Electronic Journal of Plant Breeding, 9 (2) : 682-691 (June 2018) DOI: 10.5958/0975-928X.2018.00082.0
ISSN 0975-928X

Research Article

Genetic variability and association studies for yield and its attributes in super-early pigeonpea (*Cajanus cajan* (l.) Millsp.) Genotypes

M.S. Ranjani[1], C. Vanniarajan[1], C V Sameer Kumar[2,] R. K. Saxena[2], R. Sudhagar[3] and *Anupama J. Hingane[2]

[1]Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Madurai-625104

[2]Pigeonpea Breeding, International Crop Research Institute for the Semi-Arid Tropics, Patancheru-502324
[3]Department of Forage Crops, TamilNadu Agricultural University, Coimbatore -641003

***E-mail : h.anupama@cgiar.org**

(Received: 05 Jun 2018; Revised: 26 Jun 2018; Accepted:26 Jun 2018)

Abstract

Twenty-nine super-early pigeonpea genotypes along with an early duration check were evaluated for 12 quantitative traits to assess genetic variability, cause and effect for yield as well as yield contributing traits. High PCV and GCV was observed for the traits *viz.* plant height, number of branches per plant, pod bearing length, number of clusters per plant, number of number of pods per plant and single plant yield. High heritability associated with high genetic advance as per cent of mean (GAM) was observed for the traits like plant height, pod bearing length, number of clusters per plant and number of branches per plant indicating that these traits were controlled by additive gene action and selection for above traits is advisable. Correlation coefficient analysis revealed that the traits *viz.* number of number of pods per plant, pod length, number of seeds per pod and days to fifty per cent flowering can be the best selection indices for breeding programme as they show significant positive correlation in favour of single plant yield. Path coefficient analysis showcased the traits with direct and indirect effect on single plant yield as number of pods per plant, plant height, days to maturity, number of branches per plant and days to fifty per cent flowering.

Keywords

Super-early pigeonpea, heritability, correlation, path coefficient analysis.

Introduction

Pigeonpea (*Cajanus Cajan (L.) Millsp.*) is a versatile plant species rich in protein. Globally pigeonpea is cultivated in about 5.41 M ha with a production of 4.48 M tonnes and yielding an average of 724 kg/ha (FAOSTAT, 2016). India is the largest producer of pigeonpea followed by Myanmar, Malawi, United Republic and Kenya. Pigeonpea is the second largest pulse grown in India next to chickpea. It can fix up to 235 kg nitrogen per hectare and produce more nitrogen per unit area than any other legumes, thus being a source for sustainable agriculture (Peoples *et al*, 1995). Pigeonpea is a perennial crop by its habitat and domesticated as annual crop due its commercial demand. However, due to increased cropping period, monocropping is prevailing in pigeonpea cultivation. The super early lines developed at ICRISAT, Patancheru, Hyderabad reach maturity within 100 days creating an opportunity to intensify cropping system, overcome monocropping and dodging climate changes (Srivastava *et al*, 2012). Hingane (2016) stated that the super early genotypes can adapt to various agro-ecological zones due to its thermo and photo insensitivity whereas the shorter crop period aids in escaping from extreme variants of biotic and abiotic stresses. The genotypes show synchronized maturity enhancing mechanical harvesting, thereby aiding timeliness and reduced resource input in crop production. Hence, the study was undertaken to assess variability, correlation and path coefficients which enroute in selecting superior lines, thus leading to crop improvement in super-early lines of pigeonpea.

Materials and Methods

The study was conducted at International Crop Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Hyderabad during *kharif* 2017. The study involved 29 super-early pigeonpea genotypes which include non-determinate (NDT) and determinate (DT) types developed at ICRISAT and one early duration pigeonpea, MN1 as check. MN1 is also one of the parents involved in the development of super-early lines (Srivastava *et al,* 2012). The details of the super-early genotypes are furnished in Table 1. The latitudinal and longitudinal position of the experimental plot is 17.51°N and 78.27° E respectively. The experimental plot is located at an altitude of 545 meters above MSL with an annual rainfall of 877.82 mm. The soil type is alfisol. The experimental design was randomized complete block design (RCBD) with 3 replications. The genotypes were raised in a broad bed of 4m length and 1m breadth with a spacing of 30 cm × 10 cm.

