

Research Article

Genetic Variability and Inter-Relationship among Yield Contributing Characters In Advance Lines of Pigeonpea [*Cajanus Cajan* (L.) Millsp.] Grown at Different Altitudes

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Abstract

To utilize pigeonpea gene pool effectively, experiment on genetic variability, heritability, genetic advance, correlation and path coefficient analysis of yield and its component traits, were conducted during during *kharif*- 2015 with 19 advance lines and 3 checks on three locations. In general, PCV were higher than the corresponding GCV values for all the characters in all environments. None of the trait showed high GCV and PCV in any of the environments. Over all the environments, high estimates of heritability (>60 %) coupled with high genetic advance as percent of mean (>20 %) was observed for seed yield/plot, no. of pods/plant, no.of primary branches/plant and plant height whereas rest of the traits were under category of high heritability with low to moderate genetic advance as percent of mean. Correlation study suggested that seed yield was positively correlated with no. of pods/plant and 100-seed weight and these traits are under governance of additive gene action. Direct selection for no. of seeds/plant and 100-seed weight may be rewarding for improvement in yield as these traits have direct effects on yield in respect of the any environments.

Keywords: Genetic Variability, Heritability, Correlation and Path analysis, Pigeonpea

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Introduction

Pigeonpea or red gram [*Cajanus cajan* (L.) Millsp] is one of the important *kharif* pulse crop of subsistence agriculture. Globally, pigeonpea is cultivated worldwide in developing countries under tropical and subtropical climatic conditions with variety of cropping systems. Generally, split seeds of pigeonpea is used as dhal (dry, dehulled, split seed used for cooking) which fulfills requirement of dietary protein. Besides its main use as dhal, tender green seeds are used as a vegetable, while crushed dry seeds serve as animal feed, green leaves as fodder, and stems as fuel wood and to make huts, baskets, *etc.* [1]. Globally, it is grown in about 5.52 mha area with an annual production of 4.32 m tons with an average productivity around 790 kg/ha. In India, pigeonpea is the second important legume crop after chickpea. In India, it is cultivated on 3.78 mha area with an annual production of 2.80 m tons with productivity around 740 kg/ha which is lower than global average [2]. Pigeonpea plays a vital role in vegetarian diet as seeds constitutes protein, vitamins, and mineral elements such as potassium, phosphorus, zinc and magnesium and also serves as a good source of carbohydrate and food fibres.

Pigeonpea has significant contribution in Indian agriculture economy but despite of research efforts the productivity of pigeonpea is very low and stagnated at 750kg/ha. The major constraints for achieving higher yields are inherently low yielding potential of the varieties that lack genetic variability, inefficient plant type and low yielding potential, absence of suitable ideotypes for different cropping systems, poor harvest index, low level of crop management, more competition with weeds and susceptibility to biotic and abiotic stresses [3]. Yield is a complex trait controlled by polygenes and highly sensitive for environmental factors hence it is not efficient character for selection. The efficacy of selection depends upon the existence and magnitude of genetic variability for yield and yield contributing traits in the breeding material. For yield improvement selection of superior parents possessing better heritability and genetic advance for yield contributing traits is an essential prerequisite. Heritability in conjunction with genetic advance is more useful than heritability alone in the prediction of resultant effect of selecting the best individual [4, 5]. It is therefore essential for plant breeder to know the extent of relationship between yield and its various contributing components, which will be inevitably, facilitate selection of desirable characteristics. The information on nature and magnitude of correlation coefficient give idea to the breeders which help to decide the traits

to be given importance in selection. Based on correlation coefficients, breeders can make the selection criteria for simultaneous improvement of various characters along with the seed yield. Interrelationship of various yield components is important in predicting the correlated response to direct and indirect selection and in the identification of traits with much effect on yield. Correlation coefficient provides information on interrelationship of various yield components but when more characters are involved in the association analysis it becomes difficult to ascertain which really trait contributes towards yield. Thus correlation analysis is not enough to give an exact picture of relative importance of direct and indirect influence of each of the component characters on seed yield. Path coefficient analysis provides an effective means of partitioning correlation coefficients into unidirectional pathways and alternative pathways thus permitting a critical examination of specific factors that produce a given correlation, which can be successfully employed in formulating an effective selection programme for dependent trait *i.e.* seed yield.

To utilize pigeonpea gene pool effectively, study was carried out to assess genetic variability, heritability, genetic advance, correlation and path coefficient analysis in some advance lines of pigeonpea.

