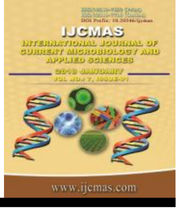
Int.J.Curr.Microbiol.App.Sci (2018) *7*(1): 867-873

International Journal of Current Microbiology and Applied Sciences
ISSN: 2319-7706 **Volume 7 Number 01 (2018)**
Journal homepage: http://www.ijcmas.com



Original Research Article https://doi.org/10.20546/ijcmas.2018.701.105

Genetic Association Estimates Using Third and Fourth Degree Statistics in Early Segregating Generations of Cowpea

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ABSTRACT

Correlation and presence of genetic interactions was studied using F_2 and F_3 generations in two cowpea 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 from the generation to generation in cowpea crosses. Cross A (C-152 × V-16) was found better than crossB (C-152 × V-57817) in providing high yielding segregants displaying parental diversity. Number of branches and 100 seed weight were positively skewed in both crosses and in both the generation. Number of seeds per pod and seed yield per plant was positively skewed in cross A while number of pods per plant was positively skewed in cross B. which is a true indication of complementary gene interaction with other genes governing these characters. Whereas, plant height was negatively skewed in both cross this indicates duplicate gene interaction. 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.

Keywords

Correlation, Cowpea, Gene interaction, Kurtosis, Skewness

Article Info

Accepted:
10 December 2017
Available Online:
10 January 2018

Introduction

Cowpea [Vignaunguiculata (L.) Walp., Fabaceae (2n=2x=22)] is grown as one of the most important widely adapted, stress tolerant grain legume, vegetable and fodder crop in tropical and sub-tropical regions of Africa, Asia, Nigeria and America (Ehlers and Hall, 1997; Singh *et al.*, 1997).Productivity of cowpea compared to cereals is very low. Hence, productivity can be increased by suitable breeding programmes. But, progress in breeding programme depends on amount of variability created during hybridization. First and second degree statistics *viz.*, range, variance and standard error were commonly used to assess the variability for yield. But these are not sufficient in identifying plants with desirable expression of traits under selection. As yield is a complex trait, which is influenced by many other important yield contributing traits controlled by polygenes and also environmental factors. The information on frequency distribution of different traits will also help in identifying plants with desirable expression of traits under selection (Preetha and Raveendren 2008). Therefore, improvement in yield could be brought about by effecting indirect selection procedures by considering other component characters, which are highly heritable and show strong correlation with yield. With this points in view, the present study was aimed at studying the genetic association of different traits using third and fourth degree statistics in early segregating generations of cowpea.

Materials and Methods

The study was conducted at Department of Genetics and Plant Breeding, College of Agriculture, V. C. Farm, Mandya, University of Agricultural Sciences (UAS), Bengaluru, India. Materials used for this study consisted of F_2 and F_3 generations from two crosses of cowpea namely C-152 × V-16 (Cross A) and C-152 × V-57817 (Cross B).

The early segregating generations, F_2 and F_3 were raised by selfing. These crosses were performed in order to combine high yielding ability of C-152 with Bacterial Leaf Blight resistant variety V-16 and cowpea mosaic virus (CpMV) resistant variety V-57817, which were released from Indian Agricultural Research Institute, New Delhi. Observations were recorded at physiological maturity on the yield and its attributes like, plant height (cm), number of branches per plant, number of pods per plant, number of seeds per pod, 100 seeds weight (gm) and seed yield per plant (gm).

The association between yield and its associated characters was worked out as a simple phenotypic correlation coefficient following the method suggested by Pearson (1895). Skewness (K_3), the third degree statistics and kurtosis (K_4), the fourth degree statistics were estimated (Snedecor and Cochron, 1967) using PAST statistical software (Hammer *et al.*, 2001) to understand the nature of distribution of different traits.

$$K3= \frac{n}{(n-1)(n-2)} \sum_{j=1}^{n} (Yj-\bar{Y})^3$$

$$K_4 = \frac{n}{(n-1)(n-2)(N-3)} \left\{ (n-1) \sum_{j=1}^{n} (Y_j-\bar{Y})4- \frac{3(n-1)}{n} \left[\sum_{j=1}^{n} (Y_j-Y)^2 \right] \right\}$$

Where, n-sample size, Yj – observational value of j^{th} 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). Three types of kurtosis are recognized based on the kurtosis value which depends on distribution curve (Robson, 1956).