Standard cultural practices were followed as per recommendation to maintain good crop health status.

The study involved 12 quantitative characters for exploring the genetic variability, cause and effect of yield and yield attributes. The quantitative characters *viz.* days to fifty per cent flowering (DFF), days to maturity (DM), plant height (PH, cm), number of branches per plant (NBR, no's), pod bearing length (PBL, cm), number of clusters per plant (NCPL, no's), number of number of pods per plant (PPC, no's), pod length (PL, cm), number of seeds per pod (NSPP, no's), 100- seed weight (HSW, g), shelling percentage (SP, %) and single plant yield (SPY, g). The readings were taken from five single competitive plants of each genotype over three replications.

The statistical analysis was carried out utilizing GENRES v 7.01 software. Phenotypic and genotypic coefficients of variation were computed based on the formulae suggested by Burton (1952). Heritability in broad sense was calculated following the method proposed by Lush (1940). Genetic advance as percent of mean was estimated using formula formulated by Johnson *et al.* (1955). Correlation analysis was carried out according to the method suggested by Johnson *et al.* (1955) and path analysis was based on the method provided by Dewey and Lu (1959).

Results and Discussion

The existence of variability among the individuals of a population is inevitable for crop improvement. Variability is an apparent index for choosing superior material in a plant breeding programme. Variability can be estimated by various methods. Measuring the components of variability is the primary step in reckoning variability. The study of analysis of variance (ANOVA) showed significant differences for all the traits studied. The estimated ANOVA is presented in Table 2.

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) shows ascendency in representing the variability. The PCV and GCV of super-early genotypes are presented in Table 3. PCV and GCV were high for characters like pod bearing length (44.49, 45.70) followed by number of clusters per plant, single plant yield, number of pods per plant, number of branches per plant and plant height. It was low for shelling percentage, number of seeds per pod, pod length, days to maturity, days to fifty percent flowering and 100- seed weight. High PCV and GCV indicate that the corresponding characters can be subjected to selection to explore beneficial traits, whereas low PCV and GCV manifest that the selection of the trait shows no singularity. PCV was higher than GCV in all the studied characters. However, the magnitude of discrepancy between PCV and GCVwas very low representing that they were majorly under genetic control and the influence of environment was negligible. Similar findings were reported by Rajamani *et al*., (2015), Kesh *et al*., (2017), Mallesh *et al.,* (2017) and Deepak *et al*., (2018).The proportion of variability due to genetic cause is projected as heritability. Heritability imprints on the transmission of traits from parents to offspring. High heritability was recorded in case of plant height (98.48%), days to maturity (97.01%), pod bearing length (94.7%), days to fifty per cent flowering (78.08%), pod length (77.32%), number of clusters per plant (70.18%) and number of branches (63.15%). Moderate heritability was observed in case of number of seeds per pod (58.63%), number of pods per plant (49.58%), 100- seed weight (47.05%) and single plant yield (39.45%) whereas shelling percentage exhibited low heritability (17.78%). The genetic advance is represented as per cent of mean. High genetic advance as per cent of mean (GAM) was recorded in case of pod bearing length (89.17%) followed by number of clusters per plant (68.16%), plant height (43.25%), number of pods per plant (39.44%), number of branches (33.75%) and single plant yield (32.82%). Moderate genetic advance was espied in case of days to fifty per cent flowering (12.7%), 100- seed weight (11.47%) and days to maturity (10.46%), whereas low genetic advance was recorded for characters like pod length (9.01%), number of seeds per pod (7.22%) and shelling percentage (2.74%).

The characters *viz.* plant height, pod bearing length, number of clusters per plant and number of branches exhibited high heritability combined with high genetic advance representing that they are controlled by additive gene action and selection is effective for these traits. The additive gene action was also reported for plant height and number of branches per plant by Bhadru (2010) and Meena *et al*., (2017), whereas for number of branches alone by Kesh *et al*., (2017). Moderate heritability in combination with high genetic advance was showcased by traits like days to fifty per cent flowering, number of pods per plant, 100- seed weight and single plant yield expressing the fact that they can also be subjected to selection, however it is not as effective as the above case and experiences some influence from biotic and abiotic factors. High heritability and low genetic advance was observed in case of traits like pod length and number of seeds per pod. High heritability and low genetic advance indicates that the trait is controlled by non-additive gene action and selection would not be rewarding. Shelling percentage shows low heritability along with low genetic advance exhibiting that it is highly influenced by environment and selection in this case is ineffective.

