



Research Article

TO STUDY THE DIRECT AND INDIRECT CONTRIBUTION OF VARIOUS CHARACTERS INFLUENCING SEED YIELD IN PIGEONPEA GERMPLASM ACCESSIONS

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Abstract: The path coefficient analysis showed that, the number of pod clusters per plant had the highest direct effect on seed yield. Hence, this character seems to be important contributor of seed yield and must be considered in selection for high seed yield. Whereas, the characters namely number of pod clusters per plant and days to maturity had the highest indirect effect on seed yield. Hence, the indirect selection of these traits may lead to be the development of high yielding genotypes.

Keywords: Path coefficient analysis, yielding genotypes

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Introduction

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is the major pulse crop of India after chickpea which contributes significantly to nourishment of a sizeable population. It belongs to the family of 'Fabaceae' and is also known as 'Arhar' or 'Tur', generally used in preparing dal which is rich in protein and minerals and eaten by majority of Indian population. It is an important legume of the tropics and subtropics because of multifarious uses viz., source of food, fodder and fuel wood; material for fencing, for soil improvement through N fixation and wind barriers. It is the fourth most important pulse crop in the world where in, India alone accounts for 85 per cent of the world supply [1]. It is grown as a field crop as well as backyard crop in more than 80 countries [2].

Materials and Methods

Experimental Detail

The experimental material was comprised of 45 pigeonpea germplasm accessions. The experiment was laid out in Randomized Complete Block Design (RBD) in two replications during *khariif*-2010-11. Experimental site has heavy (vertisol) soil. A fertilizer dose of 20N: 50P: 20K kg / ha was applied. Each entry was sown in two rows of four meter length keeping 60 cm between rows and 15 cm between plants spacings. All the recommended package of practices was adopted to raise a good crop.

Observations Recorded

Observations on metric traits were recorded on single plant basis from five randomly selected competitive plants from each genotype separately. Observations on flowering and maturity were recorded on plot basis as per the descriptors developed by IBPGR and ICRISAT for pigeonpea.

Days to flower initiation

This was noted in terms of days from the date of sowing to the opening of first flower.

Days to 50% flowering

It was noted in days from the date of sowing to the opening of first flower on approximately 50 % plants in each plot.

Days to maturity

It was noted in terms of days from the date of sowing to the stage when over 90 % pods have matured.

Plant height (cm)

The height of plant was measured in cm from ground level to the tip of main axis of physiologically matured plants.

Number of primary branches per plant

Total numbers of primary branches were counted at physiological maturity.

Number of pods per plant

All the effective pods were counted from each selected plant at physiological maturity.

No of pods per cluster

Total numbers of pods were counted from each selected plant at physiological maturity.

No of pod clusters per plant

Total numbers of clusters were counted from each selected plant at physiological maturity.

Number of seeds per pod

Total numbers of seeds from the effective pods each selected plant were counted at physiological maturity.

100 seed weight (g)

Test weight of dried 100 healthy seeds in grams at 10 per cent (air dry) moisture content was recorded.

Seed yield per plant (g)

The selected plants were harvested, threshed and winnowed separately. Finally the seeds were weighed in grams after drying them to appropriate moisture level.

Statistical Analysis

Analysis of variance

The data obtained from the individual plant observations from randomized block design experiment were analyzed statistically as per the procedure given in 1957 [3].

Table-1 List of germplasm accessions

S	Germplasm Accessions	Source of material
1	ICPL-87119	IIPR, Kanpur
2	BDN-2	IIPR, Kanpur
3	UPAS-120	IIPR, Kanpur
4	ICPL-6992	CRISAT, Patancheru
5	ICPL-6994	ICRISAT, Patancheru
6	ICPL-6995	ICRISAT, Patancheru
7	ICPL-6996	ICRISAT, Patancheru
8	ICPL-6997	ICRISAT, Patancheru
9	ICPL-6999	ICRISAT, Patancheru
10	ICPL-7000	ICRISAT, Patancheru
11	ICPL-7001	ICRISAT, Patancheru
12	ICPL-7002	ICRISAT, Patancheru
13	ICPL-7003	ICRISAT, Patancheru
14	ICPL-7004	ICRISAT, Patancheru
15	ICPL-7005	ICRISAT, Patancheru
16	ICPL-7349	ICRISAT, Patancheru
17	ICPL-7358	ICRISAT, Patancheru
18	ICPL-7359	ICRISAT, Patancheru
19	ICPL-7362	ICRISAT, Patancheru
20	ICPL-7363	ICRISAT, Patancheru
21	ICPL-7364	ICRISAT, Patancheru
22	ICPL-7366	ICRISAT, Patancheru
23	ICPL-7367	ICRISAT, Patancheru
24	ICPL-7373	ICRISAT, Patancheru
25	ICPL-7374	ICRISAT, Patancheru
26	ICPL-7376	ICRISAT, Patancheru
27	ICPL-7379	ICRISAT, Patancheru
28	ICPL-7382	ICRISAT, Patancheru
29	ICPL-7384	ICRISAT, Patancheru
30	ICPL-7385	ICRISAT, Patancheru
31	ICPL-7387	ICRISAT, Patancheru
32	ICPL-7388	ICRISAT, Patancheru
33	ICPL-7389	ICRISAT, Patancheru
34	ICPL-7391	ICRISAT, Patancheru
35	ICPL-7392	ICRISAT, Patancheru
36	ICPL-7393	ICRISAT, Patancheru
37	ICPL-7397	ICRISAT, Patancheru
38	ICPL-7398	ICRISAT, Patancheru
39	ICPL-7404	ICRISAT, Patancheru
40	ICPL-7405	ICRISAT, Patancheru
41	ICPL-7406	ICRISAT, Patancheru
42	ICPL-7409	ICRISAT, Patancheru
43	ICPL-7420	ICRISAT, Patancheru
44	ICPL-7429	ICRISAT, Patancheru
45	ICPL-7430	ICRISAT, Patancheru

