean values and stability parameters for yield and its component traits in 22 genotypes of pigeonpea

S. No.	Genotypes	Days to 50% flowering			Days to maturity			Plant height (cm)		
		Mean	b_i	S^2d_i	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i
1	PA 374	74.67	1.08	-0.07	136.90	0.28*	0.07	144.00	0.67	-6.24
2	PA 414a	75.00	0.99	-0.05	137.60	0.42	4.23***	136.40	0.61	-14.45
3	PA 415	76.89	0.89*	-0.07	133.30	0.06	3.11***	135.70	0.37**	-20.38
4	PA 429a	73.67	0.72	0.13	136.80	0.40	3.47***	164.30	1.61	10.96
5	PA 435	71.78	0.64	0.11	132.80	0.40	3.47***	166.30	1.88*	-17.71
6	PA 439	71.00	0.93	-0.03	135.00	0.05	9.18***	144.40	0.96	-10.00
7	PA 441	69.56	0.77	0.22*	132.80	0.03	12.68***	145.90	0.85	-18.94
8	PA 443	70.67	0.60	-0.01	134.00	-0.13	22.35***	136.00	0.77	22.69
9	PA 444	71.56	0.83	0.06	134.40	0.12	11.15***	168.80	1.22	30.20
10	PA 300	73.78	0.85	1.09***	146.90	1.93	3.79***	181.40	1.43	7.16
11	PA 337	75.89	0.86	0.59**	145.00	2.27	12.75***	182.40	0.98	-12.30
12	PA 402	74.89	0.80	1.27***	146.20	2.00	6.94***	184.70	1.02	-15.72
13	PA 406	73.11	0.76	0.88***	141.20	1.21	1.10*	169.80	1.10	-8.98
14	PA 409	71.44	1.00	0.61**	141.60	1.60	3.43***	174.10	1.03	-19.66
15	PA 414b	72.00	1.26	-0.05	142.90	1.78	5.30***	166.30	0.67	11.33
16	PA 419	72.11	0.76	0.88***	146.40	1.52	0.74*	168.60	0.73	-19.25
17	PA 421	72.33	1.19	2.96***	138.30	1.47	4.06***	181.90	1.09	-16.88
18	PA 426	74.11	0.76	0.88***	146.90	1.93	3.79***	188.80	1.08	-12.71
19	PA 429b	71.78	0.73	0.21*	143.40	1.47	0.98*	184.70	0.76	-12.27
20	PUSA 992	72.11	1.31	4.63***	136.10	0.99	-0.18	182.40	0.69	52.03
21	PA 291	76.22	1.71	7.97***	141.40	0.76	1.95***	197.00	1.65	-4.95
22	UPAS 120	79.00	2.57	18.02***	146.00	1.44	2.78***	180.40	0.82	106.05*
	Mean	73.34	1.00		139.80	1.00		167.50	1.00	
	S.E.	0.98	0.27		1.70	0.30		3.30	0.20	

*, **, *** = Significance at 5%, 1% and 0.1% probability levels, respectively

S. No.	Genotypes	Number of primary branches/plant			Number of secondary branches/plant			Number of pods/plant		
		Mean	b_i	S^2d_i	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i
1	PA 374	13.11	0.52	-0.61	5.67	0.92	0.18	100.10	0.82	-29.76
2	PA 414a	11.00	0.82	-0.61	5.44	1.18	-0.13	101.80	0.39	1.83
3	PA 415	14.00	0.41	-0.42	6.11	1.23	3.04***	101.80	0.20	35.93
4	PA 429a	11.89	0.99	0.30	5.33	0.54	0.33	97.70	0.31	-2.55
5	PA 435	12.00	0.82	-0.70	5.78	0.54	-0.04	84.00	0.18	32.76
6	PA 439	9.56	0.85	-0.71	4.78	0.60	0.75*	98.40	0.54	-7.48
7	PA 441	11.44	0.25	-0.15	5.78	0.11	2.15***	106.20	0.55	-0.97
8	PA 443	10.44	0.94	1.50	4.44	-0.05	0.38	88.40	0.57	-21.66
9	PA 444	11.00	0.96	-0.62	4.89	0.00	0.83**	87.90	0.30	0.23
10	PA 300	16.11	0.52	-0.08	6.56	2.14	4.71***	153.10	1.63	140.91*
11	PA 337	15.11	1.20	1.20	5.78	2.04	0.45*	143.70	1.07	101.65
12	PA 402	13.67	1.23	-0.65	5.44	0.81	-0.13	109.20	1.31	162.10*
13	PA 406	14.78	1.28	-0.67	6.44	0.70	0.10	145.70	1.76	12.17
14	PA 409	14.67	0.96	-0.31	6.11	1.18	-0.13	142.30	2.23	284.43**
15	PA 414b	14.33	1.30	-0.48	5.22	0.97	-0.11	144.90	2.18	295.13**
16	PA 419	12.00	1.57	-0.46	6.00	0.54	0.33	126.30	0.79	109.36*
17	PA 421	14.67	1.30	0.15	5.78	1.77	1.09**	142.40	1.73	51.14

