

Original Research Article

<https://doi.org/10.20546/ijcmas.2018.712.210>

Genetic Variability for Plant Type and Seed Yield Components among Recombinant Inbred Lines in Pigeon pea

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ABSTRACT

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is one of the significant grain legume crops of rainfed agriculture generally grown in sub-tropical and semi-arid regions of the world. It is having a genome size of 852Mb. The number of chromosomes is $2n = 2x = 22$. Pigeonpea is used as a substitute for animal protein in developing countries of subtropical and semi-arid regions. Mapping population, RIL was used for the study was derived through SSD method from the cross between H2001-4 and ICP 7035. The cross was further advanced to F₆₋₇ generation. Parental ones were contrasting for all the characters included in the study of the plant type and seed yield components. Parents under the study were showing remarkable differences with respect to one another. ICP 7035 was a moderately resistant variety (Anita Kumari *et al.*, 2010). ICP 7035 was a semi-compact medium duration one and show moderate resistance to pod borer, Hubner. But the H2001-4 was having indeterminate plant growth matures early. The field evaluation was carried out during *Kharif*, 2014-15 (Environment-1) and 2015-16 (Environment-2). Around 318 recombinant inbred lines were sown in augmented RBD design (Federer, 1956) in six blocks with parents (ICP 7035 and H2001-4). Seven checks were used for the assessing the performance of the different inbred lines which were viz., Pusa 992, Pusa 991, Pusa 2001, Pusa 2002, Pusa 2012, Pusa 855 and V114. Earliness is an important character for developing early maturing varieties. Compact semi erect and compact erect characters help for enhancing the cropping density of the Pigeonpea. Genetic parameters show that there is significant variation with in the population that was studied the descriptive statistics studied were also shows a range of variation for all the traits under study. There is significant variability in the two populations that had been studied. The difference between the GCV and PCV is less indicating the influence of the environment is less and the differences under the study will give the valuable information about the genes governing the traits of interest.

Keywords

Genetic variability,
Descriptive
statistics, GCV,
PCV, Heritability,
Genetic advance
and genetic advance
over mean

Article Info

Accepted:
15 November 2018
Available Online:
10 December 2018

Introduction

Cajanuscajan is a significant grain legume which is mainly cultivated in the tropical and semiarid regions of the world. Before the

genomic revolution and new molecular techniques *Cajanus cajan* was considered as the “orphan legume” as the availability of the genomic resources was limited. *Cajanus cajan* was abstemiously and nutritionally efficient

legume crop. It is having a genome size of 852Mb(1). The number of chromosomes is $2n = 2x = 22$. India is the centre of origin for Pigeonpea, as many wild relatives and a large amount of natural genetic variation is found in India (2). Even though the area under production is the highest in India, the productivity is low (kg/ha) in terms of the average productivity, when compared to the world (751 kg/ha) (3). Low productivity is mainly due to underutilization of the valuable information in terms of genes hidden in the genetic resources of the Pigeonpea, sensitivity to biotic and abiotic stresses, and lack of plant type that is high yielding and short duration and that fits into suitable cropping system in a crop season. Yield attributing traits of the Pigeonpea are plant height, number of primary branches per plant, number of secondary branches per plant, average number of pods per plant, average number seeds per plant and seeds size (4). Plant type characters include plant height, number of primary branches, number of secondary branches, days to flowering, and days to maturity (7). Compact semi erect and compact erect characters help for enhancing the cropping density of the Pigeonpea. Genetic parameters show that there is significant variation with in the population that was studied the descriptive statistics studied were also shows a range of variation for all the traits under study. There is significant variability in the two populations that had been studied. The difference between the GCV and PCV is less indicating the influence of the environment is less and the differences under the study will give the valuable information about the genes governing the traits of interest.

Materials and Methods

Development of the mapping population

Two contrasting parents ICP 7035 and H2001-4 chosen and F_{6-7} recombinant inbred lines were developed in the Division of Genetics.

