

Quantitative analysis of fruit size and fruit number in *Solanum aethiopicum* group**O.T. Adeniji^{1, 2*}, P. M. Kusolwa¹ and S.W.O.M Reuben¹**¹*Department of Crop Science and Horticulture, Sokoine University of Agriculture P.O. Box 3005, Chuo Kikuu, Morogoro, Tanzania*²*Department of Crop Science and Horticulture, Federal University Oye Ekiti, Nigeria***Abstract**

Fruit length and width, fruits per cluster and fruit clusters per plant are components of fruit yield in fruit vegetable. Inheritance studies in scarlet eggplant is limited due to inadequate research, and *Solanum aethiopicum* in an underutilized crop. The objectives of this study were to evaluate inheritance and genetic action, heritability and heterosis for fruit length and diameter, fruits per cluster and fruit cluster per plant in *Solanum aethiopicum* Gilo and Shum groups. Six generations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) from intra species hybridization were evaluated in a compact family block design with six blocks in three replications. Significant scaling and joint scaling tests for fruits clusters per plant and fruits per clusters indicated inadequacy of additive-dominance model. Additive gene action was important for fruit length and fruit clusters per plant, while dominance gene action moderates inheritance of fruit diameter and fruits per cluster. With dominance gene, hybrid breeding is worthwhile to undertake. The opposite signs of dominance and dominance by dominance digenic interaction for fruit clusters per plant showed a duplicate type of epistasis. Positive heterosis for Absolute Mid Parent Heterosis and Relative Mid Parent Heterosis implied sufficient divergence for fruit length and a platform for genetic improvement. High narrow sense heritability for traits predicts a better effectiveness of selection.

Keywords: *Solanum aethiopicum*, Joint scaling test, Generation mean, Heritability, Heterosis, Digenic interaction, fruit yield improvement

Introduction

Scarlet eggplant belongs to the family Solanaceae and in the subfamily Solanoideae. It is underutilized and indigenous leaf and fruit vegetable in sub-Saharan Africa (Bukonya-Ziraba, 2004; Sunseri et al. 2010). In the species *aethiopicum*, four groups (Aculeatum, Gilo, Kumba and Shum) have been recognized based on distinct morphological features (Plate 1). The Aculeatum group was probably developed from hybridization between Kumba group and *S. Anguivi* (Shippers, 2002), its fruits are medium-sized, round to flattened shape and in clusters of 5 and 8, with 4 to 10

locules. The Gilo group evolved from the Shum group through hybridization and selection (Anaso, 1991). Gilo fruits are round or egg-shaped, smooth or grooved, cream or green colour at commercial harvest, medium to large, smooth or slightly lobed with few to moderate fruits per plant. The leaves and fruits of *S. aethiopicum* Kumba group are used widely in Mali and Mossi empires, northern Ghana and Nigeria for medicinal purpose (Shippers, 2002). The fruits of the Kumba group are large, flattened and multilocular. In contrast, the fruits of the Shum group (Nakati) are small, usually between 12 to 18 mm and 2-3 locules per fruits.

Accessions in the Shum group performed better than the Gilo, Kumba and Aculeatum groups for fruit number, fruits per infructescence and fruit infructescence

per plant. On the other hand fruits of the Shum group are small to medium in size (Adeniji, 2012, 2013).



Plate 1. *Solanum aethiopicum* sub groups (Shum, Kumba, Gilo and Aculeatum)

The fruits of scarlet eggplant are consumed fresh with or without groundnut paste. Also, fruits can be stewed with other vegetables. Both leaves and fruits of the scarlet eggplant are a reliable source of micro and macro nutrients and medicinal uses (Bukenya-Ziraba and Bonsu, 2004; Hedges and Lister, 2007; Tiwari *et al* 2011). At physiological maturity, 100 g of eggplant fruit contains 92.70 per cent moisture, 0.1 g fat, 5.7 g carbohydrate and 1.0 g protein, vitamins and minerals (B1, B6, folate, copper, manganese, magnesium, potassium and fibre (USDA Nutrient Database, 2005). Harvested fruits and leaves of *S. aethiopicum* are increasingly important in ensuring food security and nutrition balance in sub-Saharan Africa. In 2008, about 147,000 ha of eggplants fruits were harvested in African countries (FAO, 2009). In northern Tanzania, a maximum of three production cycles are possible per year, usually under monoculture (Adeniji and Aloyce, 2012). In sub-Saharan Africa, the production of *Solanum aethiopicum* is far below the market demand, growers expect to harvest 32 t ha⁻¹ in Tanzania (Bukenya, 2002). Fruit yield from farmers' fields is low due to absence high yielding varieties and biotic stresses. Low productivity in *Solanum aethiopicum* is sequel to little research attention in comparison to

