

## Studies on genetic variability and inter-relationship among yield contributing characters in pigeonpea grown under rainfed lowland of eastern region of India

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(Received: August 26, 2013 ; Accepted: March 6, 2014)

### ABSTRACT

Genetic variability and interrelationship for yield and yield contributing characters among 38 genotypes of pigeonpea [*Cajanus cajan* (L.) Millsp.] were studied in present investigation for twelve characters. The genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability ( $h^2_b$ ), genetic advance ( $\bar{G}_a$ ) and correlation for yield and its attributes were computed. The minimum difference between PCV and GCV values for all characters indicated minimum environmental influence. Moderate to high PCV and GCV were recorded for days to fifty percent flowering (DFF) (27.41, 25.64), number of pods per plant (30.69, 2.06), number of seed (19.39, 18.23), grain yield (34.13, 29.42) and straw yield (26.24, 25.03). High heritability and genetic advance was observed for number of pods (0.94, 27.14), plant height (0.90, 21.43), test weight, days to maturity (0.84, 23.02) and primary and secondary branches per plants (0.90, 11.32) which indicated that these traits are controlled by additive gene action and emerged as ideal traits for improvement through selection. The characters viz. DFF, test weight, pod length and number of primary branches showed high heritability along with moderate or low genetic advance and could be improved by inter mating superior genotypes of population developed from combination breeding. Out of 38, eight genotypes viz., ICPL 87 (3.72 t/ha), Manak (3.59 t/ha), BSMR-736 (3.67 t/ha), BSMR-853 (3.36 t/ha), MAL-13 (3.15 t/ha), GC-11-39 (3.17 t/ha), NDA-1 (2.92 t/ha) and Virsa Bahar (2.81 t/ha) were found promising for yield and yield contributing traits as they had shown more test weight, number of pods per plant, number of seed per pod and harvest index.

**Key words:** *Cajanus cajan* L., Correlation, Genetic variability, Pigeonpea, Yield improvement

Pigeonpea, [*Cajanus cajan* (L.) Millsp.] is the second important pulse crop of India and has diversified uses as food, feed, fodder and fuel. It has been recognised as valuable source of protein for the vegetarian people in their daily diet. Pigeonpea is a cross-pollinated (with 20–70% cross pollination) species with a diploid number of  $2n=2x=22$  and genome size of 858 Mbp. In Asia, pigeonpea is grown in 4.33 million ha area with a production of 3.8 million tons. In India, it is an important pulse crop grown throughout the northern and central region for grains. Pigeonpea is one of the most nutritious food legumes and ranks next only to chickpea. Besides its utilisation as *dal*, whole or dehulled grains are also used in various preparations. In India, the average

productivity of pigeonpea is 760.3 kg per ha which is very low. Several reasons have been suggested for low productivity of this crop, which include inherent low potential of yield and damages caused by several diseases like wilt and sterility mosaic. For higher productivity, availability of genetic variability in the existing pigeonpea germplasm is required. The potential for improvement exists within the germplasm as evidenced by the yield attained in experimental field. The existing variability needs to be utilised in crop improvement programme (Bhadru 2010) as yield is a complex character controlled by polygenes. Therefore, selection made on the basis of its phenotypic expression alone is likely to be ambiguous. Grain yield is a dependent trait, which is influenced by many independent traits. The inter-relationship among the yield and yield contributing characters provides reliable information on nature and direction of selection and also useful as a basis for selecting desirable plant type (Bhadru 2010). Knowledge about the nature and extent of existing genetic variability as well as correlation amongst the characters to be improved is prerequisite before setting up any breeding programme for yield improvement through selection. Phenotypic and genotypic correlation coefficient enables to identify characters or combination of characters, which might be useful as indicator of high yield as it provides reliable information on the consequence of selection for simultaneous improvement of desirable yield component characters. Keeping in view the above facts, the present study was undertaken with objective to identify the nature and extent of genetic variability and interrelationship of yield and yield contributing traits for pigeonpea improvement programme.

### MATERIALS AND METHODS

**Experimental site:** Field experiments were carried out at the experimental farm of ICAR Research Complex for Eastern Region, Patna, India (latitude 25. 30° N, longitude 85.15° E) during kharif 2010 and 2011. The experimental site is typical rainfed having clay loam soil with pH 7.5, organic carbon 0.67%, bulk density 1.47 mg/m<sup>3</sup>, electrical conductivity 0.26 dS/m, available nitrogen 227 kg/ha, available phosphorous 28.4 kg/ha, and exchangeable potassium 218 kg/ha.

