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Genetic analysis of fruit yield in Scarlet (*Solanum aethiopicum* L.) Gboma (*S. macrocarpon* L.) and *S. anguivi*

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ABSTRACT

Fruit yield is a complex trait and its improvement is facilitated by improving component traits. The objectives of this study were to estimate the mode of inheritance and genetic control of fruit yield, magnitude of heterosis and heritability in inter and intra specific cross among *S. aethiopicum*, *S macrocarpon* and *S. anguivi*. The test population were grown in compact family block design with six blocks in three replications in two years. Data were collected on fruit yield and analyzed for adequacy of the additive-dominance model and fit of the five and six parameter models. Both additive and non-additive genes were found for fruit yield. Disparities in the type of gene action for fruit yield suggest restricted recurrent selection to mop-up several digenic effects. The additive gene effect predominates inheritance of fruit yield in intra species cross Ab_2 ♂ x Var 19 ♀ and CR001 ♂ x Var 53 ♀, and inter species cross Db_3 ♂ x Fovembot ♀. Therefore selection among segregating population may rapidly isolate homozygous lines. Hence repeated selection of homozygous lines may not be necessary. Relative Mid-Parent Heterosis (RMPH) was 75.67% in CR001 x Var 53. This provided the potential for improvement in fruit yield. Inheritance of fruit yield was polygenic. A low heritability for fruit yield implied selective breeding activities to improve fruit yield might be less effective in early generations. Genetic improvement in the tested species can be facilitated through early selection and recurrent selection methods.

Keywords: African eggplants, genetic studies, additive – dominance model, recurrent selection, heterosis and heritability

INTRODUCTION

Solanum aethiopicum L, *Solanum macrocarpon* L and *Solanum anguivi* L (2n=24) (aptly referred to as African eggplant) are relatives of the eggplant (*S. melongena* L). They are cultivated widely and consumed in sub-Sahara Africa. The fruits are consumed in various culinary preparations and are recommended as an excellent remedy for liver and diabetic complaints (Hedges and Lister, 2007; Sabolu *et al.*, 2014). A 100 g of eggplant fruit contains 92.70 per cent moisture, 0.1 g fat, 5.7 g carbohydrate and 1.0 g protein. Also, numerous vitamins and minerals, such as B1, B6, folate, copper, manganese (0.25 mg), magnesium (14 mg) and potassium (230 mg) are present in eggplant (USDA Nutrient Database, 2005). The fruits of *Solanum aethiopicum* Gilo are elongated, grooved with a thin rind, greenish or greenish white fruit colour at commercial harvest (Shippers, 2002). On the other hand, *Solanum macrocarpon* fruits are flabby, wider than long, thick rind with cream, greenish or purple fruit colour, while fruits of *Solanum anguivi* are small in size. African eggplants displayed high variation for and fruit yield (Shippers, 2002) and shape (Adeniji and Aloyce, 2012). In Tanzania, growers harvest 32 t/ha of fresh fruits (Bukenya, 2004), and 55 fruits/plant (ranged from 55 to 65) in *S. aethiopicum.* In addition, 252 fruits (ranged from 245 to 260) were counted in Fovembot 3 *(Solanum anguivi*), and 15 fruits/plant (between 9 and 21) in *Solanum macrocarpon* (Adeniji, *et al.*, 2012; Adeniji, 2013).

In East and Southern Africa, Ab_2 and Db_3 (*Solanum aethiopicum* Gilo) are commercial varieties. The fruits are harvested, sorted, graded (big, medium and small), cleaned and sold in grocery stores. Growers and consumers of *Solanum aethiopicum* and *Solanum macrocarpon* have shown interest in fruit size, this is an important market trait (Adeniji and Aloyce, 2013). Fruit yield is the end product of series of interacting process that is genetically complex and invariably influenced by environmental factors. Fruit yield and fruits/plant vary among African eggplants, both traits are positively correlated (Adeniji, 2012). *Solanum anguivi* is characterized by high fruits/plant with low fruit yield. In contrast, S*olanum macrocarpon* have few fruits/plant and high fruit yield. While fruits/plant and fruit yield are moderate in *Solanum aethiopicum* groups. Generation mean analysis is a simple, but useful technique for estimating gene effects, its greatest merit lie in its ability to estimate epistatic gene effects (Singh and Singh, 1992). Besides gene effects, it is important to know how much of the variation in a crop is genetic and to what extent this variation is heritable. The efficiency of selection depends on additive genetic variance, influence of the environment and interaction between genotype and environment.

