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Evaluation of heritability, genetic advance, correlation and genetic components of variance in pigeonpea

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Abstract

The present study was conducted on the Evaluation of Heritability, Genetic advance, correlation and Genetic components of Variance in Pigeon pea. The experiment took two crop seasons viz. *Kharif* 2014-15 and *Kharif* 2015-16. During the *kharif* season of 2014-2015, 12 parental lines i.e. 7 lines and 5 testers were sown in a Randomized Block Design (R.B.D.) with three replications to obtain data on eleven different traits for yield and yield attributes. Simultaneously. The present experimental study revealed that secondary branches, number of pods/plant and primary branches showed high heritability along with high genetic advance as% of mean manifesting that the selection for these traits is likely to accumulate more additive genes leading to further improvement of their performance, primary branches and plant height had a positive phenotypic correlation coefficient with each other. Also, secondary branches and primary branches had a positive association with each other. Significant and positive phenotypic correlation coefficient was observed between pods/plant and primary branches. Pod/plant exhibited positive and significant phenotypic correlation coefficient with secondary branches and the major role of non-additive component was evident for plant height, days to 50% flowering, primary branches, secondary branches, number of pods / plants, 100 seed weight and green pod yield / plant; as the magnitude estimated dominance (σ^2D) component of variance was higher than that of the additive (σ^2A) component of variance. For the character number of pods per cluster and number of seeds per pod, equal importance of additive and non-additive components was observed.

Keywords: Heritability, genetic advance, correlation, genetic components & variance

Introduction

Pigeonpea [*Cajanus cajan* (L.) Millsp], ($2n=2x=22$) also known as arhar, tur and red gram, is nutritionally balanced and an exceptional source of protein in both green pea and dried grain (Faris and Singh, 1990) [8]. Along with protein, pigeonpea also renders carbohydrates and Vitamin A and C (Faris *et al.* 1987) [9]. Pigeonpea seeds are rich in proteins (generally within a range of 18 to 25% and as high as 32%), carbohydrates (57.6%), fiber (1.5%), minerals (3.5%), amino acids, methionine and cystine (Birk, 1993) [4]. Because of its rich source of protein, it is an ultimate addition to traditional cereal, banana or tuber-based diets of poor farmers that are protein deficient. Its ability to produce economic yield under limited moisture conditions makes it an important crop of dryland agriculture.

Globally the area and production of pigeonpea have increased from 2.86 million ha and 1.96 million tons in 1980 to 4.36 million ha and 3.46 million tons in 2006, respectively (FAO Stat, 2008) [5]. Pigeonpea represents about 5% of world legume production and more than 70% is being produced in India.

Pigeonpea is the second most important pulse crop of India which accounts for 20% of the total pulse production in India. In India, pigeonpea is grown in an area around 4.04 million hectares with a production of approximately 2.65 million tons (Anonymous, 2012) [2]. It has registered a production of 4.02 million tons in the year 2017-18 (All India Coordinated Research Project on Pigeonpea, Annual Report 2017-18). As 'dal', pigeonpea is an important constituent of the Indian meal. Of the total pigeonpea production in the world, India alone contributes nearly 92 per cent of it.

In India average productivity of pigeonpea is lower (671 kg/ha) compared to the world average productivity (742 kg/ha) even though it leads the world in area and production (FAOSTAT, 2010) [7]. Production of pigeonpea in India is still short which cannot fulfil the present consumption of ~19 million tonnes thereby compelling to import pulses to a range of 1.5-2.0 million tons annually (<https://www.agricoop.nic.in>, accessed on Feb. 28, 2013). WHO recommendation of per capita availability of protein is 80 g/day, while it is only 28 g/day in India which does the ultimate problem of the malnutrition exist among the poor people. The chasm between per capita availability of protein in India and WHO recommendation can be bridged through pulses, which are a rich source of protein.

The importance of pulses in Indian agriculture cannot be denied. Of the total pulses, red gram or pigeonpea takes an important place among rainfed resource poor farmers as it provides quality food, fertilizer, fuel wood and fodder. Despite its immense importance in sustainable agriculture its global production per hectare has remained static over the last three decades. Lack of efficient management practices coupled with biotic and abiotic stresses has widened the gap between the potential yield and on-farm yield.

The conventional breeding procedures followed in pigeon pea brought improvement in seed yield and resistance to diseases and pests. However, for further boost in productivity, the possibility of producing pigeon pea hybrids and identification of superior hybrids through line x tester mating design open up new avenues. In a breeding programme, the most important steps are the selection of suitable genotypes as parents for hybridization. Selection of parents on the basis of phenotype is not a sound procedure since phenotypically superior line may yield poor recombinants in the segregating generation. Therefore, selection of parents on the basis of their genetic values is necessary. Generally, parents are chosen on the basis of gene action involved in the expression of quantitative characters.

