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## Estimation of genetic variation components in sponge gourd (*Luffa cylindrica* (L.) Mj. Roem)

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### Abstract

The investigation were carried out in two years with aims to determine gene action involving 9 parental lines viz., NDSG-1, NDSG-20, NDSG-22, NDSG-24, NDSG-26, NDSG-28, NDSG-30, NDSG-32 and Pusa Chikni of sponge gourd and their 36 F<sub>1</sub> hybrids at MES, Vegetable Science, N.D.U.A.&T., Kumarganj, Faizabad (U.P.) during crop seasons of summer (*Zaid*) 2014 and 2015. The experiments were laid out in RBD with three replications having each experimental unit of single row with spacing of 3m x 0.5m. High genetic advance observed for node number to first staminate flower anthesis, node number to first pistillate flower anthesis, vine length at last harvest, number of primary branches/per vine at last harvest, number of fruits per plant and marketable fruits yield/plant, which suggested additive gene action for improvement of these characters selection may be effective. The remaining characters showed low to moderate genetic advance which suggested non-additive gene action. The proportion of genes in the parents were less than 0.25 for all the traits except days to first pistillate flower anthesis, days to first fruit harvest and number of nodes/vine at last harvest in Y<sub>1</sub> indicating asymmetrical distribution of alleles at loci showing dominance in the both years.

**Keywords:** Gene action, pistillate flower anthesis, vine length, additive gene action

### Introduction

In India, a number of major and minor cucurbits are cultivated which share about 5.6 per cent of the total vegetable production. They are consumed in various forms *i.e.*, salad (cucumber, gherkins, long melon), sweet (ash gourd, pointed gourd), pickles (gherkins), and deserts (melons). In India, several research institutes and State Agriculture Universities (SAU's) have utilized a number of cultivated and wild species to develop parental lines, improved varieties and hybrids. About 112 open pollinated varieties of cucurbits have been recommended for cultivation at national and state levels. Among these, 48 improved varieties in 8 major cucurbits have been identified and recommended through All India Coordinated Vegetable Improvement Project. Similarly, 26 hybrids and 7 disease resistant varieties of major cucurbits have also been developed. Sponge gourd is an annual and monoecious cucurbit plant. The inflorescences of staminate flowers are raceme, while pistillate flowers are solitary and short long pendunculate. It is commonly grown for its tender fruits for vegetable purpose as well as for sponge of mature fruits which is used for scrubbing of body skin as a bath sponge increased blood circulation and utensils purposes. The tender fruits are rich in vitamin A, vitamin C and iron (Yawalkar, 2004) [6]. In sponge gourd, large amount of variation has been observed for many economically important traits. For the development of high yielding hybrid varieties in sponge gourd or any crop, the information on various genetic aspects in respect of important plant characters is essential for planning and execution of a successful breeding programme. Genetic advance is most useful estimate as it is the improvement in the genotypic value in the new population in contrast to base population.

### Materials and Methods

The present investigation entitled "Estimation of genetic variation components in sponge gourd (*Luffacylindrica* (L.) Mj. Roem)" was conducted during crop season of summer (*Zaid*) 2014 and 2015 to evaluate the components of genetic variation in sponge gourd (*Luffacylindrica* (L.) Mj. Roem) using diallel mating design (excluding reciprocals) at the Main Experiment Station (MES) of the Department of Vegetable Science, N.D. University of Agriculture & Technology, Kumarganj, Faizabad (U.P.) India. The selected parental lines viz., NDSG-1 (P<sub>1</sub>), NDSG-20 (P<sub>2</sub>), NDSG-22 (P<sub>3</sub>), NDSG-24 (P<sub>4</sub>), NDSG-26 (P<sub>5</sub>), NDSG-28 (P<sub>6</sub>), NDSG-30 (P<sub>7</sub>), NDSG-32 (P<sub>8</sub>) and Pusa Chikni (P<sub>9</sub>) (national check) were crossed in the all

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possible combinations, excluding reciprocals, during summer, 2014 to get 36 F<sub>1</sub> seeds for the study of gene action for 14 fruit yield and yield attributing traits.