Fruit yield is not a major research objective of eggplant breeding in sub Saharan Africa. Genetic information on the mode of inheritance, genetic control, heritability and heterosis for fruit yield in Scarlet, Gboma and *Solanum anguivi* is limited compared to tomato and pepper. Hence, the absence of commercial varieties (open pollinated and hybrids). Because of complex interactions between yield and yield contributing traits, it is difficult to improve yield through breeding. Intra species (*S. aethiopicum* Gilo) and inter species (*S. aethiopicum* Gilo and *S. anguivi*) hybridization will develop segregating population upon which selection for fruit yield and fruit number can be made. This study intends to evaluate the mode of inheritance and genetic control of fruit yield, determine the magnitude of heritability and heterosis of fruit yield in intraspecies and interspecies hybridization.

MATERIALS and METHODS

Materials, Field management and Measurements

Three genotypes of *Solanum aethiopicum* (Ab_2 and Db_3 and Var 19), two accessions of *S. macrocarpon* (CR001 and Var 53) and one accession of *S. anguivi* (Fovembot) were used in intra species (Ab_2 ♂ x Var 19 ♀, CR001 ♂ x Var 53 ♀) and inter species hybridization (Db_3 ♂ x Fovembot ♀). Five ((P_1, P_2, F_1, F_2 and F_3) and six generations (P_1, P_2, F_1, F_2, BCP_1 and BCP_2) were developed. Field experiment was carried out at the research field of the Horticultural Training Research Institute, Arusha (Latitude 4^0.88"S, Longitude 3^0.78''E; Altitude 1290 m) with an annual rainfall of 700 – 1000 mm; soil type was clay loam with a pH between 6.0 and 6.5. Field experiment was laid out in a compact family block design with six blocks, each block included three rows of 7 meters long and 0.75meters between rows for each non-segregating generation and six rows for each segregating population and replicated four times. Seedlings were raised in multicell seedling trays for four weeks and thereafter transplanted to the sides of the ridges at 0.45m between plants. Plants were fertilized with NPK (20-10-10) at the rate of 90 Kg N/ha, 45 Kg P_2O_5/ha and 45 Kg K_2O/ha. Urea fertilizer was applied at the rate of 120Kg N/ha in three splits i.e. one week after transplanting, at flowering and three weeks thereafter. Ridomyl® (Matalxyl) WP (fungicide) was sprayed against damping off in the field at the rate of 20g/15 liters of water, 12 days after transplanting. Selecron EC (insecticide) was sprayed 2 weeks after transplanting at the rate of 20 mls/20 liter of water to control cutworms and other insects on the field. The experiment was furrow-irrigated every two days for the first two weeks after transplanting, then once a week thereafter. Weeding was carried out manually and frequently with hoes to maintain weed-free plots.

Data Collection, Test of homogeneity, Scale tests and Genetic studies

75 plants were established for each parent, 200 plants for F_1 generation, 300 plants for F_2 generation and 150 plants for each backcross generation. Harvested fruits from the net plot were counted, weighed and processed for determination of fruits yield/plot (kg ha^{-1}). Weight (g) was determined on a sensitive electronic scale (Wagtech International limited ADP 1200l. UK). Homogeneity of variances of non-segregating generations was tested using Bartlett's test (Bartlett, 1937). Analysis of variance over years using GLM procedure of SAS (2009) was conducted prior to generation mean analysis. If the source of variation for genotype was significant, generation mean analyses were carried out for each year as well as across years. Data for four replications were pooled for the computation of generation means, while variances for each generation were calculated by averaging variances of each replication of the same generation. The variance of the mean for each generation was obtained by its variance divided by the number of plants in each generation. The scale tests and variances (Mather, 1949) were computed under the assumption that observed variation was due to additive and dominance effects with no epistasis or linkage. The scale test and its variance were computed as;

