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**Research Article**

# Gene Action for yield attributing characters in segregating generation ($M_2$) of Sorghum (*Sorghum bicolor* L.)

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**Abstract :**
Gamma rays was used as a physical mutagen to create variability and to study the gene action through mutation in Grain sorghum variety CO(S) 28.The LD $_{50}$ for germination was observed as 35 kR and the treatment doses *viz*., 25 kR, 35 kR and 45 kR were fixed for creating variability. The $M_1$ generation of all the three treatment doses was raised and selfed plants were forwarded as $M_2$ generation. Approximately 1500 $M_2$ plants were raised in each treatment for recording observations. The frequency distribution for the yield and yield attributing traits *viz*., panicle length, number of primary branches per panicle, number of grains per panicle, 100 grain weight and grain yield per plant were obtained. The Skewness and Kurtosis estimate were calculated to study the gene action. The traits *viz*., number of grains per panicle and grain yield per plant recorded positive Skewness value in all the three irradiated doses. This indicates the presence of complementary epistatic gene action for these traits and if selection will be made intensively in the segregating generations the gain will be faster and mild selection resulted in slower gain.

**Key words:**
Gene action – Mutated Population - sorghum

## Introduction

Sorghum is cultivated predominantly in USA, China, India and Africa for both human and animal consumption. The industrial demand for the grain sorghum as a raw material is increasing and the future demand of the same is 4.00 M.T. in near future. In recent years, the length of the rainy season and the corresponding crop growing season has reduced. Due to water deficit there will be a shift in cropping pattern towards drought tolerant food crops which is inevitable. Grain sorghum is one of the drought tolerant millet among grain crops making it an ideal choice for grain production in low rainfall areas. The major problem in grain sorghum cultivation is low productivity when compared to other cereals.

Improving the productivity of grain sorghum by means of producing hybrids depends upon the availability of CMS lines. However, owing to the genetic vulnerability, it is not safe to depend only on a single source of male sterile lines for the production of hybrids in sorghum. To overcome these difficulties induced mutation through Gamma rays is one of the viable options in sorghum to identify superior genotypes through studying the gene action. (Brunner 1992, and Bhaskar Rao and Reddi, 1975). The objective of the present study is to identifying the gene action of yield attributing characters in grain sorghum by studying the segregating $M_2$ generation.

## Materials and methods

Pedigreed Seeds of CO(S) 28 grain sorhum were used for the induced mutation. CO(S) 28 is a non lodging short duration sorghum variety. Gamma rays were employed as physical mutagen. Well filled, hand picked and uniform sized seeds with the moisture content of 10 per cent were randomly chosen for irradiation. The seeds were packed in butter paper covers and placed in the gamma cell and treated with gamma irradiation at gamma chamber installed at CPBG, TNAU, Coimbatore. Cobalt 60 was the source of gamma rays with the strength of 2700 curies. The seeds of the CO(S) 28 variety were treated with 20, 30, 40, 50, 60 and 70 kR of gamma radiation and effect of radiation on germination was observed in glass house. Based on the observations the $LD_{50}$ value for germination to gamma rays was arrived at 35 kR for CO(S) 28 grain sorghum. Hence, the treatment doses *viz*., 25 kR, 35 kR and 45 kR were chosen for conducting the field experiment. Bordoli and Talukdar (1999) observed promising micro mutants for different characters in rice varieties exposed to three lower doses of gamma rays.

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The $M_1$ generation was raised during Rabi 2002. The seeds subjected to gamma radiation were sown in the field along with the control in RBD with 3 replications. In each treatment, a total of 300 seeds were sown in four rows per replication with the row length of 4 m by adopting a uniform spacing of 45 X 15 cm. In each treatment thirty plants were randomly selected to raise the $M_2$ generation. The $M_2$ generation was raised during summer 2003 along with the control. The seeds of single $M_1$ plants were sown in two rows with the row length of 4 m without replication since $M_2$ population is a segregating one. The spacing was 45 X 15 cm. Observations on yield attributing characters *viz.* panicle length, number of primary branches per panicle, number of grains per panicle , 100 grain weight and grain yield per plant were recorded from 1500 $M_2$ plants in each treatment. 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.

## Results and discussions

The gene action for the quantitative traits in the mutated segregating generations was found 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 indicated 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 indicated 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).