If kurtosis value = 0 = Normal curve = Mesokurtic,

If kurtosis value > 0 = Leaping curve = Leptokurtic and

If kurtosis value < 0 = Flat curve = Platykurtic

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

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

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

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

Results and Discussion

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, all the traits *viz*., number of branches, number of seeds per pod, 100 seed weight and seed yield per plant were positively skewed except plant height was negatively skewed in both the crosses. But, number of pods per plant was negatively skewed in cross A and positively skewed crosses B (Table 1).

In F_3 generation, all the traits *viz*., plant height, number of branches, number of pods per plant, number of seeds per pod, 100 seed weight and seed yield per plant were positively skewed in cross-A and cross-B except number of seeds per pod and seed yield per plant were negatively skewed in cross B (Table 2).

Distribution curves of seed yield in $F_2$and F_3generation of cross-A and cross-B are presented in Figure 1. Distribution curve of F_2 generation (Table 1) showed that all the traits in cross A and cross B were platykurtic except number of branches in cross B was leptokurtic. In F_3 generation, all the traits showed leptokurtic distribution in cross A except number of branches and 100 seed weight showed platykurtic distribution (Table 2). In cross B, except number of pods per plant showed platykurtic distribution while other traits showed leptokurtic distribution.

Traits *viz*., number of branches and 100 seed weight were positively skewed in both crosses and in both the generation. Number of seeds per pod and seed yield per plant was positively skewed in cross A while number of pods per plant was positively skewed in cross B.

This positively skewed distribution is an indication of complementary gene interaction. Whereas, plant height was negatively skewed in both cross and number of seeds per pod and seed yield per plant was negatively skewed in F_3 generation of cross B which indicates duplicate gene interaction. This result is in agreement with the earlier studies (Sulistyowati, 2015).

Selection intensity and progress in improving population performance may be greater under complementary interactions than under duplicate interactions (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 (Samak *et al.*, 2011).

Positive coefficient of kurtosis for above mentioned traits 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 (Nandini, *et al.*, 2017). The variation recorded in seed yield, coefficient of skewness and kurtosis (Table 1 and 2) has decreased in F_2 over F_3 in both the crosses.

Table.1 Skewness, kurtosis and variance for yield and its traits in F_2 generation of two crosses of cowpea

Sl. No	Traits	Variance		Skewness		Kurtosis	
		Cross A	Cross B	Cross A	Cross B	Cross A	Cross B
1	**Plant height (cm)**	167.84	140.74	-0.11	-0.03	-0.53	-0.44
2	**Number of branches**	2.99	2.13	0.17	0.49	-0.27	0.02
3	**Number pods per plant**	62.12	53.09	-0.03	0.13	-0.65	-0.78
4	**Number seeds per pod**	1.73	4.98	0.06	0.19	-0.66	-0.46
5	**100 seed weight**	7.23	6.48	0.37	0.26	-0.29	-0.64
6	**Seed yield per plant**	104.00	87.43	0.44	0.51	-0.50	-0.42

Note: Cross A: C-152 × V-16 Cross B: C-152 × V-57817

Table.2 Skewness, kurtosis and variance for yield and its traits in F_3 generation of two crosses of cowpea

Sl. No	Traits	Variance		Skewness		Kurtosis	
		Cross A	Cross B	Cross A	Cross B	Cross A	Cross B
1	**Plant height (cm)**	21.46	100.07	0.67	0.96	1.29	1.46
2	**Number of branches**	0.33	0.71	0.01	0.30	-0.15	0.26
3	**Number pods per plant**	7.56	15.54	0.83	0.18	0.73	-0.23
4	**Number seeds per pod**	1.53	2.00	0.54	-0.39	1.13	0.65
5	**100 seed weight**	0.58	15.80	0.04	11.21	-0.51	134.98
6	**Seed yield per plant**	4.25	7.55	0.30	-0.15	0.50	0.70