A=2B1-F1-P1 V (A) = 4V (B1) +V (P1) +V (F1)

B=2B2-F1-P2 V (B) = 4V (B2) +V (P2) +V (F1)

C=4F2–2F1-P1-P2 V(C) = 16VF2) +4V (F1) +V (P1) +V (P2)

Significance of individual scales was assessed by a Student's t-test using degrees of freedom equal to the sum of degrees of freedom for the generation involved in each scale. If the scales are adequate, the values of A, B, and C should be zero within the limits of their respective standard errors. On the other hand, significance of any one of these scales indicates the presence of non-allelic interaction. The three-parameter model (m, [a] and [h]) of Jinks and Jones (1958) was used to test the adequacy of the additive-dominance model in the absence of non-allelic gene interaction. The six parameter and 6 -parameter models (Hayman, 1974) based on perfect fit result (m = mean, [d] = additive effect, [h] = dominant effect, [aa] = additive x additive type of gene interaction, [ad] = additive x dominance type of gene interaction and [dd] = dominance x dominance type of gene interaction was used to estimate various gene effects including the non-allelic interaction. A Student's t-test at (k-p) degrees of freedom was used to test significance of parameter estimates. The computed $\chi 2$ value was compared at (k-p) degrees of freedom to tabular values. Narrow-sense heritability was estimated using method proposed by Warner

(1952). The quantitative estimate of the minimum number of effective factors contributing to agronomic traits was computed using

1. Wright (1968) = $(P_1 – P_2)2 / [8(VF_2 – VF_1)]$ and
2. Cookerham (1986) = $[(P_1 - P_2)^2 - VP_1 - VP_2/ 8(VF_2\text{-}VE)]$ Where; P_1, P_2 = Parent cultivars;

F_1, F_2 = First and second filial generations;

BC_1, BC_2 = First and second backcrosses.

VP_1, VP_2= Variance of parents 1 and 2

VE= Environmental variance (VE= ¼(VP_1 +VP_2+ VF_1)

VF_2= Variance of the F_2 population

SE = Standard Error.

When these assumptions do not apply, the formula gives a value that may be much smaller than the true gene number. Absolute Mid-Parent Heterosis (AMPH) was calculated as = F1 – MPV, Relative Mid-Parent Heterosis (RMPH) = [F1 – MPV/MPV] 100. Absolute High-Parent Heterosis (AHPH) = F1 – HPV. Absolute High Parent Heterosis (RHPH) = [F_1 – HPH/HPH] 100.

RESULTS

The genotypes showed significant mean squares ($P < 0.01$) for fruit yield in all the cross combinations for each year and combined (Table 1). In contrast, insignificant mean squares ($P> 0.05$) were recorded for replication and year

.

Table 1: Mean squares estimate for fruit yield in three cross combinations

Source of Variation	df	AB_2 x Var 19	CR001[d] x Vat 53	Source of Variation	df	Db_3 x Fovembot
Year 1				**Year 1**		
Replication	2	235.34	595.38	Replication	2	64.92
Genotype	5	2305.13**	113484.22**	Genotype	4	5976.50**
Error	10	273.34	1057.72	Error	20	36.02
CV (%)		17	8	CV (%)		10.49
Mean		103.67	386.77	Mean		57.20
Year 2				**Year 2**		
Replication	2	92.72	78.72	Replication	2	5.44
Genotype	5	2203.14**	112136.72**	Genotype	4	6283.98**
Error	10	71.72	1062.25	Error	20	17.51
CV (%)		8	8.38	CV (%)		7.36
Mean		109.21	388.72	Mean		56.82
Combined				**Combined**		
Year	1	266.77	34.02	Year	1	1.04
Replication	4	164.11	337.05	Replication	4	35.18
Genotype	5	4475.84**	225571.51**	Genotype	4	12240.77**
Error	25	362.11	857.87	Error	20	507.56
CV (%)		11.31	8.0	CV (%)		8.83
Mean		106.39	387.75	Mean		57.04