Correlation coefficient explains the relationship between various variables. It aids in the selection of traits having significant effect on yield and other desirable characters thereby offering a successful crop improvement scenario. The result of correlation analysis is presented in Table 4. Single plant yield had significant and positive correlation with plant height (r=0.988, p<0.01), pod bearing length (r=0.978, p<0.01) number of clusters per plant (r=0.988, p<0.01), number of number of pods per plant (r=0.981,p<0.01), pod length (r=0.438, p<0.05), number of seeds per pod (r= 0.547, p<0.01), days to fifty per cent flowering (r=0.871, p<0.01) and days to maturity (r=0.481, p<0.01). Similar research proofs were provided by Saroj *et al.*, (2013), Ram *et al.*, (2016) and Narayana *et al.*, (2018). Significant and negative correlation was registered for single plant yield in case of number of branches per plant (r=-0.947, p<0.01), 100-seed weight (r=-0.679, p<0.01) and shelling percentage (r=-0.987, p<0.01). Thus, single plant yield can be improved by focusing on traits with significant and positive association with it based on correlation analysis.

Days to maturity exhibited significant positive correlation with plant height (r=0.891,p<0.01), pod bearing length (r=0.825,p<0.01), number of clusters per plant (r=0.827,p<0.01), number of number of pods per plant (r=0.881,p<0.01), pod length (r=0.482,p<0.01), number of seeds per pod (r=0.743,p<0.01) and days to fifty per cent flowering (r=0.998,p<0.01). Days to maturity was correlated in the opposite direction with traits like number of branches (r=-0.614, p<0.01), 100- seed weight (r=-0.615, p<0.01) and shelling percentage (r=-0.890, p<0.01). The above was in confirmation with the results of Narayana *et al.*, (2018).

Plant height had significant and positive correlation with pod bearing length(r=0.966,p<0.01), number of clusters per plant(r=0.988,p<0.01), number of number of pods per plant(r=0.987, p<0.01), number seeds per pod(r=0.630, p<0.01), days to fifty per cent flowering (r=0.896, p<0.01), days to maturity(r=0.891, p<0.01) and single plant yield (r=0.988, p<0.01), however it was significant and negatively correlated with number of branches per plant (r=-0.841, p<0.01), shelling percentage (r=-0.509,p<0.01) and 100- seed weight (r=-0.798, p<0.01).

The experimental material was developed with an idea of reduced days to maturity thereby offering an opportunity to overcome the drawbacks so far in pigeonpea cultivation. Therefore, trait of focus is days to maturity and single plant yield. The traits like plant height, pod bearing length, number of clusters per plant, number of number of pods per plant, pod length, number of seeds per pod and days to fifty per cent flowering can be selection indices used in a breeding programme for improvement of yield and earliness based on correlation studies.

Path coefficient analysis splits the correlation coefficient into direct and indirect effects thus making selection process more precise for improvement of a trait. Path analysis was carried out for genotypic correlation of single plant yield. The results are presented in Table 4. The effects were rated according to Lenka and Mishra (1973). The traits like number of pods per plant (0.883), days to maturity (0.836), number of branches per plant (0.636), pod bearing length (0.613), plant height (0.363) and pod length (0.356) exhibited high direct effect in the positive direction. Moderate direct effect on single plant yield was reported in case of pod length (0.274) and number of seeds per pod (0.225). 100- seed weight and shelling percentage projected low direct effect on single plant yield. The trait like days to fifty per cent flowering showed high direct effect but in the negative direction.