**Plant materials and experimental design:** In the present study, thirty eight pigeonpea genotypes were evaluated in randomized block design with three replications. The

pigeonpea genotypes used under present study were obtained from Indian Institute of Pulses Research, Kanpur, under pigeonpea improvement programme. Experimental field was thoroughly prepared and levelled with laser leveller machine. Each plot consisted of single row of 4 metre length with inter and intra row spacing of 75 and 20 cm respectively. In each plot uniform plant stands were maintained and recommended package of practices and plant protection measures were followed for raising a good crop. Agro-morphological observations of yield and yield contributing traits were recorded on randomly selected ten plants per genotype per replication for the characters *viz.*, days to 50% flowering, days to maturity, plant height (cm), plant spread (cm), primary and secondary branches, number of pods per plant, seed grain yield, seeds per pod, pod length (cm), straw yield and test weight (100 seed). Plant height, seeds per pod and pod length were recorded at maturity stage.

**Statistical Analysis:** The genotypic and phenotypic coefficients of variation were calculated as per the formula suggested by Burton and De vane (1953). Heritability (broad sense) as per Honson *et al.*, (1951) and genetic advance as per Johnson *et al.*, (1955) were also worked out. Phenotypic and genotypic correlation coefficients were worked out for all possible combinations of characters as per the procedure outlined by Panse and Sukhatme (1985).

## RESULTS AND DISCUSSION

**Genetic Parameters:** Significant variation was observed among the test cultivars for all important traits used under the present study. Genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advances for all the characters were studied. Higher PCV were observed than GCV for all the characters except pod length under this study, indicating that they interacted with the environment with same degree. These finding was in conformity with those of Bhadru (2011). Moderate to high PCV and GCV were recorded for days to fifty percent flowering (DFF) (27.41, 25.64), number of pods per plant (30.69, 2.06), number of seeds (19.39, 18.23),

grain yield (34.13, 29.42) and straw yield (26.24, 25.03) indicating presence of considerable genetic variability and minimum influence of environment on the expression of characters. Similar results were also reported in earlier studies of Satish *et al.* (2006) and Bhadru (2010). Plant height, pod length, harvest index and test weight showed low GCV and PCV values (Table 1). Thus, these characters emerged as ideal traits for improvement through selection owing to their transmissibility and variability. The results confirmed the finding of Satish *et al.* (2006) for days to 50 % flowering and days to maturity. Number of pods per plant, plant height, days to maturity, test weight and primary and secondary branches per plant showed high heritability ( $h^2b$ ) with high genetic advance ( $G_a$ ), indicating the expression of these traits are controlled by additive gene action. Panse (1957) reported that the additive gene effect is responsible for the inheritance of those quantitative characters having high heritability and genetic advance as percent over mean in broad sense and such characters could be improved through selection. High heritability along with high genetic advance for these traits has also been reported by Deshmukh *et al.* (2000) and Basavarajaiah (2000). Days to 50% flowering and pod length showed high heritability but low genetic advance, indicating that preponderances of non-additive gene action in the inheritance of these traits. The characters showing high heritability along with moderate or low genetic advance can be improved by inter mating superior genotypes of population developed from combination breeding (Samadia 2005).

### Response of yield and yield components

Yield performances of all genotypes were recorded and on average, the test genotypes showed 1.67 t/ha grain yield. However, range of grain yield was 0.79-3.72 t/ha among different genotypes. The genotypes ICPL 87 (3.72 t/ha), Manak (3.59 t/ha), BSMR-736 (3.67 t/ha), BSMR-853 (3.26 t/ha), MAL-13 (3.15 t/ha), GC-11-39 (3.17 t/ha), NDA-1 (2.92 t/ha) and Virsa Bahar (2.81 t/ha) were found promising in respect of yield and yield contributing traits over check as well as other genotypes in respect of high test weight, number of pods per plant, number

