

Skewness and Kurtosis Study in F_3 Population of Four Groundnut Crosses

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Received 1 December 2016; Accepted 3 January 2017; Published online 16 January 2017

Abstract Third order statistics i.e., skewness and kurtosis were investigated in F_3 generation of four crosses (C1, C2, C3 and C4) in groundnut involving five parents viz., ICGV 05163, ICGV 06045, ICGV 93261, TCGA 913 and TCGS 1043 for the five characters viz., SCMAR (SPAD Chlorophyll meter reading), SLA (Specific leaf area), total biomass (g), shelling out-turn (%) and harvest index (%). The distribution was near normal for SCMAR in the two crosses, C3 and C4 and for rest of the crosses there was role of non-additive gene interaction, dominance and epistasis.

Except in C2 skewness was positive for SLA which is almost opposite to that of SCMR. F_3 distributions for total biomass indicate that this trait is quantitative and governed by both additive and non-additive variance. Positively skewed distribution of this trait could be due to favorable allelic interaction i.e., dominance and epistasis of both the parents involved. For HI, the distribution was near normal indicating greater influence of additive variance except in C4. For shelling out-turn, distributions were highly negatively skewed indicating non-allelic interactions in all the four crosses.

Keywords Skewness, Kurtosis, SCMR, SLA, HI.

Introduction

Sometimes, even if two measures like mean (μ) and standard (σ) deviation are same for the two distributions still the shape of two curves may differ. One curve may be symmetric and other may be asymmetric. So we can define symmetric and asymmetric curve for uni-modal (having one defined peak) frequency distribution along with the shape of curve with the help of descriptive statistics or third order statistics using the measures of skewness and kurtosis [1]. Skewness tells the amount and direction of skew (departure from horizontal symmetry). If the bulk of the data is at the left and the right tail is longer, we say that the distribution is skewed right or positively skewed; if the peak is toward the right and the left tail is longer, we say that the distribution is skewed left or

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Table 1. Representing skewness and kurtosis. Where, n–Population size, g_1 –Co-efficient of skewness, b_1 –Co-efficient of kurtosis, g_2 –Measure of kurtosis.

Character	cross	(n)	(g_1)	(b_1)	(g_2)
SCMR	C1	240	-0.470**	3.140	0.140
	C2	242	-0.529**	3.311	0.311
	C3	241	-0.081	2.947	-0.052
	C4	214	0.065	2.636	-0.363
SLA	C1	240	1.174**	4.144**	1.144
	C2	242	-0.207	1.858**	-1.141
	C3	241	1.018**	4.377**	1.377
	C4	214	0.773**	4.420**	1.420
Total biomass	C1	240	0.734**	3.154	0.154
	C2	242	1.434**	6.172**	3.172
	C3	241	1.283**	5.011**	2.011
	C4	214	0.776**	3.498	0.494
Shelling out turn	C1	240	-0.967**	5.470**	2.470
	C2	242	-0.833**	3.738*	0.738
	C3	241	-0.582**	3.634*	0.634
	C4	214	-2.130**	12.330**	0.334
Harvest index	C1	240	-0.051	2.484**	-0.515
	C2	242	0.141	2.174**	-0.825
	C3	241	0.027	2.484*	-0.515
	C4	214	-0.601**	2.972	-0.027

negatively skewed. Kurtosis tells how tall and sharp the central peak is, relative to a standard bell curve [2]. It is applied for testing of normality. Many statistical inferences require distribution be normal or nearly normal [3]. The author wish to thank Department of Genetics and Plant Breeding, Regional Agricultural Research Station (RARS), Tirupati and ANGRAU, Hyderabad, for the providing the research material, land, labor and other support for research.

Materials and Methods

The present investigation was carried out during *kharif* 2013 at Regional Agricultural Research Station, Tirupati. The experimental material consisted of four F_3 populations derived from four crosses; C1, C2, C3 and C4 and five parents involved viz., ICGV 05163, ICGV 06045, ICGV 93261, TCGS 913 and TCGS 1043. F_3 population in each cross was derived from raising seeds obtained from single pods picked up from each plant in F_2 population. Four F_3 populations and five parents were sown in unreplicated plot maintaining 15 rows of 5 m length for F_3 populations and 4 rows of 15 m length for parents. The parents and the

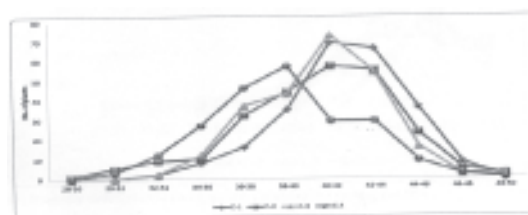


Fig. 1. F_3 frequency distribution of four crosses in groundnut for SCMR.