tomato, pepper, and maize, where crop improvement strategies have culminated in the development of hybrids and open-pollinated varieties by exploiting genetic variation in landraces. In Scarlet eggplant agronomic variation (Adeniji *et al.* 2012a), morphological variation (Adeniji *et al.* 2013), genetic diversity (Adeniji *et al.* 2012b) and association between fruit yield and yield component traits (Adeniji *et al.* 2013) are pre-requisites for the development of hybrids and open-pollinated varieties. If agronomic variation (fruit number, fruit per cluster, fruit cluster per plant, fruit weight) is properly harnessed through hybridization and selection, promising hybrids and open-pollinated varieties will be developed.

The generation mean analysis (GMA) is an important tool to understand the mode of inheritance and genetic control of agronomic traits. This statistical procedure has been extensively used to understand inheritance pattern and gene effects for agronomic traits in different crops (Cavalli, 1952; Mather, 1949; Warner, 1952; Kathiria *et al.*, 1998; Jha, 2003). Statistical procedure as the Generation Mean Analysis (GMA) is useful technique for estimating gene effects for agronomic traits, its greatest merit lies in its ability to estimate epistatic gene effects such as additive x additive [i], dominance x

dominance [l] and additive x dominance [j] effects (Mather, 1949; Mather and Jinks, 1949; 1982). Further, breeders would also like to know how much of the variation for a trait is genetic and to what extent this variation is heritable, because efficiency of selection depends mainly on additive genetic variance and influence of the environment. Whereas dominance gene action would favour production of hybrids, additive gene action implied that standard selection procedures would be effective in bringing about improvement in traits. Additionally, non-allelic interaction in quantitative traits serves as pointer to the type of selection to be advanced in subsequent generations. The presence of epistasis may bias estimates of heritability, heterosis and number of genes controlling a trait. Inheritance studies in scarlet eggplant is limited due to inadequate research, and *Solanum aethiopicum* in an underutilized crop. Genetic information on the mode of inheritance, genetic control, heritability and heterosis for fruit yield and

yield component traits are important for effective breeding strategy and development of hybrids and open-pollinated varieties. This investigation was undertaken to evaluate inheritance and genetic action (additive and dominant gene), non-allelic gene interaction (epistasis), heritability and heterosis for fruit length and diameter, fruits/cluster and fruit cluster/plant.

Materials and Methods

Materials, Field management and Measurements Variety 24 (*S. aethiopicum* Gilo) is a donor parent for fruit length and diameter (Table 1), while *Solanum aethiopicum* Shum group outperform other accessions for fruits/cluster and fruit clusters/plant. Intraspecies hybridization was done between Var 24 ♂ x Ab₂ ♀, Var 24 ♂ x Var 19 ♀, Shum ♂ x Db₃ ♀ to develop six generations (P₁, P₂, F₁, F₂, BCP₁ and BCP₂) (Table 1).

Table 1: Cross combinations investigated for fruit yield component traits

Trait	Cross combination	Species
Fruit length	Var 24 ♂ x Ab ₂ ♀	<i>S.aethiopicum</i> x <i>S.aethiopicum</i> gilo
Fruit diameter	Var 24 ♂ x 19♀	<i>S.aethiopicum</i> x <i>S.aethiopicum</i> gilo
Fruit clusters per plant	Shum ♂ x Db ₃ ♀	<i>S.aethiopicum</i> Shum x <i>S.aethiopicum</i> gilo
Fruits per cluster	Shum ♂ x Db ₃ ♀	<i>S.aethiopicum</i> Shumx <i>S.aethiopicum</i> gilo

The Field evaluation was carried out at Horticultural Training Research Institute, Arusha (latitude 4.88 S, longitude 3.78 E; altitude 1290 m) with an annual rainfall of 700 – 1000 mm. A compact family block design and with four replications was used. A total of six plots constitute a replicate, each plot was allotted to a generation. Experimental plots with three rows of 7 meters long and 0.75 meters between rows was allotted to each non-segregating generation (P₁, P₂ and F₁). While plots with six rows was allotted to each

segregating population (F₂, B₁ and B₂). Seedlings were raised in seedling trays for four weeks, thereafter vigorous seedlings were transplanted to the research field at a spacing of 0.45 m between plants. Split application of inorganic fertilizer NPK (20:10: 10) was applied at the rate of 90 Kg N/ha, 45 kg /ha of P₂O₅ and 45 kg /ha of K₂O. Urea was added at the rate of 120 kg /ha of N at the transplanting and flowering stages. Selecron (EC) was sprayed at the rate of 20 ml/20 I of water at 2 weeks after transplanting to control

pests including cutworms. Weeding was done manually using hoes.