**Table 1. Components of genetic variability in pigeonpea genotypes**

Attributes	Unit	Mean	Range	CD (5%)	PCV	GCV	Heritability	Genetic Advance
DFF	Days	87.49	49-122	3.88	27.41	25.64	0.63	7.63
Plant Height	Cm	179.70	122-280	5.17	9.25	08.66	0.90	21.43
Pods	No. per plant	138.14	69-238	9.83	30.69	28.06	0.94	72.14
Seeds	No. per pod	4.70	3.0-7.0	0.63	19.39	18.23	0.72	31.68
Test weight	Gram	9.28	6.12-13.69	1.03	2.61	1.73	0.86	2.52
Days to maturity	Days	179.70	122-280	3.55	22.38	19.93	0.84	23.02
Pod length	Cm	4.2	3.5-5.1	0.28	1.97	2.13	0.73	1.62
Primary branches	No. per plant	9.6	3.9-14.7	1.04	15.83	13.41	0.87	8.26
Secondary branches	No. per plant	22.7	12.6-35.6	1.85	21.55	18.34	0.90	11.32
Grain yield	t/ha	1.67	0.79-3.72	0.17	34.13	29.42	0.69	9.48
Straw yield	t/ha	5.65	2.13-7.90	0.51	26.24	25.03	0.78	27.16
Harvest index	Percent	27.65	23.14-35.24	1.57	10.35	08.72	0.81	15.17

DFF: Days to 50 percent flowering; PCV: Phenotypic coefficient of variation; GCV: Genotypic coefficient of variation; CD: critical difference at 5%

of seed per pod, number of primary and secondary branches per plant and harvest index. BSMR-736 showed high test weight (13.69) followed by ICPL 87 (12.83) and MAL-13 (13.04). Highest number of primary branches/ plant was observed in BSMR-736 (14.77) followed by BSMR-853 (13.52) and ICPL 87 (13.27) whereas, highest secondary branches per plant was found in MAL-13(35.61) followed by BSMR-736 (33.87) and Manak (32.46). Pigeonpea genotype MAL-13 showed highest number of seed/pod followed by ICPL 87 and BSMR-736. Therefore, promising pigeonpea genotypes for different characters may be utilised as good genetic donors for exploitation in future breeding programme.

**Correlation studies among grain yield and yield attributes:** Inter-relationship between grain yield and its contributing traits has been determined by correlation matrix studies (Table 2). At the genotypic and phenotypic level primary and secondary branches per plant, number of pods, number of seeds per pod and harvest index showed significantly positive correlation with seed grain yield. The results are in conformity with the earlier findings of Mahamad *et al.* (2006) for number of branches and number of pods per plant and Satish *et al.* (2006) for all these characters. Mahajan *et al* (2007) also

reported similar results for earliness, pods per plant and plant height. Plant height was found positively and significantly correlated with pods/plant (0.346) and primary (0.42) and secondary branches (0.389). Moreover, primary and secondary branches/plant had positive significant correlation with number of pods per plant (0.74, 0.68) whereas, positive significant correlation was also found between pod length and number of seed/ pod (0.579). Similarly, number of primary branch/plant was also positively correlated with number of secondary branch / plant (0.437) while it was negatively correlated with days to maturity. On the other hand, days to 50% flowering showed significant negative genotypic association with plant height (-0.278), primary branches (-0.001), secondary branches (-0.004) and test weight (g) (-0.041). Such results were also reported earlier by Singh *et al.* (1990) and Sewak *et al.* (2012) in chickpea. At both genotypic and phenotypic levels, plant height was negatively associated with days to 50% flowering. Similarly, significant and positive correlation was observed between test weight and harvest index (r=0.386). Likewise, Straw yield was also positively associated with number of pods / plant, number of seed per pod, primary and secondary branches/plant.

**Table 2. Genotypic and phenotypic correlation between different traits of Pigeonpea**

Traits	DDF (days)	PH (cm)	Pods length (cm)	Pods per plant	Seeds per pod	Primary branch per plant	Secondary branch per plant	Days to maturity	Test weight	Grain yield	Straw yield	Harvest index
DDF (days)	1.000	-0.278**	0.034	-0.128	0.065	-0.001	-0.004	0.617**	-0.041	0.048	0.104	-0.031
Plant height (cm)		1.000	-0.167	0.346**	0.289	0.426**	0.389**	0.064	0.203	0.315**	0.249**	0.273**
Pods length (cm)			1.000	0.095	0.579**	0.078	0.062	0.036	0.053	-0.04	0.092	-0.066
Pods per plant				1.000	0.482**	0.741**	0.684**	-0.026	-0.015	0.545**	0.532**	0.339**
Seeds per pod					1.000	-0.057	0.089	0.083	-0.076	0.399**	0.383**	0.198
Primary branch per plant						1.000	0.437**	-0.341	0.131	0.305**	0.343**	0.292
Secondary branch per plant							1.000	0.043	0.261	0.418**	0.297**	0.284
Days to maturity								1.000	-0.044	-0.093	-0.009	0.015
Test weight									1.000	0.146	-0.124	0.386**
Grain yield										1.000	0.903**	0.801**
Straw yield											1.000	0.482**
Harvest index												1.000