The indirect effect in case of number of pods per plant was high and positive for plant height, pod bearing length, number of clusters per plant, days to fifty per cent flowering and days to maturity whereas, it was high and negative for traits like number of branches per plant, hundred seed weight, and shelling percentage. The pod bearing length, number of number of pods per plant, pod length, number of seeds per pod, days to fifty per cent flowering and days to maturity had high and positive indirect effect on plant height, whereas number of branches per plant, 100-seed weight, number of clusters per plant, shelling percentage had negative indirect effect on plant height. Days to maturity experienced moderate to high indirect affect *via* other traits. Based on the path coefficient analysis, the traits like number of number of pods per plant, plant height, days to maturity, number of branches per plant and days to fifty per cent flowering can be considered in a breeding programme for improvement of single plant yield**.** Similar findings were reported by Narayana *et al.*, (2018)

The study of genetic parameters showcased the fact that characters *viz.* plant height, pod bearing length, number of clusters per plant and number of branches exhibited high variability in combination with high heritability and genetic advance as per cent of mean. Hence the selection for above traits can be strictly considered while crop improvement in super early pigeonpea for single plant yield (g). The cause and effect analysis implied that the traits like number of number of pods per plant, pod length, number of seeds per pod, days to maturity and days to fifty per cent flowering showed positive association and direct effect towards single plant yield thus they can be a selection index for improving single plant yield.

References

Burton, G.W. 1952. Quantitative inheritance in grasses. *Proc. 6th Int. Grassland Cong.*, **1**: 277 - 283.

Bhadru, D. 2010. Studies on genetic parameters and interrelationships among yield and yield contributing traits in pigeonpea (*Cajanus cajan (L.) Mill Sp*.). *Legume Res.,* **33(1)**:23-27.

Dewey, R. D. and Lu, K.H. 1959. A Path coefficient analysis of components of creasted wheat grain seed production. *Agron. J.,* **51**: 515-518.

Deepak, P., Verma, S.K., Panwar, R.K., Arora, A. and Gaur, A. K. 2018. Correlation and Path Analysis Studies in Advance Lines of Pigeonpea [*Cajanus cajan (L.) Millspaugh*] under Different Environments. *Int.J.Curr.Microbiol.App.Sci***., 7(04)**: 378-389.

FAOSTAT. 2016. Retrieved from (http://www.fao.org/faostat/en/#data/QC)

Hingane, A. J. 2016. Super-early pigeonpea: dodging climate change in the drylandshttp://www.icrisat.org/super-early-pigeonpea-dodging climate-change-in-the-drylands/

Kesh, H., Yadav, A. S., Sarial, A.K., Khajuria, S. and Jain,B.T. 2017. Genotypic Variability and Character Association among Yield and Yield contributing Traits in Pigeonpea (*Cajanus cajan L. Millsp*). *Research Journal of Agricultural Sciences*, **8(1):** 194-198.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. 1955. Estimation of genetic variability and environmental variability in soybean. *Agron. J*., **47**: 314 - 318.

Ram, K., Saxena, K., Tushar, M. S.and Geeta, B. 2016. A Study on Genetic Variability, Correlation and Path Analysis in Pigeon pea [*Cajanus cajan L. Millspaugh*]. *International Journal of Agriculture Science,* **8(51):** 2287-2289.

Lenka, D. and Mishra, B. 1973. Path coefficient analysis of yield in rice varieties**.** *Indian J. Agric. Sc.,* ***43*****:** 376-379.

Lush, J.L. 1940. Intra – sire correlation and regression of offspring on dams as a method of estimating heritability of characters. In**:** Proc. of "*American Society of Animal Production"*, **33**: 293-301.

Narayanan, S. L., Manivannan, N. and Mahalingam, A. 2018. Correlation and Path Analyses of Yield and its Component Traits in Pigeonpea [*Cajanus cajan (L.) Millsp*.]. *Int.J.Curr.Microbiol.App.Sci*., **7(03):** 614-618.

Mallesh, P., Nanda, H.C., Durgaraju, Ch., Kumar, C.V.S., Mohan, N.Z. and lee, J. 2017. Variability, Heritability and Genetic Advance for Quantitative Traits in Pigeonpea (*Cajanus cajan* (L.) Mill sp.). *Int. J. Pure App. Biosci.,* **5(5):**25-28.

Peoples, M. B., Herridge, D. F.,Ladha, J. K. 1995. Biological nitrogen fixation: An efficient source of Nitrogen for sustainable agricultural production? Plant and Soil**, 174**:3-28.

Rajamani, S., Sreekanth, M. and Koteswara Rao, Y.2015. Evaluation of Pigeonpea Genotypes for their Genetic Variability, Heritability and Genetic advance. *J. Res. ANGRAU*.**, 43(3&4):** 96-98.

