Indian J. Genet., 76(2): 181-186 (2016)
DOI: 10.5958/0975-6906.2016.00022.5

Genetic association and frequency distribution in segregating generations derived from pigeonpea crosses

B. C. Ajay*[1], M. Byregowda, G. N. Veerakumar, K. N. Ganapathy[2], Murlidhar Meena[1], H. Prashanth Babu and M. Reena

AICRP on Pigeonpea, University of Agricultural Sciences, GKVK, Bengaluru 560 065; [1]Directorate of Groundnut Research, Junagadh 362 001; [2]Directorate of Sorghum Research, Hyderabad

(Received: April 2015; Revised: March 2016; Accepted: April 2016)

Abstract

Correlation and presence of genetic interactions was studied using F_2 and F_3 generations in three pigeonpea crosses for yield and its component traits. Most of the characters studied were positively skewed and were being governed by several genes indicating quantitative inheritance. Variance, skewness and kurtosis have also indicated that homozygosity has increased over the generation in pigeonpea crosses. Cross BRG 1 x ICP 8863 was found better than other two crosses (TTB 7 x ICP 8863 and TTB 7 x ICPL 87119) in providing high yielding segregants displaying parental diversity. Seed yield and other associated characters such as plant height and number of pods per plant had complementary gene action with other genes governing these characters. Yield increase is possible by following rigid selection for yield and its component characters. A shift in correlation coefficients between the generations was recorded which is likely to be attributed to difference in gene complementation of linkage blocks and an indication of unstable nature of breeding population.

Key words: Correlation, skewness, kurtosis, gene interaction, pigeonpea

Introduction

Pigeonpea (*Cajanus cajan* L. Millsp.) is an important leguminous short lived perennial shrub cultivated as annual crop in semi-arid tropical and subtropical regions of the world. Productivity of pigeonpea worldwide in comparison to cereals is very low. This low productivity is attributed to its low harvest index and limited man made selections (Ganapathy et al. 2009). Progress in breeding programme depends on amount of variability created during hybridization. Simple measures of variability *viz.,* range, variance and standard error were commonly used to assess the variability for yield. The information on frequency distribution of different traits will help in identifying plants with desirable expression of traits under selection (Preetha and Raveendren 2008). Breeding for high yield is the main objective of any crop improvement programme. Since yield is polygenically controlled and highly influenced by environment, selection based on yield alone is not effective. Therefore, improvement in yield could be brought about by effecting indirect selection through component characters, which are highly heritable and show strong correlation with yield. The present study was aimed at studying the genetics of different traits, association of yield and its component traits using third and fourth degree statistics in segregating generations of pigeonpea.

Materials and methods

The study was conducted at All India Co-ordinated Research Project (AICRP) on Pigeonpea, University of Agricultural Sciences (UAS), Bengaluru, India. Materials used for this study consisted of F_2 and F_3 generations from three crosses of pigeonpea namely BRG-1×ICP-8863 (Cross-A), TTB-7×ICP-8863 (Cross-B) and TTB-7×ICPL-87119 (Cross-C). F_2 and F_3 generations were raised by selfing under insect proof nylon net. These crosses were performed in order to combine high yielding ability of TTB-7 and BRG-1 with *Fusarium* wilt resistance available in genetic stocks, ICP-8863 and ICPL-87119. At maturity observations were recorded on primary branches (PB), secondary

