Gene effects studies in sponge gourd for earliness, yield and its component traits

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ABSTRACT

Gene action was studied in indigenous and under exploited vegetable sponge gourd utilizing six high yielding F_1s, their F_2, B_1 and B_2 generation population following generation mean analysis. Preponderance of additive gene effects was noticed for earliness, while dominance gene effects for number of fruits per plant, fruit length, fruit weight and total yield per plant. High dominance effect was observed in crosses DSG-6 × PSG-9 (41.22), DSG-6 × NSG-1-11 (36.60) and DSG-7 × NSG-1-11 (27.95) for number of fruits per plant, while DSG-7 × NSG-1-11 DSG-6 × Pusa Sneha and DSG-6 × CHSG-2 for average fruit weight (69.00, 46.33 and 41.33, respectively). The dominance component was comparatively less for total yield per plant and DSG-6 × PSG-9 (6.64), DSG-7 × NSG-1-11 (5.47) and DSG-6 × NSG-1-11 (5.43) exhibited highest dominance effect among the crosses. Additive × additive interaction was higher in magnitude in desirable positive direction for total yield per plant and DSG-6 × PSG-9 (3.53) exhibited the highest followed by DSG-7 × Pusa Sneha (3.38) and DSG-7 × NSG-1-11 (3.01). Majority of the crosses showed duplicate type of epistasis. One cross DSG-6 × CHSG-2 showed complementary epistasis indicating the positive gain in yield enhancement through heterosis breeding. The study suggested the need of adoption of cross specific (parent specific) breeding programme for different traits. Simple mass selection would result in progress for characters governed by additive gene effects like earliness, heterosis breeding for characters governed by dominance gene effects like number of fruits and yield per plant and breeding plan based on restricted selection by way of intermating the most desirable segregants followed by selection and/or diallel selective mating system would be most appropriate for characters where duplicate epistasis was predominant.

Key words: Generation mean analysis, gene action, epistasis, sponge gourd.

INTRODUCTION

Sponge gourd (*Luffa cylindrica* Roem., 2n = 2x = 26) is an indigenous and genetically under exploited vegetable, belongs to family cucurbitaceae and is a popular vegetable in the tropical and subtropical regions. The young, tender fruits are used as vegetable, while mature fruits produce organic *Luffa* for cleaning, washing and filteration. As a vegetable, it is high in demand during spring-summer and rainy seasons, when temperate vegetables are short in supply and growers fetch good return. The fruits are low in calorific value and have medicinal as well as industrial properties (Porterfield, 10). They are annual, luscious, high climbing or trailing vines, clothed with dark green leaves and yellow flowers. They are monoecious in nature, male flowers in cluster of 7-8 appear first followed by individual female flower. The tender fruit is used as vegetable and the mature, dry fruit consists of a hard shell surrounding a stiff, dense network of cellulose fibres (sponge), which is a good source of fiber used in industries for filter and cleaning the motor car, glassware, kitchen utensil, bath and body bathing accessories (Oboh and Aluyor, 7). Sponge gourds are also used as absorbent (Altinisik *et al.*, 1). The breeding work on sponge gourd is mostly relied on mass selection from land races. Despite its importance for diversified use, systemic work on sponge gourd for yield and related traits has been very few which is evidenced by the absence of hybrid and sufficient number of open-pollinated varieties at national level. The knowledge of the nature and magnitude of gene action controlling inheritance of characters related to earliness and productivity in the breeding population would aid in the choice of most suitable breeding methods and selection strategy, thus accelerating the pace of its genetic improvement. Though generation mean analysis has been extensively used to understand the gene effects in different crops, but practically no reports are available on the use of this technique for understanding the gene effects in sponge gourd, hence, the present study was undertaken.

MATERIALS AND METHODS

The present investigation was carried out at research farm of Division of Vegetable Science, IARI, New Delhi. Seven sponge gourd lines (5 cultivated

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varieties, *viz*., Pusa Sneha, PSG-9, NSG-1-11, CHSG-1, CHSG-2 and two advanced breeding lines, *viz*., DSG-6 and DSG-7) were used to create non-reciprocal hybrids, where cultivated varieties and advanced breeding lines were used as paternal and maternal parents, respectively, as they exhibited better performance than the cultivated varieties. The cultivated varieties were collected from the seed producing organizations and there by sibbing to produce lines (s>4), those were subsequently used to create 10 F_1 hybrid combinations. The six sets of F_1s were advanced to F_2 (F_1s selfed), B_1 ($F_1 \times P_1$) and B_2 ($F_1 \times P_2$) generations.