F_3 populations were sown following a spacing of 30 cm between the rows and 10 cm between the plants within a row. The crop was fertilized at 20 kg N, 40 kg P_2O_5 and 50 kg K_2O and 500 kg gypsum ha^{-1} in the form of urea, single super phosphate and murate of potash respectively. Five characters were taken into consideration viz., SCMR (SPAD Chlorophyll meter reading), SLA (Specific leaf area), total biomass (g), shelling out-turn (%) and harvest index (%). SPAD chlorophyll meter reading (SCMR) was recorded using SPAD meter (SPAD-502, Minotla Corporation, Ramsey, NJ) on 3rd leaf from the top of main axis of each individual plant after 60 DAS. Leaf area was recorded at 60 DAS using leaf area meter (Li-COR Model-3100). Specific leaf area is the ratio of leaf area to the leaf dry weight of third leaf of each individual plant. Whereas for remaining characters data were recorded at the time of harvest. Skewness and kurtosis were calculated for above said characters. Individual plants of F_3 population were grouped into different classes by taking a suitable class interval. The skewness for a normal distribution is zero and any symmetric data should have skewness near zero. Negative values for the skewness indicate data that are skewed left and positive values for the skewness indicate data that are skewed right. By skewed left, we mean that the left tail is long relative to the right tail. Similarly, skewed right means that the right tail is long relative to the left tail [1]. The coefficient of skewness is denoted by g_1 . The shape of the vertex of curve is known as kurtosis (can be leptokurtic, mesokurtic and platykurtic). Simple estimates of the coefficient of skewness (g_1) and kurtosis (b_1) and the amount of kurtosis (g_2) were computed for each F_3 population as per [4]:

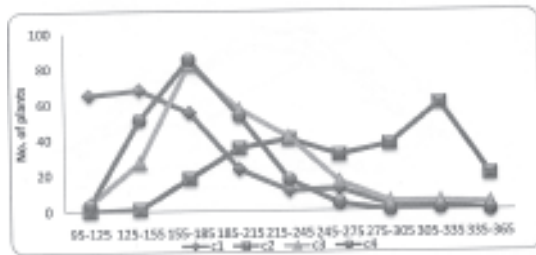


Fig. 2. F_3 frequency distribution of four crosses in groundnut for SLA.

$$g_1 (\sqrt{b_1}) = m_3 / (m_2 \sqrt{m_2})$$

$$b_2 = m_4 / m_2^2$$

$$g_2 = b_2 - 3$$

Where, $m_3 = h_3 - 3h_1 h_2 + 2h_2^3$, $m_2 = h_2 - h_1^2$, $m_4 = h_4 - 4h_1 h_3 + 6h_1^2 h_2 - 3h_1^4$.

U = deviation from the arbitrary mean/width of the class interval

$$h_1 = \sum f U / n$$

$$h_2 = \sum f U^2 / n$$

$$h_3 = \sum f U^3 / n$$

$$h_4 = \sum f U^4 / n$$

Results and Discussion

Frequency distribution for each of the five traits in different crosses was shown in the form of graph to draw conclusion about the mode of inheritance of characters. Frequency distribution is depicted in Figures (1—5). Skewness and kurtosis, values are indicated in table (Table 1). For SCMR, the distribution was unimodal in all the four crosses but F_3 distribution was asymmetric and negatively skewed in crosses C1 and C2 while skewness was negligible and almost near normal in crosses C3 and C4 indicating the SCMR is a quantitative trait. Parents in the crosses C1 and C2 are diverse. The female parent, TCGS 1043 is a line with moderate SCMR while ICGV 05163 and ICGV 06045 had high SCMR values. This could be due to some unfavorable non-additive interactions i.e., epistasis and dominance or due to coming together of unfavorable or negative alleles in more number of

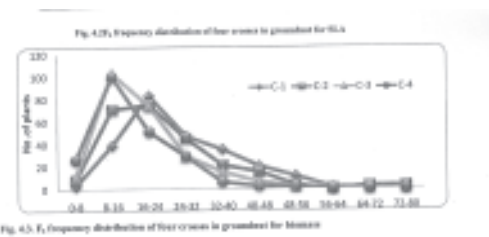


Fig. 3. F_3 frequency distribution of four crosses in groundnut for biomass.