---

*Corresponding author's e-mail: ajaygpb@yahoo.co.in

Published by the Indian Society of Genetics & Plant Breeding, F2, First Floor, NASC Complex, PB#11312, IARI, New Delhi 110 012
Online management by indianjournals.com

branches (SB), plant height (PH), number of pods per plant (PP), pod yield/weight per plant (PY), seeds per pod (SPP), 100 seed weight (100SW), seed yield per plant (SY) and shelling per cent (SHP). The association between yield and its associated characters was worked out as a simple phenotypic correlation coefficient following the method suggested by Goulden (1939). Skewness (K_3), the third degree statistics and kurtosis (K_4), the fourth degree statistics were estimated (Snedecor and Cochron) using PAST statistical software (Hammer et al. 2001) to understand the nature of distribution of different traits

$$K_4 = \frac{n}{(n-1)(n-2)(N-3)}$$

$$\left\{(n+1)\sum_{j=1}^{n}(Yj-\bar{Y})4 - \frac{3(n-1)}{n}\left[\sum_{j=1}^{n}(Yj-Y)^2\right]\right\}$$

where, n-sample size, Yj – observational value of jth sample, Y-sample mean.

For a normal distribution, skewness is equal to zero in absence of gene interaction; it is greater and smaller than zero in presence of average complementary and duplicate interactions respectively. Also, gene interactions can be detected by studying fourth degree statistics, kurtosis which is always negative or near to zero in absence of gene interaction and positive only in presence of gene interaction (Choo and Reinbergs 2008).

The standard error for coefficient of skewness and kurtosis were estimated as per Fisher (1950) as follows;

$$SEK3 = \sqrt{\frac{6n(n-1)}{(n-2)(n+1)(n+3)0}}$$

$$SEK4 = \sqrt{\frac{24(n-1)^2}{(n-3)(n-2)(n+5)(n+3)}}$$

Frequency distribution for each trait significantly deviated from zero ($P \leq 0.05$) probability level if that value was greater than twice of its standard error

Results and discussion

Skewness and kurtosis

The study of distribution using skewness and kurtosis provides information about nature of gene action and number of genes controlling the traits (Samak et al. 2011; Nachimuthu et al. 2014). Positive skewness is associated with complementary gene action while negative skewness is associated with duplicate (additive × additive) gene interactions. Kurtosis is negative or close to zero (platykurtic) in absence of gene interaction and positive in presence of gene interaction (leptokurtic) (Nachimuthu et al. 2014). Studies on gene interactions are needed to increase the efficiency of selection in breeding program.

In F_2 generation, days to flowering was positively skewed in all three crosses whereas 100 seed weight was positively skewed in cross-B and cross-C and negatively skewed in cross-A (Table 1). PH was negatively skewed in all the three crosses. PB, SB, SPP, SYL and PPP were positively skewed in all the three crosses. SHP was negatively skewed in cross-B and cross-C. In F_3 generation (Table 2), DFF and PH were positively skewed in cross-A and cross-C whereas 100SW and PB were positively skewed in cross-A and cross-B. SB, SHP, SYL and PPP were positively skewed in all three crosses. SPP were positively skewed in cross-B and cross-C.

Distribution curves of pod yield in F_2 generation of cross-A, cross-B and cross-C are presented in Figs. 1a, 1b and 1c, respectively. Distribution curves of pod yield in F_3 generation from these crosses is also depicted in Figs. 1d, 1e and 1f, respectively. Distribution curve of F_2 generation (Table 1) showed that PH, PB were platykurtic in cross-A and cross-C; DFF in all three crosses with kurtosis values less than '0'. Distribution curve was leptokurtic for SB in cross-A and cross-B; PPP and SHP in all three crosses; SPP, 100SW and SYL in cross-A and cross-C. Distribution curve of F_3 generation (Table 2) showed that PH was platykurtic in cross-B and cross-C; DFF, SYL in cross-A and cross-B; PPP in cross-A and cross-C with kurtosis values less than '0'. Traits namely PB, SB and 100SW were leptokurtic in all three crosses; SHP in cross-A and cross-B and SPP in cross-A and cross-C. The traits, namely, DFF, PB, SB, PPP, SPP and PYL (Fig. 1a, 1b and 1c) and SYL were positively skewed in F_2 generation which is an evidence for complementary gene interactions, whereas PHT was negatively skewed indicating duplicate gene interaction. The SHP and 100SW showed duplicate gene interaction in some particular cross and complementary interactions in other crosses. In F_3 generation traits, namely, DFF, PHT, PB, SPP and 100SW had duplicate interactions in some cross and complementary interactions in other crosses, whereas SB, PPP, PYL (Fig. 1d, 1e and 1f) and SYL had positive skewness with complementary gene interactions in all the crosses. Selection intensity and

