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Research Note

Genetic variability for plant type and seed yield components among recombinant inbred lines in pigeonpea

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Abstract

Genetic variability for plant type and seed yield components among 318 recombinant inbred lines of Pigeonpea [*Cajanus cajan* (L.) Millspaugh] was studied during the *Kharif* season of 2017-18 and 2018-19. The characters studied include plant height, the number of primary branches, the number of secondary branches, days to flowering, and days to maturity, the number of pods per plant, the number of seeds per pod, pod bearing length and branching angle with the main axis. Significant genetic variability was observed among the recombinant inbred lines. Remarkable genotypic differences were found for many of the traits under study. The recombinant inbred line population studied under two environments showed less genotype and environment interaction. The difference between the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) is less indicating high heritability of the traits under study and control of additive gene action. The genetic advance over the percentage of the mean was also high for all the traits under study. From the study, it was inferred that genotypes with determinate plant types with a greater number of pod and primary branches early flowering and early maturing with high seed weight and acute branching angle play a significant role in enhancing the yield.

Keywords: Genetic variability, descriptive statistics, GCV, PCV, heritability, genetic advance, and genetic advance over mean.

Cajanus cajan is an important grain legume which is mainly cultivated in the tropical and semi-arid regions of the world. Before the genomic revolution and new molecular techniques, *Cajanus cajan* was considered an "orphan legume" owing to the availability of limited genomic resources. The number of chromosomes is $2n = 2x = 22$ and the genome size is 852 Mb (Singh *et al.*, 2012). India is the centre of origin for Pigeonpea, like many wild relatives and a large amount of natural genetic variation is found in India (Van der Maesen, 1980). Even though the area under production is the highest in India, the average productivity remained low (760.33 kg/ha), when compared to the world (762 kg/ha) (www.fao.com, 2015-16). Low productivity is mainly due to underutilization of the valuable information in

terms of genes hidden in the genetic resources of the pigeon pea, sensitivity to biotic and abiotic stresses and lack of plant type that is high yielding and short duration and that fits into the suitable cropping system in a crop season. Yield attributing traits of the pigeon pea are plant height, the number of primary branches per plant, the number of secondary branches per plant, the average number of pods per plant, average number of seeds per plant and seeds size (Niranjana kumara *et al.*, 2016). Plant type characters include plant height, the number of primary branches, the number of secondary branches, days to flowering and days to maturity (Giriraj kumawat *et al.*, 2012). First genetic map of pigeon pea was developed by Yang *et al.* (2011) which has given information about different genomic regions of pigeon

pea. Compact semi-erect and compact erect characters help for enhancing the cropping density of the Pigeonpea. Hence, breeding for plant types is very essential for developing a variety that can be planted with high density (Techale *et al.*, 2013). A study of the genetic parameters of variability showed that there was significant variation within the population. The descriptive statistics study showed that there was a noticeable range of variation for all the traits under study. The difference between the GCV and PCV was less indicating high heritability and additive gene action of the traits.

The experiment was conducted at IARI research farms during the *Kharif* season years 2017-18 and 2018-19. A total of 318 recombinant inbred lines that were derived from the cross H-2001-4 and ICP 7035 which is moderately resistant to pod borer (Anitha kumari, 2005) were tested for genetic variability for plant type and seed yield components. They were sown in the augmented design (Federer, 1956) along with checks and parents. Different checks utilized were Pusa 992, Pusa 991, Pusa 2001, Pusa 2002, Pusa 2012, Pusa 855 and V114. All the necessary agronomic practices were followed for raising fabulous crop stands. In each row, 10 plants were chosen randomly from each line and observations were recorded on plant height (cm), the number of primary branches/plant, the number of secondary branches/plant, days to 50% flowering, days to maturity, the number of pods/plant, the number of seeds/pod, pod bearing length on the main axis, 100 seed-weight (g) and branching angle with the main stem (Dhanasekhar *et al.*, 2007). The data of the branching angle with the main is was transformed with suitable transformation (arcsine transformation) and subjected to analysis of variance (ANOVA) by Windostat version 9.3 Indostat services Hyderabad. Phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance over per cent of the mean was calculated.