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 *khariif*, 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 were statistically analysed to estimate genetic variability, heritability (broad sense), expected genetic advance as percent of mean, correlation coefficients and path coefficients. The phenotypic and genotypic coefficient of variability (PCV, GCV) were computed according to the method suggested by Burton (1952) [6], heritability (h^2) and genetic advance as percent of mean (GA) as suggested by Allard (1960) [7]. The correlation coefficients at phenotypic and genotypic levels were estimated from the analysis of variance and covariance as given by Searle (1961) [8]. Direct and indirect effects of various characters on seed yield were estimated with the help of path coefficient analysis as suggested by Wright (1921) [9] and Dewey and Lu (1959) [10].

Results and Discussion

Analysis of Variance (ANOVA)

The results of ANOVA for three different environments are presented in **Table 2** showed that all the characters except number of seeds/pod exhibited significant difference among genotypes which indicated sufficient variability exists among the genotypes and hence desirable improvement can be brought through selection for different characters. Number of seeds/pod gave the insignificant results in the EII while in EIII and EI, this trait recorded significant result at 5 % and 1% level of significance, respectively. [11], [12], [13] and [14] also reported sufficient genetic variability for these characters.

PCV, GCV, h^2 and GA: In general, higher estimates of PCV were measured for all the characters in all the environments than that of the corresponding GCV. It indicates the positive influence of environmental factors in expression of different morphological traits under different environments. Estimates of GCV, PCV, h^2 and GA were given in Table 2. Similar results were also reported by [15], [16], [17] and [18]. The PCV and GCV estimates were lower in EI as compared to EII and EIII for all characters except number of seeds/pod. The minimum magnitude difference in PCV and GCV for days to 50% flowering, days to maturity and 100-seed weight in all the three environments were explained that the trait are mostly governed by genetic factors with little role of environment in the genetic expression of these characters. Thus the selection of these traits on of the basis of the phenotypic value may be effective. In case of EI, the maximum value of GCV was recorded for number of pods/plant (17.26) while GCV was lowest for days to maturity (1.94). In EI, PCV ranges from 2.12 for days to maturity to 17.81 no. of pods per plant. In case of EII and EIII, PCV were lowest for days to 50% flowering and values were 4.46 and 3.74, respectively while seed yield/plot recorded highest values for PCV with 31.39 and 36.69, respectively. For EII and EIII, GCV were lowest for days to 50% flowering and values were 4.43 and 3.72, respectively while seed yield/plot recorded highest values for PCV and values were as 30.13 and 35.60, respectively. High estimates of GCV (>20 %) was observed for no. of secondary branches/plant in EII (20.52), for no. of pods per plant in EII and EIII (23.01 and 23.40) and for seed yield/plot in EII and EIII (30.13 and 35.60) which indicates better chances for selection to the specific traits. Lower estimates of GCV (<10 %) was recorded in all the environments for days to 50% flowering and days to maturity, for no. of seeds/pod in EII and EIII and for no. of secondary branches/plant and 100 seed weight under EI while, for rest of the traits in different environments moderate estimates of GCV (10-20 %) were recorded. Lower estimates for PCV (<10 %) was recorded for days to 50 % flowering and days to maturity in all three environments and for 100 seed weight in EI. Higher estimates for PCV (>20 %) was recorded in EII and EIII for seed yield/plot (31.39 and 36.69) and for no. of pods per plant (24.40 and 25.41). Only for EII, PCV was higher for no. of primary and secondary branches/plant (21.63 and 23.31, respectively) while, rest of the traits recorded moderate for different environments. Similar kind of results for different characters were also reported by [13], [19], [20], [21] and [22].

Higher magnitude of broad sense heritability (>60 %) in all the environments was observed for days to 50 % flowering, days to maturity, plant height, no of primary branches/plant, no of pods/plant, 100-seed weight and seed yield/plot and values are given in Table 2. Broad sense heritability was lowest (16.66) for the number of seeds/pod in EII while, rest of the traits in corresponding environments recorded moderate values for heritability. Differences between GCV and PCV for no. of seeds/pod were also found maximum, indicating that these traits were highly affected by environment. Therefore, lower values for heritability and genetic advance percent of mean for the trait validated that the trait is under environmental influence. Selection for such trait will not be effective. High heritability indicated that selection may be effective for isolating superior genotypes. For these characters, high heritability estimates were also reported by [12], [20], [23-24] and [26].