In each cross combination 75 plants were maintained for each parent, 100 plants for F₁ population, 200 plants from each F₁ generation, and 300 plants for each F₂ generation, 150 plants each for backcross generation-1 and backcross generation-2. At maturity, five fruits were randomly picked from ten plants in each generation for determination of fruit length and fruit girth. Fruit length (cm) was measured from the base to tip of the fruit whereas, fruit girth (cm) was measured at the widest diameter of the fruit. Fruits per cluster was estimated by counting the number of fruits in each fruit cluster, while fruit clusters per plant was measured by counting the number of fruit clusters on each plant.

Statistical analysis

Homogeneity of variances of non-segregating generations was tested for using Bartlett's test (Bartlett, 1937). Analysis of variance was done for each year and combined as described by GLM procedure of SAS (2009). Significant mean squares for genotype necessitate analysis of generation mean for each year and pooled. The individual scaling test of Mather (1949) was computed based on the assumption that the populations have non-homogenous variances (Mather and Jinks, 1971). Thereafter the joint scaling test (Mather and Jinks, 1949) which evaluates the goodness - of -fit of the 3-parameter model (mean, additive and dominance effects) to the observed data was done.

The generation mean was computed using Hayman (1974) method which makes use of the multiple linear regression method to fit a six parameter model described by Gamble's (1963). The notations for the six parameter model are the population mean [m]; the pooled additive effects [a]; the pooled dominance effects, [d]; the pooled additive x additive epistatic effects, [aa]; the pooled additive by dominance epistatic effects, [ad]; and the pooled dominance x dominance epistatic effects, [dd]. Narrow sense heritability (H_{2n}) was computed using the formula described by Warner (1952) as $H_{2n} = [2F_2 - (VB_1 - VB_2)] / VF_2$ ($2F_2 - (VB_1, VB_2)$). While the minimum number of effective factors contributing to the inheritance of agronomic traits was calculated using the formula described by Cookerham (1986) and Wright (1968).

Results and Discussion

The analysis of variance showed significant ($P \leq 0.05$) mean squares for fruit length, fruit diameter, fruits/cluster and fruit clusters/plant among the population (Table 2). Year effect recorded significant mean squares for fruits/cluster and fruit clusters/plant. This indicates that the phenotypic performance of the population was influenced by environmental factors. With significant ($P \leq 0.05$) genotypic effects for fruit length, fruit diameter, fruits/cluster and fruit clusters/plant, individual scaling test of Mather (1949), joint scaling test and generation mean analyses were conducted for each year and then two years were combined.

Table 2. Mean square value for fruit length and diameter, fruits/cluster and fruit clusters/plant

Source of Variation	df	Fruit length Var 24 ♂ x Ab ₂ ♀	Fruit diameter Var 24♂x Var 19♀	Fruit clusters/plant Shum ♂ x Db ₃ ♀	Fruits/cluster Shum ♂ x Db ₃ ♀
2011					
Replication	2	0.43	0.02	12.38	1.05
Genotype	5	5.87**	3.10**	425.52**	20.88**
Error	10	0.67	0.39	6.32	0.79
CV (%)		12	12.71	5.31	16.31
Mean		6.86	4.92	47.27	5.44
2012					
Replication	2	0.49	0.07	3.39	9.72**
Genotype	5	5.03**	3.42**	527.25**	21.78**
Error	10	0.74	0.20	16.12	0.32
CV (%)		12	9.27	7.66	9.04
Mean		7.07	4.88	52.38	6.28
Combined					
Year	1	0.33	0.02	235.111**	6.25**
Replication (Year)	4	0.46	0.05	7.88	5.38**
Genotype	5	10.60**	6.49**	939.46**	41.96**
Error	25	0.59	0.25	(4)11.64	0.59
CV (%)		11	10.10	6.84	13.08
Mean		6.97	4.90	49.83	5.81