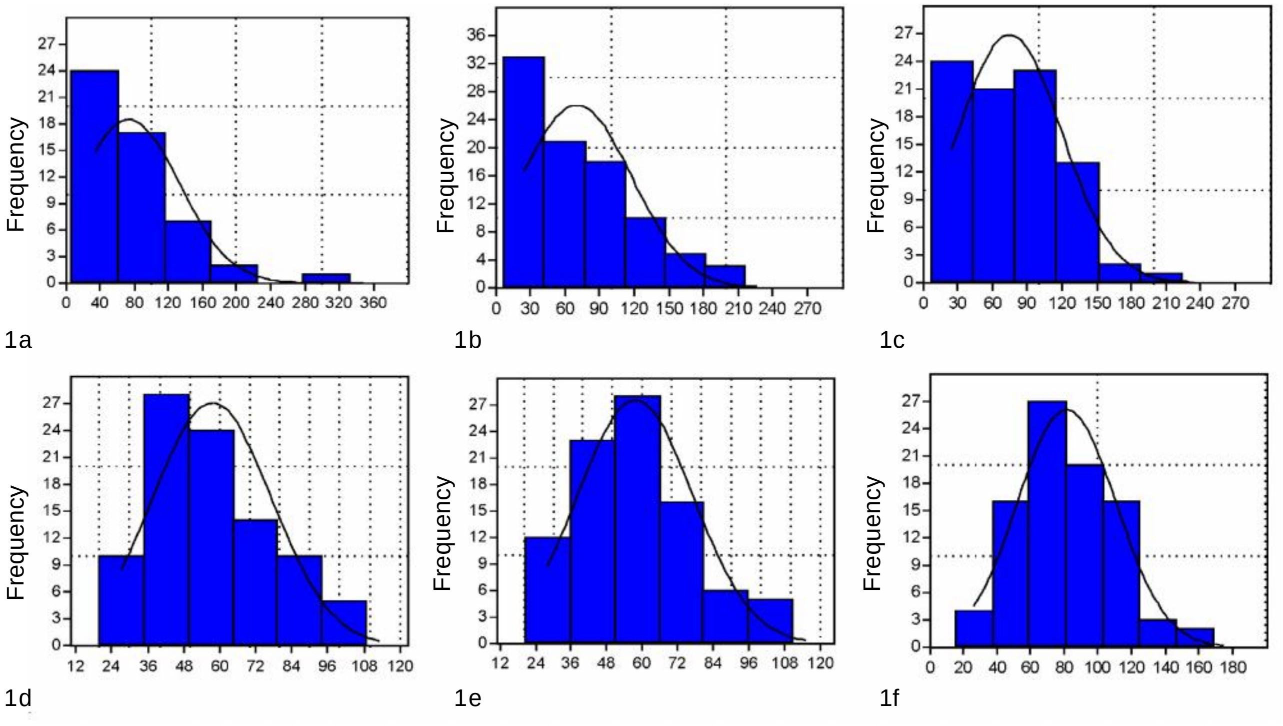
Table 1. Skewness and kurtosis for yield and its component traits in F_2 generation of three pigeonpea crosses