DDF: Days to 50 percent flowering; PH: Plant height;\*\* significant at 5% level significance.

**Table 3. Direct (diagonal) and indirect effect of yield component characters to grain yield in Pigeonpea**

Traits	DDF (days)	PH (cm)	Pods length (cm)	Pods per plant	Seeds per pod	Primary branch per plant	Secondary branch per plant	Days to maturity	Test weight (g)	Grain yield
DDF (days)	0.0309	0.0016	0.0061	-0.0032	0.0062	-0.0004	0.0003	0.0192	-0.0015	0.1794
Plant height (cm)	-0.0028	-0.0194	-0.0241	0.0411	-0.0034	0.1184	0.0976	-0.0137	0.0096	0.1357
Pods length (cm)	0.0074	0.0029	-0.1232	0.0184	0.0011	0.0015	0.0068	0.0063	0.0029	0.0002
Pods per plant	0.0058	0.0003	0.0028	0.0177	0.0094	0.1639	0.1174	0.0002	0.0021	0.3457**
Seeds per pod	-0.0095	-0.0024	0.0008	-0.002	-0.0462	-0.0037	0.0095	-0.0019	0.0019	0.4096**
Primary branch per plant	-0.0003	-0.0069	-0.0142	0.1337	0.0027	0.2753	0.04857	-0.0004	0.0053	0.4772**
Secondary branch per plant	0.0002	-0.0047	-0.0117	0.1592	0.0012	0.2294	0.1233	0.0027	0.0142	0.5285**
Days to maturity	-0.0122	0.0052	-0.0094	0.0002	0.0096	-0.0516	-0.0148	0.0197	0.0005	0.0048
Test weight	0.0003	-0.0071	0.0005	0.0008	0.0016	0.03761	0.02984	0.0009	0.0497	0.2265**

DDF: Days to 50 percent flowering; PH: Plant height;\*\* significant at 5% level significance.

As simple correlation does not provide the true association of the characters with each other as these attributes are interrelated among themselves and considerably influence each other. Path coefficient analysis helps in understanding the magnitude of direct and indirect contribution of each character on grain yield and provides the actual contribution of an attributes and its influence through other characters (Lavanya and Toms 2009). Number of seed/pod (0.409), number of pods/plant (0.345), number of primary branches/plant (0.477), number of secondary branches/plant (0.528) and test weight (0.226) showed positive direct effect on grain yield (Table 3) and indicated that selection for higher yield on the basis of the above said characters could be reliable. Mahajan *et al.* (2007) also reported similar findings in pigeonpea for number of pods per plant and earliness.

Present study reveals the importance of yield component traits in increasing grain yield. On the basis of present findings it may also be emphasized that the existence of genetic variation for grain yield and yield contributing characters in the pigeonpea population showed differential reaction of cultivars in their relative adaptation to environment. The minimum difference between phenotypic coefficients of variation (PCV) and genotypic coefficient of variation (GCV) values indicated minimum environmental influence on yield and yield contributing traits. The correlation study indicated that numbers of pods/plant, number of seed /pod and primary and secondary branches were more important yield contributing traits and showed positive and significant direct association with grain yield. Direct selection of these traits would be worthwhile for yield improvement in pigeonpea. The characters like days to fifty percent flowering, test weight, pod length and number of primary branches can be improved by inter-mating superior genotypes of population developed from combination breeding. Therefore, it may be concluded that traits *viz.* number of pod, number of seed, grain yield and number of primary and secondary branches showed high PVC, GCV, heritability and genetic advance can be improved through competent breeding programme of pigeonpea. Promising pigeonpea genotypes for different characters may also be utilised as good genetic donors for exploitation in future breeding programmes.

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