**= significant at 1% probability; d=donor parent, r=recipient parent, CV (%) = Coefficient of Variability

In the cross Ab_2 ♂ x Var 19 ♀, the F_1 hybrid mean was not intermediate in performance between the two parents, while the F_2 population mean was larger than the mid parent (Table 2). The individual scaling tests indicates involvement of non-allelic interaction among genes contributing to fruit yield. In the cross Ab_2 ♂ x Var 19 ♀, all scaling tests (A, B, C and D) were insignificant. Overwhelming evidence of non-allelic interaction for each year and combined in the cross between CR001 ♂ x Var 53 ♀, due to significant ($P < 0.01$) A, B and C –scale tests, was found in intra species. However, the D- scale test showed insignificant ($P> 0.01$) estimates for each year and combined. The C

– scale test was significant (2010 and combined) and insignificant (P> 0.05) during 2011 in the cross Db$_3$ ♂ x Fovembot-2 ♀.

Table 2: Generation means, standard error and individual scaling test for parents and offspring generations (F$_1$, F$_2$, F$_3$ BC$_1$ BC$_2$) for fruit yield

Cross	Year 1	Year 2	Combined
Ab$_2$[d]	134.67±6.74	136.67±5.55	135.97±3.93
Var 19[r]	71.63±6.36	75.63±6.35	73.17±4.10
F$_1$	97.60±8.95	111.30±6.49	104.50±5.81
F$_2$	124.67±13.04	132.30±7.13	128.50±6.15
BC$_1$	122.0±11.27	122.33±4.98	122.17±5.51
BC$_2$	73.67±7.17	77.00±2.83	74.33±4.95
MP	103.15	105.84	104.57
A	11.73±25.17	-3.31±13.12	4.17±31.99
B	-25.59±18.07	-32.30±25.76	-29.01±26.78
C	97.80±55.93	94.33±32.46**	96.17±55.93
D	55.66±32.43	65.33±11.23**	60.50±45.93
[m]	214.33±55.93**	236.55±55.93**	225.42±69.42**
[a]	31.67±4.93**	30.83±7.31**	31.25±6.95**
[h]	-242.00±155.93	-291.57±40.93**	-226.75±159.46
X^2	X^2 [3] = 9.00	X^2 [3] = 8.74	X^2 [3] = 9.05
CR001[d]	537.66±12.17	528.33±12.41	533.00±7.32
Var 53[r]	171.67±12.25	176.66±11.79	172.66±7.62
F$_1$	617.67±14.35	622.00±12.50	619.83±8.55
F$_2$	363.33±20.45	363.00±18.48	359.83±14.31
BC$_1$	486.67±18.59	492.00±17.52	489.33±11.48
BC$_2$	150.33±10.13	153.00±10.14	151.33±9.05
MP	354.67	350.44	352.83
A	-182.19±41.60**	166.33±39.22**	-174.17±25.54**
B	-488.88±56.18**	-489.00±26.58**	-489.33±21.43**
C	-518.00±88.33**	-494.00±79.84*	-506.0±59.47**
D	76.33±55.93	80.67±55.93	78.50±55.93
[m]	507.23±232.64**	512.33±223.39**	509.83±55.77**
[a]	185.00±14.96**	177.33±14.82**	180.16±13.57**
[h]	-713.00±495.00	-707.00±476.10	-710.00±435.82
X^2	X^2 [3] = 11.46	X^2 [3] = 12.00	X^2 [3] = 14.87
Db3 [d]	122.33±2.05	124.67±0.87	123.50±0.92
Fovembot[r]	4.33±1.34	3.47±0.91	3.90±0.75
F$_1$	29.00±1.45	29.0±1.00	29.17±1.14
F$_2$	59.67±9.33	59.33±2.40	59.83±3.50
F$_3$	67.33±3.76	70.00±4.04	68.67±2.59
MP	63.33	64.07	63.70
C	67.33±37.50	39.86±9.90**	53.59±32.22
[m]	-	-	-
[a]	59.99±1.71**	60.00±1.10**	59.79±1.54**
[h]	-	-	-
X^2	X^2 [3] = 4.10	X^2 [3] = 4.23	X^2 [3] = 4.34

**= significant at 1% probability; [d] =donor parent, [r] = recipient parent, [m] =mean, [a] = additive, [d] = dominance A, B, C= Individual Scaling test of Mather (1949).

