Research Article

Study on Some Genetic Parameters for Yield and Related Traits in Pigeonpea [*Cajanus cajan* (L.) Millspaugh] Genotypes

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Abstract

The present investigation was undertaken with the objectives to assess variability, heritability, genetic advance, correlation and path coefficients among one forty four (144) pigeonpea genotypes. The experiment was conducted during *kharif* 2016-17 in Randomized Complete Block Design (RCBD) with three replications at Norman E. Borlaug Crop Research Centre, G. B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand. The analysis of variance (ANOVA) showed that the mean sum of squares were highly significant for all the characters. In general, the phenotypic coefficients of variation were higher than the respective genotypic coefficients of variation for all the traits under study. The GCV of various characters varied from 4.35 to 25.45 while the PCV varied from 5.73 to 33.86. High broad sense heritability was observed for days to maturity, days to 50% flowering, number of pods per plant, plant height and number of seeds per pod. The high estimates of genetic advance as percent of mean were observed for number of pods per plant, seed yield, number of seeds per pod and plant height.

Significant and positive correlation of seed yield with days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant and number of seeds per pod at both phenotypic and genotypic level were observed. The number of pods/plant and days to maturity had shown high direct effects on seed yield/plant and hence direct selection for these traits may contribute towards improvement in seed yield/plant.

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

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Introduction

Pigeonpea [*Cajanus cajan* (L.) Millspaugh] also known as arhar, tour or red gram is a drought tolerant pulse crop suitable for rainfed farming. In India it is considered as second most important pulse crop after chickpea. Pigeonpea belongs to family Fabaceae, sub family Papilionaceae, tribe Phaseoleae, sub-tribe *Cajanae*, genus *Cajanus* and species *cajan*. It is a drought tolerant and often cross pollinated food legume crop with diploid chromosome number 2n=2x=22. It is a very hardy crop with wider adaptability and with large temporal variation (97-299 days) for grain maturity [1]. Almost all plant parts of this crop are used for one or other purposes the grains are used both as human food and animal feed, leaves can be used as animal fodder; green pods are used as vegetable in western India and after harvesting the grains the woody remains are used for fuel. The seed of pigeonpea contains 20-22% protein along with some reasonable amounts of essential amino acids [2]. India is the largest producer, consumer and the importer of pigeonpea today and this crop plays an important role in providing food security, balanced diet and alleviation of poverty particularly in rural areas [3].

Even after four decades of green revolution both the productivity as well as grain yield per unit area of pigeonpea has not increased much. This stagnation is caused due to many factors like non availability of quality seed of suitable varieties, climatic changes, various biotic and abiotic stresses and the emergence of new biotypes of insect pests and different diseases. Therefore, there is an urgent need of improved genotypes having high yield potential with multiple resistances to important diseases and insect pests and hence the study of variability, heritability, genetic advance, correlation and the cause and effects relationship among seed yield and yield contributing traits is absolutely essential in chalking out an effective pigeonpea breeding programme. The knowledge on available variability, heritability and the expected genetic advance is necessary for selecting improved genotypes. Seed yield is a polygenic or complex trait so the direct selection for seed yield may not be effective. The information about the nature and extent of relationship between various morphological traits would be helpful in developing an ideal plant type. Path coefficient analysis partitioned the correlation coefficients of independent variables on dependent variable into the direct and indirect effects. The study of path analysis is helpful in determining whether the association of these components is

due to their direct effects on yield or as a consequence of their indirect effect through some other component traits. Hence the correlation and path coefficient analysis helps to find out association among various characters and also the direct and indirect contribution of different traits towards seed yield. Therefore, the present study was conducted with the aim to estimate genetic variability, heritability, genetic advance, relationship between yield and its various contributing components and the direct and indirect effects of different component traits towards the grain yield so that the desired information can be obtained and be used the future pigeonpea breeding programmes.

Materials and Methods

The experimental material comprised of one hundred forty four genetically diverse genotypes of pigeonpea. All the genotypes were sown in Randomized Complete Block Design (RCBD) with three replications in a six row plots of four meter length during *Kharif*, 2016-17 crop season at Norman E. Borlaug Crop Research Centre, G. B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand. The row to row distance was maintained at 60 cm and the plant to plant distance was maintained at 15 cm. The recommended packages of agronomic practices relevant to the crop were followed throughout the crop period.

Observed traits and sampling measurements

From each plot in each replication, five plants were randomly selected and observations were recorded for nine component characters, *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100- seed weight (g) and seed yield per plant (g). The mean values computed from the observations for each replication were used for statistical analysis.