Table-2 The skeleton of analysis of variance for Randomized Complete Block Design (RBD)

Source	D.F.	SS	MSS	F value
Replications	(r-1)	SSR	MSR	MSR / MSE
Genotypes	(t-1)	SST	MST	MST / MSE
Error	(r-1)(t-1)	SSE	MSE	
Total	rt-1	TSS		

Where, r = Number of replications. t = number of genotypes.

To test the significance of treatment, the calculated value of 'F' was compared with tabular value of 'F' at 5 and 1 per cent levels of probability against error degree of freedom, i.e. (r-1) (t-1).

Estimation of genetic parameters of variation

Mean

Mean of the character was estimated by summing up of all the observation and dividing the sum by the number of observations.

$$\bar{X} = \frac{\sum X_i}{N}$$

Where,

$\sum X_i$ = Summation of all the observations

N = Number of observations

Range

Range is the difference between the least and the greatest terms of a series of observation and thus provides the information about the variability present in the genotypes.

Estimation of coefficients of variation

The coefficient of variation for different characters was estimated by Burton (1952)

$$GCV (\%) = \frac{\sqrt{\sigma^2 g}}{\bar{X}} \times 100$$

$$PCV (\%) = \frac{\sqrt{\sigma^2 p}}{\bar{X}} \times 100$$

Where,

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

X = Mean of character

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

The estimates of genotypic and phenotypic coefficient of variance were classified as low, moderate and high as suggested in 1973 [4].

< 10% = Low

10% to 20% = Moderate

< 20% = High

Genetic advance

Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. The expected genetic advance was calculated by the formula given in 1955 [5] as described below.

$$GA = K \cdot h^2 \cdot \sigma_p$$

Where,

GA = Genetic advance

K = Constant (Standardized selection differential) having the value of 2.06 at 5 per cent level of selection intensity.

h^2 = Heritability

σ_p = Phenotypic standard deviation

The genetic advance as percentage of mean was estimated as per the below formula

$$\frac{GA}{\bar{X}}$$

Genetic advance as percentage of mean = $\frac{GA}{\bar{X}} \times 100$

Where,

$\bar{X}$ = Grand mean

GA = Genetic advance

The magnitude of genetic advance as percentage of mean was categorized as high (> 30%), moderate (30% - 10%) and low (< 10%).

Estimation of Heritability

Heritability in broad sense (h^2 bs) defined as the proportion of the genotypic variance to the total variance (phenotypic) was calculated as per the formula suggested in 1956 [6].

$$h^2 (bs) \% = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,

$h^2 (bs)$ = Heritability in broad sense,

$\sigma^2 g$ = Genotypic variance,

$\sigma^2 p$ = Phenotypic variance

The broad sense heritability estimates were classified as low (<50%), moderate (50-70%) and high (>70%) as suggested in 1966 [7].

Table-1 Genotypic path coefficient of various characters influencing seed yield/plant

Character	Days to flower initiation	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/plant	No. of pods/plant	No. of pod clusters/plant	Pod length (cm)	No. of seeds/pod	100 seed weight (g)	Genotypic Correlation Coefficient
Days to flower initiation	-0.558	-0.433	-0.279	0.057	-0.084	-0.119	-0.167	-0.107	0.065	0.053	-0.110
Days to 50% flowering	0.375	0.483	0.342	-0.039	0.062	0.110	0.109	0.009	-0.093	0.019	-0.088
Days to maturity	-0.294	-0.417	-0.589	-0.097	-0.139	-0.246	-0.243	-0.180	0.126	-0.081	0.059
Plant height (cm)	0.016	0.012	-0.025	-0.154	-0.049	-0.040	-0.021	-0.022	0.010	-0.001	0.078
No. of primary branches/plant	0.019	0.016	0.029	0.040	0.124	0.048	0.024	0.023	-0.030	0.018	0.319*
No. of pods/plant	0.071	0.076	0.138	0.085	0.127	0.331	0.240	0.073	-0.008	0.036	0.643**
No. of pod clusters/plant	0.166	0.125	0.230	0.075	0.105	0.405	0.557	0.051	0.022	-0.041	0.546**
Pod length (cm)	0.097	0.010	0.155	0.072	0.095	0.111	0.046	0.505	0.082	0.160	0.340*
No. of seeds/pod	0.023	0.038	0.042	0.013	0.048	0.005	-0.008	-0.032	-0.199	-0.007	-0.006
100 seed weight (g)	-0.004	0.002	0.006	0.000	0.006	0.005	-0.003	0.014	0.002	0.043	0.224

