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Genetics of Quantitative Traits in muskmelon (*Cucumis melo* L.)

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ABSTRACT: To unravel genetics of quantitative traits (QTs), most researcher's attempts are based either on first or second degree statistics, and rarely both. Use of both first and second degree statistics provide the most comprehensive mode of action of genes controlling QTs in crop plants. Meanwhile, genetic analysis based on third and fourth degree statistics is powerful and useful in detecting and characterizing the nature of epistasis. Genetics of fruit yield and its component traits (including TSS as quality trait) was unravelled using a combination of first and second degree and also third and fourth degree statistics in muskmelon. The results based solely on first and second degree statistics were contradictory. While, first degree statistics suggested the predominance of genes with dominance effects, second degree statistics indicated the predominance of additive gene effects in controlling the inheritance of most QTs investigated. However, the combination of first and second degree statistics revealed the importance of both additive and dominance genetic effects in the inheritance of average fruit weight, TSS and fruit cavity size in the genetic background of 21KGSB-258 × 21KGSB-93. High magnitude of estimates of additive gene effects [d] and additive genetic variance (σ^2_A) coupled with low magnitude / non-significant dominance gene effects [h] and non-significant dominance genetic variance (σ^2_D) suggested high frequency of increasing effect genes controlling the inheritance of average fruit yield, average fruit weight, fruit cavity size and TSS in the genetic background of 21KGSB-218 × 21KGSB-54. Bi-parental mating in F_2 generations before exercising selection is suggested to reduce dominance genetic effects to increase the effectiveness of selection for fruit weight, TSS and cavity size in the cross 21KGSB-258 × 21KGSB-93. Simple selection in F_2population is expected to result in rapid genetic gains for average fruit yield, average fruit weight, fruit cavity size and TSS in the genetic background of 21KGSB-218 × 21KGSB-54.

Keywords: Muskmelon, Quantitative traits, Additive effect, Additive genetic variance, Dominance effect, Dominance genetic variance.

INTRODUCTION

Muskmelon (*Cucumis melo* L.) is one of the most economically important fruit crops, belongs to the family Cucurbitaceae. Muskmelon is widely cultivated around the world for its sweet, juicy flesh and refreshing flavour, making it a favourite in many cuisines and a staple of summer diets. Muskmelon provides numerous health benefits as they are rich in vitamins A and C, potassium, and dietary fibre (Chakrabarti *et al.*, 2001). They are known for their hydrating properties. The fruit juice is nutritive and acts as demulcent and diuretic drink. Juice is also remedy for skin diseases, tan freckles and in case of dyspepsia. The seeds are edible and its kernel is rich in oil (40-44%). In addition to their nutritional value, muskmelons are also appreciated for their delicious taste and refreshing qualities, making them a popular choice during the summer season. Breeding for quantitative traits in muskmelon is essential for achieving significant advancements in yield. Efficient collection of genetic information and a rapid application of this information to breeding, is clearly a priority in a crop like melon. This is true of quantitative traits, which have genetic complexity and are subjected to environmental fluctuations. Through targeted selection and breeding, breeders can develop muskmelon varieties that meet the needs of farmers, consumers, and the agricultural industry as a whole. The effectiveness of breeding muskmelon hinges on comprehensive information on genetics of target traits. To elicit such genetic information, it is necessary to understand the nature and magnitude of genetic variation using appropriate genetic models.

Genetics of productivity per se traits could be unravelled employing first-, second-, third- and fourth-degree statistics. Developing and testing digenic epistasis-independent (additive-dominance model) and epistasis-inclusive models are popular methods of unravelling genetics of productivity per se traits at first

degree statistics level (popularly known as generations mean analysis). Reported literature indicates the use of either first degree or second-degree statistics-based approaches and rarely both for genetic analysis of quantitative traits in crop plants. However, analysis of first- and second-degree statistics are not mutually exclusive alternatives. They are genetically complementary to each other (Mather and Jinks 1982; Kearsey and Pooni 1996). Joint application of both approaches provides complementary and comprehensive information about genetic control of quantitative traits (Kearsey and Pooni 1996). Meanwhile, skewness, the third-degree statistics and kurtosis, the fourth-degree statistics are also powerful and useful in detecting and characterizing the nature of gene action. However, such studies have not yet been attempted in muskmelon. Under these premises, the present study was carried out with an objective to unravel, interpret and discuss muskmelon breeding implications of genetic parameters estimated based on first-, second-, third- and fourth-degree statistics