**Result and Discussion**

The diallel cross analysis was carried out separately over both the years for all the 14 characters, using analytical approach in terms of components of variation i.e.  $\hat{D}, \hat{H}_1, \hat{H}_2, \hat{F}, \hat{h}^2$  and  $\hat{E}$  along with their respective errors. The estimates of these components have been presented in Table 1. These genetic parameters were used in estimation of dominance  $(\hat{H}_1/\hat{D})^{1/2}$ ,

proportion of dominant and recessive genes (KD/KR) in parents i.e.  $(4\hat{D}\hat{H}_1)^{1/2} + \hat{F} / (4\hat{D}\hat{H}_1)^{1/2} - \hat{F}$  and number of gene groups which control the character and exhibit dominance  $(\hat{h}^2/\hat{H}_2)$ . The coefficient of correlation (r) between parental order of dominance (Wr-Vr) and parental measurements (Yr) was calculated to get an idea about the dominance genes with positive and negative effects. The non-significant values of t<sup>2</sup> indicates validity of assumptions pertaining to diallel analysis, while significant values of t<sup>2</sup> showed failure of hypothesis for diallel cross analysis. The findings on the genetic components recorded character wise are presented as follows:

**Table-1:** Estimates of components of variation and their related statistics in 9x 9 diallel crosses of sponge gourd over two years (Y<sub>1</sub>, Y<sub>2</sub>)

Components of variation and related statistics	Years	Node number to first staminate flower anthesis	Node number to first pistillate flower anthesis	Days taken for anthesis of first staminate flower	Days taken for anthesis of first pistillate flower	Days to first fruit harvest	Number of Node per vine at last harvest	Inter Nodal Length (cm)
		1	2	3	4	5	6	7
$\hat{D}$ (Additive effect)	Y <sub>1</sub>	12.20** ±0.96	13.30** ±2.88	34.76** ±8.10	27.46** ±3.08	22.83** ±3.15	154.46** ±15.81	1.56** ±0.43
	Y <sub>2</sub>	14.84** ±0.72	19.11** ±3.01	32.75** ±6.19	25.06** ±2.92	21.12** ±3.27	141.72** ±11.80	1.78** ±0.54
$\hat{H}_1$ (Dominance effect)	Y <sub>1</sub>	4.94* ±2.11	15.57* ±6.36	42.06** ±17.87	23.97** ±6.80	18.84** ±6.95	82.53* ±34.89	5.17** ±0.95