The six generations (P_1, P_2, F_1, F_2, B_1 and B_2) of these six crosses were evaluated under randomized block design with three replications. The crop was sown in rows of 1.2 m with 60 cm spacing between the plants. A single non-experimental row was planted on either sides of each block, so as to minimize environmental error due to border effect. Data were recorded on 10 randomly tagged plants in parents and F_1 hybrids, 15 plants in B_1 and B_2 and 30 plants in F_2 from each replication on six quantitative characters, *viz.,* days to first female flower opening, days to first fruit harvest, fruit weight (g), number of fruits per plant, fruit length (cm) and fruit yield per plant (kg). The data thus obtained were subjected to scaling test (Hayman, 2) to identify the interacting and non-interacting crosses. The generation means of P_1, P_2, F_1, F_2, B_1 and B_2 were used for scaling tests and estimation of gene effects. The data from interacting crosses were analyzed through 6-parameters model (Hayman, 2; Jinks and Jones, 4). The estimates of mean and gene effects for interacting crosses, *i.e*., mean (*m*), additive (*d*), dominance (*h*), additive × additive (*i*), additive × dominance (*j*) and dominance × dominance (*l*) were obtained for yield and its components. The data from non-interacting crosses were analysed using three parameters (*m*, *d* and *h*) model of Jinks and Jones (4).

RESULTS AND DISCUSSION

The interacting and non-interacting crosses out of selected six crosses have been identified by presence or absence of non-allelic interactions (epistasis) through their significance or non-significance in scaling test (Mather, 5). In scaling test, four tests (*A*, *B*, *C* and *D*) for scale effects have been used. When the scale is adequate, the values of *A*, *B*, *C* and *D* would be non-significant. When the scales are significant, *A* and *B* indicated additive × dominance (*j*), *C* dominance × dominance (*l*) and *D* additive × additive (*i*) type of gene interactions. The results of the scaling tests are presented in Table 1.

The perusal of data from Table 1 indicated that all the characters were governed by inter allelic interaction and simple additive dominance model won't suffice to explain the inheritance of traits. However, three crosses showed non-significance for three different traits, like DSG-6 × Pusa Sneha for fruit length, DSG-6 × CHSG-2 for days to first fruit harvest and DSG-7 × Pusa Sneha for days to first female flowering. Fruit weight, fruit length and fruit yield had maximum number of significant scales. Therefore, inheritance of these characters is presumed to be more complex. The gene effects for three quantitative characters in non-interacting crosses have been presented in Table 2.

The cross DSG-7 × Pusa Sneha exhibited positive dominance (*h*) and additive (*d*) gene effects and *h* component was higher in magnitude but in undesirable positive direction suggesting minimal role of heterosis breeding for imparting earliness involving the parental population. For days to first fruit harvesting, the cross DSG-6 × CHSG-2 showed additive gene effects in desirable negative direction but the dominance effect was in undesirable positive direction and it was higher in magnitude compared to the additive effects. The simple nature of inheritance of earliness was earlier corroborated by Singh and

Table 1. Scaling tests in selected crosses for six quantitative traits in sponge gourd.

Cross combination	Days to 1st female flower opening	Days to 1st fruit harvest	Fruit weight (g)	No. of fruits per plant	Fruit length (cm)	Fruit yield per plant (kg)
I. DSG-6 × Pusa Sneha	*B*	*B*	*A, B, C, D*	*D*	NS	*D*
II. DSG-6 × PSG-9	*B, C*	*C*	*B, C, D*	*B, C*	*A, B, D*	*C*
III. DSG-6 × NSG-1-11	*B*	*B*	*A, B, C, D*	*B, D*	*B, C, D*	*A, B, D*
IV. DSG-6 × CHSG-2	*B*	*NS*	*A, B, C, D*	*B, C, D*	*A*	*B, C, D*
V. DSG-7 × Pusa Sneha	*NS*	*D*	*A, B, C, D*	*A, B*	*A, B, C, D*	*A, B, C, D*
VI. DSG-7 × NSG-1-11	*B*	*B*	*A, B, C, D*	*B, D*	*A, B, C, D*	*A, B, D*

NS = Non-significant

Table 2. Estimates of gene effects in non-interacting crosses (3-parameter model).