MATERIAL AND METHODS

Basic experimental material and development of experimental material. The basic material consisted of two pairs of parental genotypes (1) P_1 (21KGSB-258) and P_2 (21KGSB-93); (2) P_1 (21KGSB-218) and P_2 (21KGSB-54) contrasting for yield and component traits including total soluble solids (TSS) as quality trait (Table 1). Involving these four parents, two crosses *viz*., C_1 (21KGSB-258 × 21KGSB-93) and C_2 (21KGSB-218 × 21KGSB-54) were affected. The two crosses constituted the experimental material. For affecting the crosses, the designated male and female flowers were bagged a day prior to anthesis (emasculation of designated female flower has to be done if and romonoecious). On the next day morning, female buds/emasculated flowers were pollinated using the pollen grains collected from designated male parents of afore-mentioned two planned crosses (C_1 and C_2) during rabi season 2021. The seeds of the four parents and all the F_1 seeds germinated and survived to maturity during summer 2022. F_1 plants of both crosses were raised and selfed to produce F_2 generation as well as backcrossed to corresponding parents to produce BC_1 and BC_2 generations. Six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) for each of the two crosses were evaluated for four QTs (average fruit yield, average fruit weight, TSS and fruit cavity size) at the experimental plots of Namdhari Seeds, Pvt. Ltd., Itakudibbanahalli, Tumkur, during *Kharif* 2022 and the experimental site is located at 13.8162° N, 77.3166° E and 787m above mean sea level.

Data recording. Data was recorded on four quantitative traits *viz*., average fruit yield, average fruit weight, TSS and fruit cavity size on five plant of the parents and F_1, and for each of the F_2 and backcrossed plants of two crosses (C_1 and C_2) following the methodology detailed in Table 2.

Statistical analysis. Means and variances in respect of above-mentioned fruit traits were calculated for each population using the data recorded on individual plants as detailed below

$$\text{Mean} = \bar{X}\ \Sigma\ \frac{X_i}{n}$$

$$\text{Variance} = \frac{\Sigma\ X_1^2 - \left(\frac{\Sigma x^2}{n}\right)}{n-1}$$

$$\text{Standard error (SE)} = \sqrt{\text{Variance of polulaton} / n}$$

Where,

x_i = i^{th} observation of a population

n = Number of observations

Mean of the data recorded on five plants in P_1, P_2, F_1 and data recorded on individual F_2, BC_1 and BC_2 plants were used for the following statistical analysis.

Estimation of first-degree statistics-based gene effects: First degree statistics-based gene effects were estimated using the following perfect-fit solutions based on six parameter model (Hayman, 1958).

Mean $= \hat{m} = \frac{1}{2}\bar{P}_1 + \frac{1}{2}\bar{P}_2 + 4\bar{F}_2 - 2\overline{BC}_1 - 2\overline{BC}_2$

Additive gene effect = $[\hat{d}] = \frac{1}{2}\bar{P}_1 + \frac{1}{2}\bar{P}_2$

Dominance gene effect = $[\hat{h}] = 6\overline{BC}_1 + 6\overline{BC}_2 - 8\bar{F}_2 - \bar{F}_1 - \frac{3}{2}\bar{P}_1 - \frac{3}{2}\bar{P}_2$

Additive × Additive gene effect = $[\hat{i}] = 2\overline{BC}_1 + 2\overline{BC}_2 - 4\bar{F}_2$

Additive × Dominance effect = $[\hat{j}] = 2\overline{BC}_1 - \bar{P}_1 - 2\overline{BC}_2 + \bar{P}_2$

Dominance × Dominance effect = $[\hat{l}] = \bar{P}_1 + \bar{P}_2 + 2\bar{F}_1 + 4\bar{F}_2 - 4\overline{BC}_1 - 4\overline{BC}_2$

Statistical significance of gene effects was examined using 't' test (Mather and Jinks, 1982).