Note: Cross A: C-152 × V-16 Cross B: C-152 × V-57817

Table.3 Correlation coefficient matrix among yield related characters in F_2 generation of two crosses of cowpea

Characters	Crosses	Plant height	Number of branches	Number pods per plant	Number Seeds per pod	100 seed weight	Seed yield per plant
Plant height (cm)	A	1.000	0.340^{**}	0.086	0.073	0.153^{*}	0.033
	B	1.000	0.818^{**}	-0.002	0.052	0.049	-0.081
Number of branches	A		1.000	-0.022	-0.056	0.225^{**}	0.144^{*}
	B		1.000	-0.011	0.044	0.039	-0.129
Number pods per plant	A			1.000	0.058	-0.009	-0.023
	B			1.000	0.105	-0.044	-0.022
Number Seeds per pod	A				1.000	0.131^{*}	-0.069
	B				1.000	-0.051	0.091
100 seed weight	A					1.000	0.025
	B					1.000	-0.190^{**}
Seed yield per plant	A						1.000
	B						1.000

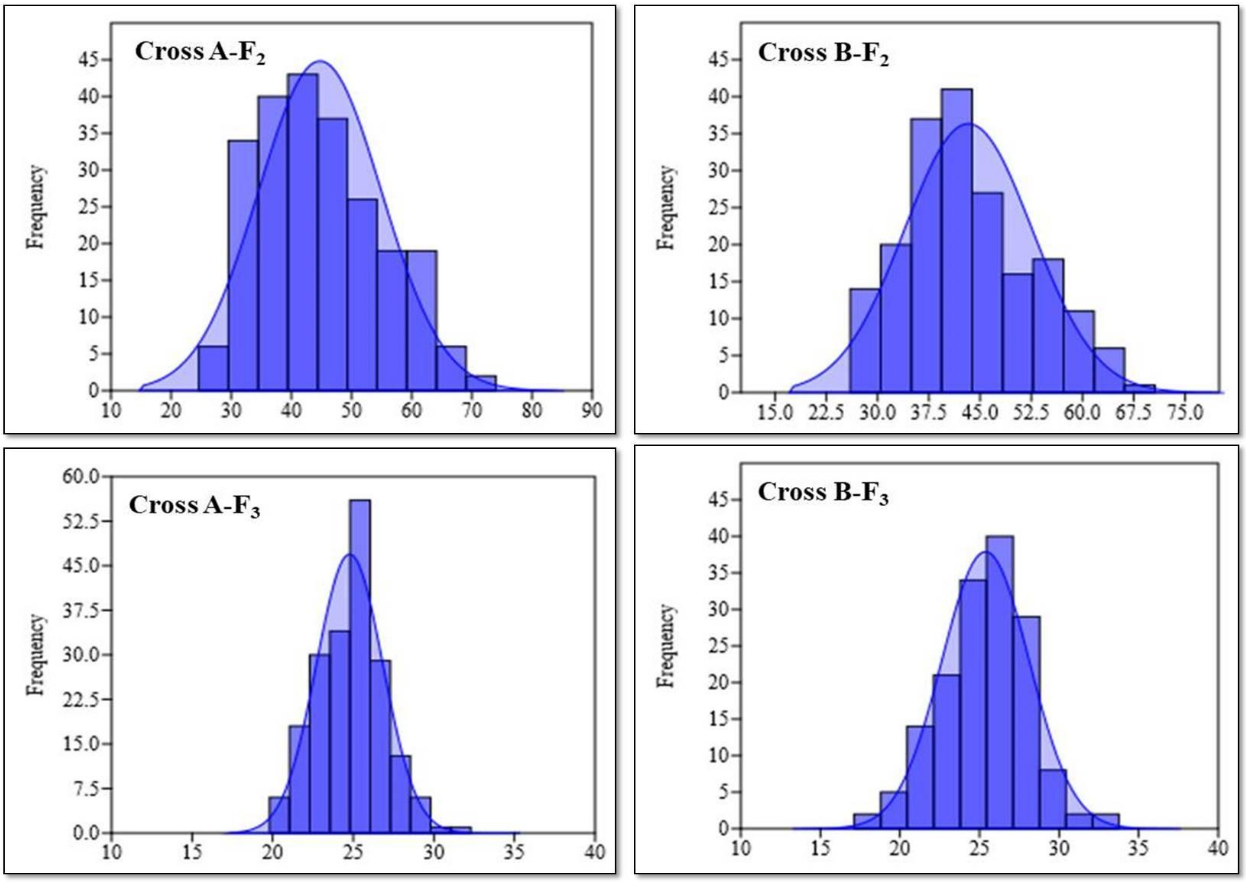
Note: Cross A: C-152 × V-16 Cross B: C-152 × V-57817