Parents under the study were showing remarkable differences with respect to one another. ICP 7035 was a moderately resistant variety (5). ICP 7035 was a semi-compact medium duration one and show moderate resistance to pod borer, Hubner. But the H2001-4 was having indeterminate plant growth matures early (Table 1). Till 6 generation single seed descent method had been followed for the generation of recombinant inbred lines. 318 recombinant inbred lines were taken for the study over two seasons 2014 and 2015. The field evaluation was carried out during *Kharif*, 2014-15(Environment-1) and 2015-16(Environment-2). Around 318 recombinant inbred lines were sown in augmented RBD design (6) in six blocks with parents (ICP 7035 and H2001-4). Seven checks were used for the assessing the performance of the different inbred lines which were viz., Pusa 992, Pusa 991, Pusa 2001, Pusa 2002, Pusa 2012, Pusa 855 and V114. Plate-1 depicts the parental genotypes used.

Traits phenotyped in the mapping population

Recording of the observation was made for the traits related to plant type. The traits under study include plant height (cm), number of secondary branches on the primary branches, number of primary branches on the main stem, days to flowering, days to maturity, number of pods per plant, seeds per pod, pod bearing length on main axis, 100 seed weight and branching angle with respect to main stem. Observations on 10 randomly sampled plants were recorded and mean was calculated for morphological traits.

Observations recorded in the following manner

Plant height (cm): At maturity plant height was measured from basal portion of the plant to the tip of the grown plant.

Primary branches per plant: Number of branches directly arising from the plant was recorded.

Secondary branches per plant: Number of branches that were arising on the primary branches was recorded.

Days to flowering: Number of days taken from the date of sowing to the appearance and opening of the flowers in 50% of the plants in a row.

Days to maturity: Number of days taken from the flowering date to maturity of the developing pods till they give a sign of yellowing nature.

Number of pods per plant: Number of pods per plant was noted on each single plant from 10 plants

Seeds per pod: Numbers of seed present in 5 pods of each of the 10 sampled plants was noted and mean value was recorded as seeds per pod.

Pod bearing length: Length of the main axis bearing the pods was recorded on 10 sampled plants and mean was recorded as pod bearing length.

100 seed weight: Weight of the randomly sampled 100 seed was taken which reflect the seed mass and, dry matter production.

Branching angle: The angle between the main stem and the primary branches was taken with the help of protractor at five nodes leaving the basal two nodes.

Mean value over the 10 plants was recorded as branching angle. Phenotypic data was statistically analysed by the Windostat version 9.3 Indostat services Hyderabad.

Results and Discussion

Plant height (cm)

Variation for plant height ranged from 92.31 cm to 193.62 cm in environment one and in environment two it ranged from 94.32 cm-191.42 cm. Study of the genetic parameters of variation for plant height suggested that there is significant variability in the population and the intervention of the environment is less as the difference between the PCV (15.17%) and GCV (15.16%) is less. The character under study also showed high heritability (0.99) (Table 2 and 3). *Number of primary branches per plant:* The range of the primary branches was from 6.11 to 15.76 among the recombinant lines in first environment and 6.54 to 15.19 in second environment. Study of the genetic parameters suggested that there was significant variability in the population and the difference between the PCV and GCV was low indicating that the influence of the environment was low and the heritability of the character is high (0.98) (Table 2 and 3). *Number of secondary branches per plant:* For number of secondary branches, the range was from 2.04 to 6.32 in first environment and 1.82 to 6.24 in the second environment. The heritability of the trait was high (0.91 and 0.67) in both the environments and difference between the PCV and GCV also was very low indicating the mapping population is fixed for the locus under study (Table 2 and 3). *Days to flowering:* The range in first environment was from 79.83 to 153.02 and second environment it was from 80.83 to 154.26. Study of the genetic parameters showed that there is significant variability in the population. The heritability of the character under study was high (0.99) (Table 2 and 3). *Days to maturity:* The range in first environment was from 122 to 173.4 and in second environment it was from 120.09 - 174.34. The heritability of the character was high (0.98). The difference between the PCV