*, **= significant at 5% and 1% probability; d=donor parent, r=recipient parent, CV= Coefficient of Variability

Fruit length

Fruit length was monitored in the cross Var 24 ♂ x Var 19♀, the mean of F₁ hybrid population was higher than the average recorded for fruit length among the mid-parent (Table 3). Also, the F₂ generation means were consistently larger in magnitude than the corresponding means of the F₁, P₁, P₂ population and MP for each year and combined. Insignificant Mather (1949) scaling test (A, B, C, and D) and joint scaling tests indicates the absence of inter-allelic interactions. Therefore, the possibility of explaining the inheritance of fruit length within the additive–dominance model. The three-parameter model recorded significantly (P < 0.05) positive additive gene. The Hayman six parameter model showed that additive gene was positive and significant (Table 4). On the other hand, dominance gene [d], additive x additive [aa], additive x dominance [ad] and dominance x dominance [dd] digenic interactions

recorded insignificantly positive or negative estimates. Rao (2003) has emphasized the importance of additive gene action for fruit length in *Solanum melongena*. In contrast, Chaudhary and Pathania (2001) and Jha (2003) had reported dominance gene action for fruit length in *Solanum melongena*. Additive gene [d] action in the cross Var 24 ♂ x Ab₂ ♀ provides that fruit length can be improved by simple selection scheme like pedigree selection method. In addition, early selection among segregating generation could rapidly develop new varieties with improved fruit length compared to the donor or mid parent. A significantly positive dominance [d] gene for fruit length indicates that the higher scoring parent was responsible for the increase in fruit length of the F₁ population over the donor and mid-parent. A non-significant digenic interaction ([aa], [ad] and [dd]) suggest no evidence of non-allelic interaction, implying additive gene

action for fruit length. The narrow sense heritability estimate for fruit length was high for each year and combined (Table 5). This indicates that fruit length is consistent with the preponderance of additive genetic variance, which is a fixable component of genetic variation.

AMPH, RMPH and AHPH, RHPH recorded opposite signs. Positive heterosis for AMPH and RMPH suggests that there was sufficient variation for fruit length in the parents, thus providing a platform for genetic improvement.

Table 3. Comparison of means for fruit length and fruit diameter, fruits/cluster and fruit clusters/plant

Fruit length	Year 1	Year 2	Combined	Fruit diameter	Year 1	Year 2	Combined
Var 24[d]	6.73±0.32	6.78±0.31	6.75±0.02	Var 24[d]	5.57±0.19	5.77±0.23	5.83±0.13
Ab ₂ [r]	4.77±0.26	4.77±0.29	4.70±0.18	Var 19[r]	3.76±0.23	3.66±0.22	3.72±0.14
F ₁	6.43±0.39	6.77±0.33	6.55±0.19	F ₁	5.83±0.17	5.83±0.21	5.84±0.13
F ₂	7.80±0.61	7.87±0.58	7.83±0.37	F ₂	4.27±0.18	3.91±0.18	4.12±0.18
BC ₁	8.73±0.54	8.54±0.38	8.63±0.30	BC ₁	5.80±0.23	5.93±0.26	5.87±0.16
BC ₂	7.19±0.45	7.17±0.49	7.18±0.30	BC ₂	4.00±0.14	4.07±0.24	4.03±0.13
MP	5.75	5.78	5.73	MP	4.67	4.72	4.78
A	4.30±1.04**	2.97±1.58	3.63±1.99	A	0.13±0.51	0.26±0.62	0.08±0.40
B	2.71±1.04	2.92±1.23	2.82±1.52	B	-1.59±0.41	-1.35±1.10	-1.49±1.35
C	6.96±4.59	2.93±1.38	6.45±3.63	C	-4.27±2.81	-5.11±3.26	-4.68±2.53
D	-0.02±0.70	0.01±0.70	-8.81±8.70	D	1.27±1.01	2.00±1.69	-1.63±1.19
[m]	5.65±4.97	6.15±4.61	5.89±4.32	[m]	2.30±4.09	0.12±2.40	1.51±3.52
[d]	1.05±0.35*	1.35±0.69*	1.19±0.53*	[d]	1.06±0.24**	1.05±0.27**	1.05±0.23**
[h]	7.67±0.41	10.00±0.57	9.00±0.50	[h]	4.33±10.06	8.02±5.62	6.18±7.40
χ ²	Ns	ns	Ns	χ ²	ns	ns	ns
Fruit clusters/plant				Fruits/cluster			
Shum[d]	66±1.21	71±3.23	69±6.70	Shum[d]	7.67±0.41	10.00±0.57	9.00±0.50
DB ₃ [r]	30±0.43	32±4.33	31±4.67	DB ₃ [r]	2.33±0.47	3.00±0.47	2.37±0.44
F ₁	44±2.33	48±2.33	46±6.97	F ₁	6.00±0.57	6.33±0.57	6.16±0.50
F ₂	47±21.32	57±26.89	52±49.87	F ₂	7.33±0.88	7.67±0.67	7.50±0.57
BC ₁	52±12.45	60±14.44	56±14.27	BC ₁	7.00±0.57	7.33±0.57	7.17±0.48
BC ₂	43±14.55	46±22.26	44±29.07	BC ₂	2.00±0.57	3.33±0.57	3.00±0.41
MP	48	52	50	MP	5.00	6.33	5.67
A	4.30±1.04**	2.97±0.90*	3.63±1.68*	A	0.33±1.35	-1.67±1.46	-0.83±0.28*
B	3.71±1.04*	3.92±1.08*	3.82±1.52*	B	-2.33±1.89	-2.67±1.65	-2.33±0.65**
C	6.96±2.59*	5.93±2.46*	6.45±1.63*	C	7.66±4.18	5.00±0.72	6.33±1.02**
D	-0.02±0.70	0.01±0.70	-8.81±8.70	D	-5.00±1.53**	4.67±0.72**	4.83±1.51*
[m]	5.65±4.97	6.15±4.61	5.89±4.32	[m]	14.83±2.89**	5.83±8.13*	15.33±16.42*
[d]	1.05±0.35*	1.35±0.69*	1.19±0.53*	[d]	5.17±0.58**	3.50±0.28**	3.33±0.81*
[h]	7.67±0.41	10.00±0.57	9.00±0.50	[h]	-21.17±6.97*	-23.16±14.10	-22.17±14.37
χ ²	**	*	**	χ ²	*	*	*

