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# Estimates of genetic components of variation in sponge gourd (*Luffa cylindrica* Roem.)

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Sponge gourd (*Luffa cylindrica* Roem.), also known as dishrag gourd, dishcloth gourd, loofah gourd, and smooth loofah (Whitaker and Davis, 1962), is a popular low cost vegetable in the tropical and subtropical regions. It is an important component of crop rotation during *pre-kharif* and *kharif* seasons in North Indian condition and is cultivated both on commercial scale and in kitchen gardens. India is considered as the centre of origin of *Luffa* species (Choudhury, 1996) and exhibits considerable amount of genetic diversity with respect to different characters. The improvement programme of sponge gourd is based mainly on exploiting natural sources of germplasm by means of selection and hybridization followed by selection.

Development of high yielding varieties mainly depends upon genetically superior parents, coupled with suitable breeding methodology. To formulate any breeding method, it is imperative to have knowledge of gene action involved in inheritance of various traits. Selection and hybridization are two basic methods for crop improvement. The success of selection mainly depends upon the extent of genetic variability. Therefore, a higher genetic base should be utilized for faster and higher magnitude of success. Utilization of divergent germplasm in hybridization creates such broad genetic base (Singh *et al*., 1998).

A detailed knowledge about the magnitude and nature of genetic variation in a specific population is of prime importance for the effective prediction of the most effective breeding programme (Debnath, 1988). The numerical analysis of diallel provides detailed account of additive and dominance components and the allied statistics. The genetics largely depends upon the relative magnitude of these two components. The genetic model on which the analysis of diallel tables is based involve certain assumptions *viz.* (i) segregation is diploid; (ii) there are only environmental differences between reciprocal crosses; (iii) absence of epistasis; (iv) the parents are homozygous; (v) there are no multiple alleles (vi) that the genes are independently distributed and that there is no genotype interaction with locations and years (Walton, 1968).

In spite of exhibiting considerable amount of genetic diversity with respect to different characters little attention has been given for improvement of this crop. Hence, an attempt was made to investigate the gene action (inheritance pattern) of yield and yield attributing traits.

The present investigation was carried out during spring summer and *kharif* season of 2010 at research farm of Division of Vegetable Science of Indian Agricultural Research Institute, New Delhi. Eight genetically diverse inbreds of sponge gourd *viz*. Pusa Sneha ($P_1$), Pusa Supriya ($P_2$), NSG 1-11 ($P_3$), PSG 9 ($P_4$), CHSG 1 ($P_5$), CHSG 2 ($P_6$), NSG 28 ($P_7$) and Pusa Chikni ($P_8$) were crossed in 8 x 8 half-diallel (excluding reciprocals) mating scheme (Hayman, 1954). The resulting 28 $F_1$ hybrids along with 8 parental lines were evaluated in a randomized block design with three replications. The seeds were sown in rows of 2.5m with 0.75 m spacing between the plants. All the recommended package of practices was followed to grow a successful crop. Out of 12 plants, 10 were marked for taking observations. Observations on individual plant basis were recorded on nine quantitative characters *viz.* days to first male flower anthesis, days to first female flower anthesis, days to first fruit harvest, fruit length (cm), fruit diameter (cm), average fruit weight (g), number of fruits per plant, vine length (m) and total fruit yield per plant (kg). Gene action was studied by the diallel method of numerical approach given by Hayman (1954). If the estimates of average degree of dominance $[(H_1/D)^{½}]$ is '0' denote no dominance, 0 to 1, partial dominance; 1, complete

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dominance and > 1, over dominance. The maximum values of $H_2/4H_1$ shall be 0.25 when u = v = 0.05. If the relative frequency of dominant and recessive genes $[(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F]$ in parents =1, means nearly equal proportion i.e. symmetrical distribution; u = v = 0.5. Any deviation from 1 shows asymmetry of distribution (u < v) as > 1 refers to excess of dominant genes and minority of recessive genes (u > v) and <1 means minority of dominant genes and excess of recessive (u < v).

The estimates of genetic components of variation and various statistical parameters for different characters were represented in Table 1. The genetic component of variation for days to first female flower anthesis, the estimates of D, $H_1$, $H_2$ and $h^2$ were highly significant. The value of $H_1$ was more than D, which signify that dominant genes were more than additive genes. The environmental influence (E) on the inheritance of this was non-significant. The mean degree of dominance $(H_1/D)^{1/2}$ was greater than one (1.74) and indicated role of over dominance for this trait. The proportion of genes with positive and negative effects $(H_2/4H_1)$ in the parents was found to be less than 0.25 (0.23), denoting asymmetry at the loci showing dominance. The proportion of dominant and recessive gene as indicated by $[(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F]$ was 10.01 while the group of genes, which controlled the characters $(h^2/H_2)$ and exhibited dominance was 5.42. Narrow sense heritability being 16.15% showed preponderance of non-additive gene action.