Genetic variation among genotypes and relation between major yield contributing traits are of great vital importance in the breeding programme that aims to produce improved genotype.

Yield is a complex character, which is the product of interaction of many traits. Therefore, it is necessary to have the knowledge of the contribution of different characters towards yield through correlation. Basic information of the nature and extent of inter-relationships between yield and its attributes will be of great utility for the choice of characters in the selection programme.

Utilization of the cross as commercial hybrid is possible if the specific cross has high heterosis and the observations made are true for an economic character like yield, provided there exist cytoplasmic genetic male sterility and fertility restoration system. Analysis of combining ability is considered as the most potent tool for identifying the suitable parents for a hybridization programme. Selection of parents with high general combining ability (GCA) effect and cross combinations with high specific combining ability (SCA) is necessary for heterosis breeding. Therefore, the present investigation was undertaken to study the combining ability of parents and cross combinations as well as to evaluate the nature and magnitude of heterosis for green pod yield and its components.

Pigeon pea is an often-cross pollinated crop and therefore, amenable to genetic improvement by following breeding methods suitable for both allogamous and autogamous crops. Understanding the nature and magnitude of genetic variance implies an appropriate breeding procedure for isolation of a suitable genotype that has maximum useful alleles.

Materials and Methods

The experiment entitled “Combining ability analysis for vegetable yield and its components in pigeonpea [*Cajanus cajan* (L.) Millsp.]” was carried out during *kharif* seasons in 2014-15 and 2015-16 at the experimental farm of Department of Genetics and Plant Breeding, School of Agricultural Sciences and Rural Development, Nagaland University, Medziphema campus, which is located at 23° 45' 49" N latitude, 90° 33' 04" E longitude at an altitude of 305 m above sea level bearing sub-tropical climate and the experiment took two crop seasons viz. *Kharif* 2014-15 and *Kharif* 2015-16. During the *kharif* season of 2014-2015, 12 parental lines i.e. 7 lines and 5 testers were sown in a Randomized Block Design (R.B.D.) with three replications to obtain data on eleven different traits for yield and yield attributes. Simultaneously, the five testers and seven parental lines were grown during *kharif* 2014-15 in a crossing plot. F₁ hybrids were produced following Line X Tester mating system involving 7 lines and 5 testers by hand emasculation and pollination technique. In the next crop season i.e., *Kharif* 2015-16, all the seeds of 35 F₁ cross combinations (7 lines x 5 testers) with the 12 parental lines (7 lines and 5 testers) totalling 47 treatments were grown in a Randomized Block Design (RBD) with three replications.

Heritability

Heritability in broad sense (h^2_b) was calculated according to the formula suggested. It was computed as the ratio of genotypic variance σ_g^2 to the phenotypic variance σ_p^2 and expressed in% age.

$$h^2_b = \sigma_g^2 / \sigma_p^2 + \sigma_e^2$$

Where,

σ_g^2 = genotypic variance

σ_e^2 = environmental variance

Genetic Advance (GA)

The expected genetic advance was calculated by using the formula suggested by Johnson *et al.* (1955).

$$GA = K\sigma_p h_b^2$$

Where,

K = selection differential at 5% selection intensity, the value is 2.06

σ_p = phenotypic standard deviation

h_b^2 = heritability in broad sense

The genetic advance was expressed as% of the mean to facilitate the comparison between different characters under study.

Correlation studies

The correlation coefficient at phenotypic, genotypic and environmental levels was determined according to the formula given.

Genotypic correlation coefficient between character x and y

$$r_{gxy} = \frac{Cov.xy(g)}{\sqrt{Var.x(g) \times Var.y(g)}}$$

Phenotypic correlation coefficient between character x and y

$$r_{pxy} = \frac{Cov.xy(p)}{\sqrt{Var.x(p) \times Var.y(p)}}$$

Environmental correlation coefficient between character x and y

$$r_{xy} = \frac{Cov.xy(e)}{\sqrt{Var.x(e) \times Var.y(e)}}$$

Where,

$cov.xy(g)$, $cov.xy(p)$, and $cov.xy(e)$ denote genotypic, phenotypic and environmental co-variance for characters x and y, respectively $Var.x(g)$, $Var.x(p)$ and $Var.x(e)$, denotes genotypic, phenotypic and environmental variance for character x $Var.y(g)$, $Var.y(p)$ and $Var.y(e)$, denotes genotypic, phenotypic and environmental variance for character y