*, **= significant at 5% and 1% probability; d=donor parent, r=recipient parent, [m] = mean, [d] = additive, [h] = dominance, A, B, C and D = Individual Scaling test of Mather (1949)

Fruit diameter

The fruit diameter in F₁ hybrid of the cross Var 24 ♂ x Ab₂ ♀ is wider compared to the mid-parent (F₁ > MP) (Table 2). The generation mean for fruit diameter decreased over F₁ and F₂ generations. On the other hand, the mean for fruit diameter in the BC₁ generation was closer to the donor parent. The A, B, C and D scale tests of Mather (1949) and joint scaling test are insignificant (P > 0.05) (Table 3). This suggests additivity for fruit diameter and the absence of digenic interaction. The three parameter model showed

preponderance of additive gene [d] compared to dominance gene [h]. The main effects ([a] + [d]) are positive and significant (P < 0.01) (Table 4), but dominance gene [d] recorded high magnitude compared to additive gene [a]. For each year and combined, additive x additive [aa] digenic interaction had positive and significant (P < 0.01) estimates. However, dominance gene [h] predominates inheritance of fruit diameter compared to additive gene [a]. With dominance gene [h] hybrid breeding is worthwhile to undertake. In another investigation, Chaudhary and Pathania

(2001) and Jha (2003) had reported dominance gene action for fruit diameter in *Solanum melongena*. Heritability estimates in narrow sense for fruit diameter are high, the AMPH, RMPH,

AHPH and RHPH recorded positive estimates, and a maximum of five genes are involved in the inheritance of fruit diameter (Table 5).

Table 4: Estimates of genetic effects for fruit length, fruit diameter, fruit clusters/plant and fruits/cluster