Results pertaining to days to first fruit harvest the estimates of D, $H_1$, $H_2$ and $h^2$ were highly significant where E and F were non-significant. The value of $H_1$ was greater than D, suggesting the presence of dominant alleles in parents. The negative value of F showed recessive alleles was more frequent. The mean degree of dominance $(H_1/D)^{1/2}$ being 2.96 indicating over-dominance. The proportion of genes with positive and negative effects $(H_2/4H_1)$ was 0.25, showing dominance. The proportion of dominant and recessive genes $[(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F]$ in the parents was 3.74, while the group of dominant genes $(h^2/H_2)$ was 6.20. Narrow sense heritability being 12.82% exhibited predominance of non-additive gene action.

Results pertaining to fruit length the estimates of D, $H_1$, $H_2$ and $h^2$ were highly significant. The value of $H_1$ was more than D, exhibiting non-additive gene action. The positive F value indicated more prevalence of dominant alleles in parents. The mean degree of dominance $(H_1/D)^{1/2}$ was 1.65 indicating over-dominance. While the proportion of genes with positive and negative effects $(H_2/4H_1)$ in parents was found to be 0.18 denoting asymmetry at loci showing dominance. The proportion of dominant and recessive genes $[(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F]$ in parents was 13.93 whereas the number of genes $(h^2/H_2)$ which controlled the character and exhibit

**Table 1.** Estimates of genetic components of variation and various statistical parameters for different characters

| Genetic parameters | Days to first female flower anthesis | Days to first fruit harvest | Fruit length (cm) | Fruit diameter (cm) | Average fruit weight (g) | Number of fruits per plant | Vine length (m) | Total fruit yield per plant (kg) |
|---|---|---|---|---|---|---|---|---|
| (D) Additive effect | 2.72** ± 0.60 | 16.43** ± 3.90 | 8.32** ± 1.78 | 0.10 ± 0.04 | 94.63 ± 41.42 | 1.82 ± 0.61 | 1.10 ± 0.30 | 0.21 ± 0.05 |
| (H) Dominance effect | | | | | | | | |
| $H_1$ | 8.24** ± 1.38 | 144.13** ± 6.67 | 22.70** ± 4.09 | 0.26* ± 0.09 | 761.49** ± 141.19 | 9.21** ± 1.41 | 2.95** ± 0.70 | 0.45** ± 0.04 |
| $H_2$ | 7.80** ± 1.20 | 145.76** ± 5.80 | 16.81** ± 3.56 | 0.27* ± 0.08 | 656.45** ± 122.83 | 8.62** ± 1.23 | 2.28** ± 0.61 | 0.43** ± 0.03 |
| $h^2$ | 42.27** ± 0.81 | 903.17** ± 3.89 | 77.93** ± 2.39 | 1.41** ± 0.05 | 2275.15** ± 82.38 | 43.69** ± 0.82 | 11.19** ± 0.41 | 2.16** ± 0.01 |
| (F) Gene distribution | -0.49 ± 1.42 | -3.78 ± 6.85 | 14.06** ± 4.20 | 0.10 ± 0.09 | 133.63 ± 145.42 | 0.23 ± 1.45 | 0.40 ± 0.72 | -0.01 ± 0.05 |
| (E) Environmental effect | 0.76 ± 0.20 | 2.87 ± 0.97 | 0.79 ± 0.50 | 0.14 ± 0.01 | 14.59 ± 20.47 | 0.63 ± 0.20 | 0.31 ± 0.10 | 0.02 ± 0.02 |
| $(H_1/D)^{1/2}$ | 1.74 | 2.96 | 1.65 | 1.61 | 2.83 | 2.24 | 1.63 | 1.46 |
| $H_2/4H_1$ | 0.23 | 0.25 | 0.18 | 0.25 | 0.21 | 0.23 | 0.19 | 0.23 |
| $(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F$ | 10.01 | 3.74 | 13.93 | 0.53 | 403.51 | 7.99 | 3.31 | 0.61 |
| $h^2/H_2$ | 5.42 | 6.20 | 4.64 | 5.22 | 3.47 | 5.07 | 4.91 | 5.02 |
| Heritability % (ns) | 16.15 | 12.82 | 21.22 | 19.86 | 14.53 | 18.95 | 23.64 | 26.35 |

*Significant at P = 0.05, **Significant at P = 0.01

dominance was 4.64. Narrow sense heritability (21.22%) showed preponderance of non-additive gene action.