	Skewness			Kurtosis			Variance		
	Cross A	Cross B	Cross C	Cross A	Cross B	Cross C	Cross A	Cross B	Cross C
DFF	0.72*	0.52*	0.89*	–0.79	–0.82	–0.51	65.5	60.1	35.7
PH	–0.03	–0.04	–0.66*	–0.05	0.15	–0.31	376.9	443.4	352.6
PB	0.36	0.03	0.28	–0.41	–0.32	0.76	20.2	24.9	40.3
SB	1.10*	0.73*	0.26	0.73	0.20	–0.17	66.7	106.7	76.3
PPP	1.22*	1.16*	0.78*	2.39*	1.22*	0.96	9446.8	10619.0	12603.0
SPP	0.13	0.16	0.45	0.29	–0.14	0.28	0.2	0.1	0.2
SHP	0.26	–0.81*	1.34*	1.87*	1.95*	8.90*	683.3	566.2	123.5
100SW	–0.55	0.08	0.37	2.22*	–0.02	2.32*	2.6	2.0	2.0
PYL	1.89*	0.83*	0.58*	5.61*	0.05	0.13	3635.8	2597.4	2136.1
SYL	1.99*	0.95*	0.37	6.35*	0.31	–0.76	1536.0	1355.8	767.8

Cross A = BRG-1×ICP-8863; Cross B = TTB-7×ICP-8863; Cross C = BRG-1×ICPL-87119

progress in improving population performance may be greater under complementary interaction than under duplicate interaction (Reynolds 2009; Ajay et al. 2012). For all the above traits with duplicate gene action rapid genetic gain could be observed under mild selection using existing variability, whereas for traits with complementary gene action selection has to be strict for enhanced genetic gain which is in agreement with the earlier studies (Zhang and Zhou et al. 2006; Samak et al. 2011).

Positive coefficient of kurtosis for PPP, SHP, and PYL (Fig. 1a, 1b and 1c) in F_2 generation and PB, SB, 100SW in F_3 generation indicates the presence of gene interaction and further it also indicates that these traits are governed by fewer numbers of dominant genes with majority having increasing effect. Traits such as PHT, PB, SB, SPP, 100SW and SYL



1a 1b 1c

1d 1e 1f

Fig. 1. Normality distribution of pod yield in F_2 and F_3 generations of three pigeonpea crosses

in F_2 generation and DFF, PHT, PPP, SPP, SHP, PYL (Fig 1d, 1e and 1f) and SYL in F_3 generation had positive coefficient of kurtosis in some crosses and negative kurtosis in other crosses indicating the presence gene interactions for these traits and are governed by many genes. Ajay et al. (2012) using 5 generation mean analysis have observed duplicate interaction for plant height, whereas PYL and SYL

Table 2. Skewness and kurtosis for yield and its component traits in F_3 generation of three pigeonpea crosses

	Skewness			Kurtosis			Variance		
	Cross A	Cross B	Cross C	Cross A	Cross B	Cross C	Cross A	Cross B	Cross C
DFF	0.92*	–0.10	0.74*	–0.01	–1.11*	2.65*	28.26	25.16	0.16
PH	–0.68*	0.40	–0.09	2.00*	–0.20	–0.33	201.98	146.55	118.72
PB	0.08	0.23	–0.46	0.01	0.48	1.49*	7.09	5.86	8.50
SB	1.57*	1.10*	0.80*	2.90*	0.93	1.24*	20.83	31.55	24.95
PPP	0.52*	0.56*	0.23	–0.18	0.03	–0.36	1155.60	1512.20	4203.50
SPP	–0.09	0.32	0.14	0.41	–0.24	1.10*	0.09	0.04	0.06
SHP	–1.02	–0.10	–0.60*	2.68*	–0.07	0.65	65.59	36.02	56.02
100SW	0.30	0.11	–3.03*	0.44	0.28	19.95*	0.94	0.87	0.87
PYL	0.51*	0.54*	0.34	–0.17	–0.09	0.14	400.42	386.84	872.33
SYL	0.46	0.53*	0.37	–0.53	–0.05	0.98	159.91	186.09	346.56

Cross A = BRG-1×ICP-8863; Cross B = TTB-7×ICP-8863; Cross C = BRG-1×ICPL-87119

Table 3. Correlation coefficient matrix among yield related characters in F_2 generation of three pigeonpea crosses