Fruit length	Year 1	Year 2	Combined	Fruit diameter	Year 1	Year 2	Combined
Var 16 x Var 19				Var 16 x Var 19			
[m]	7.80±0.37**	7.82±0.39**	7.83±0.37**	[m]	4.27±0.18**	3.97±0.16**	4.12±0.19**
[a]	1.83±0.67**	1.35±0.70**	1.59±0.84**	[a]	1.80±0.52*	1.83±0.36*	1.85±0.28**
[d]	0.78±2.32	0.53±2.51	0.65±1.58	[d]	3.53±1.82*	5.11±1.31**	4.32±1.02**
[aa]	-0.03±2.31	-0.03±2.48	-0.00±1.55	[aa]	2.53±1.77	4.00±1.27**	3.27±0.90**
[ad]	0.78±0.74	0.02±0.76	0.40±0.49	[ad]	0.73±0.57	0.81±0.41	0.70±0.31
[dd]	-7.03±3.46	-5.27±3.65	-6.45±4.30	[dd]	-0.80±2.65	-2.90±1.98	-1.35±1.45
Fruit clusters/plant Shum x Db3				Fruits/cluster Shum x Db3			
[m]	47.23±5.31**	24.34 2.85**	53.33 1.19**	[m]	7.33±0.88**	7.66±0.67**	7.55±0.32**
[a]	10.00±2.00**	14.00±3.27**	14.16±0.44**	[a]	4.33±0.75**	4.00±0.46**	4.17±0.44**
[d]	-21.65±7.38*	-20.00±6.70*	-9.16±1.53**	[d]	-8.83±2.88**	-9.50±1.65**	-9.18±0.58**
[aa]	-1.33±7.17	-17.33±1.35**	-9.17±1.53**	[aa]	-10.00±2.51**	-9.33±1.60**	-9.67±1.53**
[ad]	-8.00±2.28**	-5.06±1.60*	-4.83±0.09**	[ad]	1.16±0.81	0.50±0.51	0.83±0.49
[dd]	-6.67±0.67**	-4.33±1.03*	-13.00±1.60*	[dd]	12.33±3.76	13.17±2.40***	13.00±2.50**

*, ** = significant at 5% and 1% probability, [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

Table 5: Estimates of narrow sense heritability and heterosis for fruit length, fruit diameter, fruit clusters/plant and fruits/cluster

Fruit length Var 24 ♂ x Ab ₂ ♀	Year 1	Year 2	Combined	Fruit diameter Var 16 ♂ x Var 19 ♀	Year 1	Year 2	Combined
Hn (%)	64	85	74	Hn (%)	136	52	75
AMPH	0.85	1.00	0.82	AMPH	1.16	1.11	1.05
RMPH	9.91	17.33	14.31	RMPH	24.84	23.51	21.97
AHPH	-0.31	-0.01	-0.20	AHPH	0.26	0.06	0.01
RHPH	-4.45	-0.14	-2.96	RHPH	0.05	10.29	0.17
N1	1.11	0.70	0.73	N1	0.31	4.83	0.97
N2	1.10	0.70	0.73	N2	0.30	4.83	0.98
Fruit clusters/plants 55 ♂ x 52 ♀				Fruits/cluster Shum ♂ x Db ₃ ♀			
Hn (%)	158	93	113	Hn (%)	72	117	75
AMPH	-3.66	-3.50	-3.75	AMPH	1.00	-0.33	0.33
RMPH	-7.57	-6.79	-7.51	RMPH	20.00	-5.21	5.82
AHPH	-21.66	-22.67	-22.33	AHPH	-1.67	-4.00	-3.00
RHPH	-32.65	-32.08	-32.60	RHPH	-21.77	-40.00	-33.33
N1	14.52	8.35	3.97	N1	2.50	5.75	11.83
N2	15.26	8.14	3.86	N2	2.50	5.72	11.69

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))

Fruit clusters/plant

Shum is a donor parent for fruit clusters/plant (Table 2). In the cross Shum ♂ x Db₃ ♀, the mean for fruit clusters/plant among the F₁ population skewed to mean of the recipient parent (Db₃). While the

mean of BC₁ generations was located closer to the donor parent. Mather (1949) individual scale tests (A, B and C) and joint scaling tests were significant (P < 0.01) (Table 3). Significant Mather (1949) A, B and C scale tests and joint scaling

tests imply that additive-dominance model was inadequate to explain the inheritance of fruit clusters/plant. The fit of the six parameter model showed significantly ($P < 0.05$) positive additive gene effects, dominance [d] was negative and significant ($P < 0.05$). Dominance in direction of the lesser parent for fruit clusters is undesirable (Table 4). Non-allelic interaction (additive x additive [aa], additive x dominance [ad], dominance x dominance [dd] are significantly ($P < 0.05$) positive or negative. Significantly positive additive x dominance digenic [ad] digenic interaction indicates an increasing effect of fruit clusters, while complementary

epistatic gene implies that fruit clusters/plant skewed to the recipient parent. Therefore, the preponderance of dominance towards the parent with fewer fruit clusters. With epistatic gene action for fruit diameter, early selection among segregating generation is not worthwhile. Estimates of narrow sense heritability are high (113%, 158%, and 93%), the magnitude and direction of heterosis for fruit clusters/plant varied (positive or negative) (Table 5). RHPH and AHPH marked high values compared to AMPH and RMPH. Inheritance of fruit clusters/plant was governed by 3.97 and 15 genes