Srivastava, R. K., Vales, M. I., Sultana, R., Saxena, K. B., Kumar, R. V., Thanki, H. P., Sandhu, J. S. and Chaudhari,K. N., 2012.Development of "super -early" pigeonpeas with good yield potential from early × early crosses. *An Open Access Journal published by ICIRSAT***. 10.**

Saroj, S. K., Singh, M. N., Kumar, R., Singh, T. and Singh, M.K. 2013. Genetic variability, correlation and path analysis for yield attributes in pigeonpea. *The Bioscan*., **8(3)**: 941-944.

Meena, S. S., Verma, S. K., Choudhary, R., Panwar, R. K. and Singh, J. P. 2017. Genetic Variability and Inter-Relationship among Yield Contributing Characters in Advance Lines of Pigeonpea [*Cajanus Cajan* (L.) Millsp.] Grown at Different Altitudes. *Chem Sci Rev Lett.,* **6(22)**:1120-1128.

Table 1. List of super-early pigeonpea genotypes under study

NAME OF GENOTYPES	GROWTH HABIT	DAYS TO MATURITY
ICPL 20328	NDT	93
ICPL 11244	NDT	95
ICPL 11296	NDT	93
ICPL 11276	NDT	90
ICPL 11279	NDT	92
ICPL 11301	NDT	91
ICPL 11300	NDT	92
ICPL 20329	NDT	95
ICPL 20327	NDT	97
ICPL 20325	NDT	99
ICPL 20333	NDT	90
ICPL 11245	NDT	91
ICPL 11326	NDT	92
ICPL 11242	NDT	91
ICPL 11285	NDT	95
ICPL 20326	NDT	95
ICPL 11292	NDT	88
ICPL 11303	NDT	92
ICPL 11298	NDT	87
ICPL 11249	DT	84
ICPL 11255	DT	86
ICPL 11273	DT	85
ICPL 20340	DT	84
ICPL 20341	DT	82
ICPL 11253	DT	84
ICPL 20336	DT	84
ICPL 20338	DT	83
ICPL 11252	DT	84
ICPL 11256	DT	88
MN1(CHECK)	DT	95

Table 2. Analysis of variance for 12 quantitative characters in super-early pigeonpea genotypes

Source of Variation	df	Mean Sum of Squares											
		PH	**NBR**	**PBL**	**NCLP**	**PPC**	**PL**	**NSPP**	**HSW**	**SP**	**DFF**	**DM**	**SPY**
Replication	2	53.69	0.76	133.40	237.86	456.20	0.00	0.00	5.14	47.87	3.01	4.80	52.19
Treatment	29	1091.35**	11.36**	1918.89**	514.96**	965.19**	0.18**	0.11**	1.09**	35.12**	50.89**	65.06**	35.99**
Error	58	5.59	1.85	35.08	63.88	244.53	0.02	0.02	0.3	21.30	4.37	0.66	12.18

** Significance at 1% probability level

Table 3. Genetic parameters for 12 quantitative characters in super-early pigeonpea genotypes

Characters	Mean	Range		GCV*	PCV*	h^2	GA%
		Maximum	**Minimum**				
PH	89.92	120.52	59.67	21.16	21.32	98.48	43.25
NBR	8.64	12.80	5.67	20.68	25.94	63.15	33.75
PBL	56.34	83.40	20.40	44.49	45.71	94.71	89.17
NCLP	31.05	50.20	12.53	39.48	47.14	70.18	68.16
PPC	57.02	87.80	27.40	27.19	38.62	49.58	39.44
PL	4.72	5.17	4.28	4.97	5.65	77.32	9.01
NSPP	3.70	4.11	3.27	4.58	5.98	58.63	7.22
HSW	6.33	7.33	5.17	8.12	11.84	47.05	11.47
SP	67.94	74.29	59.87	3.16	7.49	17.78	2.74
DFF	56.38	62.33	49.00	6.99	7.91	78.03	12.71
DM	89.89	98.67	82.00	5.15	5.23	97.01	10.46
SPY	11.11	17.07	5.70	25.37	40.49	39.45	32.82

*GCV-Genotypic coefficient of variation: PCV- Phenotypic coefficient of variation: ECV: Environmental coefficient of variation:H^2 -Heritability: GA%- Genetic advance as per cent of mean