	Cross	DFF	PH	PB	SB	PPP	SPP	TWT	SHP	PYL
PH	A	0.003	1							
	B	–0.09	1							
	C	–0.29**	1							
Pb	A	0.09	0.14	1						
	B	–0.15	0.41**	1						
	C	–0.41**	0.22*	1						
SB	A	0.03	0.36**	0.41**	1					
	B	–0.083	0.32**	0.24*	1					
	C	–0.05	0.28**	0.29**	1					
PPP	A	–0.13	0.50**	0.32*	0.51**	1				
	B	–0.11	0.47**	0.29**	0.41**	1				
	C	–0.21*	0.41**	0.13	0.23*	1				
SPP	A	–0.17	0.14	–0.001	0.11	0.036	1			
	B	–0.16	0.12	0.14	0.14	0.14	1			
	C	–0.10	0.14	0.21*	0.18*	0.29**	1			
TWT	A	–0.06	0.07	0.23	0.38**	0.15	0.06	1		
	B	–0.002	0.20*	0.15	0.03	0.004	0.03	1		
	C	–0.026	0.13	0.15	0.16	–0.10	–0.08	1		
SHP	A	–0.07	–0.13	–0.31*	–0.22	–0.29*	–0.25*	–0.09	1	
	B	0.06	–0.15	–0.11	–0.08	–0.19*	–0.09	0.003	1	
	C	0.01	–0.14	–0.06	–0.14	–0.39**	–0.14	–0.01	1	
PYL	A	–0.13	0.51**	0.30*	0.51**	0.98**	0.08	0.19	–0.28*	1
	B	–0.14	0.54**	0.31**	0.38**	0.96**	0.19*	0.13	–0.19*	1
	C	–0.19*	0.36**	0.17	0.24*	0.93**	0.31**	0.01	–0.43**	1
SYL	A	–0.15	0.52**	0.25*	0.49**	0.96**	0.05	0.18	–0.24*	0.99**
	B	–0.13	0.52**	0.31**	0.36**	0.94**	0.20*	0.15	–0.05	0.98**
	C	–0.26**	0.43**	0.21*	0.25**	0.92**	0.26**	0.05	–0.26**	0.96**

Cross A - BRG-1×ICP-8863; Cross B – TTB-7×ICP-8863; Cross C - BRG-1×ICPL-87119 revealed complementary gene interaction in some crosses and duplicate gene interaction in other crosses. The variation recorded in seed yield, coefficients of skewness and kurtosis (Table 1 and 2) has decreased in F_3 over F_2 in all the crosses. It indicates that over the generation variability in population has decreased due to increase in homogygosity. In F_2 generation, cross-A had higher variance (1536), coefficient of skewness (1.99) and kurtosis (6.35) compared to cross-B and cross-C. It indicates that there is a better chance of identifying high yielding segregants from cross-A

Table 4. Correlation coefficient matrix among yield related characters in F_3 generation of three pigeonpea crosses