	Y <sub>2</sub>	8.38** ±1.60	16.59* ±6.64	45.20** ±13.66	35.91** ±6.44	37.96** ±7.21	74.56** ±26.05	5.99** ±1.19
$\hat{H}_2$ (Dominance indicating asymmetry of +/- effect of genes)	Y <sub>1</sub>	4.51* ±1.81	13.55* ±5.47	36.25* ±15.36	23.92** ±5.85	19.30** ±5.97	84.04** ±29.99	2.91** ±0.82
	Y <sub>2</sub>	6.01** ±1.37	14.35* ±5.71	41.01** ±11.74	34.32** ±5.53	31.61** ±6.20	72.35** ±22.40	3.35** ±1.03
$\hat{F}$ (Mean Fr over arrays)	Y <sub>1</sub>	1.81 ±2.23	6.34 ±6.72	6.23 ±18.89	-4.69 ±7.19	-10.80 ±7.34	4.98 ±36.87	3.04** ±1.00
	Y <sub>2</sub>	6.56** ±1.69	11.54 ±7.02	3.29 ±14.43	-3.74 ±6.80	-3.11 ±7.62	3.10 ±27.54	3.49** ±1.26
$\hat{h}^2$	Y <sub>1</sub>	0.11 ±1.21	0.31 ±3.66	-0.39 ±10.29	1.28 ±3.92	-1.69 ±4.00	8.79 ±20.09	1.36* ±0.55
	Y <sub>2</sub>	2.62** ±0.92	7.30 ±3.82	4.32 ±7.87	7.82* ±3.71	2.15 ±4.15	9.29 ±15.00	0.84 ±0.69
$\hat{E}$ (Environmental component)	Y <sub>1</sub>	0.08 ±0.30	0.18 ±0.91	2.90 ±2.56	3.06** ±0.97	7.75** ±1.00	7.52 ±5.00	0.12 ±0.14
	Y <sub>2</sub>	0.09 ±0.23	0.28 ±0.95	3.02 ±1.96	3.08** ±0.92	4.74** ±1.03	7.78* ±3.73	0.11 ±0.17
$(\hat{H}_1/\hat{D})^{1/2}$ (Mean degree of dominance)	Y <sub>1</sub>	0.64	1.08	1.10	0.93	0.91	0.73	1.82
	Y <sub>2</sub>	0.75	0.93	1.17	1.20	1.34	0.73	1.84
$\hat{H}_2/4\hat{H}_1$ (Proportion of genes with +/- effects in parents)	Y <sub>1</sub>	0.23	0.22	0.22	0.25	0.26	0.25	0.14
	Y <sub>2</sub>	0.18	0.22	0.23	0.24	0.21	0.24	0.14
$(4\hat{D}\hat{H}_1)^{1/2} + \hat{F} / (4\hat{D}\hat{H}_1)^{1/2} - \hat{F}$ (Proportion of dominant and recessive genes in parents)	Y <sub>1</sub>	1.26	1.56	1.18	0.83	0.59	1.05	3.32
	Y <sub>2</sub>	1.83	1.96	1.09	0.88	0.90	1.03	3.30
$\hat{h}^2/\hat{H}_2$ (Number of gene groups)	Y <sub>1</sub>	0.02	0.02	-0.01	0.05	-0.09	0.10	0.47
	Y <sub>2</sub>	0.44	0.51	0.11	0.23	0.07	0.13	0.25
R (Correlation coefficient)	Y <sub>1</sub>	0.84	0.34	0.30	0.60	0.57	0.91	0.65
	Y <sub>2</sub>	0.92	0.51	0.05	0.71	0.73	0.94	0.42
t <sup>2</sup>	Y <sub>1</sub>	0.03	0.50	0.60	0.16	2.66	0.91	0.21
	Y <sub>2</sub>	0.12	0.26	0.09	0.03	1.27	5.46	0.01