Table 4. Genotypic and phenotypic correlation between 12 quantitative characters in super-early pigeonpea genotypes

Correlation		PH	NBR	PBL	NCLP	PPC	PL	NSPP	HSW	SP	DFF	DM	SPY
PH	**G**	1.000	-0.814**	0.966**	0.988**	0.987**	0.378*	0.630**	-0.540**	-0.797**	0.896**	0.891**	0.988**
	P	1.000	-0.619**	0.934**	0.828**	0.719**	0.339*	0.489**	-0.363*	-0.323*	0.794**	0.874**	0.675**
NBR	**G**		1.000	-0.912**	-0.963**	-0.873**	-0.446**	-0.783**	0.549**	0.368*	-0.654**	-0.614**	-0.947**
	P		1.000	-0.691**	-0.510**	-0.309*	-0.268	-0.364*	0.329*	0.180	-0.361*	-0.470**	-0.253
PBL	**G**			1.000	0.989**	0.985**	0.383*	0.652**	-0.566**	-0.679**	0.826**	0.825**	0.978**
	P			1.000	0.874**	0.762**	0.344*	0.489**	-0.389*	-0.260	0.732**	0.797**	0.719**
NCLP	**G**				1.000	0.943**	0.477**	0.710**	-0.601**	-0.900**	0.809**	0.827**	0.988**
	P				1.000	0.872**	0.380*	0.457**	-0.333*	-0.303	0.715**	0.710**	0.860**
PPC	**G**					1.000	0.282	0.539**	-0.832**	-0.866**	0.854**	0.881**	0.981**
	P					1.000	0.203	0.308*	-0.357*	-0.161	0.652**	0.654**	0.938**
PL	**G**						1.000	0.616**	0.046	-0.529**	0.524**	0.482**	0.438**
	P						1.000	0.594**	0.014	-0.305	0.439**	0.424**	0.253
NSPP	**G**							1.000	-0.590**	-0.572**	0.730**	0.743**	0.547**
	P							1.000	-0.276	-0.147	0.491**	0.549**	0.313*
HSW	**G**								1.000	0.062	-0.641**	-0.615**	-0.679**
	P								1.000	0.128	-0.425**	-0.432**	-0.202
SP	**G**									1.000	-0.805**	-0.890**	-0.987**
	P									1.000	-0.450**	-0.356*	-0.034
DFF	**G**										1.000	0.986**	0.871**
	P										1.000	0.907**	0.563**
DM	**G**											1.000	0.868**
	P											1.000	0.585**
SPY	**G**												1.000
	P												1.000

** ,*Significance at 1% & 5% probability level respectively.

Table 5. Direct (diagonal) and indirect effect of eleven quantitative characters on single plant yield in super-early pigeonpea genotypes

CHARACTERS	**PH**	**NBR**	**PBL**	**NCLP**	**PPC**	**PL**	**NSPP**	**HSW**	**SP**	**DFF**	**DM**	**SPY**
PH	**0.363**	-0.518	0.593	-0.140	0.825	0.135	0.191	-0.083	-0.103	-0.916	0.745	0.966**
NBR	-0.295	**0.636**	-0.559	0.136	-0.821	-0.159	-0.238	0.084	0.047	0.733	-0.514	-0.947**
PBL	0.351	-0.580	**0.613**	-0.142	0.864	0.137	0.198	-0.087	-0.087	-0.905	0.690	0.987**
NCLP	0.358	-0.612	0.617	**-0.141**	0.809	0.170	0.215	-0.092	-0.117	-0.880	0.691	0.985**
PPC	0.372	-0.555	0.604	-0.133	**0.883**	0.100	0.163	-0.128	-0.112	-0.951	0.737	0.981**
PL	0.137	-0.283	0.235	-0.0674	0.861	**0.356**	0.187	0.007	-0.068	-0.829	0.403	0.438**
NSPP	0.228	-0.498	0.399	-0.100	0.692	0.219	**0.303**	-0.090	-0.074	-0.854	0.621	0.547**
HSW	-0.196	0.349	-0.347	0.084	-0.768	0.016	-0.179	**0.154**	0.008	0.713	-0.514	-0.679**
SP	-0.289	0.234	-0.416	0.127	-0.812	-0.188	-0.174	0.009	**0.129**	0.874	-0.745	-0.988**
DFF	0.325	-0.416	0.506	-0.114	0.796	0.187	0.222	-0.098	-0.104	**-0.981**	0.850	0.871**
DM	0.323	-0.391	0.505	-0.117	0.730	0.172	0.225	-0.095	-0.115	-0.907	**0.836**	**0.868****