The study depicted that there was a significant amount of variability among the recombinant inbred lines for the plant type and seed yield components in both seasons (**Table 1 and Table 2**). The general mean of parental lines, range and standard deviation of recombinant inbred lines were tabulated (**Table 3 and Table 4**). Plant height followed by days to 50% flowering showed a high range of variation and seeds /pod and secondary branches / plant showed a low range of variation. The genetic parameters of the two seasons, genotypic and phenotypic coefficient variation (GCV and PCV), heritability (H^2) and genetic advance over per cent of the mean for two seasons were depicted in **Table 1 and Table 2**. The phenotypic coefficient of variation was slightly higher when compared to the genotypic coefficient of variation. The difference between PCV and GCV was found to be low indicating less influence from the environment. PCV for all the characters under study ranged from 9.27 to 34.10 per cent. High PCV was observed for seed weight (34.10 %) followed by primary branches /plant (28.00 %) during the first season. In the second season, high PCV was observed for seed weight (33.60%) followed by branching angle (28.81%). Low PCV was observed for nodes /plant (9.27%) and days to maturity (9.31%) during the first season and nodes /plant (9.32 %) and days to maturity (9.40 %) during the second season. GCV values are high for seed weight (33.10 %) followed by primary branches /plant (27.76 %) during the first season. In the second season, seed weight (33.06 %) followed by branching angle (28.52 %) exhibited high GCV. Low GCV was observed for a number of pods /plants (9.19 %) and days to maturity (9.28 %) during the first season. In the second season, the same characters nodes /plant (8.64 %) and days to maturity (9.30 %) exhibited low GCV. High heritability accompanied by a high GCV value enhances the efficiency of selection (Burton, 1952, Ritesh Sharma *et al.*, 2014). During phenotypic selection, high heritability, genetic advance and high GCV are considered which

Table 1. Genetic parameters of variation for the traits under study in first season

S. No.	Characters	PV	GV	EV	GCV (%)	PCV (%)	H^2 (%)	GA	GA as % of the mean
1	PH	499.67	498.75	0.92	15.16	15.17	0.99	45.58	30.88
2	PB	8.96	8.81	0.15	27.76	28	0.98	6.04	56.5
3	SB	1.38	1.26	0.12	26.72	27.96	0.91	2.02	48.09
4	DF	337.235	336.13	1.1	14.09	14.11	0.99	37.45	28.78
5	DM	218.92	217.41	1.51	9.28	9.31	0.99	30.17	18.97
6	NPP	177.5	174.5	3	9.19	9.27	0.98	26.89	18.72
7	SPP	0.9	0.83	0.07	19.93	20.75	0.92	1.79	39.16
8	PBL	74.06	73.66	0.4	25.02	25.09	0.99	17.55	51.18
9	SW	13.8	13.0	0.8	33.10	34.10	0.94	7.02	64.50
10	BA	98.87	99.47	0.4	25.89	25.94	0.99	20.38	73.67

PH: Plant height, PB: Number of primary branches, SB: Secondary branches, DF: Days to flowering, DM: Days to maturity, NPP: Number of pods per plant, SSP: Seeds per pod, PBL: Pod bearing length on the main axis, SW: 100 Seed weight, BA: branching angle with main stem.

Table 2. Genetic parameters of variation for the traits under study in second season

S. No.	Characters	PV	GV	EV	GCV (%)	PCV (%)	H ² (%)	GA	GA as % of the mean
1	PH	501.11	491.66	9.45	15.15	15.3	0.98	45.19	30.89
2	PB	8.83	8.26	0.57	24.58	25.41	0.93	5.69	48.67
3	SB	1.32	0.89	0.43	22.24	27.09	0.67	1.58	37.26
4	DF	347.22	342.77	4.45	14.01	14.1	0.98	37.61	28.46
5	DM	226.27	223.81	2.46	9.3	9.4	0.98	30.36	18.99
6	NPP	176.73	152.25	21.48	8.64	9.32	0.86	23.55	16.51
7	SPP	0.89	0.81	0.08	20.5	21.58	0.91	1.76	40.27
8	PBL	76.25	70.56	5.69	25.23	26.23	0.92	16.54	49.68
9	SW	12.45	12.01	0.44	33.06	33.6	0.96	6.48	65.29
10	BA	98.92	96.99	1.93	28.52	28.81	0.98	20.07	58.14