Statistical analysis

The recorded data were analysed to calculate genotypic and phenotypic coefficients of variation (GCV and PCV), heritability (broad sense), expected genetic advance as percent of mean, correlation coefficients and direct and indirect effects of component characters on seed yield per plant. The genotypic and phenotypic coefficients of variation (GCV and PCV), for various component traits were calculated by the formula suggested by [4]. Heritability in broad sense and genetic advance as percent of mean (GA) was calculated by formula given by [5]. The phenotypic and genotypic coefficients of correlation were estimated from the analysis of variance and covariance according to formula suggested by [6]. Path coefficients to find the direct and indirect effects of various characters on seed yield were computed by using the formula suggested by [7] and [8].

Results and Discussion
Analysis of Variance (ANOVA)

The analysis of variance (ANOVA) showed that the mean sum of squares were highly significant (**Table 1**) for all the characters indicating the presence of sufficient genetic variability among the different genotypes under study and hence desirable improvement can be brought through selection for different component traits.

Table 1 Analysis of Variance for nine characters in 144 genotypes of pigeonpea

Mean squares										
Source of variation	d.f.	Days to 50 % flowering	Days to maturity	Plant height (cm)	No. of primary branches/ plant	No. of Pods/plant	Pod length (cm)	No. of seeds/pod	100- Seed weight (g)	Yield per plant (g)
Replication	2	34.17**	41.92**	28.97	32.148**	28.197	0.61*	0.26	14.36**	316.39
Treatment	143	54.83**	226.27**	2,503.95**	8.306**	7,077.54**	0.34**	1.03**	3.85**	695.91**
Error	286	1.09	1.34	331.06	4.060	445.92	0.17	0.16	0.92	142.13
*, **: Significant at 5% and 1% probability levels, respectively										

Genotypic and Phenotypic coefficients of variation (GCV and PCV), Heritability (broad sense) h^2 and Genetic Advance (GA)

A close perusal of (**Table 2**) indicated a wide range of phenotypic variation in the experimental material. In general, high phenotypic coefficient of variation (PCV) was reported than the corresponding genotypic coefficient of variation (GCV) for all the characters under study. The higher PCV indicated a positive influence of environmental factors in

expression of different morphological traits. High PCV estimates than the corresponding GCV estimates for different traits were also reported earlier by [9], [10], [11], [12] and [13]. The GCV estimates of various characters varied from 4.35 for pod length to 25.45 for seed yield/plant. High estimates of GCV (>20 %) was observed for seed yield/ plant (25.45) and number of pods/plant (23.53), which indicates presence of high degree of genetic variation in the experimental material. For rest of the traits under study the GCV estimates were moderate or low. The PCV estimates for various traits ranged from 5.73 for days to 50% flowering to 33.86 for grain yield per plant. High estimates of PCV were recorded for grain yield per plant (33.86), number of pods / plant (25.80) and number of primary branches / plant (21.65). Moderate to Low estimates of PCV were recorded for rest of the traits in the present study. Similar kinds of results for different traits were also earlier reported by [9], [10], [11], [12] and [13].

Although GCV indicates the existence of high genetic variation but the estimates of heritability and genetic gain are still needed to find out that how much portion of that variation is heritable. High broad sense heritability (>60 %) was observed for days to maturity (98.24), days to 50% flowering (94.29) number of pods per plant (83.21) plant height (68.63) and number of seeds per pod (64.89). High estimates of heritability indicated that these traits can be improved through selection. Moderate estimates of heritability were recorded for 100-seed weight (51.58) yield per plant (56.49) whereas low estimates were recorded (< 40%) for the pod length (26.09) number of primary branches (25.85). High heritability estimates for these different traits were also reported High genetic advance coupled with high heritability estimates were observed for plant height, number of pods / plant and the grain yield per plant by [14], [15], [16], [17] and [18].

For effective selection high heritability estimates coupled with high genetic advance is a better criterion as suggested by [19]. Genetic advance is dependent upon the heritability of trait, genetic variability and intensity of selection [20]. In the present investigation high magnitude of genetic advance as percent of mean (>20 %) were observed for number of pods/plant (44.23), seed yield/plant (39.41), number of seeds per pod (22.32) and plant height (20.30), whereas, moderate (10-20%) for 100-seed weight (18.75), days to maturity (12.72), number of primary branches/plant (11.53) and days to 50 % flowering (11.13). The low (<10 %) genetic advance as percent of mean was observed for pod length (4.58). High genetic advance coupled with high heritability estimates were observed for plant height, number of pods / plant and the grain yield per plant in the present study indicating that these traits are governed by additive gene and therefore, selection based on phenotypic performance is likely to give beneficial results in improving these characters. High genetic advance coupled with high heritability estimates for plant height, number of pods / plant and the grain yield per plant were also reported by [14], [15] and [18].