In intra specie cross CR001 ♂ x Var 53 ♀, the F_1 hybrid mean was larger in magnitude compared to the mid parent value, donor and recipient parents for each year and combined. The generation means in the cross combinations Ab_2 ♂ x Var 19 ♀ and CR001 ♂ x Var 53 ♀ decreased over F_1 to F_2 population. None of the mean of the segregating population equaled the mean of the F_1 hybrid. The generation mean increased over F_1 to F_2 and F_3 generation in the cross Db_3 ♂ x Fovembot ♀. Clearly the F_1 generation mean did not equal the mid-parent value, but are larger than the poor fruit yielding parent. This confirms the individual scaling test results. The three-parameter model showed a significant additive gene [a] and insignificant ($P > 0.05$) dominance gene [d] for fruit yield in the cross Ab_2 ♂ x Var 19 ♀ for each year and combined. However, goodness of fit tests for fruit yield implies the existence of non-allelic interaction in the cross Ab_2 ♂ x Var 19 ♀, CR001 ♂ x Var 53 ♀ and Db_3 ♂ x Fovembot ♀. There is therefore, the need to incorporate additional parameters.

All the five and six-parameter model showed significantly ($P < 0.05$) positive additive gene [a] and dominance by dominance [dd] digenic interaction for CR001 x Var 53 and Ab2 x Var 19 (Table 3). While dominance [d] gene and additive by additive [aa] digenic interaction were significant ($P < 0.05$) though estimates were negative in direction. Among the digenic interaction, the dominant by dominant [dd] digenic interaction predominates. However, duplicate epistatic interaction was found in the inheritance of fruit yield. In addition, estimates of narrow sense heritability were high for each year and combined. The values for AHPH and RHPH were negative for each year and combined. The number of factors affecting fruit yield ranged from 6 to 39 (Table 3). In the cross CR001 ♂ x Var 53 ♀, the additive gene [a] effect, dominance x dominance digenic [dd] interaction, and additive by dominance [ad] digenic were positive and significant ($P < 0.01$). In contrast, additive by additive [aa] digenic interaction were negative and statistically different from zero ($P < 0.05$). The narrow sense heritability estimates were high for fruit yield. The four heterotic models tested for fruit yield showed positive and high values (14.88 to 267.00). The estimates of AMPH were larger in magnitude than their corresponding AHPH. The estimates of RMPH were smaller than RHPH. The number of effective factors affecting fruit yield ranged from 6 to 11. The five -parameter model applied to inter species cross Db_3 ♂ x Fovembot ♀ showed significantly ($P < 0.01$) positive additive gene [a] effect. While dominance gene [d] effect and additive by dominance digenic [ad] were significantly different from zero. Dominance [d] of fruit yield was in direction of the parent with low fruit yield. The estimates recorded for AMPH, RMPH, AHPH and RHPH were negative for each year and combined. The number of effective factors affecting fruit yield ranged from 7 to 36.

Table 3: Estimates of genetic effects for generation means fitted into 5 and 6 parameter model heritability and heterosis for fruit yield