Fisher *et al* (1942) showed that, for one locus 2 alleles system, the Skewness of the frequency distribution of $F_2 = M_2$ Plants is equal to $-3/4\ hd^2$, where "d" is additive genetic effect and "h" is the dominance effect. Thus by studying he Skewness of frequency distribution of $F_2$ (or) $M_2$ generation plants , one can determine whether the average "h' is positive it will make the frequency distribution skewed to the left indicating that the increasing alleles are dominant where as negative average 'h" produces rightward Skewness with the decreasing alleles being dominant.

Kurtosis will occur if either a 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 indicated leptokurtic curve and negative kurtosis indicated platykurtic curve.

The skewness and kurtosis values for the yield attributing characters *viz,* panicle length, number of primary branches per panicle, number of grains per panicle, 100 grain weight and grain yield per plant in $M_2$ generation were given in the Table 1.The traits number of grains per panicle, 100 grain weight and grain yield per plant recorded positive skewness values in all the three irradiated doses. This indicates the presence of complementary epistatic gene action for these traits and if selection will be made intensively in the segregating generations for number of grains per panicle, 100 grain weight and grain yield per plant, the gain will be faster and mild selection resulted in slower gain. Patil *et al* (1995) reported the significant positive correlation between grain yield per plant and number of grains per panicle in sorghum. The remaining traits *viz*., panicle length, number of primary branches per panicle showed inconsistent values for skewness over mutagenic treatments indicated that the genetic equilibrium of these characters were disturbed by the irradiation. The inconsistent trend in frequency distribution suggests that besides selection pressure, other genetic factors might have influenced the induction and expression of mutation. (Gaul and Aesteveit, 1966)

The kurtosis estimate for the traits panicle length and 100 grain weight recorded positive values over the three treatments indicated that these characters are controlled by few segregating genes only. It confirms the hypothesis that the genes governing panicle length and 100 grain weight are disturbed by irradiation.

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**Table 1. Variance, coefficient of variability, heritability, genetic advance, skewness and kurtosis for yield attributing characters in $M_2$ generations of CO(S) 28 grain sorghum.**

| Sl No | Character | Gamma Dosage | Variance | | Coefficient of variability | | Heritability | Genetic advance | Skewness | Kurtosis |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | G | P | G | P | | | | |
| 1 | Panicle Length | 25 kR | 14.78 | 23.08 | 15.29 | 19.10 | 64.03 | 6.33 | 0.04 | 0.31 |
| | | 35 kR | 3.89 | 12.19 | 7.96 | 14.09 | 31.91 | 2.22 | -.012 | 1.78 |
| | | 45 kR | 14.4 | 22.70 | 14.91 | 18.72 | 63.43 | 6.18 | -1.31 | 3.20 |
| 2 | Number of Primary Branches per panicle | 25 kR | 147.87 | 214.57 | 24.21 | 29.17 | 68.90 | 20.51 | -.012 | -0.10 |
| | | 35 kR | 80.07 | 146.77 | 16.87 | 22.84 | 54.50 | 13.47 | -0.29 | 0.66 |
| | | 45 kR | 36.69 | 103.39 | 10.37 | 17.42 | 35.48 | 7.33 | 0.13 | 2.40 |
| 3 | Number of grains per panicle | 25 kR | 159449.2 | 6456617.5 | 38.44 | 33.35 | 49.69 | 811.05 | 1.06 | 1.77 |
| | | 35 kR | 114011.66 | 600179.9 | 28.05 | 64.36 | 18.99 | 287.26 | 1.01 | 1.14 |
| | | 45 kR | 21746.6 | 507914.9 | 13.20 | 63.80 | 4.28 | 62.83 | 0.42 | -0.26 |
| 4 | 100 grain weight | 25 kR | 0.0295 | 0.0595 | 6.73 | 9.56 | 49.57 | 0.24 | 0.51 | 1.77 |
| | | 35 kR | 0.0575 | 0.0875 | 9.51 | 11.73 | 65.71 | 0.39 | 0.12 | 0.87 |
| | | 45 kR | 0.0511 | 0,0811 | 9.22 | 11.62 | 63.00 | 0.36 | 0.25 | 0.99 |
| 5 | Grain yield per plant | 25 kR | 55.37 | 322.42 | 27.71 | 66.87 | 17.17 | 6.28 | 0.99 | 0.86 |
| | | 35 kR | 172.27 | 439.32 | 44.59 | 71.21 | 39.21 | 16.83 | 1.11 | 1.69 |
| | | 45 kR | 25.30 | 292.35 | 19.13 | 65.03 | 8.65 | 2.81 | 0.36 | -.046 |