Cross	m	d	h
1. Days to first female flower opening DSG-7 × Pusa Sneha	44.67 ± 7.08*	0.01 ± 0.55	8.00 ± 16.28
2. Days to first fruit harvest DSG-6 × CHSG-2	46.00 ± 8.72*	-3.00 ± 1.14*	35.00 ± 20.87
3. Fruit length DSG-6 × Pusa Sneha	17.43 ± 7.73*	-0.40 ± 0.43	-0.27 ± 16.71

*Significant at 5% level of significance

Ram (13) in bitter gourd. But they observed greater role of additive component than that of the dominance effects, which is contrary to the present finding. DSG-6 × Pusa Sneha showed adequacy of simple additive-dominance model for fruit length, both the additive and dominance effects were in undesirable negative direction and additive effect was higher in magnitude compared to dominance effect. Rao *et al*. (11) reported the dominance role of additive gene effect for fruit length in *Luffa.* Hedau and Sirohi (3) stated that in ridge gourd fruit length was governed by additive and dominant factors.

The significance of one or more components in scaling test (Table 1) indicated the presence of complex reaction in the inheritance of traits. The analysis of gene effects and interaction component revealed significant involvement of one or more gene effects and interactions in the inheritance of different traits (Table 3).

For days to first female flowering all the crosses showed desired negative additive gene effect and undesired positive dominance gene effect except DSG-6 × NSG-1-11, which had desired dominance effect. Among the epistatic interaction additive × additive (*i*) interaction was in undesired negative direction and dominance × dominance (*l*) interaction was in desired negative direction except in DSG-6 × NSG-1-11. Sanandia *et al*. (12) indicated the presence of higher order interaction for days to first female flower in sponge gourd. The result of the present findings substantiated the earlier report of Pal *et al*. (8) in bottle gourd; and Singh and Ram (13) in bitter gourd. The trend was similar for days to first fruit harvest too. Hybrid DSG-7 × Pusa Sneha showed undesired *d* gene effect. None of the crosses showed desired *i* epistatic interaction and all of them showed desired *l* effect. These reports were supported by the earlier report of Tyagi *et al*. (15) in ridge gourd; Singh and Ram (13) in bitter gourd, and Maurya *et al*. (6) in bottle gourd.

In case of number of fruits per plant *h* and *l* gene effect and interaction were higher in magnitude than the other gene effects and interaction except in DSG-6 × CHSG-2 were *i* component was higher in magnitude but in negative direction. The *h* effect was in positive direction but the *l* interaction was in negative direction except in DSG-6 × CHSG-2. Additive gene effect was significant in desirable direction in three crosses and *h* effect in four crosses for fruit weight. Both the gene effects were in desired positive direction in all the crosses. In all the crosses, epistasis was duplicate type.

For fruit length additive effect was significant in desirable direction in three crosses, while dominance effect was significant in desirable direction in only one cross. DSG-6 × NSG-1-11 exhibited comparatively higher magnitude of *h* and *l* effects, but the epistasis was duplicate type. Importance of additive gene action in some crosses and non-additive and epistatic interaction in other crosses for fruit characters were earlier reported by Tyagi *et al*. (15), Pandey *et al*. (9) in luffa; Maurya *et al*. (6); Pal *et al*. (8), and Sit and Sirohi (14) in bottle gourd.

In the present study, *h* component was positive in all the crosses and significant in three crosses. Among all the gene components *h* exhibited comparatively higher value in desired direction indicating the rapid scope for improvement of this trait following heterosis breeding. However, the presence of duplicate epistasis indicated the decreased gain through heterosis breeding only. The presence of positive *d* and *i* component in five crosses suggested considerable scope for improvement through selection of desirable alleles in positive direction. The epistasis was duplicate type in all the crosses except cross DSG-6 × CHSG-2, where it was complementary type. Additive effect was found to have minimal role, while dominance effect played a predominant role. Hence, heterosis breeding was a better choice. However, duplicate epistasis was noticed in most of the crosses, therefore biparental mating or recurrent selection to generate heritable variation followed by intermating the most desirable segregants would be appropriate. The result is inconsonance with the earlier findings of Rao *et al*. (11), Tyagi *et al*. (15), and Hedau and Sirohi (3) in ridge gourd.