Diagonal values are direct effect, Residual effect = 0.3128

Results and Discussion

Path coefficient analysis

Path coefficient analysis is simply a standardized partial regression coefficient, which splits the correlation coefficient into direct and indirect effects. Following method given in 1959 [9] has been used to estimate the magnitude and direction of direct and indirect effects of various yield and yield contributing characters. Correlation coefficients along with path coefficients together provide more reliable information, which can be effectively predicted in crop improvement programme. If the correlation between yield and a character is due to direct effect of a character, it reveals true relationship between them and direct selection for this trait will be rewarding for yield improvement. However, if the correlation coefficient is mainly due to indirect effects of the character through another component trait, indirect selection through such trait will be effective in yield improvement. If the direct effect is positive and high, but the correlation is negative, in such situation direct selection for such trait should be practiced to reduce the undesirable indirect effect.

Direct effect of attributes on seed yield

The results of present study presented in [Table-3] showed that number of cluster per plant had the highest direct effect (0.557) on seed yield. It also had significant positive association with seed yield, compiled with high heritability and genetic advance. Hence, this character seems to be important contributor of seed yield and must be considered in selection for high seed yield. Other important characters having considerable direct effects were pod length (0.505), days to 50% flowering (0.483) and number of pods per plant (0.331). The character number of pods per plant also exhibited high positive association with yield with high heritability and genetic advance. Hence, direct selection for these traits may lead to the development of high yielding genotypes from pigeonpea germplasm accessions of Bastar origin. The number of pods per plant showed significant correlation ($r=0.643$) and its direct effect on seed yield per plant was (0.331) which is mainly due to the indirect effects via number of pod clusters per plant (0.240) and days to maturity (0.138). Similarly, number of primary branches per plant had positive correlation with seed yield per plant ($r=0.319$) and its direct effect on seed yield per plant was (0.124) which is mainly due to the nullifying effects via number of pods per plant (0.048), plant height (0.040), days to maturity (0.029), number of pod clusters per plant (0.024) and pod length (0.023). Hence, indirect selection of these traits may increase more number of primary branches per plant which ultimately lead to be development of high yielding genotypes. Similar results were reported in 1980 [8], 1991 [9], 1993 [10], 1991 [11], 2010 [12], 1999 [13], 2007 [14], 2009 [15], 2010 [16] 2017 [17], 2018 [18].

Conclusion

The path coefficient analysis showed that the number of cluster per plant had the highest direct effect on seed yield. It also had significant positive association with seed yield, compiled with high heritability and genetic advance. Hence, this

character seems to be important contributor of seed yield and must be considered in selection for high seed yield. Moreover, other important characters having considerable direct effects were pod length, days to 50% flowering and number of pods per plant may lead to the development of high yielding genotypes from pigeonpea germplasm accessions of Bastar origin. Direct effect of the number of pods per plant on seed yield per plant was mainly due to the indirect effects via number of pod clusters per plant and days to maturity. Similarly, number of primary branches per plant had positive correlation with seed yield per plant and its direct effect on seed yield per plant was mainly due to the nullifying effects via number of pods per plant, plant height, days to maturity, number of pod clusters per plant and pod length. Hence, indirect selection of these traits may increase more number of primary branches per plant which ultimately lead to be development of high yielding genotypes. The path coefficient analysis showed that the number of cluster per plant had the highest direct effect on seed yield. Hence, this character must be considered in selection for high seed yield. Moreover, other important characters having considerable direct effects were pod length, days to 50% flowering and number of pods per plant may lead to the development of high yielding genotypes from pigeonpea germplasm accessions of Bastar origin. Whereas, indirect selection of the traits number of pod clusters per plant, days to maturity, number of pods per plant, plant height and pod length may increase more number of primary branches per plant which ultimately lead to be development of high yielding genotypes.

Application of research: Direct selection for number of clusters per plant, pod length, days to 50% flowering and number of pods per plant may lead to the development of high yielding genotypes from pigeonpea germplasm accessions of Bastar origin.

Research Category: Germplasm and Path analysis

Abbreviations:

PCV: Phenotypic coefficient of variation

GCV: Genotypic coefficient of variation

GA: Genetic advance

RBD: Randomized Block Design

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Study area / Sample Collection: Indira Gandhi Krishi Vishwavidyalaya, Raipur, 492012, Chhattisgarh

Cultivar / Variety / Breed name: Pigeonpea [*Cajanus cajan* (L.) Millsp]

Conflict of Interest: None declared

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.

Ethical Committee Approval Number: Nil

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