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Research Note

Gene action for oil yield contributing characters in backcross population of sunflower (*Helianthus annuus* L.)

Chandirakala, R., Ameena Premnath and N. Manivannan
Department of Oilseeds, Tamil Nadu Agricultural University, Coimbatore - 641003.
***E-mail** : chandirakala2009@gmail.com

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Abstract

An investigation was carried out to study the measure of symmetry (skewness) in BC_2F_1 population of a cross involving TNHSF 239-61-2-4-1, an elite restorer line with low oleic content and HO 5-13, a high oleic inbred line. Analysis for third order statistics was done for the traits, *viz.*, plant height, head diameter, volume weight, seed yield, oil content, oil yield and oleic acid content. Skewness and kurtosis estimates were calculated to study the gene action. The traits *viz.*, seed yield and oil yield recorded positive skewness. This indicates the presence of complementary epistatic gene action for these traits and if selection is made intensively in the segregating generations, the gain will be faster and mild selection results in slower gain.

Key words
Sunflower, backcross, skewness, kurtosis, gene action.

Sunflower (*Helianthus annus* L.) is an important oilseed crop. It ranks third after soybean and palm oil in worldwide vegetable oil production (Iqbal *et al*., 2009). The understanding and knowledge of genetic variation and genetic similarities present within individuals or populations are useful for the efficient use of genetic resources in breeding program (Safavi *et al*., 2010). Sunflower oil is considered as premium oil due to its light color, mild flavor, low level of saturated fatty acids and ability to withstand high cooking temperatures (Robert *et al.*, 1993). Quality of sunflower oil is judged on the basis of the oleic and linoleic acid content. It has been determined that their contents are genetically controlled and are heavily influenced by environmental factors. Breeding programs depend on the knowledge of key traits, genetic systems controlling their inheritance, and genetic and environmental factors that influence their expression. To plan an efficient development program, it is necessary to have an understanding on the gene action of the characters and effective breeding systems.

The study material comprised of BC_2F_1 population of TNHSF 239 -61-2-4 x HO 5-13 which was developed using TNHSF 239 -61-2-4 (an elite restorer line with low oleic content) as recurrent parent crossed with HO 5-13 (a high oleic inbred line) as donor parent. The population was evaluated at Department of Oilseeds, Tamil Nadu Agricultural University, Coimbatore along with parents during *Rabi* 2014-15. Recommended crop production practices for Tamil Nadu were followed to ensure good crop health. Observations were recorded on single plants for 7 traits *viz.*, plant height (cm), head diameter (cm), volume weight (g/100 ml), seed yield (g/plant), oil content (%), oil yield (g/plant) and oleic acid content (%). Quality of sunflower oil is judged on the basis of the ratio of oleic and linoleic acid. The most frequent fatty acid composition in sunflower oil is 55 - 65% of linoleic acid, 20 -30% of oleic acid and the remainder is including other fatty acids, primarily palmitic and stearic. The oil content and fatty acid profile of the genotypes were assessed using Near-Infrared spectroscopy. The objective of the present study was to identify the gene action of yield attributing characters in sunflower by studying the segregating generation. Based on the observations, the skewness and kurtosis estimates were calculated by using the formula suggested by Fisher *et al.* (1942) to study the gene action.

The main objective of sunflower breeding is to produce high oil yielding lines which will be involved in breeding programmes. The prerequisite to achieve this goal is the presence of sufficient amount of variability where desired lines can be selected for further manipulation to achieve the yield target. The present study was conducted to assess the presence of variability for oil yield contributing characters. The geneaction for the quantitative traits in the segregating generations was worked out based on the frequency distribution of traits through third and fourth order statistics *viz.* skewness and kurtosis.