** ,* Significance at 1% & 5% probability level respectively.

Residual Effect – 0.185

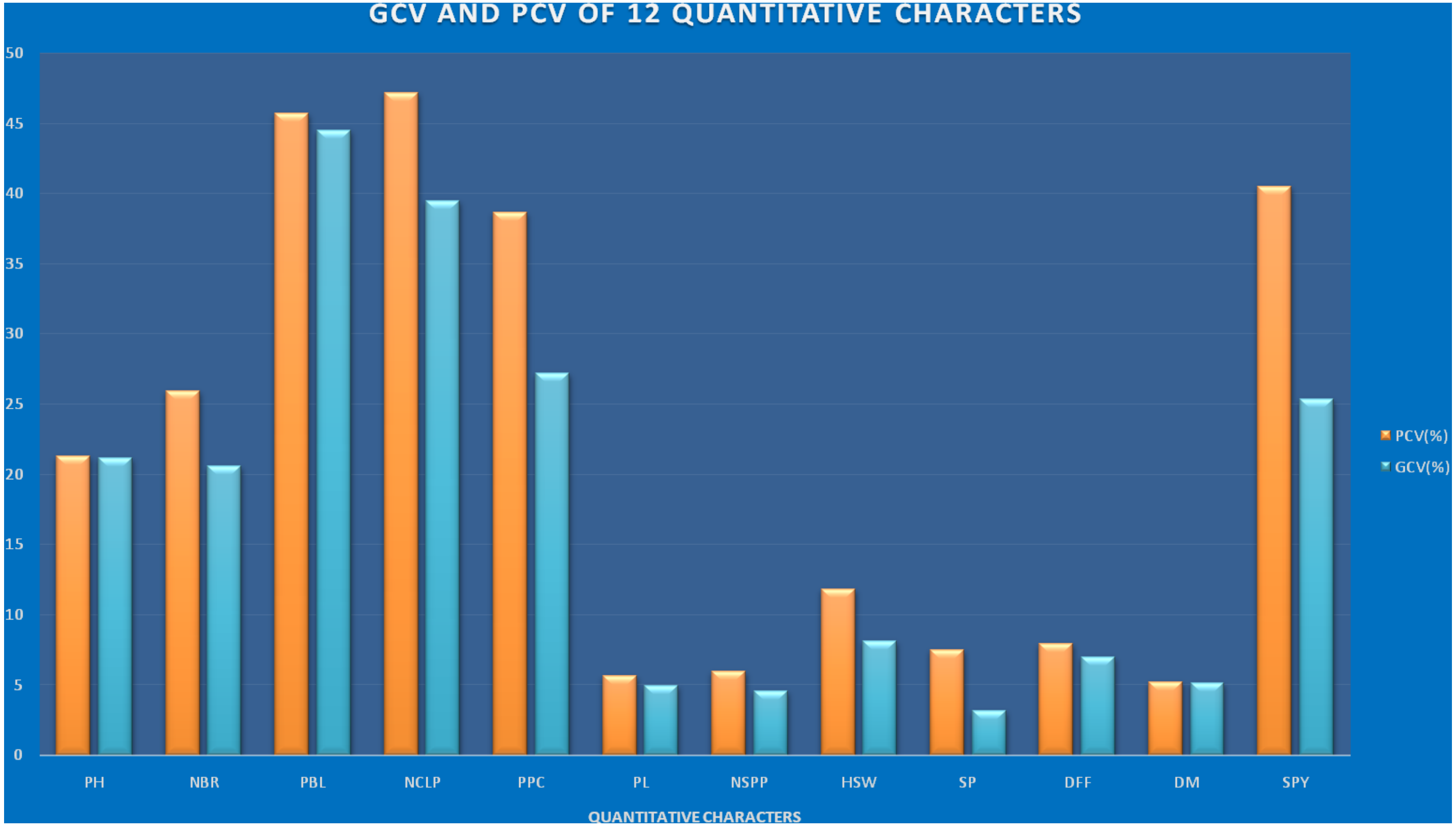

Fig. 1. PCV and GCV for 12 quantitative characters in super-early pigeonpea genotypes