The genetical parameters like $H_1$, $H_2$ and $h^2$ were significant while D was non-significant for fruit diameter. The value of $H_1$ was greater than D indicating presence of non-additive genes. The positive value of F indicated that the dominant allele were more frequent in parents. The mean degree of dominance $(H_1/D)^{½}$ being 1.61 exhibited over-dominance. The proportion of genes with positive and negative effects $(H_2/4H_1)$ was noted 0.25 indicating asymmetry at loci showing dominance. The proportion of dominant and recessive genes $[(4DH_1)^{½} + F/ (4DH_1)^{½} - F]$ in the parents was 0.53 whereas the number of dominant group of genes $(h^2/H_2)$ was 5.22. Narrow sense heritability (19.86%) showed preponderance of additive type of gene action for this trait.

For fruit weight, the estimated value of $H_1$, $H_2$ and $h^2$ were highly significant while other parameters *viz.* D, E and F were non-significant. The estimated value of $H_1$ was greater than D which revealed that non-additive genes were more than additive genes. Positive value of F indicated predominance of dominant alleles. The mean degree of dominance $(H_1/D)^{½}$ being 2.83 showed over-dominance. The proportion of genes with positive and negative effects $(H_2/4H_1)$ was 0.21, which denotes asymmetry at loci. The proportion of dominance and recessive genes $[(4DH_1)^{½} + F/ (4DH_1)^{½} - F]$ was 403.51 whereas number of group of genes exhibiting dominance and controlling character was 3.47. The narrow sense heritability (14.53%) indicated the dominant type of gene action for expression of this character.

The genetic component of variation for number of fruits per plant *viz.* $H_1$, $H_2$ and $h^2$ were highly significant whereas estimate of D, E and F were non-significant. The value of $H_1$ was more than D which showed more prevalence of dominant genes. The positive value of F suggested predominance of dominant alleles in the parents. The degree of dominance $(H_1/D)^{½}$ was 2.24 revealed role of over-dominance. The proportion of genes with positive and negative effects $(H_2/4H_1)$ was 0.23 exhibiting dominance. The proportion of dominant and recessive genes $[(4DH_1)^{½} + F/ (4DH_1)^{½} - F]$ was 7.99 whereas the number of group of genes $(h^2/H_2)$ which showed dominance was 5.07. Narrow sense heritability (18.95%) indicated non-additive gene action.

For vine length, the estimated value of $H_1$, $H_2$ and $h^2$ were highly significant while other parameters *viz.* D, E and F were non-significant. The estimated value of $H_1$ was greater than D which revealed that non-additive genes were more than additive genes. Positive value of F indicated predominance of dominant alleles. The mean degree of dominance $(H_1/D)^{½}$ being 1.63 showed over-dominance. The proportion of genes with positive and negative effects $(H_2/4H_1)$ was 0.19, which denotes asymmetry at loci. The proportion of dominance and recessive genes $[(4DH_1)^{½} + F/ (4DH_1)^{½} - F]$ was 3.31 whereas number of group of genes exhibiting dominance and controlling character was 4.91. The narrow sense heritability (23.64%) indicated the dominant type of gene action for expression of this character.

Results pertaining to components of genetic variation for total yield per plant revealed that estimate of $H_1$, $H_2$ and $h^2$ were highly significant while other parameters *viz.* D, E and F were non-significant. The value of $H_1$ was greater than D indicating the presence of more dominant genes than additive ones. The negative value of F showed preponderance of recessive alleles for this trait in parents. The value of $(H_1/D)^{½}$ was higher (1.46) indicating over-dominance. The proportion of genes with positive and negative effects $(H_2/4H_1)$ in parents was found to be 0.23 (less than 0.25), which denoted asymmetry at loci showing dominance. The proportion of dominance and recessive genes $[(4DH_1)^{½} + F/ (4DH_1)^{½} - F]$ was 0.61. The number of group of genes $(h^2/H_2)$ exhibiting dominance and controlling the character was 5.02. The narrow sense heritability (26.35%) indicated that non-additive type of gene action played an important role in the inheritance of this trait. In accordance to the present findings, Sarkar and Sirohi (2005) reported over-dominance for fruit length, fruit diameter and fruit weight in 45 cucumber $F_1$ crosses. In all these characters, the dominance component of genetic variance was higher than additive component of genetic variance. Munshi *et al.* (2006) reported predominance of non-additive genetic variance (over-dominance) and low narrow sense heritability for characters like days to first fruit harvest, number of fruits per plant and yield per plant. These results were also on conformity with the findings consonance with findings of Hedau and Sirohi (2004), Tyagi *et al.* (2010) in ridge gourd.

The results of present investigation showed dominance and over-dominance gene actions for all quantitative traits under study. Average degree of dominance was found to be more than 1 and narrow sense heritability was found to be less than 0.5 for all the characters suggesting the preponderance of non-additive gene action. Thus, in the present investigation, the predominance of non-additive gene action and low narrow sense heritability was observed for most of the important yield contributing characters which suggested the importance of heterosis breeding to get higher gain in sponge gourd.

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