Table 2 Phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2) and genetic advance (GA) for different traits in pigeonpea

Characters	Heritability (%)	Genotypic Coefficient of Variation (GCV)	Phenotypic Coefficient of Variation (PCV)	Genetic Advance (GA)	Genetic Advance as (%) of Means
Days to 50 % flowering	94.29	5.56	5.73	8.46	11.13
Days to maturity	98.24	6.232	6.28	17.68	12.72
Plant height (cm)	68.63	11.89	14.36	45.29	20.30
Number of primary branches/plant	25.85	11.00	21.65	1.24	11.53
Number of pods per Plants	83.21	23.53	25.80	88.35	44.23
Pod length (cm)	26.09	4.35	8.51	0.25	4.578
Number of seeds per pod	64.89	13.45	16.70	0.89	22.32
100-Seed weight (g)	51.58	12.67	17.65	1.46	18.75
Yield/Plant (g)	56.49	25.45	33.86	21.03	39.414
*, **: Significant at 5% and 1% probability levels, respectively					

Correlations and Path Analysis

The relationship among different plant traits can be measured by using correlation coefficient. It also helps in deciding the component traits on which selection may be based for genetic improvement in yield. In the present study, the estimates of genotypic correlations, in general, were found higher than the corresponding phenotypic correlation coefficients (**Table 3**). The high values of genotypic correlation coefficients than the corresponding phenotypic correlation coefficients indicated that there is strong association between these two characters but the phenotypic values are lessened by the influence of environment. High values of genotypic correlation coefficients than the

corresponding phenotypic correlation coefficients for different characters were also reported earlier by [13], [21], [22], [23], [24] and [25].

Table 3 Phenotypic (P) and Genotypic (G) correlation coefficients among different yield contributing traits in pigeonpea

Traits		Days to 50% flowering	Days to maturity	Plant height	Number of primary branches	Number of pods/ plant	Pod length	Number of seeds /pod	100-Seed weight	Yield/ plant
Days to 50%	P	1.000	0.851**	0.212**	0.428**	0.705**	-0.053	0.663**	0.050	0.670**
flowering	G	1.000	0.866**	0.265**	0.893**	0.787**	-0.139**	0.838**	0.045	0.919**
Days to maturity	P		1.000	0.220**	0.486**	0.834**	-0.028	0.795**	0.018	0.755**
	G		1.000	0.267**	0.979**	0.920**	-0.061	0.986**	0.026	1.015**
Plant height	P			1.000	0.143**	0.195**	0.069	0.170**	-0.120*	0.206**
	G			1.000	0.353**	0.249**	0.038	0.269**	-0.200**	0.272**
Number of primary	P				1.000	0.481**	0.009	0.439**	0.023	0.472**
branches/plant	G				1.000	1.082**	0.023	1.130**	-0.032	1.175**
Number of	P					1.000	-0.023	0.760**	0.114*	0.768**
pods/plant	G					1.000	-0.074	1.039**	0.124*	1.121**
Pod length	P						1.000	-0.033	-0.015	-0.065
	G						1.000	-0.077	-0.056	-0.072
Number of seeds	P							1.000	0.056	0.677**
/pod	G							1.000	0.094	1.151**
100-Seed weight	P								1.000	0.082
	G								1.000	0.125**
Yield/plant	P									1.000
	G									1.000
*, **: Significant at 5% and 1% probability levels, respectively										

In the present study the seed yield had shown significant and positive correlations with days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant and number of seeds per pod at both phenotypic and genotypic level, indicating that these characters are useful for taking them as the basis of selection for high yield. Similar results were also obtained by [21], [22] and [23]. 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 on these traits. The 100 seed weight had shown positive and significant correlation with number of pods per plant, however it showed negative and significant correlation with plant height. Similar, kind of results for correlation of 100 seed weight with other characters were also reported by [13] and [25].

It is also clear from the Table 3 that number of seeds per pod exhibited positive and significant relationship with days to 50% flowering, days to maturity, plant height, number of primary branches, number of pods per plant and seed yield per plant. This is quite clear that an increase in these components will results in an increase in the number of seeds per pod. A close perusal of results on correlation studies showed that number of pods per plant exhibited positive and significant association with days to 50% flowering, days to maturity, plant height, number of primary branches, number of seeds per pod and seed yield per plant at both phenotypic and genotypic level indicating a strong association of pods per plant with these component characters. Positive and significant association of pods / plant with these different characters were also reported by [13] and [24]. Similarly, number of primary branches per plant showed positive and significant association with days to 50% flowering, days to maturity, plant height, number of seeds per pod and seed yield per plant at both phenotypic and genotypic level indicating that there is strong association of primary branches per plant with these different component characters, however, primary branches per plant exhibited on significant association at both, the phenotypic and genotypic level with pod length and 100 seed weight. [21], [22] and [24] also reported similar kind of results for these different characters.

