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# Assessment of genetic variability, heritability in sesame (*Sesamum indicum* L.)

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**Abstract**
The present investigation was conducted during Kharif 2018 at Agricultural Research Station, Yellamanchili, Andhra Pradesh, India. Analysis of variance showed highly significant differences among 114 genotypes for all the characters studied showing the presence of genetic variability among the materials studied. The genetic variability studies revealed that the present material under investigation has potential variability and can be exploited for effective breeding programme. High heritability was recorded for all the parameters under study. The seed yield per plant showed high heritability coupled with high genetic advance indicated the role of additive gene action.

**Keywords:** Sesame, variability, heritability, gene action

## Introduction
Sesame (*Sesame indicum* L.) belongs to the family pedaliaceae (2n=26). It is grown in subtropical and tropical countries. It is grown in subtropical and tropical climatic situations. Sesame is grown in 10.56 m ha world wide with a production of 5.46 million tonnes (FAOSTAT 2015) [5]. The major sesame growing countries are Tanzania, China, Myanmar & India. Sesame oil used as edible oil, for industrial use, cosmetics and seeds for confectionary purpose. Sesame seed consists of 45-55% of oil. It is popularly known as simsim, til, gingelly. It is a part and parcel of our food system from times immemorial. The success of the crop improvement programme is mainly dependent on the presence of wide genetic variability present in the genotypes employed in the breeding programme for seed yield or any yield attributing characters. At this juncture, studies on heritability, phenotypic coefficient of genetic variation, genetic advance gives us a clear vision of the characters under study and help us to know their gene action and breeding methods to be adopted. In this present study, we know the heritability, variability, genetic advance as per cent mean, gene action is explained.

## Materials and Methods
The present investigation was carried out during Kharif 2018 at Agricultural Research Station, Yellamanchili, Viskhapatnam district of Andhra Pradesh. The Agricultural Research Station is located at 17.57013 $^{0}$ N and 82.84775 $^{0}$ E. The type soil is light texture sandy loam. The experiment was conducted with 114 genotypes. The accessions were collected from all over the country. Some of the germplasm lines were collected from National Bureau of Plant Genetic Resources, New Delhi. The experiment was laid in randomized block design with two replications. Each plot consisted of three rows each of 4.5 m row length with 30 X 15 cm spacing. Observations were recorded on five randomly selected plants for seven parameters *viz.*, days to 50% flowering, plant height (cm), number of branches per plant, number of capsules per plant, number of seeds per capsule, days to maturity and seed yield per plant (g). The mean data of all the parameters were used for the statistical analysis. All the statistical analysis was carried out using SAS package.

### Statistical Designs
### Analysis of Variance
The data for different characters was statistically analyzed on the basis of the model given by Cochran and Cox (1950) for randomized block design.

$Y_{ij} = \mu + b_i + t_j + e_{ij}$

Where, $Y_{ij}$ = Performance of the $j^{th}$ genotype in the $i^{th}$ block; $\mu$ = general mean
$b_i$ = effect of $i^{th}$ block; $t_j$ = effect of $j^{th}$ genotype
$e_{ij}$ = random error associated with $i^{th}$ block and $j^{th}$ genotype

**Coefficient of variation**
Phenotypic and Genotypic coefficients of variation (PCV and GCV) were computed according to Burton (1952).

$$PCV = \frac{\text{Phenotypic standard deviation } (\sigma_p)}{\text{General mean } (\overline{X})} \times 100$$

$$GCV = \frac{\text{Genotypic standard deviation } (\sigma_g)}{\text{General mean } (\overline{X})} \times 100$$

GCV and PCV were categorized into:- Low = Less than 10% ; Moderate = 10-20% ; High =More than 20% (as suggested by Sivasubramanian and Menon,1973).

**Heritability (**$h^2$ b)
Heritability in broad sense was estimated as per Lush (1940) and Allard (1960) [1].

$$h^2 (b) = \frac{\text{Genotypic variance } (\sigma^2_g)}{\text{Phenotypic variance } (\sigma^2_p)} \times 100$$

$h^2$ (b) estimates were categorized into:- Low =0 – 30%; Moderate=31-60%; High=61% and above (as suggested by Johnson *et al.* (1955) [8].

**Genetic advance as per cent of mean (GAM)**

$$GAM = \frac{\text{Genetic advance}}{\text{Grand mean } (\overline{X})} \times 100$$

The range of genetic advance as per cent of mean was classified:- Low=Less than 10%; Moderate=10-20%; High=More than 20% (as suggested by Johnson *et al.* (1955) [8].