Table 3. Descriptive statistics of ten traits among parents and recombinant inbred lines in first season

S. No.	Trait	Parents		RILs	
		H 2001-4	ICP 7035	Range	Mean±SD
1	PH	129.71	175.42	92.31-193.62	147.95±23.93
2	PB	8.34	12.77	6.11-15.76	10.68±2.90
3	SB	4.55	3.47	2.04-6.32	4.20±1.08
4	DF	116.63	99.83	79.83-153.32	130.1±16.39
5	DM	149.75	136.33	122-173.4	158.78±17.02
6	NPP	142.99	166.55	110.34-179.11	143.68±12.27
7	SPP	5.11	3.93	2.43-6.3	4.57±0.90
8	PBL	31.37	21.28	19.88-55.05	34.28±8.48
9	SW	10.85	7.78	5.43-15.94	10.88±2.30
10	BA	23.17	50.80	20.65-56.64	38.51±10.28

Table 4. Descriptive statistics of ten traits among parents and recombinant inbred lines during the second season.

S. No.	Trait	Parents		RILs	
		H 2001-4	ICP 7035	Range	Mean±SD
1	PH	133.17	177.66	94.32-191.42	148.45±23.09
2	PB	8.04	10.17	6.54-15.19	10.77±2.94
3	SB	4.46	3.01	1.82-6.24	4.22±1.14
4	DF	113.63	106.00	80.83-154.26	131.51±16.94
5	DM	151.55	139.03	120.09-174.34	159.96±17.58
6	NPP	142.99	159.14	112.89-170.44	143.12±12.40
7	SPP	4.98	3.72	2.34-6.12	4.52±0.89
8	PBL	30.37	25.92	20.01-56.03	34.54±8.27
9	SW	10.46	7.75	5.51-16.02	11.06±2.27
10	BA	21.17	51.35	21.47-56.22	35.43±11.16

PH: Plant height, PB: Number of primary branches, SB: Secondary branches, DF: Days to flowering, DM: Days to maturity, NPP: Number of pods per plant, SSP: Seeds per pod, PBL: Pod bearing length on the main axis, SW: 100 Seed weight, BA: branching angle with main stem.

gives an opportunity for improving the traits. Yield-related traits viz., seeds /pod, the number of pods/plant and 100-seed weight exhibited high heritability. Ritesh Sharma *et al.* (2014), Linge *et al.* (2010) and Patel and Patel, (1998) reported similar results. Genetic progress can be made only by considering genetic gain and heritability together during selection (Johnson *et al.*, 1955). The number of pods/plant exhibited moderate genetic advance over per cent of the mean and high heritability indicating the predominance of additive gene action.

The population under study was recombinant inbred lines which were believed to be fixed at almost all the loci. Hence, broad sense heritability estimates are reliable. Higher estimates of broad sense heritability for all the traits under study were observed. The genetic advance over per cent of mean was also high for all the traits under study intriguing that preliminary selection is productive in bringing about the maximum per se performance of the genotypes. The descriptive statistics showed that there was a remarkable range of variability in the mapping population (Table 4). The descriptive statistics also predominantly showed that there were significant differences between the two parents chosen and the range of the recombinant inbred lines in terms of their mean values, was greater than the mean values of parental ones indicating the phenomena of transgressive segregation. The plant parameters studied under two different environments showed no significant difference in terms of their mean values. The range of mean values depicted that the characters were controlled by multiple genes and exhibited normal distribution.

The plant parameters studied showed that there was high heritability and genetic advance over per cent of the mean. So, the selection for early maturing, compact erect and compact semi-erect plant types with high seed 100 seed weight will assist us in identifying desirable genotypes for per se performance. The results are reliable and reproducible as the population under study is fixed recombinant inbred lines.

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