Plant height depicted a significant and positive association with traits like days to 50 percent flowering, days to maturity, number of primary branches per plant, number of pods per plant, number of seeds per pod and seed yield per plant and negative and significant association with 100 seed weight at both phenotypic and genotypic level which indicated strong association of plant height with these different component characters in different directions. This indicated that an increase in plant height may result in an increase in these characters except 100 seed weight. Similar results of association of plant height with different characters were earlier also reported by [22] and [25]. Days to maturity showed positive and significant association with days to 50% flowering, plant height, primary branches per plant, number of pods per plant, number of seeds per pod and seed yield per plant indicating that an increase in

maturity may result in an increase in seed yield. [21], [22] and [24] also reported positive and significant association of days to maturity with days to 50% flowering, plant height, primary branches per plant, number of pods per plant, number of seeds per pod and seed yield per plant earlier.

Correlation does not tell anything related to the cause and effect relationship [26]. Knowledge of correlation alone is often misleading as the correlation observed may not be always true. Path coefficient analysis is a very powerful statistical tool that indicates about the effect of independent variables (causes) on dependent variables (seed yield), while recognizing the impacts of multi colinearity [27]. Correlation only measures the mutual association without considering causation while the path coefficient analysis not only measures the relative importance of the characters but also specifies the cause.

In present study the seed yield per plant was taken as dependent character while other traits as independent. Perusals of **Table 4** revealed that number of pods/plant (0.394) and days to maturity (0.218) not only had high direct effects on seed yield/plant but also had positive and significant correlation with seed yield/plant at phenotypic level. Number of pods/plant not only had high direct effect on seed yield but also shown high positive indirect effect via days to maturity (0.181). Besides high positive direct effect, days to maturity exhibited high positive indirect effect via number of pods per plant (0.328). It indicated that these two characters are truly associated with seed yield per plant and may be useful in improving the seed yield. High direct effect of these two characters on seed yield per plant was also earlier reported by [28], [29] and [30]. Pod length exhibited negative direct effects on seed yield/plant and negative indirect effects through other traits like days to 50% flowering days to maturity, number of pod per plant, number of seed per pod, 100-seed weight. The residual effect estimates were found to be 0.35141 which is a clear cut indication that there are some more characters which contribute towards the seed yield/plant.

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 | Correlation With seed yield/plant | Direct effects | Indirect effects *Via* | | | | | | | |
			Days to 50% flowering	Days to maturity	Plant height	No. of primary branches/ plant	No. of pods/ plant	Pod length	No. of seeds /pod	100-Seed weight
Days to 50% flowering	0.670**	0.095		0.186	0.008	0.038	0.278	0.002	0.061	0.001
Days to maturity	0.755**	0.218	0.089		0.009	0.043	0.328	0.001	0.074	0.0004
Plant height	0.206**	0.039	0.020	0.048		0.012	0.076	-0.003	0.015	-0.003
No. of primary branches/ plant	0.472**	0.089	0.040	0.105	0.006		0.189	-0.0003	0.04	0.0005
No. of Pods/plant	0.768**	0.394	0.067	0.181	0.007	0.042		0.001	0.070	0.002
Pod length	-0.065	-0.046	-0.005	-0.006	0.002	0.0007	-0.008		-0.003	-0.0003
No. of seeds /pod	0.677**	0.093	0.062	0.173	0.006	0.039	0.299	0.0015		0.0014
100-Seed weight	0.082	0.025	0.0047	0.004	-0.0046	0.00208	0.0448	0.0006	0.0051	

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

Conclusion

The present study revealed the presence of wide range of genetic variability for almost all the traits under investigation. In general, the genotypic correlation coefficients were greater than the phenotypic correlation coefficients in magnitude and were in similar direction. High broad sense heritability was observed for days to maturity, days to 50% flowering, number of pods per plant and number of seeds per pod. High heritability indicates the scope of genetic improvement of these characters through selection. The high genetic advance were observed for plant height, number of pods per plant, number of seed per pod and seed yield. The seed yield had significant and positive correlation with days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant and number of seeds per pod at both phenotypic and genotypic level. The number of

pods/plant and days to maturity had shown high direct effects on seed yield/plot hence direct selection for these traits may contribute towards increase in seed yield/plant.

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