Plate 2. Segregating populations (F₁ and F₂) for Fruits/cluster

Fruits/cluster

In intraspecific cross Shum ♂ x Db₃ ♀, the donor parent (Shum ♂) had higher fruits/cluster compared to Db₃ (Table 3). The fruits/cluster in F₂ population is greater than the F₁ hybrid mean. The first backcross generation recorded higher fruits/cluster compared to second backcross generation. The A, B, C and D scale tests of Mather (1949) and Joint scaling test had significant ($P < 0.01$) estimates. This result signifies both additive and non-additive gene for fruits/cluster. Additive gene [a] predominates the expression of fruits/cluster in the cross Shum ♂ x Db₃ ♀, due to positive and significant ($P < 0.01$) estimates (Table 4). With additive gene for fruits/cluster, early selection among the

segregating generation is worthwhile, despite gene pairs for fruits/cluster being associative among the parents, and this trait was largely depressed among the segregating population. On the other hand, dominance gene [d] was negative and significant ($P < 0.01$) for each year and combined. Digenic interaction components showed greater manifestation in the expression of fruits/cluster compared to the main effects. Among the digenic interaction components, dominance x dominance digenic [dd] interaction was significantly positive and larger in magnitude compared to additive x additive [aa] and additive x dominance digenic interaction [ad]. Duplicate type of epistasis in the inheritance of fruits/cluster, the breeding implication of this type of epistasis is that difficulties might be

encountered in the process of developing new varieties with improved fruits/cluster. Therefore, to circumvent this early selection among segregating generations should be mild and intense in the later generations. Duplicate epistatic gene effects for fruit clusters/plant was reported by Jha (2003), Patel (2003) and Aswani and Khandelwal (2005) in *Solanum melongena*. With duplicate epistasis, recurrent selection scheme in which large populations are carried forward to later generations is a worthwhile breeding procedure. This allows for the fruit diameter gene to be in the homozygous state before selection. High narrow sense heritability for fruit clusters suggest a large proportion of variability was additive, with minimal influence of the environment. Also, individual's superior for fruit diameter possess desirable genes and should transmit fruit diameter gene to their offspring leading to homozygosity in the later generations (Prabhu et al. 2009). With positive heterosis for F₁ hybrid over mid-parent, a considerable improvement of fruit yield is expected. However, breeder companies may consider the exploitation of heterosis in this cross to develop hybrids with high fruits per cluster. On the other hand, fruits resulting from this cross, Shum ♂ x Db₃ ♀ are small sized fruits. Hence backcrossing to Db₃ and selection may recover considerable fruit length and diameter in subsequent generations due to additive gene action for these traits. High heritability in narrow sense for fruit clusters/plant (Table 5) signifies a high proportion of additive gene [d] action and low influence of environmental factors and dominance. The superiority of the F₁ hybrid over the mid-parent for fruit clusters/plant indicates that the F₁ population is closer to the dominant parent, and selection of this cross may be worthwhile for successful exploitation for the commercial hybrid production. This is reflective of preponderance of partial dominance gene action.

Conclusions

The individual scaling test A, B, C, and D and joint scaling test of Hayman (1974) revealed that additive and dominance gene action and inter-allelic interactions (duplicate epistasis) in inheritance of fruit length, fruit diameter, fruit clusters/plant and fruits/cluster. With additive gene action for fruit length, pedigree selection is a worthwhile procedure for development of new varieties with improved fruit length and fruit cluster. Duplicate type of epistasis found for fruit diameter, fruits/cluster and fruit clusters/plant limit the progress in developing new varieties. Therefore restricted recurrent selection through inter-mating among desirable segregates for fruit diameter, fruit clusters and fruits/cluster, followed by selection or diallel selective mating or biparental mating in early segregating generations could be promising for genetic improvement for these traits. With high heritability and heterosis for fruit length, fruit diameter, fruit clusters/plant fruits/clusters, selection would be effective for development of open-pollinated varieties and commercial exploitation of heterosis for fruit yield.

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