	Cross	DFF	PH	PB	SB	PPP	SPP	TWT	SHP	PYL
PH	A	0.35^{**}	1.00							
	B	0.36^{**}	1.00							
	C	–0.08	1.00							
PB	A	0.16	0.41^{**}	1.00						
	B	0.40^{**}	0.22^{*}	1.00						
	C	$–0.21^{*}$	0.34^{**}	1.00						
SB	A	0.34^{**}	0.09	0.35^{**}	1.00					
	B	0.38^{**}	0.17	0.37^{**}	1.00					
	C	0.15	0.30^{**}	0.15	1.00					
PPP	A	0.25^{**}	0.38^{**}	0.32^{**}	0.42^{**}	1.00				
	B	0.23^{*}	0.25^{**}	0.39^{**}	0.52^{**}	1.00				
	C	–0.15	0.13	0.34^{**}	0.45^{**}	1.00				
SPP	A	–0.07	0.25^{**}	–0.05	-0.30^{**}	0.08	1.00			
	B	–0.05	0.20^{*}	0.02	0.02	0.19^{*}	1.00			
	C	$–0.20^{*}$	–0.16	–0.07	-0.07	0.13	1.00			
TWT	A	0.15	0.174^{*}	0.207^{*}	0.01	0.06	0.208^{*}	1.00		
	B	0.24^{*}	0.29^{**}	0.28^{**}	0.34^{**}	0.22^{*}	0.09	1.00		
	C	–0.17	–0.06	–0.14	$–0.23^{*}$	–0.06	0.18^{*}	1.00		
SHP	A	–0.01	–0.11	0.09	0.00	$–0.30^{**}$	$–0.19^{*}$	–0.11	1.00	
	B	–0.15	–0.05	–0.07	–0.10	–0.15	0.09	–0.02	1.00	
	C	0.08	0.06	–0.02	–0.06	$–0.23^{*}$	–0.03	0.24^{*}	1.00	
PYL	A	0.22^{*}	0.39^{**}	0.31^{**}	$.036^{**}$	0.91^{**}	0.24^{*}	0.18^{*}	$–0.43^{**}$	1.00
	B	0.33^{**}	0.32^{**}	0.46^{**}	0.63^{**}	0.91^{**}	0.25^{**}	0.47^{**}	–0.15	1.00
	C	–0.16	0.11	0.36^{**}	0.44^{**}	0.93^{**}	0.17	0.01	$–0.27^{**}$	1.00
SYL	A	0.25^{**}	0.41^{**}	0.38^{**}	0.39^{**}	0.88^{**}	0.19^{*}	0.18^{*}	–0.09	0.93^{**}
	B	0.28^{**}	0.31^{**}	0.45^{**}	0.60^{**}	0.87^{**}	0.27^{**}	0.47^{**}	0.10	0.96^{**}
	C	–0.12	0.17	0.36^{**}	0.46^{**}	0.90^{**}	0.16	0.03	0.01	0.95^{**}

Cross A = BRG-1×ICP-8863; Cross B = TTB-7×ICP-8863; Cross C = BRG-1×ICPL-87119

Character association

SYL had significantly positive correlation with PB, SB and PPP in all the crosses of both the generations. Similar associations of these characters with SYL have been reported previously by several workers in their study (Sodavadiya et al. 2009; Sawargaonkar et al. 2011; Rao et al. 2013). Hence selection could be practiced for these component characters to increase seed yield. PPP had positive association with PB, SB and PH in all the three crosses in both generations, except in F_2 generation of a cross-B. Similar observations were made by Ganapathy et al. (2009) and Rao et al. (2013). DFF had positive association with SB, PPP and PH in cross-A and cross-B; while cross-C had significant negative association for above characters. This difference in association of DFF with other component characters is due to the fact that, cross-C is late flowering type in comparison to other two crosses. PH was positively associated with PB, SB, PPP and DFF in all the three crosses which is in agreement with the reports of earlier workers (Sodavadiya et al. 2009; Rao et al. 2013). SHP had significant negative association with PPP in both the generations of three crosses. The study revealed that some characters changed in magnitude of association from generation to generation. For instance, association of DFF was significant with SB, PPP and PH in cross-A in F_3 generation but not in F_2 generation. Similarly, PB had negative significant association with SHP in F_2 generation, but in F_3 generation it was positive and non significant in the cross-A. This kind of shifts in correlation coefficients between generations was attributed to difference in gene complementation of linkage blocks and an indication of unstable nature of breeding population (Preetha and Raveendren 2008). It is concluded that yield contributing traits such as SB, PPP, PYL and SYL are governed by complementary gene action. Since these characters are inter-correlated among themselves, selection in any one of these traits will result in the improvement of other trait and hence expected to result in increased yield.