Skewness describes the degree of departure of a distribution from symmetry and kurtosis characterizes the peakedness of a distribution. In a frequency distribution of a segregating generation, skewness could result when certain combinations of genes are lethal, presence of incomplete linkage of certain genes, presence of epistasis and one gene has a much larger effect than others. Sign of skewness helps us to draw the conclusion about the gene action for a particular trait. The positive skewness indicates the presence of complementary epistatic gene action for that trait. The gain is slower with the mild selection and faster with intensive selection for that particular trait. The negative skewness indicates the presence of duplicate epistatic gene action and the gain is faster with mild selection and less rapid with intense selection (Snape and Riggs, 1975). By studying the skewness of frequency distribution of F_2 generation, one can determine that the frequency distribution is skewed to the left indicating that the increasing alleles are dominant where as rightward skewness with the decreasing alleles being dominant (Fisher *et al*., 1942).

Kurtosis will occur if either few genes are contributing to the phenotypic distribution or there are inequalities in the additive genetic effects at different loci. Traits showing leptokurtic distribution are usually under the control of few segregating genes and traits showing a platykurtic distribution usually represent characters that are controlled by many genes. The positive values of kurtosis indicates leptokurtic curve and negative kurtosis indicates platykurtic curve.

The mean, range, variance, skewness and kurtosis values for the oil yield attributing characters *viz.*, plant height (cm), head diameter (cm), volume weight (g/100 ml), seed yield (g/plant), oil content (%), oil yield (g/plant) and oleic acid content (%) inBC_2F_1 generation of TNHSF 239 -61-2-4 x HO 5-13 are given in the Table 1.

Among the different traits studied, higher amount of variance was accounted by plant height and oleic acid content and moderate amount of variance for seed yield. Due to the wide range of variation between the low oleic (<20%) and high oleic lines (>80%) found in the segregating generation, higher variance (300.58) was observed for oleic acid content in BC_2F_1 generation.

The traits such as seed yield and oil yield showed significantly positive skewness in backcross population (Table 1). This indicates that larger number of individuals possessed less *per se* performance for these traits. Selection need not be exercised and the materials may be forwarded to further generations. This result was supported by the findings of Premnath *et al.* (2014). This indicates the presence of complementary epistatic gene action for these traits and if selection will be made intensively in the segregating generations for these traits the gain will be faster and mild selection will result in slower gain. This was supported by Jayaramachandran *et al.* (2010). Significantly negative skewness was observed for the traits *viz.,* plant height and volume weight in backcross generation. Hence, mild selection could be effective to improve the *per se* performance of these traits.

The traits *viz.,* volume weight, seed yield and oil yield recorded leptokurtic nature. Due to narrow variability, selection may not improve the *per se* performance of these traits. The kurtosis estimate for the traits *viz.*, volume weight, seed yield and oil yield recorded significantly positive values. The kurtosis estimate for these traits indicated that these characters are controlled by few segregating genes only. This result was in accordance with the result of Jayaramachandran *et al.* (2010).

From this study, it could be concluded that the large genetic variation among the progenies in the backcross populations could be useful for selecting genotypes in terms of better oil yield for investigation of oil quality in further generations.

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Table1. First, second and third order statistics for oil yield traits in backcross generation of sunflower

Descriptive statistics	Plant height (cm)	Head diameter(cm)	Volume weight (g/ 100 ml)	Oil content (%)	Oleic acid content (%)	Seed yield (g/plant)	Oil yield (g/plant)
Mean	167.39	18.30	7.39	31.11	43.72	25.16	7.88
Standard Error	2.05	0.36	0.11	0.26	2.04	1.30	0.42
Range	86.80	14.10	6.14	10.70	76.92	59.56	18.03
Minimum	110.50	11.30	3.21	25.54	12.23	3.38	1.04
Maximum	197.30	25.40	9.35	36.24	89.15	62.94	19.06
Standard deviation	17.38	3.02	0.96	2.24	17.34	10.99	3.59
Variance	302.07	9.11	0.91	5.00	300.58	120.77	12.87
Kurtosis	0.81	-0.19	6.44**	-0.14	-0.57	1.64**	1.19*
Skewness	-1.12**	-0.07	-1.71**	-0.44	0.21	0.75*	0.74*

* - Significance at 5% level
** - Significance at 1% level