Estimation of second-degree statistics-based genetics (components of genotypic variation)

Estimation of additive genetic variance(σ^2_A) and dominance genetic variance(σ^2_D)

σ^2_A and σ^2_D were estimated using the following equations (Mather and Jinks 1982)

$\sigma^2_A = 2[2VF_2 - (VB_1 + VB_2)]$

$\sigma^2_D = 4[(VB_1 + VB_2) - VF_2]$

Estimation of third- and fourth-degree statistics-based genetics. Skewness, the third-degree statistic and kurtosis, the fourth-degree statistic were estimated as per Snedecor and Cochran, (1994) using the 'SPSS version 16' software program to understand the nature of distribution of F_2 and back cross population for average fruit yield, average fruit weight, total soluble solids (TSS) and fruit cavity size.

Kurtosis indicates the relative number of genes controlling the traits (Robson, 1956). Three types of kurtosis are recognized based on the value which depends on distribution curve.

If kurtosis value = 3 = Normal curve = Mesokurtic

If kurtosis value > 3 = Leaping curve = Leptokurtic

If kurtosis value < 3 = Flat curve = Platykurtic

Genetic expectation of coefficient of skewness of distribution of $F_2$and backcross population is a function of number of genes and parameters that specify their

additive main genetic and digenic additive × additive epistatic interaction effects (Pooni *et al*., 1977). The co-efficient of skewness values which range from -3 to +3. The type of distribution based on the skewness values are as follows.

If skewness value is zero = symmetrical distribution

If skewness value is negative = negatively skewed distribution

If skewness value is positive= positively skewed distribution

Table 1: Description of fruit traits of commercial importance among parents used to derive crosses in muskmelon

Parents	Fruit yield (Kg plant^{-1})	Fruit weight (Kg fruit^{-1})	TSS (^{0}Brix)	Fruit cavity size(cm)
21KGSB-258	3	0.7	5	1.5
21KGSB-218	0.9	0.9	13	0.9
21KGSB-93	10	1.2	7	2.96
21KGSB-54	3	0.6	9	1

Table 2: Description on method of recording observation of fruit traits of commercial importance.

Sr. No.	Trait	Method of Observation	References
1.	Fruit yield (Kg plant^{-1})	The yield of harvested fruits of all pickings from 5 plants from P_1, P_2, $F_1$and the average fruit yield per vine was calculated and for each plant in F_2, BC_1 and $BC_2$was taken.	(Gaikwad *et al*., 2016; Feyzian *et al*., 2009; Rodriguez *et al*., 2002)
2.	Fruit weight (Kg fruit^{-1})	Weight of randomly chosen 3 individual fruits harvested at maturity from each of 5 plants in P_1, P_2, $F_1$and 3 fruits from each individual of F_2, BC_1 and $BC_2$was recorded. Mean fruit weight was calculated and expressed in Kilograms fruit^{-1}from each plant.	(Ibrahim, 2012; Fergany *et al*., 2011; Mishra *et al*., 2017)
3.	TSS (^{o} Brix)	Flesh of three fruits in each of 5 plants from P_1, P_2, $F_1$and 3 fruits from each individual of F_2, BC_1 and BC_2 were crushed separately and a drop of juice was placed on hand refractometerand the reading was noted and expressed in percentage/^{o}Brix.	(Stepansky *et al*., 1999; Rodriguez, 2002)
4.	Fruit cavity size (cm)	Three fruits from each of 5 plants in P_1, P_2, $F_1$and 3 fruits from each individual of F_2, BC_1 and BC_2 were taken and cavity size was measured using a centimetre scale after making a transverse cut across the melon fruit.	(Ahmed, 2009; Javanmard *et al*., 2018)

Table 3: Interpretation based on combination of additive genetic effects [a] and additive genetic variance (σ^2A).

Additive genetic effects [a]	Additive genetic variance (σ^2A)	Interpretation
Small	Large	Dispersion of increasing and decreasing alleles between parents. Hence mutual cancellation of effects of increasing and decreasing alleles
Large	Large	Prevalence of large additive gene effects
Large	Small and Non-significant	Effects of individual gene controlling trait are very small (<1.0).

RESULTS AND DISCUSSION

Estimates of quantitative trait means for average fruit yield, average fruit weight, fruit cavity size and TSS among parental lines and segregating populations derived from C_1 and C_2 crosses. Mean fruit yield among parents ranged from 0.92 Kg (21KGSB-93) to 11.50 Kg (21KGSB-218). Average fruit weight ranged from 0.67 Kg in 21KGSB-54 to 1.04 in 21KGSB-218. Mean TSS was greater for fruits produced by the parental line 21KGSB-93 (12.50°Brix) while, 21KGSB-258 produced fruits with lower TSS (5.10 °Brix). 21KGSB-93 produced smaller cavity

sized fruits (0.91 cm) compared to 21KGSB-218 (2.96 cm). Large differences in means across quantitative traits among parental lines substantiate their use in deriving segregating populations used in present investigation (Table 5).