Acknowledgements

Authors express their gratitude to the Government of India (Rashtriya Krishi Vikas Yojana, RKVY) for supporting this project.

References

Ajay B. C., Gnanesh B. N., Ganapathy K. N., Byregowda M., Prasad P. S., Veerakumar G. N., Venkatesha S. C., Abdul Fiyaz R. and Ramya K. T. 2012. Genetic analysis of yield and quantitative traits in pigeonpea (*Cajanus cajan* L. Millsp.). Euphytica, **186**: 705-714.

Ajay B. C., Prasad P. S., Byregowda M., Ganapathy K. N., Gnanesh B. N., Abdul Fiyaz R., Veerakumar G. N., Prashanth babu H., Venkatesha S. C. and Ramya K. T. 2013. Inheritance of resistance to Bangalore race of Fusarium wilt disease in pigeonpea (*Cajanus cajan* L.). Aust. J. Crop Sci., **7**: 1520-1524.

Samak A. N. R., Hittalamani S., Shashidhar N. and Hanumareddy B. 2011. Exploratory studies on genetic variability and genetic control for protein and micronutrient content in F_4 and F_5 generations of rice (*Oryza sativa* L.). Asian J. Plant Sci., **10**: 376-379.

Fisher R. A. 1950. Statistical methods for research workers. 11th edn., Oliver and Bond London.

Ganapathy K. N., Byregowda M., Venkatesha S. C., Ramachandra R., Gnanesh B. N. and Girish G. 2009. Identification of AFLP marker linked to sterility mosaic disease in pigeonpea *Cajanus cajan* (L.) Millsp. Int. J. Integr. Bio., **7**: 145-149.

Goulden C. H. 1939. Methods of statistical analysis. John Wiley and Sons, New York.

Gupta S. P. 2011. Skewness, moments and kurtosis. *In*: Statistical methods Sultan Chand and Sons, India.

Hammer Ø., Harper D. A. T. and Ryan P. D. 2001. PAST: Paleontological statistics software package for education and data analysis. Palaeontologia Electronica, **4**: article 4 9pp.

Nachimuthu V. V., Robin S., Sudhakar D., Raveendran M., Rajeswari S. and Manonmani S. 2014. Evaluation of rice genetic diversity and variability in a population panel by principal component analysis. Indian J. Sci. Technol., **7**: 555-562.

Preetha S. and Raveendren T. S. 2008. Genetic appraisal of yield and fibre quality traits in cotton using interspecific F_2, F_3 and F_4 populations. Int. J. Integr. Biol., **3**: 136-142.

Rao P. J. M., Malathi S., Reddy D. V. V. and Upender M. 2013. Genetic studies of association and path coefficient analysis of yield and its component traits in pigeonpea (*Cajanus Cajan* L. Millsp.). Int. J. Sci. Res. Publ., **3**: 1-5.

Reynolds M., Manes Y., Izanloo A. and Langridge P. 2009. Phenotyping approaches for physiological breeding and gene discovery in wheat. Ann. Appl. Biol., **155**: 309-320.

Sawargaonkar S. L., Saxena K. B., Madrap I. A. and Rathore A. 2011. Stability analysis of yield and related traits in pigeonpea hybrids Indian J. Genetics, **24**: 184-193.

Snedecor G. W. and Cochron W. G. 1967. Statistical methods 6th edition Oxford and IBH publishing Co. Pvt. Ltd., New Delhi, India, pages: 553.

Sodavadiya P. R., Pithia M. S., Savaliya J. J., Pansuriya A. G. and Korat V. P. 2009. Studies on characters association and path analysis for seed yield and its components in pigeonpea (*Cajanus cajan* (L.) Millsp.). Legume Res., **32**: 203-205.

Zhang G. and Zhou W. 2006. Selection intensity and progress in improving population performance may be greater under complementary interaction than under duplicate interaction. J. Genetics, **85**: 45-51.