The estimates obtained from each crosses for different traits indicated the need of observing each cross individually while formulating the breeding methodology for further improvement of a particular trait. However, the overall result showed that dominance gene effect, additive × additive and dominance × dominance component were higher in magnitude in interacting crosses for almost all the

Table 3. Estimates of gene effects in interacting crosses (6-parameter model).

Cross combination	m	d	h	i	J	l
1. Days to first female flower opening						
DSG-6 × Pusa Sneha	44.67 ± 1.76*	-4.33 ± 0.67*	8.50 ± 7.35	18.00 ± 7.18*	-3.50 ± 1.38*	-31.67 ± 8.17*
DSG-6 × PSG-9	48.00 ± 1.15*	-3.33 ± 2.05*	20.33 ± 6.46*	20.00 ± 6.18*	-1.67 ± 2.38	-26.00 ± 10.15*
DSG-6 × NSG-1-11	57.33 ± 2.73*	-5.33 ± 2.33*	-4.00 ± 11.97	-8.00 ± 11.87	-3.33 ± 2.65	1.33 ± 14.68
DSG-6 × CHSG-2	47.33 ± 2.03*	-9.67 ± 3.18*	12.33 ± 10.56	19.33 ± 10.31	-7.00 ± 3.50*	-32.67 ± 15.76*
DSG-7 × NSG-1-11	48.33 ± 1.86*	-6.67 ± 2.29*	3.83 ± 8.90	10.67 ± 8.72	-5.50 ± 2.37*	-18.33 ± 12.30*
2. Days to first fruit harvest						
DSG-6 × Pusa Sneha	56.67 ± 1.20*	-4.00 ± 0.47*	4.17 ± 5.06	12.00 ± 4.90*	-3.17 ± 1.01*	-24.3 ± 5.74*
DSG-6 × PSG-9	58.67 ± 0.88*	-2.00 ± 2.49	14.50 ± 6.24*	14.67 ± 6.11*	0.17 ± 2.65	-17.00 ± 10.87
DSG-6 × NSG-1-11	62.33 ± 2.96	-4.33 ± 1.56*	12.83 ± 12.35	10.00 ± 12.26	-2.83 ± 1.85	-19.00 ± 13.74
DSG-7 × Pusa Sneha	54.00 ± 1.15*	0.33 ± 2.26	2.00 ± 6.53	12.67 ± 6.46*	0.67 ± 2.35	-18.67 ± 10.32
DSG-7 × NSG-1-11	58.00 ± 1.00	-7.33 ± 2.40*	1.67 ± 6.61	9.33 ± 6.25	-6.33 ± 2.52*	-19.33 ± 11.25
3. Number of fruits per plant						
DSG-6 × Pusa Sneha	21.07 ± 1.06*	2.30 ± 2.02	11.33 ± 6.16	1.27 ± 5.86	-1.60 ± 2.12	-5.87 ± 9.90
DSG-6 × PSG-9	15.47 ± 1.91*	1.93 ± 1.67	41.22 ± 8.39*	24.93 ± 8.33*	-5.05 ± 1.79*	-30.7 ± 10.35*
DSG-6 × NSG-1-11	17.80 ± 1.04*	2.93 ± 1.88	36.60 ± 5.67*	23.60 ± 5.62*	-3.37 ± 1.98	-41.2 ± 8.73*
DSG-6 × CHSG-2	26.90 ± 1.44*	0.60 ± 1.92	-2.30 ± 7.06	-16.3 ± 6.92*	-4.83 ± 2.03*	7.53 ± 10.00
DSG-7 × Pusa Sneha	21.00 ± 1.54*	-2.77 ± 1.96	27.88 ± 7.33*	19.53 ± 7.30*	-5.68 ± 2.02*	-49.5 ± 10.05*
DSG-7 × NSG-1-11	21.47 ± 1.95*	-1.23 ± 2.27	27.95 ± 9.06*	10.33 ± 9.04	-6.56 ± 2.32*	-24.0 ± 12.03*
4. Fruit weight						
DSG-6 × Pusa Sneha	150.0 ± 4.16*	9.00 ± 5.56	46.33 ± 20.68*	16.67 ± 20.02	4.67 ± 6.22	-87.33 ± 29.65*
DSG-6 × PSG-9	146.0 ± 2.89*	12.67 ± 5.33*	42.83 ± 16.30*	-6.67 ± 15.72	-2.17 ± 5.91	-27.00 ± 25.75