and GCV was less indicating the influence of environment is less (Table 2 and 3). *Number of pods per plant*: The range for the character under study was from 110.34 to 179.11 and in second environment it was from 112.89 - 170.44. The genetic parameters of variations study indicated that there was significant variability in the population. The heritability of the character is also high (0.98 and 0.86). The difference between the PCV and GCV was less indicating the character is less influenced by the environment (Table 2 and 3). *Seeds per pod*: Study of the genetic parameters showed that there was variability among the recombinant inbred lines. The difference between the GCV and PCV is less which indicated that there was less influence of the environment, and high heritability (0.92 and 0.91). The range in first environment was from 2.43 to 6.3 and in second environment it was from 2.34 - 6.12 (Table 2 & 3). *Pod bearing length on main axis (cm)*: The range in first environment was from 19.88cm - 55.05cm, and in second environment it was from 20.01cm - 56.03cm. The study of the genetic parameters showed that there is significant variability in the population and

the heritability of the character is high (0.99 and 0.92) the difference between the PCV and GCV was less indicating the less influence of environment over the character (Table 2 & 3). *100 seed weight*: This is very important character in the seed yield components which reflects the seed mass and is one of the significant components in the dry matter production and harvest index. The frequency distribution of the trait ranged from 5.43 to 15.94 in first environment and in second environment 5.51 to 16.02. The heritability of the trait was high (0.99 and 0.99) in both the environments and the difference between the PCV and GCV was less indicating the influence of the environment is low (Table 2 & 3). *Branching angle with main axis (Degrees)*: Angle was studied as the compact erect with less plant height are important characters of plant for higher yields. and the range was from 20.65 to 56.64 in first environment and it was from 21.47 to 56.22 in the second environment. The heritability of the trait is high (0.99 and 0.98) (Table 2 & 3). The descriptive statistics showed that there was remarkable range of variability in the mapping population (Table 4 and 5).

Table.1 Phenotypic characters of parental genotypes ICP 7035, H 2001-4

Trait	H-2001- 4 (female)	ICPL 7035 (male)
Plant height (cm)	218	130
No of primary branches	16	6.6
No of secondary branches	3.9	12
Days to flowering	120	96
Days to maturity	160	130
No of pods per plant	165	230
No of seeds per pod	3.5	5.5
Pod bearing length on main axis (cm)	30.5	20.5
100 seed weight (g)	8.5	13.5
Branching angle with main axis of the stem (Degrees)	45	25
Pod wall thickness (mm)	Thin	Thick
Pod borer resistance	Susceptible	Moderately resistance
Plant type	Spreading	Compact

Table.2 Genetic parameters of variation for the traits under study in environment one (E1)

Genetic parameters E1												
S. No.	Characters	Mean	Range min	Range max	Pv	Gv	Ev	Gcv (%)	Pcv (%)	H ²	GA	GA as % of mean
1	PH	147.27	92.31	193.62	499.67	498.75	0.92	15.16	15.17	0.99	45.58	30.88
2	PB	10.69	6.11	15.76	8.96	8.81	0.15	27.76	28	0.98	6.04	56.5
3	SB	4.2	2.04	6.32	1.38	1.26	0.12	26.72	27.96	0.91	2.02	48.09
4	DF	130.11	79.83	153.02	337.235	336.13	1.1	14.09	14.11	0.99	37.45	28.78
5	DM	158.79	122	173.4	218.92	217.41	1.51	9.28	9.31	0.99	30.17	18.97
6	NPP	143.63	110.34	179.11	177.5	174.5	3	9.19	9.27	0.98	26.89	18.72
7	SPP	4.57	2.43	6.3	0.9	0.83	0.07	19.93	20.75	0.92	1.79	39.16
8	PBL	34.29	19.88	55.05	74.06	73.66	0.4	25.02	25.09	0.99	17.55	51.18
9	SW	10.88	5.43	15.94	10404.1	10404.05	0.05	937	956.25	0.99	208.01	1911.8
10	BA	38.52	20.65	50.08	99.87	99.47	0.4	25.89	25.94	0.99	20.38	73.67

PH: Plant height(cm), 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 main axis(cm), SW: 100 Seed weight(g), BA: branching angle with main stem (Degrees).