segregants. Earlier, Vasanthi et al. [5] reported negative skewness in F_2 population of Tirupati 4 $\times$ TCGS 647 and positive skewness in two crosses, K 134 $\times$ TCGS 647 and VR 12 $\times$ TCGS 647 and near normal distribution in TCGS 29 $\times$ TCGA 647. For SLA, the distribution was unimodal in three crosses, C3, C4 and C2 and skewness was positive in these crosses while in C1, skewness was negative and frequency of individual with low SLA values was higher and distribution was not normal. For, SCMR the frequency of individuals with higher SCMR was low in this cross. SCMR and SLA are highly correlated traits which confer water use efficiency. In this cross, skewness was negative from which it can be inferred that this could be due to same unfavorable non-additive interactions in this particular cross. Positive skewness in the other two crosses might be due to contribution of alleles that contribute for increase in SLA i.e., decrease in leaf thickness. Earlier, Nigam et al. [6] reported that relative contribution of additive and dominance gene effect for specific leaf area, a correlated trait to SCMR is different in different crosses. F_3 distribution was unimodal and continuous for total biomass in all the crosses under study indicating that it is a quantitatively inherited trait. Skewness and kurtosis were significant and positive in all the crosses which could be due to contribution of positive alleles (from both the parents) or favorable interaction of alleles (non-additive relationships such as dominance and/or epistasis). This kind of relationships could have induced asymmetry and kurtosis in F_3 population under study for total biomass. Skewness and kurtosis results were significant and positive in all

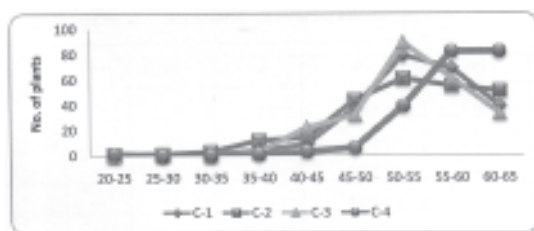


Fig. 4. F_3 frequency distribution of four crosses in groundnut for shelling out-turn.

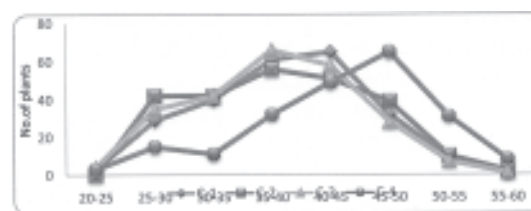


Fig. 5. F_3 frequency distribution of four crosses in groundnut for harvest index. C1: TCGS 1043 $\times$ ICGV 05163; C2: TCGS 1043 $\times$ ICGV 06045; C3: TCGS 1043 $\times$ ICGV 93261; C4: TCGS 1043 $\times$ TCGS 913; On x-axis number of plants are represented.

the crosses. Hence, the gene interactions could be similar as for total biomass. As the distribution is unimodal and continuous, the trait appears to be quantitative trait governed by additive and non-additive gene loci. F_3 distribution in the four crosses was highly variable for shelling out-turn. Results of skewness and kurtosis further confirmed the variable distribution for shelling out-turn. Though female parent is common and possesses favorable allelic combination for high shelling out-turn, the contribution of negative alleles from male parents involved might be responsible for high negative skewness in all the crosses. Further the non-additive interactions, dominance and epistasis might also be responsible for this kind of variability in distribution in different F_3 populations of the present study. In the three crosses i.e., C1, C2 and C3, the distribution was normal while in fourth cross, C4 it was significantly negatively skewed for harvest index. Kurtosis was significant in all the crosses indicating F_3 population distribution was variable in different crosses. The near-normal distribution in three crosses clearly indicates that it is quantitative trait. Negative skewness could be due to contribution of negative alleles from one or both the parents involved. From the F_3 frequency distribution, skewness and kurtosis, it could be inferred that total biomass, shoot weight per plant and harvest index are governed by polygenes and inheritance is clearly quantitative. Though non-additive gene loci contribution is there, it appears to be not predominant in the four crosses studied. Traits, SCMR, SLA and shelling out-turn appear to be influenced by both additive and non-additive gene interactions. From variability studies, total biomass, shoot weight per

plant and harvest index were found to be more under the influence of additive gene action. Non-additive gene action was found to predominantly influence SCMR while SLA was found to be governed by both additive and non-additive gene actions. Earlier, Vasanthi et al. [7] came to conclusion from their study involving five F_2 populations that SCMR could be a quasi-quantitative trait. Ajay et al. [8] studied F_3 distribution of two crosses with respect to reaction to wilt disease in pigeonpea and opined that as the distribution is continuous, it could be governed by more than two genes. He found the distribution to be positively skewed (towards susceptibility) indicating dominance of susceptibility over resistance. From the F_3 frequency distribution, skewness and kurtosis, it could be inferred that total biomass, shoot weight per plant and harvest index are governed by polygenes and inheritance is clearly quantitative. Though non-additive gene loci contribution is there, it appears to be not predominant in the four crosses studied. Traits, SCMR, SLA and shelling out-turn appear to be influenced by both additive and non-additive gene interactions.

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