Table.4 Correlation coefficient matrix among yield related characters in F_3 generation of two crosses of cowpea

Characters	Crosses	Plant height	Number of branches	Number pods per plant	Number Seeds per pod	100 seed weight	Seed yield per plant
Plant height (cm)	A	1.000	0.193***	-0.006	0.021	0.205***	-0.021
	B	1.000	0.080	-0.066	-0.020	0.000	-0.052
Number of branches	A		1.000	0.064	-0.035	0.011	-0.027
	B		1.000	0.081	0.002	0.095	-0.001
Number pods per plant	A			1.000	0.01	0.037	0.056
	B			1.000	0.134*	0.044	0.032
Number Seeds per pod	A				1.000	0.238***	0.158
	B				1.000	-0.035	-0.027
100 seed weight	A					1.000	0.115
	B					1.000	0.023
Seed yield per plant	A						1.000
	B						1.000

Note: Cross A: C-152 × V-16 Cross B: C-152 × V-57817

Fig.1 Normality distribution of seed yield in F_2 and F_3 generations of two cowpea crosses



It indicates that over the generation variability in population has decreased due to increase in homozygosity. InF_2 generation, cross A had higher variance (104.00) compared to cross B. It indicates that there is a better chance of identifying high yielding segregants from cross A. These results are in agreement with earlier references (Ajay *et al.*, 2016 and Nandini, *et al.*, 2017).

Character association

Correlation of characters serves as a measure and forms the basis of selection as it gives direction and magnitude of relationship between the characters studied. Selection for yield will be effective, only when it is considered along with yield attributes rather than relying on yield alone (Dinesh *et al.*, 2017). In cross A, number of branches and 100 seed weight showed strong relationship with plant height while number seeds per pod showed strong relationship with 100 seed weight suggesting that individual plant selections can be practiced in F_3 and advanced segregating generations with these characters which could precisely lead to improvement in plant height and 100 seed weight in the later generations (Table 3 and 4). In cross B, number of pods per plant showed strong relationship with number of seeds per pod (Table 4) suggesting that individual plant selections can be practiced in F_3 and advanced segregating generations with these characters which could precisely lead to improvement in number of pods per plant and number of seeds per pod in the later generations.

Some characters changed in magnitude of association from generation to generation. For instance association of plant height with number of branches had significant positive association in F_2 population and non-significant associations in F_3generation of cross B. Similarly, number of branches had significant positive association with 100 grain weight and seed yield per plant in F_2 population of cross A while they showed non-significant associations in F_3 generation. Similar results were observed by Ajay *et al.*, (2016) in pigeonpea segregating generations. 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 Raveendran, 2008).

It is concluded that yield contributing traits such as number of branches, number of seeds per pod and 100 grain weight 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.

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How to cite this article:

Dinesh, H.B., K.P. Viswanatha, H.C. Lohithaswa, R. Pavan and Poonam Singh. 2018. Genetic Association Estimates Using Third and Fourth Degree Statistics in Early Segregating Generations of Cowpea. *Int.J.Curr.Microbiol.App.Sci.* 7(01): 867-873.
doi: https://doi.org/10.20546/ijcmas.2018.701.105