DSG-6 × NSG-1-11	160.3 ± 4.33*	14.33 ± 5.73*	4.83 ± 21.60	-36.67 ± 20.77	-0.50 ± 6.39	-40.33 ± 31.07
DSG-6 × CHSG-2	159.0 ± 3.79*	5.00 ± 5.97	41.33 ± 19.98*	-2.00 ± 19.29	-3.67 ± 6.64	-76.00 ± 30.14*
DSG-7 × Pusa Sneha	157.7 ± 4.06*	4.00 ± 4.69	36.83 ± 19.46	13.33 ± 18.74	1.17 ± 5.56	-129.7 ± 26.94*
DSG-7 × NSG-1-11	151.3 ± 5.21*	10.67 ± 6.07*	69.00 ± 24.47*	14.67 ± 24.11	-2.67 ± 6.78	-87.33 ± 33.07*
5. Fruit length						
DSG-6 × PSG-9	17.37 ± 0.77*	4.37 ± 0.75*	-0.65 ± 3.55	-5.13 ± 3.42	4.52 ± 0.86*	3.83 ± 4.71
DSG-6 × NSG-1-11	19.33 ± 0.85	1.57 ± 0.73*	-16.0 ± 3.82*	-18.6 ± 3.71*	2.02 ± 0.81*	20.43 ± 4.87*
DSG-6 × CHSG-2	15.90 ± 0.57*	5.77 ± 1.28*	15.45 ± 3.79*	9.80 ± 3.43*	6.02 ± 1.58*	-17.4 ± 6.48*
DSG-7 × Pusa Sneha	15.63 ± 0.37*	1.20 ± 0.87	4.65 ± 2.40	4.80 ± 2.29*	1.55 ± 0.96	-17.2 ± 4.06*
DSG-7 × NSG-1-11	18.47 ± 0.44*	6.93 ± 1.02*	4.40 ± 2.75	-1.73 ± 2.70	7.73 ± 1.07*	-2.67 ± 4.57
6. Total yield per plant						
DSG-6 × Pusa Sneha	3.17 ± 0.23*	0.53 ± 0.41	2.55 ± 1.31	0.58 ± 1.25	-0.01 ± 0.43	-2.42 ± 2.06
DSG-6 × PSG-9	2.26 ± 0.30*	0.55 ± 0.34	6.64 ± 1.40*	3.53 ± 1.39*	-0.40 ± 0.35	-4.09 ± 1.84*
DSG-6 × NSG-1-11	2.85 ± 0.14*	0.78 ± 0.39*	5.43 ± 0.96*	3.01 ± 0.95*	-0.11 ± 0.40	-6.51 ± 1.67*
DSG-6 × CHSG-2	4.29 ± 0.31*	0.19 ± 0.30	0.11 ± 1.38	-2.67 ± 1.36*	-0.57 ± 0.31	0.37 ± 1.76
DSG-7 × Pusa Sneha	3.32 ± 0.33*	-0.34 ± 0.39	4.90 ± 1.53*	3.38 ± 1.53*	-0.73 ± 0.40	-10.14 ± 2.04*
DSG-7 × NSG-1-11	3.23 ± 0.18*	0.04 ± 0.41	5.47 ± 1.09	2.01 ± 1.09	-0.70 ± 0.41	-4.53 ± 1.79*

*Significant at 5% level of significance

characters studied. Duplicate epistasis was recorded in all the interacting crosses for all the characters except complementary epistasis in DSG-6 × CHSG-2 for total yield per plant. Over-dominance was noticed in the non-interacting crosses. The preponderance of non-additive and inter-allelic interaction component suggested the importance of heterosis breeding and recurrent selection for effective exploitation of dominance and epistatic component. Biparental mating and reciprocal recurrent selection technique would be effective in breaking undesirable linkage and to locate useful recombinants. The traits exhibiting higher magnitude of additive component can be increased easily through selection of desirable alleles in unidirection.

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