18	PA 426	15.78	1.15	0.77	6.33	0.27	-0.02	142.10	1.72	59.95
19	PA 429b	14.00	1.37	-0.66	5.22	0.59	-0.13	128.00	1.32	18.72
20	PUSA 992	15.56	1.12*	-0.71	6.56	2.20	0.78**	120.10	0.65	0.61
21	PA 291	14.33	1.30	-0.48	6.67	1.83	1.13**	123.60	1.25	13.93
22	UPAS 120	14.44	1.14	-0.64	6.33	1.88	0.20	150.30	0.50	424.75***
	Mean	13.36	1.00		5.76	1.00		119.90	1.00	
	S.E.	0.49	0.12		0.65	0.76		7.50	0.30	

*, **, *** = Significance at 5%, 1% and 0.1% probability levels, respectively

S. No.	Genotypes	Number of seeds/pod			100 seed weight (g)			Seed yield/plot (g)		
		Mean	b_i	S^2d_i	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i
1	PA 374	4.00	0.89	0.08	8.66	-0.74	0.08***	766.70	0.54	11990.46*
2	PA 414a	4.33	0.89	0.08	8.31	-0.51	0.09***	791.10	0.36	14253.07*
3	PA 415	4.11	2.30	-0.04	8.02	-0.83	0.11***	785.60	0.39	33538.75**
4	PA 429a	3.44	2.30	-0.04	8.86	-0.31	0.07***	750.00	0.54	14387.92*
5	PA 435	4.11	-1.49	0.02	7.83	-1.46	0.16***	846.70	0.41	20295.64*
6	PA 439	4.11	2.30	-0.04	8.09	-2.44	0.16***	852.20	0.51	715.48
7	PA 441	3.89	2.38	-0.07	8.19	-1.39	0.09***	1278.90	1.54	11693.64*
8	PA 443	4.33	-0.67	0.11	7.71	-1.60	0.11***	731.10	0.45	2682.17
9	PA 444	4.33	1.56	-0.07	8.16	-1.09	0.06***	1411.10	1.60	18162.45*
10	PA 300	4.00	0.89	0.08	9.12	1.98	0.05**	996.70	0.48	-3026.96
11	PA 337	3.67	-0.89	0.08	9.64	1.04	0.01*	1162.20	0.74	4580.06
12	PA 402	4.33	0.67	0.11	10.13	6.70	0.86***	971.10	0.50*	-3250.84
13	PA 406	3.67	3.12	-0.07	9.37	0.56	0.00	1664.40	1.89*	-2557.02
14	PA 409	4.33	-0.67	0.11	9.37	2.67	0.15***	1534.40	1.42	4197.68
15	PA 414b	4.00	1.56	-0.07	9.94	4.11	0.37***	1695.60	1.89	12334.82
16	PA 419	4.00	0.67	0.11	9.71	5.50	0.46***	1454.40	1.65	3773.77
17	PA 421	4.00	-1.56*	-0.07	9.64	2.43	0.04**	1687.80	1.81*	-3570.87
18	PA 426	3.89	3.05	0.05	9.34	2.12	0.02*	1254.40	1.19	22076.21
19	PA 429b	3.56	1.49	0.02	9.07	4.34	0.34***	1295.60	1.43**	-3619.11*
20	PUSA 992	4.33	1.56	-0.07	9.42	3.31	0.05***	1102.20	0.96	-3516.72
21	PA 291	4.00	-1.56*	-0.07	9.02	0.36	0.00	1168.90	1.08	-1845.15
22	UPAS 120	3.78	3.20	-0.04	8.52	-2.76	0.44***	1120.00	0.66	-1922.80
	Mean	4.01	1.00		8.92	1.00		1151.00	1.00	
	S.E.	0.20	0.95		0.30	1.93		72.50	0.20	