The calculated genotypic and phenotypic correlation coefficients were tested for significance by applying t-test as follows:

$$t = \frac{r\sqrt{n-2}}{\sqrt{1-r^2}} \text{ at } (n-2) \text{ degree of freedom}$$

$$Cov F.S. = \frac{(M_l - M_e) + (M_t - M_e) + (M_{lxt} - M_e)}{3r} + \frac{6r \text{ Cov H. S. (average)} - r(l+t)\text{Cov H. S. (average)}}{3r}$$

$$gca \text{ variance } (\sigma^2g) = Cov H. S. (average) = \left[\frac{1+F}{4} \right] \sigma^2A$$

sca variance (σ^2s) was calculated following

$$sca \text{ variance } (\sigma^2s) = Cov F.S. - 2 \text{ Cov H. S. (average)} = \left[\frac{1+F}{2} \right]^2 \sigma^2D$$

Where, 'F' is the coefficient of inbreeding.

In the present study, F was assumed as zero.

Results and Discussion

Essential steps in transmitting traits include selecting the correct parents and employing the appropriate breeding methods. The parents selected for the crossover procedure were evaluated based on how well their genes functioned to produce superior hybrids. An explanation of the outcomes for several field qualities is given below

The estimates of coefficient of variation, heritability and genetic advance for yield and yield related traits are given in Table 1. Akram, S., Hussian, B. M. N., Bari, Md, A., Burrit. D. J and Hossain, M.A. 2016^[1], Khan, R., Farhatullah and Khan, H. 2011^[12] & Kingslin, M., Subbaraman, N, and Vanniarajan, C. 1999^[13].

The highest genotypic coefficient of variation (GCV) was observed for number of pods/plant (43.10%) followed by secondary branches (38.87%). However, days to flowering (1.88%), 100 grain weight (3.71%) and number of pods/ cluster (4.49%) exhibited the lowest genotypic coefficient of variation. The highest phenotypic coefficient of variation (PCV) was observed for green pod yield (64.94%) followed by number of pods/ plant (46.03%) and secondary branches (41.46%). However, days to 50% flowering (2.16%), 100 grain weight

Where,

n = number of genotypes

The calculated t value was compared with t-value at 5% or 1% probability level with (n-2) degree of freedom for its significance.

Genetic components of variance

$$Cov H. S. (line) = \frac{(M_l - M_{lxt})}{rt}$$

$$Cov H. S. (tester) = \frac{(M_t - M_{lxt})}{rl}$$

$$Cov H. S. (average) = \frac{l}{r(2lt - l - t)} \left[\frac{(l-1)(M_l) + (t-1)(M_t)}{l+t-2} - M_{lxt} \right]$$

(11.49%) and number of seeds/pod (13.17%) exhibited the lowest phenotypic coefficient of variation.

High heritability estimates were observed for number of pods/plant (88.00%), secondary branches (87.86%), primary branches (76.41%) and days to 50% flowering (75.29%) whereas lowest heritability estimates were exhibited by number of pods/cluster (2.00%). The genetic advance as%age of mean was highest for number of pods/plant (83.12%) followed by secondary branches (75.04%).

The phenotypic and genotypic correlation coefficient for yield and its components are presented in Table 4.4. Primary branches and plant height had a positive phenotypic correlation coefficient (0.62) with each other. Also, secondary branches and primary branches had a positive association (0.75) with each other. Significant and positive phenotypic correlation coefficient association was observed between pods/ plant and primary branches (0.72). Pods/plant exhibited positive and significant phenotypic correlation coefficient with secondary branches (0.70). Arshad, M., Bakhsh, A., Zubiar, M. And Abdul Ghafoor. 2003^[3], Fisher, R.A. 1918^[10] & Gupta, S.K; Kaur, A.; Singh, Kuldeep and Singh, D. 2003^[11], Table 2

Genetic components of variance in intervarietal crosses of pigeonpea are presented in Table 4.9. Among the characters studied, sca variance (σ^2s) and non-additive (σ^2D) variance components were higher than genetic variance (σ^2g) and additive (σ^2A) variance for all the characters under study except for pods per cluster and seeds per pod where additive component of gene action (σ^2A) was higher than non-additive variance (σ^2D). Kumara, B.N., Santoshagowda, G.B., Nishanth, G.K. and Dharmaraj, P.S. 2013^[14], Meena, B.L., Das, S.P., Meena, S.K., Kumari, R., Devi, A.G. and Devi., H.L. 2017^[15] & Sreelakshmi, C., Kumar, C.V.S. and Shivani, D. 2010^[16], Table 3

Table 1: Variability and other genetic parameters for 9 characters in parents of pigeon pea