Table 2 Analysis of variance, general mean, range and estimated genetic parameters for 9 quantitative traits in three environments for advance lines of pigeon pea

Source of variation	d.f.	Environments	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 seeds /pod	100 seed weight (g)	Seed yield/plot (g)
Replications	2	EI	0.424	1.379	77.636	2.864	0.652	16.955	0.015	0.002	40.742
		EII	0.318	0.061	351.045	2.242	0.561	416.182	0.106	0.004	10619.697
		EIII	0.045	0.182	195.197	0.045	0.591	347.106	0.061	0.009	16704.545
Genotypes	21	EI	11.983**	21.111**	838.777**	23.568**	0.815**	784.655**	0.652**	0.439**	31564.214**
		EII	32.552**	198.968**	1260.664**	13.323**	5.799**	3468.880**	0.398	2.874**	603506.854**
		EIII	24.367**	181.100**	1482.315**	8.898**	1.683**	2599.323**	0.505*	2.896**	662313.997**
Error	42	EI	0.392	1.252	40.351	3.356	0.286	16.558	0.222	0.027	2843.155
		EII	0.128	0.346	60.649	1.528	0.513	139.071	0.249	0.004	16703.824
		EIII	0.109	0.102	61.467	1.617	0.369	145.916	0.219	0.010	13364.863

Mean, Range, SEm and Estimated genetic parameters

Range	EI	66.33-72.67	127.33-136.00	123.67-169.00	12.67-21.33	4.00-6.00	68.67-144.33	3.00-4.33	8.17-9.43	533.33-833.33
	EII	70.67-84.67	130.00-152.00	131.33-201.67	7.33-13.00	4.00-9.33	92.33-190.67	3.67-4.67	7.47-10.77	923.33-2266.33
	EIII	71.67-84.67	134.67-156.00	142.33-225.33	7.67-14.33	5.00-8.00	77.67-167.67	3.33-4.67	7.73-10.40	696.67-2086.67
Mean \pm S.E _m	EI	69.35 \pm 0.51	132.67 \pm 0.91	148.32 \pm 5.19	18.23 \pm 1.50	4.80 \pm 0.44	92.73 \pm 3.32	3.79 \pm 0.38	8.77 \pm 0.13	678.49 \pm 43.54
	EII	74.23 \pm 0.29	141.65 \pm 0.48	168.36 \pm 6.98	10.80 \pm 1.01	6.47 \pm 0.58	144.82 \pm 9.63	4.21 \pm 0.41	8.90 \pm 0.05	1468.03 \pm 105.53
	EIII	76.46 \pm 0.27	145.14 \pm 0.26	185.74 \pm 6.40	11.05 \pm 1.04	6.00 \pm 0.50	122.20 \pm 9.86	4.03 \pm 0.38	9.08 \pm 0.08	1306.36 \pm 94.39
PCV %	EI	2.97	2.12	11.80	17.43	14.16	17.81	15.95	4.62	16.42
	EII	4.46	5.76	12.75	21.63	23.31	24.40	12.98	11.02	31.39
	EIII	3.74	5.36	12.45	18.21	14.97	25.41	13.92	10.86	36.69
GCV %	EI	2.83	1.94	11.00	14.24	8.74	17.26	10.00	4.22	14.42
	EII	4.43	5.74	11.88	18.35	20.52	23.01	5.30	10.99	30.13
	EIII	3.72	5.35	11.72	14.11	11.03	23.40	7.66	10.81	35.60
h^2	EI	90.78	84.10	86.84	66.75	38.07	93.93	39.33	83.62	77.10
	EII	98.83	99.48	86.83	72.01	77.45	88.86	16.66	99.58	92.13
	EIII	98.67	99.83	88.51	60.02	54.29	84.86	30.28	98.95	94.18
GA as % of mean	EI	5.56	3.66	21.11	23.97	11.10	34.45	12.92	7.96	26.09
	EII	9.07	11.80	22.80	32.08	37.20	44.68	4.46	22.60	59.57
	EIII	7.61	11.02	22.71	22.51	16.74	44.41	8.68	22.14	71.18

*, **: Significant at 5% and 1% probability levels, respectively.

In all the three environments, high magnitude of genetic advance as percent of mean (>20 %) were observed for plant height, number of primary branches/plant, number of pods/plant, 100 seed weight and seed yield/plot (Table 2) which indicated that these characters governed by additive gene and therefore to selection based on phenotypic performance is likely to give beneficial results in improving these characters. Whereas, in general, moderate (10-20 %) or low (<10 %) genetic advance as percent of mean were observed for days to 50 % flowering, days to maturity, number of secondary branches/plant and number of seeds/pod. Values for genetic advance as percent of mean were given in Table 2.