Ab$_2$[d] x Var 19 [r]	**Year 1**	**Year 2**	**Combined**
[m]	124.67±13.04**	132.30±7.13**	128.58±6.15**
[a]	50.33±13.49**	45.33±6.891**	47.83±6.98**
[d]	-116.66±48.19**	-125.16±24.69**	-120.91±24.80**
[aa]	-111.33±46.75**	-130.67±23.95**	-121.00±24.05**
[ad]	18.66±16.08	14.50±7.73	16.58±7.88
[dd]	125.33±50.12*	166.33±35.93**	145.83±36.10**
Hn (%)	95	134	74
AMPH	-5.55	5.47	-0.08
RMPH	-5.38	5.16	-0.07
AHPH	-37.04	-25.37	-31.47
RHPH	-27.50	-18.70	-23.14
N1	12.32	39.78	6.34
N2	12.21	38.40	5.51
Type of gene action	Duplicate epistasis	Duplicate epistasis	Duplicate epistasis
CR001 [d] x Var 53[r]	**Year 1**	**Year 2**	**Combined**
[m]	363.33±20.45**	363.30±18.48**	359.83±14.31**
[a]	336.34±26.54**	338.67±26.61**	337.50±16.91**
[d]	110.33±94.81	109.67±95.02	110.00±60.38
[aa]	-152.67±91.98	-161.33±92.18	-157.00±64.31**
[ad]	153.33±29.68**	161.33±29.75**	157.33±31.09**
[dd]	823.33±137.98**	816.67±138.27**	820.84±101.46**
Hn (%)	93	80	96
AMPH	263.00	271.56	267.00
RMPH	74.15	77.49	75.67
AHPH	80.01	93.67	86.00
RHPH	14.88	17.73	16.14
N1	11.14	6.67	8.38
N2	11.00	6.65	8.38
Type of gene action	Complementary Epistasis	Complementary Epistasis	Complementary Epistasis
Db3 [d] x Fovembot-2 [r]	**Year 1**	**Year 2**	**Combined**
[m]	39.67±3.11**	55.33±2.40**	49.63±7.03**
[a]	59.00±2.68**	60.59±0.88**	59.83±12.23**
[d]	-68.00±10.72**	-54.67±3.54**	-59.89±0.59**
[aa]	-33.67±8.89**	-19.93±2.93**	-44.01±9.86**
[ad]	-	-	-
[dd]	-	-	-
Hn (%)	-	-	-
AMPH	-34.33	-35.07	-34.53
RMPH	-54.20	-54.74	-54.21
AHPH	-93.33	-95.67	-94.33
RHPH	-76.89	-76.74	-76.38
N1	7.34	125	36.22
N2	7.35	125	36.22
Type of gene action	No epistasis	No epistasis	No epistasis

*, **= significant at 5% and 1% probability, [d] = donor parent, [r] = recipient parent, m = mean, [a] = additive, [d] = dominance, [aa] = additive x additive dominance digenic interaction, [ad] = additive x dominance digenic interaction, [dd] = dominance x dominance digenic interaction, AMPH = Absolute mid parent heterosis, RMPH = Relative mid parent heterosis, AHPH = Absolute high parent heterosis, RHPH = Relative high parent heterosis, N1= Effective factors (Wright,1968), N2 = Effective factors (Cookerham, 1986).

DISCUSSION

In any breeding program for development of new varieties, fruit yield is the main criteria. The additive gene effect predominates inheritance of fruit yield in intra species cross Ab$_2$ ♂ x Var 19 ♀ and CR001 ♂ x Var 53 ♀, and inter species cross Db$_3$ ♂ x Fovembot ♀. In a separate study, additive gene [a] effect for fruit yield in *S. melongena* L. was reported by (Patel and Dalal, 1994). The gene for fruit yield is associative among the parents in each cross combination. With additive gene [d] effect, the success of selection will be higher in segregating populations. In the improvement of self-pollinated plants such as eggplant, additive variation (fixable) is of great importance and makes it possible to successfully select better individuals in segregating populations. For this reason, backcross, pedigree, single-seed descent or gametic selection methods are recommended for advancing the segregating populations (Bernado, 2003). In intra species cross Ab_2 ♂ x Var 19 ♀ and inter species cross Db_3 ♂ x Fovembot ♀, dominance of low fruit yield was observed among the generation means. Negative sign of dominance [d] in the cross Ab_2 ♂ x Var 19 ♀ and Db_3 [d] x Fovembot-2 [r] indicated that alleles from the males (Ab_2 and Db_3) are recessive to alleles from the females (Var 19 and Fovembot-2), and the parent with lower fruit yield was responsible for fruit yield. Mather and Jinks (1971, 1982) had noted that negative estimate of dominance gene effect may arise from sampling errors, while Munoz-Falcon *et al.*, (2008) reported that genotype x environment interaction may infer negative estimate of dominance. Negative and significant epistatic effects particularly the [aa] type of digenic interaction in Ab_2 ♂ x Var 19, Db3 [d] x Fovembot-2 [r] and CR001 ♂ x Var 53 ♀ is associated with dispersion and interaction between increasing and decreasing alleles for fruit yield, this is synonymous with dispersion among the inbred lines.