Arithmetic mean is a measure of central tendency and often used in summarizing the data points. It picturizes the tendency of individuals in the populations to congregate in the distribution. F_1 hybrid developed from the cross C_2 showed higher trait means for fruit yield, fruit weight, fruit cavity size and TSS in comparison to the cross C_1 (Table 5). Similarly, segregating generations (F_2, BC_1 and BC_2) derived from the cross C_2 exhibited higher trait means for all the four fruit traits of commercial importance compared to C_1 cross. Based on the comparison of trait means among two crosses, C_2 cross is better over C_1 for average fruit yield, average fruit weight and TSS as preferred by farmers and consumers and could be considered as potential cross in recovering superior segregants for these three commercially important fruit traits. Higher trait's mean indicates the presence of genes that enhances traits phenotype (Dudley, 1982, 1984; Melchinger, 1987; Bernardo, 2020) and hence maximizing the chances of recovering superior advanced breeding lines (ABLs). However, in melon smaller fruit cavity sized fruits are preferred over larger ones (Nunes *et al*., 2005). F_1 and other segregating generations derived from C_2 cross showed higher trait mean for fruit cavity size than C_1 cross, this difference could be due to the fact that one of the parents involved in (21KGSB-218 × 21KGSB-54) is 21KGSB-218 which produced fruits with larger fruit cavity (2.96 cm) and in (21KGSB-258 × 21KGSB-93), 21KGSB-93 as a parent had smaller fruit cavity size. Considering the fact that larger fruit cavity size is not preferred in the market, C_1 cross could be considered as desirable in producing fruits with smaller internal fruit cavity.

Segregating population derived from C_2 cross (21KGSB-218 × 21KGSB-54) registered high variance for average fruit yield, average fruit weight, fruit cavity size and TSS indicating the population to be promising. There by suggesting to advance individuals of this segregating population to stabilize and isolate superior breeding lines with higher fruit yield, fruit weight and TSS in advanced generations (Table 6).

First degree statistics-based genetics. Phenotypic selection in quantitative traits is slow due to segregation at numerous loci and due to effects of environment on phenotype. Hence, in order to probe into various genetic effects affecting quantitative traits in melon, six generation mean analysis (Hayman, 1958; Jinks and Jones, 1958; Mather and Jinks, 1971) was employed. Further, detection, estimation and interpretation of non-allelic interaction has progressed much farther at the level of first-degree statistics as their effects are less confounded. Kinds of experiments required for their analysis are both smaller and simpler.

In the present study, significance of joint scaling test indicated inadequacy of first-degree statistics-based simple additive-dominance (A-D) model in explaining the inheritance of average fruit yield, average fruit weight, fruit cavity size and TSS (Table 7 and 8). Non adequacy of A-D model could be attributed to the involvement of parameters specifying di-genic epistasis and/or genotype × environment interaction (GEI). We included only di-genic epistasis parameters namely additive × additive [i], additive × dominance [j] and dominance × dominance [l] in the A-D model assuming the absence of GEI or GEI is of non-crossover type (Mather and Jinks 1982).

Table 4: Interpretation based on combination of dominance genetic effects [d] and dominance genetic variance (σ^2D).

Dominance genetic effects [d]	Dominance genetic variance (σ^2D)	Interpretation
Significant, positive	Significant	Directional dominance for increasing alleles
Significant, negative	Significant	Directional dominance for decreasing alleles
Non-significant	Significant	Ambi-directional dominance
Non-significant	Non-significant	No dominance
Significant, small	Non-significant	Low dominance

Table 5: Estimates of means among six generations with their standard error derived from crosses, C_1 and C_2 for average fruit yield, average fruit weight, fruit cavity size and TSS in melon.