Selection on the basis of high heritability alone may not be rewarding in breeding programmes as broad sense heritability comprise both additive and non-additive effects. Therefore, heritability estimates were considered along with high values of genetic advance as suggested by Panse (1957) [27]. Johnson *et al.*, (1955) [4] emphasised that heritability estimates in conjugation with genetic gain would be promising to predict the resulting effect of selecting the best individuals. In the present study, high heritability coupled with high genetic advance was observed for plant height, no. of primary branches/plant, number of pods/plant, 100 seed weight and seed yield/plot in all the three environments except 100 seed weight in EI. It indicated additive genetic control in the inheritance of these traits and hence selection may be effective. For these characters, similar finding were also observed by [12], [16] and [28-31]. No. of seeds/pod showed low heritability with low genetic advance and days to 50 % flowering showed high heritability with low genetic advance indicating preponderance of non-additive genetic effects so selection would be ineffective. Thus, the genetic improvement in this trait can be achieved by hybridization followed by selection.

Correlations and Path Analysis

The data obtained from present study revealed that estimates of genotypic correlations in general were higher than the corresponding phenotypic correlation coefficients for all the traits in each environment (**Table 3**). In general directions of phenotypic and genotypic correlations were almost same for the most of the character combinations in particular environment. A positive correlation between desirable characters is favorable to plant breeder because it helps in simultaneous improvement in both the characters which is genetically correlated with the dependent character. This indicated that there was inherent association among the characters.

Over the environments, perusal of interrelationship correlation matrix revealed that the seed yield had highly significant and positive correlation with days to maturity, plant height, no. of pods per plant and 100 seed weight at both phenotypic and genotypic level, indicating that increase in these character will naturally bring an increase in seed yield and therefore to improve the seed yield, selection can be exerted for these traits. Since all these traits were associated with high heritability and conjugated with moderate to high genetic advance, therefore, seed yield can be improved by exerting direct selection pressure for these four traits. A positive and significant correlation of seed yield/plot with plant height, number of pods/plant and 100 seed weight were also reported by [14] and [32-37]. Similarly, in all environments 100 seed weight exhibited positive and significant correlation with plant height, number of primary branches/plant, number of pods/plant and seed yield/plot; number of pods/plant was significant and positively correlated with plant height, number of primary branches/plant, 100 seed weight and seed yield/plot at both phenotypic and genotypic level; number of primary branches/plant exhibited positive and significant correlation with plant height, number of pods/plant and 100 seed weight and plant height also showed significant and positive correlation with number of primary branches/plant, number of pods/plant, 100 seed weight and seed yield/plot at both phenotypic and genotypic level. Only number of seeds/pod did not exhibit significant and positive correlation with all the characters studied.

Knowledge of correlation alone is often misleading as the correlation observed may not be always true. Two characters may show correlation just because they are correlated *via* another common character. In such cases, it is necessary to study a method which considers the casual relationship between the variables in addition to the degree and direction of such relationship. Therefore, Path coefficient analysis measures the direct effects of one variable upon the other and permits partition of correlation coefficient into components of direct and indirect effects and provides better insight on character and their relationship with yield and thus forms the basis of selection to improve the yield.

Path coefficients measured vide **Table 4** of seed yield revealed that in all the three environments number of pods/plant not only had high direct effects followed by 100-seed weight but it also had positive and significant correlation with seed yield/plot and 100-seed weight at genotypic and phenotypic level. It means that slight increase in no. of pods/plant and 100- seed weight may directly contribute towards seed yield/plot. Days to 50 % flowering and days to maturity in EI, EII, EIII, no. of primary branches/ plant in EII, EIII and no. of secondary branches/ plant in EI, EII recorded negative direct effects on seed yield/plot but indirect effects through other traits were positive. Remaining traits recorded low positive direct effects on seed yield/plot. Direct selection for number of pods/plant will be rewarding for improving seed yield/plot. Our findings are in accordance with previous studies of [25] and [38-40]. The residual effect estimates were found to be moderate in EI (0.5449), EII (0.3768) and EIII (0.4398) which is a clear cut indication that there are some more characters which are contribute towards the seed yield/plot.