*, **, *** = Significance at 5%, 1% and 0.1% probability levels, respectively

The seven genotypes PA 414a, PA 415, PA 429a, PA 435, PA 439, PA 441, PA 444 exhibited low mean performance (<139.80), b_i less than 1 and S^2d_i is nearly zero for days to maturity can be assigned as suitable for poor environment, while PA 421 showed low mean (<139.80), b_i more than 1 and S^2d_i is nearly zero be adopted in rich environment. For plant height, eight genotypes PA 337, PA 402, PA 406, PA 409, PA 421, PA 419, PA 429b and PA 426 were identified desirable and stable due to high mean (>167.50), $b_i \approx 1$ and $S^2d_i \approx 0$. Stability of genotypes for plant height was also observed by [6], [21] and [15]. The genotypes PA 409, PA 426 and UPAS 120 revealed high mean (>13.36) for primary branches/plant, $b_i > 1$ and least non-significant deviation from regression suggesting suitability and stability over three environments. The results are corresponding to the findings of [5], [11] and [21]. The genotypes PA 406, PA 419 and UPAS 120 showed high mean (>5.76), $b_i \approx 1$ and least non-significant deviation from regression indicated that these genotypes were most desirable and suitable genotypes for number of secondary branches/plant over different environments. Stability of genotypes for number of secondary branches/plant was also observed by [16] and [22]. Among the test genotypes, most desirable and stable genotypes for number of pods/plant, across the environments were PA 406, PA 421, PA 426, PA 429b, PUSA 992 and PA 291 with least deviation in stability parameters ($\bar{X}_i > 119.90$, $b_i \approx 1$ and $S^2d_i \approx 0$). [5], [6], [8] and [15] reported similar results with present study. For number of seeds/pod, none of the genotype was found stable across the environments while, one genotype PA 439

with higher mean performance, high linear regression coefficient estimates ($b_i > 1$) and S^2d_i is nearly zero and one genotype PA 435 with high mean, $b_i < 1$ and S^2d_i is nearly zero were identified suitable for rich and poor environment, respectively. For 100 seed weight, genotypes PA 406 and PA 291 were identified most desirable and stable across environment due to high mean (> 8.92), $b_i \approx 1$ and least non-significant deviation from regression ($S^2d_i \approx 0$). [10], [15], [7], and [8] also observed stability of genotypes for 100 seed weight.

The genotypes PA 337, PA 409 and PA 419 showed high mean performance ($\bar{X}_i > 1151$) for seed yield/plot, regression coefficient ($b_i \approx 1$) and least non-significant deviation (S^2d_i) from regression. This indicated that these genotypes were stable over three environmental conditions for seed yield/plot. These findings were in agreement with [15], [5], [6] and [18]. These genotypes can also be utilized as parents in hybridization programme for improving the yield and wider adaptability.

Based on these parameters, components (b_i and S^2d_i) had been classified into four groups. In the first group, none of the two components were non-significant, hence, indicated total absence of the G x E interaction. Second category consisted of the genotypes, where only linear (b_i) component was significant. Thus, the performance of these genotypes in varying environment can be predicted. Third group comprised of the genotypes, where only non-linear (S^2d_i) component was significant indicated that performance of these genotypes under different environmental condition is unpredictable, and in the fourth group, both the components were significant indicated that both linear and non-linear component were responsible for significant genotypes x environment interaction.

Conclusion

From the present investigation, it may be concluded that there was no superior genotype for all the traits in all the environments. It may be due to behavior of the traits is not same in all the environmental conditions. The genotypes PA 337, PA 409 and PA 419 had high seed yield and also were found to be stable across the environments for seed yield/plot with desirable traits such as plant height, number of primary branches/plant and number of secondary branches/plant and these genotypes can also be used as a donor parent for generating new breeding material for development of variety with good stability across the different environments. However, this needs to be verified by testing the breeding lines over the season and over the locations for one more year. The identified stable genotypes could be exploited as parents in hybridization programme for developing the suitable genotypes with wider adaptability.

Acknowledgements

Authors duly acknowledge the support from the Department of Genetics and Plant Breeding of the G.B. Pant University of Agriculture and Technology, Pantnagar (Uttarakhand)-263145- India. We are extremely grateful to the Directorate of Experiment Station, G.B. Pant University of Agriculture and Technology, Pantnagar (Uttarakhand)-263145- India for providing financial assistance to conduct experiment.

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Publication HistoryReceived 24th Apr 2017Revised 20th May 2017Accepted 12th June 2017Online 30th June 2017

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