Table.3 Genetic parameters of variation for the traits under study in environment two (E2)

Genetic parameters E2												
S. No.	Charac-ters	Mean	Range min	Range max	Pv	Gv	Ev	Gcv (%)	Pcv (%)	H ²	GA	GA as % of mean
1	PH	146.27	94.32	191.42	501.11	491.66	9.45	15.15	15.3	0.98	45.19	30.89
2	PB	11.69	6.54	15.19	8.83	8.26	0.57	24.58	25.41	0.93	5.69	48.67
3	SB	4.24	1.82	6.24	1.32	0.89	0.43	22.24	27.09	0.67	1.58	37.26
4	DF	132.11	80.83	154.26	347.22	342.77	4.45	14.01	14.1	0.98	37.61	28.46
5	DM	159.79	120.09	174.34	226.27	223.81	2.46	9.3	9.4	0.98	30.36	18.99
6	NPP	142.63	112.89	170.44	176.73	152.25	21.48	8.64	9.32	0.86	23.55	16.51
7	SPP	4.37	2.34	6.12	0.89	0.81	0.08	20.5	21.58	0.91	1.76	40.27
8	PBL	33.29	20.01	56.03	76.25	70.56	5.69	25.23	26.23	0.92	16.54	49.68
9	SW	10.48	5.51	16.02	10404.26	10404.15	0.11	972.28	973.29	0.99	208.02	1984.92
10	BA	34.52	21.47	56.22	98.92	96.99	1.93	28.52	28.81	0.98	20.07	58.14

PH: Plant height(cm), 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 main axis(cm), SW: 100 Seed weight(g), BA: branching angle with main stem (Degrees).

Table.4 Descriptive statistics of ten traits among parents and recombinant inbred lines under environment one (E1)

S. No	trait	Parents		RILs	Mean±SD
		ICP 7035	H2001-4	range	
1	PH	129.17	175.42	92.31-193.62	147.95±23.93
2	PB	8.34	12.77	6.11-15.76	10.68±2.9
3	SB	4.55	3.47	2.04-6.32	4.20±1.08
4	DF	116.63	99.83	79.83-153.02	130.10±16.39
5	DM	149.55	136.33	122-173.4	158.78±17.02
6	NPP	148.99	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	7.47	5.43-15.94	10.88±2.3
10	BA	23.17	50.80	20.65-56.64	38.51±10.28

Table.5 Descriptive statistics of ten traits among parents and recombinant inbred lines under environment two (E2)

S. No	Trait	Parents		RILs	
		ICP 7035	H2001-4	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

Plate.1 Parental lines from which recombinant inbred lines are derived



Female Parent H-2001-4



Male Parent ICP

It is concluded that, the study of the genetic parameters of variability showed that there was significant variability in the mapping population of the Pigeonpea and the differences under the study will give the appreciable results. As the population is fixed at almost all the loci gene effects can be studied in an appropriate manner. The success of the genetic advance under selection mainly depends on the range of variability in the base population that is recombinant inbred lines and the genetic diversity between the parents which is reflected in the contrasting characters of the chosen parents for the development of the mapping population. The study showed that the characters are having high heritability with high genetic advance which is due to additive gene effects.

Acknowledgement

Authors express immense gratitude for the division of genetics IARI new Delhi for providing all the necessary facilities for conducting the research. I am thankful to project director of NRCPB Dr. N.K.Singh for helping me to complete my work and properly guiding me to complete my research.

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How to cite this article:

Suman Parre and Singh, N.K. 2018. Genetic Variability for Plant Type and Seed Yield Components among Recombinant Inbred Lines in Pigeon pea. *Int.J.Curr.Microbiol.App.Sci.* 7(12): 1802-1808. doi: <https://doi.org/10.20546/ijemas.2018.712.210>