Table 3 Phenotypic (P) and genotypic (G) correlation coefficients among various characters in pigeonpea genotypes in different environment

Traits	Environment		Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/plant	No. of secondary branches/plant	No. of pods/plant	No. of seeds/pod	100 seed weight (g)	Seed yield/plot (g)
Days to 50% flowering	EI	P	1.000	0.022	-0.057	0.083	0.089	0.005	-0.054	0.028	0.009
		G	1.000	0.033	-0.060	0.096	0.296*	-0.008	-0.054	0.009	0.011
	EII	P	1.000	0.267*	0.160	0.228	0.455**	0.116	0.001	-0.102	-0.275*
		G	1.000	0.270*	0.171	0.276*	0.540**	0.124	0.003	-0.104	-0.294*
	EIII	P	1.000	0.389**	0.233	0.368**	0.104	0.276*	-0.088	0.122	-0.153
		G	1.000	0.391**	0.244*	0.454**	0.140	0.296*	-0.170	0.122	-0.154
Days to maturity	EI	P	1.000	-0.430**	-0.419**	0.035	0.059	-0.201	-0.352**	-0.495**	
		G	1.000	-0.450**	-0.563**	0.101	0.096	-0.354**	-0.412**	-0.690**	
	EII	P	1.000	0.635**	0.390**	0.440**	0.793**	-0.064	0.808**	0.324**	
		G	1.000	0.683**	0.459**	0.503**	0.836**	-0.150	0.813**	0.342**	
	EIII	P	1.000	0.589**	0.361**	0.082	0.758**	-0.281*	0.762**	0.416**	
		G	1.000	0.629**	0.459**	0.116	0.825**	-0.516*	0.767**	0.428**	
Plant height (cm)	EI	P	1.000	0.763**	0.039	0.361**	0.003	0.479**	0.543**		
		G	1.000	1.017**	0.069	0.387**	-0.004	0.549**	0.675**		
	EII	P	1.000	0.368**	0.408**	0.517**	-0.131	0.590**	0.342**		
		G	1.000	0.396**	0.458**	0.570**	-0.303*	0.630**	0.355**		
	EIII	P	1.000	0.302*	0.331**	0.481**	-0.223	0.495**	0.400**		
		G	1.000	0.416**	0.368*	0.528**	-0.502**	0.524**	0.413**		
Number of primary branches/plant	EI	P	1.000	-0.011	0.257*	-0.115	0.500**	0.560**			
		G	1.000	0.228	0.331**	0.109	0.669**	0.723**			
	EII	P	1.000	0.734**	0.511**	-0.097	0.273*	0.134			
		G	1.000	0.891**	0.601**	-0.232	0.338**	0.149			
	EIII	P	1.000	0.076	0.512**	0.054	0.298*	0.085			
		G	1.000	0.126	0.677**	-0.150	0.360**	0.104			
Number of secondary branches/plant	EI	P	1.000	0.054	-0.218	-0.083	-0.063				
		G	1.000	0.080	-0.431**	-0.134	-0.070				
	EII	P	1.000	0.466**	-0.055	0.259*	0.032				
		G	1.000	0.565**	-0.372**	0.302*	0.044				
	EIII	P	1.000	0.106	-0.009	0.111	0.261*				
		G	1.000	0.119	0.339**	0.141	0.318**				
Number of pods/plant	EI	P	1.000	-0.326**	0.330**	0.270*					
		G	1.000	-0.580**	0.402**	0.284*					
	EII	P	1.000	-0.125	0.672**	0.596**					
		G	1.000	-0.255**	0.721**	0.657**					
	EIII	P	1.000	-0.170	0.659**	0.576**					
		G	1.000	-0.314*	0.723**	0.650**					
Number of seeds/pod	EI	P	1.000	-0.142	0.076						
		G	1.000	-0.348**	0.249*						
	EII	P	1.000	-0.030	-0.039						
		G	1.000	-0.054	-0.040						
	EIII	P	1.000	-0.270*	-0.146						
		G	1.000	-0.471**	-0.338*						
100 seed weight (g)	EI	P	1.000	0.429**							
		G	1.000	0.587**							
	EII	P	1.000	0.520**							
		G	1.000	0.540**							
	EIII	P	1.000	0.537**							
		G	1.000	0.554**							
Seed yield/plot (g)	EI	P	1.000								
		G	1.000								
	EII	P	1.000								
		G	1.000								
	EIII	P	1.000								
		G	1.000								

*, **: Significant at 5% and 1% probability levels, respectively.