\*, \*\* Significant at 5 per cent and 1 per cent probability levels, respectively.

Table 1: Contd....

Components of variation and related statistics	Years	Vine length (m) at last harvest	Number of primary branches per vine at last harvest	Fruit length (cm) of marketable fruits	Fruit diameter (cm)	Number of fruits per plant	Average fruit weight (g)	Marketable fruit yield per plant (kg)
		8	9	10	11	12	13	14
$\hat{D}$ (Additive effect)	Y <sub>1</sub>	2.50** ±0.09	3.16** ±0.13	41.52** ±4.13	0.27** ±0.04	53.74** ±3.88	1204.06** ±111.743	0.47** ±0.07
	Y <sub>2</sub>	2.76** ±0.09	2.84** ±0.15	47.82** ±3.40	0.19 ±0.00	38.92** ±3.96	857.55** ±115.55	0.41** ±0.12
$\hat{H}_1$ (Dominance effect)	Y <sub>1</sub>	0.82** ±0.21	0.94** ±0.30	42.79** ±9.11	0.59** ±0.08	36.46** ±8.49	881.04** ±246.63	1.09** ±0.17
	Y <sub>2</sub>	0.88** ±0.21	1.32** ±0.33	36.56** ±7.52	0.03** ±0.01	29.10** ±8.74	1016.84** ±255.05	1.22** ±0.26
$\hat{H}_2$ (Dominance indicating asymmetry of +/- effect of genes)	Y <sub>1</sub>	0.78** ±0.18	0.83** ±0.04	40.65** ±7.83	0.35** ±0.07	31.16** ±7.30	758.88** ±212.02	0.91** ±0.14
	Y <sub>2</sub>	0.81** ±0.21	1.01** ±0.28	32.43** ±6.46	0.03** ±0.01	26.17** ±7.51	733.50** ±219.25	0.95** ±0.22
$\hat{F}$ (Mean Fr over arrays)	Y <sub>1</sub>	0.21 ±0.22	-0.16 ±0.32	0.80 ±9.63	0.31** ±0.09	9.47 ±8.97	-509.14 ±260.67	-0.03 ±0.17
	Y <sub>2</sub>	0.47* ±0.22	-0.35 ±0.35	7.64 ±7.94	0.04** ±0.01	-5.04 ±9.24	-791.31 ±269.56	-0.10 ±0.28
$\hat{h}^2$	Y <sub>1</sub>	0.13 ±0.12	-0.04 ±0.17	31.37** ±5.25	0.00 ±0.05	28.53** ±4.89	950.95** ±142.03	2.12** ±0.09
	Y <sub>2</sub>	0.41** ±0.12	0.01 ±0.19	49.09** ±4.33	0.01 ±0.01	26.21** ±5.03	1266.99** ±146.87	2.08** ±0.15
$\hat{E}$ (Environmental component)	Y <sub>1</sub>	0.04 ±0.03	0.10* ±0.04	2.16 ±1.30	0.02 ±0.01	1.56 ±1.21	35.33** ±0.02	0.02 ±0.02
	Y <sub>2</sub>	0.04 ±0.03	0.09* ±0.04	2.49* ±1.07	0.02 ±0.00	1.44 ±1.25	52.74 ±36.54	0.02 ±0.03
$(\hat{H}_1 / \hat{D})^{1/2}$ (Mean degree of dominance)	Y <sub>1</sub>	0.57	0.54	1.01	1.47	0.82	0.85	1.51
	Y <sub>2</sub>	0.56	0.68	0.87	0.43	0.86	1.08	1.72
$\hat{H}_2 / \hat{H}_1$ (Proportion of genes with +/- effects in parents)	Y <sub>1</sub>	0.24	0.22	0.23	0.15	0.21	0.21	0.20
	Y <sub>2</sub>	0.22	0.19	0.22	0.22	0.22	0.18	0.19
$(4\hat{D}\hat{H}_1)^{1/2} + \hat{F} / (4\hat{D}\hat{H}_1)^{1/2} - \hat{F}$ (Proportion of dominant and recessive genes in parents)	Y <sub>1</sub>	1.16	0.92	1.02	2.26	1.24	0.60	0.96
	Y <sub>2</sub>	1.35	0.83	1.20	1.65	0.86	0.40	0.86
$\hat{h}^2 / \hat{H}_2$ (Number of gene groups)	Y <sub>1</sub>	0.17	-0.04	0.77	0.00	0.91	1.25	2.32
	Y <sub>2</sub>	0.51	0.01	1.51	0.44	1.00	1.72	2.18
R (Correlation coefficient)	Y <sub>1</sub>	0.97	0.93	0.84	0.76	0.64	0.81	0.88
	Y <sub>2</sub>	0.97	0.91	0.91	0.94	0.83	0.80	0.77
$t^2$	Y <sub>1</sub>	1.14	0.03	0.61	0.08	0.12	0.24	0.50
	Y <sub>2</sub>	1.57	0.10	0.04	0.40	1.89	1.08	1.71

\*, \*\* Significant at 5 per cent and 1 per cent probability levels, respectively.

**Result and Discussion**

The node number to first staminate flower anthesis, shows the estimates of  $\hat{D}$ ,  $\hat{H}_1$  and  $\hat{H}_2$  components were highly significant in both the years while  $\hat{F}$ ,  $\hat{h}^2$  and  $\hat{E}$  were non-significant in both years (Y<sub>1</sub> and Y<sub>2</sub>) except  $\hat{h}^2$  and  $\hat{F}$  in Y<sub>2</sub>. The highest value of  $\hat{D}$  than  $\hat{H}_1$  and  $\hat{H}_2$  in both the years indicated preponderance of additive gene action for inheritance of this trait. In case of node number to first pistillate flower anthesis, the estimates of  $\hat{D}$ ,  $\hat{H}_1$  and  $\hat{H}_2$ , were significant in both