Generations/ populations	Sample size	Fruit yield (Kg plant^{-1})		Fruit weight (Kg fruit^{-1})		Fruit cavity size (cm)		TSS(°Brix)	
		C_1	C_2	C_1	C_2	C_1	C_2	C_1	C_2
P_1	10	2.97 ± 0.05	11.50 ± 0.94	0.72 ± 0.04	1.04 ± 0.04	1.30 ± 0.05	2.96 ± 0.06	5.10 ± 0.10	7.00 ± 0.21
P_2	10	0.92 ± 0.07	3.00 ± 0.14	0.93 ± 0.04	0.67 ± 0.02	0.91 ± 0.01	1.02 ± 0.02	12.50 ± 0.34	8.80 ± 0.29
F_1	10	2.00 ± 0.04	9.16 ± 0.93	0.71 ± 0.02	0.79 ± 0.03	1.08 ± 0.05	2.54 ± 0.04	6.30 ± 0.26	7.60 ± 0.27
F_2	100	1.94 ± 0.18	3.60 ± 0.31	0.43 ± 0.04	0.75 ± 0.04	1.00 ± 0.02	2.01 ± 0.06	6.15 ± 0.12	7.08 ± 0.16
BC_1	75	3.66 ± 0.25	6.44 ± 0.51	0.56 ± 0.03	1.06 ± 0.04	1.19 ± 0.02	2.96 ± 0.06	6.60 ± 0.13	7.09 ± 0.16
BC_2	75	2.06 ± 0.13	2.43 ± 0.22	0.41 ± 0.02	0.48 ± 0.02	1.12 ± 0.02	1.75 ± 0.04	6.40 ± 0.15	6.97 ± 0.18

Table 6: Estimates of variances among six generations derived from crosses, C_1 and C_2 for average fruit yield, average fruit weight, fruit cavity size and TSS in melon.

Generations/ populations	Sample size	Variance							
		Fruit yield (Kg plant^{-1})		Fruit weight (Kg fruit^{-1})		Fruit cavity size (cm)		TSS (^{0} Brix)	
		C_1	C_2	C_1	C_2	C_1	C_2	C_1	C_2
P_1	10	0.03	8.78	0.02	0.02	0.03	0.04	0.10	0.44
P_2	10	0.05	0.19	0.02	0.01	0.002	0.004	1.17	0.84
F_1	10	0.02	8.71	0.005	0.005	0.02	0.02	0.68	0.71
F_2	100	3.46	9.50	0.18	0.15	0.03	0.35	1.42	2.66
BC_1	75	4.82	19.61	0.03	0.14	0.05	0.31	1.26	1.98
BC_2	75	1.23	3.70	0.02	0.03	0.05	0.13	1.62	2.60

Table 7: Estimates of components of generation means among six generations derived from C_1cross and test for adequacy of A-D model in the inheritance of commercially important fruit traits.

Characters	m	d	h	χ^2	P value	Adequacy of Additive-Dominance (A-D) model
Fruit yield (Kg plant^{-1})	1.94	1.03	1.06	15.91	0.001	Inadequate
Fruit weight (Kg fruit^{-1})	0.58	0.04	-0.02	226.90	0.00	Inadequate
Fruit cavity size (cm)	1.07	0.15	0.03	44.48	0.00	Inadequate
TSS (^{0} Brix)	7.16	-1.82	-1.29	232.38	0.00	Inadequate

The additive effect of genes reflects those effects which are expected to be manifested in a genotype to which the genes are being substituted for their alternate forms / alleles (Mather and Jinks, 1982; Kearsey and Pooni, 1996). Significant but low magnitude or non-significant additive genetic effects in the inheritance of most of the traits in two crosses (Table 9 and 10) could be attributed to genes with either low magnitude of additive effects or those with different degrees of nullifying increasing and decreasing effects (Mather and Jinks 1982; Kearsey and Pooni 1996).

First degree statistics is valuable for detection and estimation of additive, dominance and epistatic gene effects. However, it does have limitations. Distribution of increasing and decreasing effect genes between the parents causes serious bias to the estimates of additive and additive × additive based gene effects. However, dominance [h] and dominance × dominance [l] gene effects are independent of the degree of gene distribution due to which the combined estimates of [h] and [l] could be considered to be the best representative of sign and magnitude of individual h's and l's, respectively. Hence, practically [h] and [l] are the only components which can safely be used to determine the type of epistasis that may have influence on the observed per se performance of generations for quantitative traits (Mather and Jinks 1982; Kearsey and Pooni 1996).