Table 4 Path coefficient analysis showing direct and indirect effect of various characters on seed yield/plot at phenotypic level in pigeonpea genotypes in different environment

Traits	Envi ron men ts	Correlat ion with seed yield/plo t	Direct effects	Indirect effects Via							
				Days to 50% flowering	Days to maturit y	Plant height (cm)	No. of primar y branch es/plant	No. of seconda ry branch es/plant	No. of pods/pl ant	No of seeds/p od	100 seed weight (g)
Days to 50% flowering	EI	0.009	-0.0023	-	-0.0063	-0.0046	0.0284	-0.0028	0.0010	-0.0066	0.0026
	EII	-0.275*	-0.0436	-	-0.2304	0.0320	-0.0270	-0.0660	0.1120	0.0001	-0.0525
	EIII	-0.153	-0.2587	-	-0.0762	0.0323	-0.0799	0.0183	0.1789	-0.0002	0.0326
Days to maturity	EI	-0.495**	-0.2901	-0.0001	-	-0.0350	-0.1235	-0.0011	0.0113	-0.0243	-0.0322
	EII	0.324**	-0.8616	-0.0117	-	0.1272	-0.0462	-0.0638	0.7689	-0.0031	0.4145
	EIII	0.416**	-0.1958	-0.1007	-	0.0817	-0.0784	0.0145	0.4915	-0.0007	0.2040
Plant height (cm)	EI	0.543**	0.0813	0.0001	0.1247	-	0.2250	-0.0022	0.0695	0.0003	0.0438
	EII	0.342**	0.2004	-0.0070	-0.5469	-	-0.0435	-0.0591	0.5016	-0.0064	0.3029
	EIII	0.400**	0.1387	-0.0602	-0.1152	-	-0.0656	0.0584	0.3117	-0.0005	0.1326
Number of primary branches/ plant	EI	0.560**	0.2948	-0.0002	0.1216	0.0620	-	0.0003	0.0494	-0.0139	0.0458
	EII	0.134	-0.1184	-0.0100	-0.3359	0.0737	-	-0.1063	0.4951	-0.0047	0.1403
	EIII	0.085	-0.2170	-0.0953	-0.0707	0.0419	-	0.0135	0.3322	0.0001	0.0799
Number of secondary branches/ plant	EI	-0.063	-0.0317	-0.0002	-0.0102	0.0056	-0.0032	-	0.0103	-0.0263	-0.0076
	EII	0.032	-0.1450	-0.0199	-0.3792	0.0817	-0.0868	-	0.4514	-0.0027	0.1330
	EIII	0.261*	0.1764	-0.0268	-0.0161	0.0459	-0.0166	-	0.0688	-0.0000	0.0296
Number of pods/plant	EI	0.270*	0.1947	0.0000	-0.0170	0.0293	0.0756	-0.0017	-	-0.0393	0.0302
	EII	0.596**	0.9696	-0.0050	-0.6833	0.1037	-0.0604	-0.0675	-	-0.0061	0.3448
	EIII	0.576**	0.6485	-0.0714	-0.1484	0.0677	-0.1111	0.0187	-	-0.0004	0.1765
Number of seeds/pod	EI	0.076	0.1206	0.0001	0.0584	0.0002	-0.0340	0.0069	-0.0627	-	-0.0130
	EII	-0.039	0.0488	-0.0001	0.0555	-0.0263	0.0115	0.0080	-0.1216	-	-0.0152
	EIII	-0.146	0.0024	0.0288	0.0550	-0.0310	-0.0117	-0.0015	-0.1102	-	-0.0722
100 seed weight (g)	EI	0.429**	0.0916	-0.0001	0.1021	0.0389	0.1473	0.0026	0.0635	-0.0171	-
	EII	0.520**	0.5131	0.0045	-0.6961	0.1183	-0.0324	-0.0376	0.6515	-0.0014	-
	EIII	0.537**	0.2678	-0.0315	-0.1492	0.0687	-0.0647	0.0195	0.4273	-0.0006	-

*, **: Significant at 5% and 1% probability levels, respectively.

Conclusion

The present study revealed that pigeonpea genotypes exhibited a wide range of variation for most of the investigated traits. Present study suggests that direct selection for no. of pods/plant and 100-seed weight contributes directly towards seed yield. Seed yield, number of pods per plant and 100-seed weight is greatly influenced by the additive gene action and greater proportions of variations are heritable this results validated through high heritability coupled with high genetic advance as percent of mean. Under such circumstances, selection should be made for increased no. of pods/plant as well as 100-seed weight which will help in selecting superior genotypes, that may be directly used as the parent in hybridization program for development of high yielding varieties.

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