**Results and Discussion**
The (ANOVA) analysis of variance showed significant difference among the 114 genotype (Menzir 2012) [10] (Table 1) for all the parameters under study. In the present study (Table 2), all the parameters except days to 50% flowering, plant height and days to maturity showed high range of variation, which reveals that these parameters can be exploited in the breeding programme (Menzir 2012) [10]. The parameters days to 50% flowering, plant height and days to maturity has shown lower variability. (Solanki and Gupta 2001). Seed yield per plant showed a mean of 2.62 g ranging from 0.83 g to 6.29 g.

**Table 1:** Analysis of variance for seed yield and yield components in sesame (*Sesamum indicum* L.)

| Source | d.f. | Days to 50% flowering | Plant height (cm) | No. of branches per plant | No. of capsules per plant | No. of seeds per capsule | Days to maturity | Seed yield per plant (g) |
|---|---|---|---|---|---|---|---|---|
| | | | Mean Squares | | | | | |
| Replications | 1 | 2.74 | 0.302 | 0.00 | 0.072 | 0.09 | 0.15 | 0.007 |
| Treatments | 113 | 11.745** | 224.769** | 1.894** | 898.25** | 922.03** | 9.166** | 1.864** |
| Error | 113 | 0.962 | 36.081 | 0.046 | 17.188 | 29.768 | 0.042 | 0.275 |

** = Significance at 1% level

All the parameters under study (Table 2) showed high PCV values compared to GCV indicating the influence of environment on expression of the characters (Menzir 2012) [10]. All the characters showed high heritability indicating the significance of genetic components in their expression and low influence of environmental component (Begum and Dasgupta 2014) [2]. Genetic advance showed high values for all the parameters except for days to maturity indicating that those parameters show high selection response in the studied material (Ismaila and Usman 2012) [7]. Only days to maturity has shown low selection response due to its low value of genetic advance.
The parameters number of branches per plant, number of capsules per plant, number of seeds per capsule and seed yield per plant (g) showed high heritability coupled with high genetic advance indicating the role of additive gene action in inheritance of this trait. For these traits simple selection may be adopted in exploitation of this trait. (Gangadhara *et al*., 2012; Revathi *et al*., 2012) [6, 11] The characters days to 50% flowering and plant height recorded high heritability coupled with moderate genetic advance indicating the operation of non-additive gene action and additive gene action. Improvement of these parameters may be done by adopting mass selection, progeny selection or any modified selection method to exploit the additive gene effects. The parameter days to maturity showed high heritability coupled with low genetic advance indicating the preponderance of non-additive gene action and further improvement of this character would be possible through heterosis breeding. (Teklu *et al*., 2014) [14].

**Table 2:** Mean, genetic variability, heritability (broad sense) and genetic advance as percent of mean for seed yield and yield components in sesame (*Sesamum indicum* L.)

| S. No | Character | Mean | Range | | PCV (%) | GCV (%) | Heritability (%) | Genetic advance as % of mean |
|---|---|---|---|---|---|---|---|---|
| | | | Min | Max | | | | |
| 1 | Days to 50% flowering | 37.97 | 35 | 45 | 6.64 | 6.12 | 84.85 | 11.60 |
| 2 | Plant height (cm) | 156.43 | 125 | 179 | 7.30 | 6.21 | 72.34 | 10.87 |
| 3 | No. of branches per plant | 5.25 | 2.20 | 8.15 | 18.74 | 18.29 | 95.25 | 36.77 |
| 4 | No. of capsules per plant | 56.97 | 7.8 | 92.10 | 37.55 | 36.83 | 96.24 | 74.44 |
| 5 | Seeds per capsule | 58.27 | 7.5 | 92.90 | 37.34 | 36.25 | 93.74 | 72.29 |
| 6 | Days to maturity | 82.79 | 79 | 87 | 2.59 | 2.58 | 99.07 | 5.28 |
| 7 | Seed yield per plant (g) | 2.62 | 0.83 | 6.29 | 39.62 | 34.13 | 74.22 | 60.57 |

## Conclusions

Thus the present study indicated that the presence of high variability in the studied material and the traits, branches per plant, number of capsules per plant, number of seeds per capsule and seed yield per plant (g) showed high heritability coupled with high genetic advance indicating the role of additive gene action governing the inheritance of the these traits and can be exploited by simple selection.

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