years (Y<sub>1</sub> and Y<sub>2</sub>) while  $\hat{F}$ ,  $\hat{E}$  and  $\hat{h}^2$  were found non-significant in both the years. The magnitude of  $\hat{H}_1$  more than  $\hat{D}$ ,  $\hat{H}_2$ , and  $\hat{E}$  values indicated preponderance of non-additive gene action during only Y<sub>1</sub> for this trait. In days taken for anthesis of first staminate flower, the estimates of component,  $\hat{H}_1$ ,  $\hat{D}$  and  $\hat{H}_2$  were significant for days taken to first male flower anthesis in during both the years.  $\hat{F}$ ,  $\hat{h}^2$  and  $\hat{E}$  were found non-significant in year (Y<sub>1</sub> and Y<sub>2</sub>). The significance of  $\hat{H}_1$  during both the years and higher value of it than  $\hat{D}$  along

with non-significant values of other components in either of season suggested the role of dominance components for expression of this character. The estimates of  $\hat{D}$ ,  $\hat{H}_1$  and  $\hat{H}_2$  were significant during both the years for days to first marketable fruit harvest traits while the values of  $\hat{F}$ ,  $\hat{h}^2$  and  $\hat{E}$  were found to be non-significant in both the years ( $Y_1$  and  $Y_2$ ). The significant value of  $\hat{H}_1$ , indicated the major role of dominance component for this character. In case of vine length (m) at last harvest, the significant values of  $\hat{D}$ ,  $\hat{H}_1$  and  $\hat{H}_2$  in both years ( $Y_1$  and  $Y_2$ ) suggested the major role of dominance components in the expression of this character. The  $\hat{F}$ ,  $\hat{h}^2$  and  $\hat{E}$  were found non-significant in both years ( $Y_1$  and  $Y_2$ ) except  $\hat{F}$  and  $\hat{h}^2$  in  $Y_2$ . Number of primary branches per vine at last harvest indicates the estimates of  $\hat{D}$ ,  $\hat{H}_1$  and  $\hat{H}_2$  were significant for this trait while  $\hat{F}$  and  $\hat{h}^2$  were non-significant in both years ( $Y_1$  and  $Y_2$ ). The higher values of  $\hat{H}_1$  than  $\hat{D}$  and  $\hat{H}_2$  indicated the major role of dominance component for this character in both years ( $Y_1$  and  $Y_2$ ). The non-significant  $\hat{F}$  values showed an bidirectional dominance. In case of number of nodes per vine at last harvest, the significant values of  $\hat{D}$ ,  $\hat{H}_1$  and  $\hat{H}_2$  in both years ( $Y_1$  and  $Y_2$ ) suggested the major role of dominance components in the expression of this character. The  $\hat{F}$ ,  $\hat{h}^2$  and  $\hat{E}$  were found non-significant in both years ( $Y_1$  and  $Y_2$ ) except  $\hat{E}$  in  $Y_2$ .

### Conclusion

Highly significant values for additive ( $\hat{D}$ ) and dominance ( $\hat{H}_1$  and  $\hat{H}_2$ ) effects of components were observed for all the 14 traits in both the years except the values of  $\hat{D}$  for fruit diameter in  $Y_2$  which showed non-significant. The significant values of  $\hat{D}$ ,  $\hat{H}_1$  and  $\hat{H}_2$  indicated the importance of both additive and dominance gene action in the expression of these traits, which is in consonance with the findings of Sundharaiya and Arumugam (2006) [5] and Sundaram (2007) [4] in bitter gourd. However, additive ( $\hat{D}$ ) genetic variance components were lower in magnitude than dominant component of genetic variance for all of the traits over both the years which showed preponderance of dominance components of variance in expression of fruit yield and its attributing traits in both the years. (NDSG-20 x NDSG-22),  $P_4$  x  $P_8$  (NDSG-24 x NDSG-32) and  $P_7$  x  $P_9$  (NDSG-30 x Pusa Chikni) could be exploited as commercial hybrid in future. In sponge gourd similar findings was also recorded by Sabina *et al.* (2013) [3] Mishra *et al.* (1998) [1], Yuan *et al.* (2009) [7] and Pandey *et al.* (2012) [2].

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