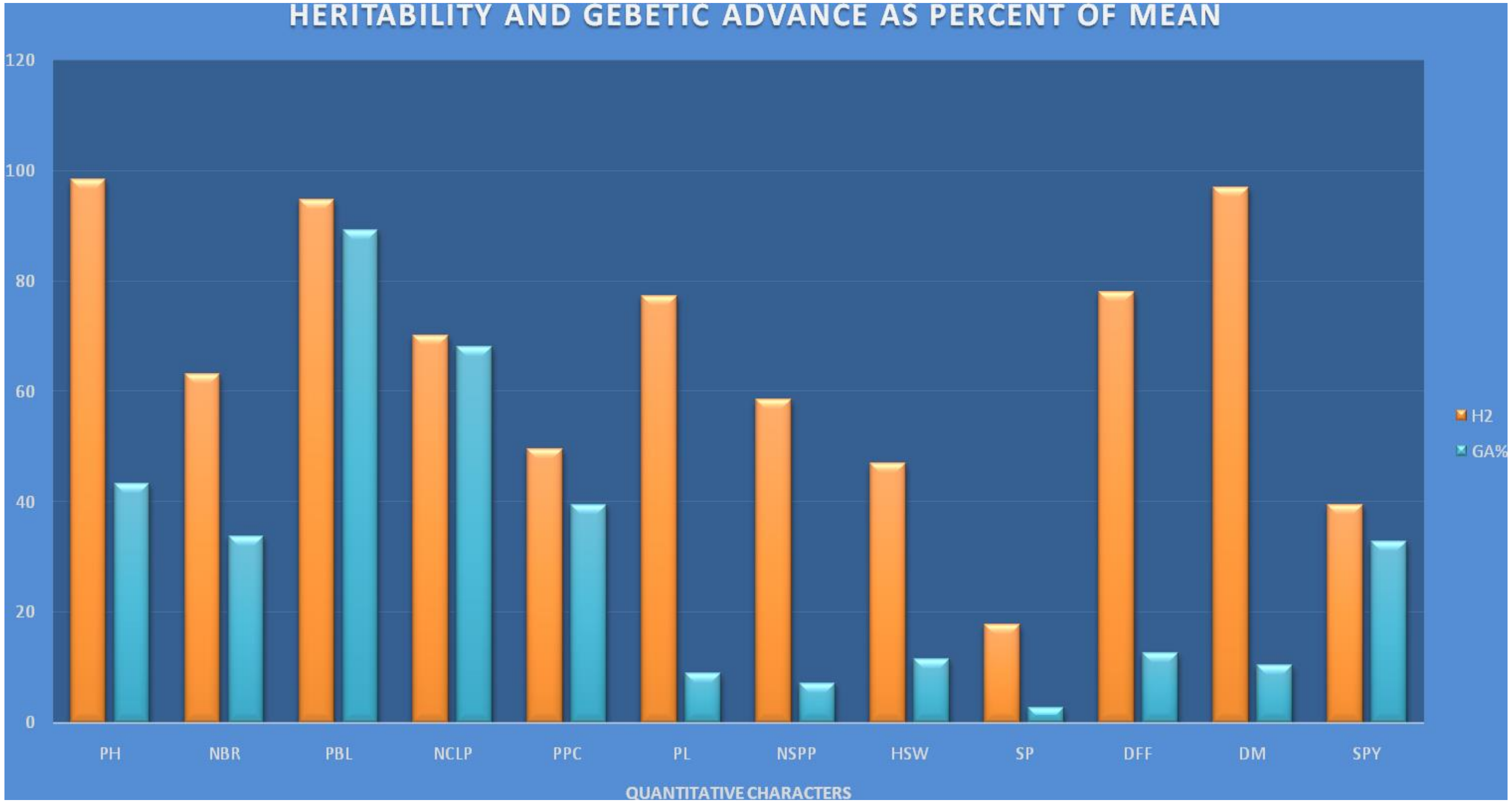

Fig. 2. Heritability and genetic advance as per cent of mean for the traits in super-early pigeonpea genotypes