The presence of epistasis has important implications for eggplant breeding. Duplicate epistasis in the cross Ab_2 ♂ x Var 19 ♀ is a function of dominance effects [d] and dominance x dominance [dd] digenic interaction. This kind of epistasis generally hinders the improvement through selection. However, population improvement approaches such as recurrent selection scheme in which large populations are carried forward to later generations will allow for favourable gene combination to be in homozygous state before selection. Also, bi-parental mating would be more effective to accumulate desirable genes and/or to break undesirable linkages. The preponderance of non-additive gene actions were reported by Singh (1981), Dixit, *et al.*, (1984). Kathiria, *et al.*, (1998), Jha (2003) and Aswani and Khandelwal (2005) for fruit yield. Duplicate epistatic gene action implied that selection should be delayed until heterozygosity is reduced in the population, this type of genetic action rapidly slow down breeding progress for development of new varieties through selection. This situation is not favourable compared to complementary type of epistasis due to realized enhanced genetic gain in breeding. In general, disparities in the type of gene action for fruit yield necessitated the choice of selection method that will mop-up several digenic effects for fruit yield gene, to form superior gene combination interacting in favourable manner, and at the same time maintain heterozygosity.

Narrow sense heritability is expression of the reliability with which phenotypic value guides to the breeding value. Moreover, it is the breeder's best estimate of breeding value as it represents the portion of phenotypic variation due to additive effects. Narrow-sense heritability estimates are based on additive genetic variance (fixable component). High narrow sense heritability for fruit yield implies greatest chance of genetic improvement (Bhutani and Dudi, 1982: Vaghasiya *et al.*, 2000). Inheritance of fruit yield gene among the cross combination was under polygenic action with six and thirty-six genes for fruit yield. High heterotic response (CR001 ♂ x Var 53 ♀) for fruit yield was associated with F_1 superiority over the mid parent, and better parent (Kearsey and Pooni, 1996). This is enhanced by positive and significant digenic action combined with dispersion of the gene pairs for fruit yield. The exploitation of heterosis in the cross CR001 ♂ x Var 53 ♀ for fruit yield could be promising for development of hybrid varieties. The result of hybrid vigour over the better parent shows high levels of heterobeltiosis for fruit yield (CR001 ♂ x Var 53 ♀). Positive and negative heterosis for fruit yield are in agreement with the results obtained from studies in *S. melongena* (Suneetha and Kathiria 2005; Munoz-Falcon *et al.,* 2008).

CONCLUSION

It can be concluded that the nature and magnitude of gene effects vary with different cross combinations for fruit yield. Hence, specific breeding strategy has to be adopted for a particular cross to get improvement in fruit yield. Findings indicated a consequence of higher magnitude of interactions, and the preponderance of non-fixable genes compared to fixable. With duplicate type of epistasis found in Ab_2 x Var 19, the selection intensity should be mild in the earlier and intense in the later generations because it marks the progress through selection. Therefore, methods that exploit non-additive gene effect and take care of non-allelic interactions like restricted recurrent selection by way of inter mating among desirable segregates, followed by selection or diallel selective mating or multiple crosses or biparental mating in early segregating generations could be promising for genetic improvement of fruit yield. In addition, few cycles of recurrent selection, followed by pedigree method may also be useful for the effective utilization of all three types of gene effects simultaneously. It will lead towards an increased variability in later generations for effective selection by maintaining considerable heterozygosity through mating of selected plants in early segregating generations.

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