Characters	Mean	Range	GCV%	PCV%	Heritability (%)	GA as% of m
Plant height (cm)	211.95	158.40-250.80	9.24	19.23	23.10	9.15
Days to 50% flowering	166.19	156.00-168.67	1.88	2.16	75.29	3.36
Primary branches	27.92	14.77-34.37	23.01	26.32	76.41	41.43
Secondary branches	101.09	33.00-166.60	38.87	41.46	87.86	75.05
Number of pods /cluster	1.58	1.33-2.33	4.49	35.77	2.00	1.16
Number of pods /plant	46.95	17.27-85.90	43.10	46.03	88.00	83.12
Number of seeds /pod	4.61	3.67-5.33	7.31	13.17	30.82	8.36
100 seed (green) weight (g)	23.66	20.74-27.24	3.71	11.49	10.44	2.47
Green pod yield /plant (g)	288.51	133.72-483.80	14.62	64.94	5.00	6.78

Table 2: Phenotypic (r_p) and genotypic correlation (r_g) correlation coefficient of yield and its contributing characters in pigeon pea

Characters	DT 50% F	Primary branches	Sec. branches	Pods /cluster	Pods/ plant	Seeds/ pods	100 seed weight	Green pod yield/ plant	
Plant height	0.08	0.62*	0.48	-0.17	0.41	0.11	-0.07	-0.38	P
	(0.01)	(0.25)	(0.23)	(0.19)	(0.18)	(-0.20)	(-0.01)	(-0.30)	G
DT 50%F	-	0.19	0.15	0.14	0.26	-0.11	-0.02	-0.07	P
	-	(0.08)	(0.06)	(0.02)	(0.12)	(-0.07)	(0.02)	(-0.05)	G
Pri. branches	-	-	0.75**	0.15	0.72**	-0.34	0.07	-0.46	P
	-	-	(0.28)	(0.28)	(0.26)	(-0.22)	(-0.13)	(-0.40)	G
Sec. branches	-	-	-	0.30	0.70*	-0.57	0.15	-0.35	P
	-	-	-	(0.21)	(0.23)	(-0.26)	(0.11)	(-0.36)	G
Pods/cluster	-	-	-	-	0.39	-0.45	-0.08	-0.21	P
	-	-	-	-	(0.32)	(-0.22)	(0.21)	(0.09)	G
Pods/plant	-	-	-	-	-	-0.44	-0.04	-0.30	P
	-	-	-	-	-	(-0.16)	(-0.03)	(-0.25)	G
Seeds/pods	-	-	-	-	-	-	-0.25	0.14	P
	-	-	-	-	-	-	(-0.17)	(0.09)	G
100 seed weight	-	-	-	-	-	-	-	0.05	P
	-	-	-	-	-	-	-	(-0.03)	G

Table 3: Genetic components of variance in intervarietal crosses of pigeon pea

	Characters	σ^2_g	σ^2_s	σ^2_g/σ^2_s	σ^2_A	σ^2_D
1	Plant height	977.65	1995.86	0.49	3910.60	7983.44
2	Days to 50% flowering	17.29	39.78	0.43	69.17	159.12
3	Primary branches	22.16	112.29	0.20	88.62	449.16
4	Secondary branches	1194.43	8216.18	0.15	4777.72	32864.71
5	Number of pods/ clusters	0.13	0.24	0.53	0.51	0.97
6	Number of pods/ plants	954.67	5428.53	0.18	3818.69	21714.10
7	Number of seeds / pods	0.09	0.12	0.75	0.35	0.46
8	100 seed weight	0.21	0.97	0.21	0.82	3.88
9	Green pod yield /plant	7000.92	42191.27	0.17	28003.68	168765.07

Conclusion

The present experimental study revealed that secondary branches, number of pods/plant and primary branches showed high heritability along with high genetic advance as percent of mean manifesting that the selection for these traits is likely to accumulate more additive genes leading to further improvement of their performance, primary branches and plant height had a positive phenotypic correlation coefficient with each other. Also, secondary branches and primary branches had a positive association with each other. Significant and positive phenotypic correlation coefficient was observed between pods/plant and primary branches. Pod/plant exhibited positive and significant phenotypic correlation coefficient with secondary branches and the major role of non-additive component was evident for plant height, days to 50% flowering, primary branches, secondary branches, number of pods / plants, 100 seed weight and green pod yield / plant; as the magnitude estimated dominance (σ^2_D) component of variance was higher than that of the additive (σ^2_A) component of variance. For the character number of pods per cluster and number of seeds per pod, equal importance of additive and non-additive components was observed.

The author's input

Each of the aforementioned authors has contributed significantly both directly and intellectually, and they have all approved the work's publication.

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Available data

The datasets used and/or examined in this investigation are available upon reasonable request from the corresponding author.

Statement of ethics

The work was approved by the Department of Genetics and Plant Breeding, School of Agricultural Sciences and Rural Development, Nagaland University, Medziphema campus

Informed agreement

The subjects provided written informed consent prior to being enrolled in the study.

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