Opposite signs in dominance [h] and dominance × dominance interaction [l] represented duplicate epistasis between alleles with dominance and increasing effects in the expression of average fruit yield and fruit cavity size and the negative dominance [h] and positive dominance × dominance interaction [l] indicated the involvement of duplicate epistasis between alleles with dominance and decreasing effects for average fruit weight and TSS in the C_1 cross (Table 9). Similarly, in the cross C_2, negative dominance [h] and positive dominance × dominance interaction [l] indicated duplicate epistasis between alleles with dominance and decreasing effects in the expression of average fruit yield, average fruit weight and TSS and positive dominance [h] and negative dominance × dominance interaction [l] indicated the duplicate epistasis between alleles with dominance and decreasing effects in the expression of fruit cavity size (Table 10).

Thus, first degree statistics-based components of generation mean suggest predominance of genes with dominance and dominance-based effects in the inheritance of most traits investigated. Estimates of [d], [h], [i] and [l] which are based on first degree statistics pose serious limitations on the interpretation due to internal cancellation of effects of genes in positive and negative direction. Thus, the estimates of genetic components of generation means are most often under estimated. This is especially true as these estimates are based on data obtained from highly selected set of parents where gene dispersion may not be an unusual phenomenon (Kearsey and Pooni 1996). However, the estimates of variances (second degree statistics) arising from additive, dominance and di-genic epistatic effects of genes are not affected by internal cancellation of gene effects in positive and negative direction (Mather and Jinks 1982; Kearsey and Pooni 1996).

Second degree statistics-based genetics. Significance of additive genetic variance [σ^2_A] in F_2 derived from C_1 and C_2 crosses suggested substantial contribution of additive effects in the inheritance of average fruit yield, average fruit weight, fruit cavity size and TSS (Table 11). Thus, contrary to first degree based statistics (which revealed predominance of dominance genetic effects), second degree statistics revealed predominance of genes with additive effects. Thus, inferences solely based on either first- or second-degree statistics-based mode of action of genes controlling target traits are most often misleading. A combination of components of means and of variances provides complementary and more comprehensive information on the true nature of genetic control of quantitative traits (Kearsey and Pooni 1996).

Interpretation of combination of first - and second-degree statistic-based genetic parameters. Significance of both [a] and [σ^2_A] in F_2 derived from 21KGSB-258 × 21KGSB-93 suggested substantial contribution of additive effects in the inheritance of average fruit yield, average fruit weight, fruit cavity size and TSS. Non-significance of both [d] and [σ^2_D] suggested absence of dominance effects in the inheritance of average fruit yield. Where significant [d] and non significant σ^2_D indicated lower dominance in the inheritance of average fruit weight, fruit cavity size and TSS (Table 11). Several researchers also reported preponderance of significant additive effects and additive genetic variance for inheritance of fruit traits *viz*., average fruit yield, fruit weight, fruit cavity size and TSS. Our results argue well with those reported by Saha *et al.* (2018); Metwally *et al*. (2015); Paris *et al*. (2008) in muskmelon.

In the genetic background of 21KGSB-218 × 21KGSB-54, significance of both [a] and [σ^2_A] suggested substantial contribution of additive effects in the inheritance of average fruit weight, fruit cavity size and TSS. Whereas, larger [a] and low/non-significant σ^2_A in the inheritance of average fruit yield indicated that the effect of individual gene controlling fruit yield is very small. Non-significance of both [d] and [σ^2_D] suggested absence of dominance effects in the inheritance of average fruit yield and average fruit weight and TSS. However, significant [d] and non-significant σ^2_D suggested lower dominance in the inheritance of fruit cavity size (Table 11).

Table 8: Estimates of components of generation means among six generations derived from C_2 cross and test for adequacy of A-D model in the inheritance of commercially important fruit traits.

Characters	m	d	h	χ2	P value	Adequacy of Additive-Dominance (A-D) model
Fruit yield (Kg plant^{-1})	6.36	3.46	-3.74	63.47	0.00	Inadequate
Fruit weight (Kg fruit^{-1})	0.81	0.29	-0.07	90.94	0.00	Inadequate
Fruit cavity size(cm)	2.00	0.99	0.51	28.89	0.00	Inadequate
TSS (^{0} Brix)	7.52	-0.51	-0.55	24.96	0.00	Inadequate

Table 9: Estimates of components of generation means among six generations derived from C_1 cross based on perfect fit solutions for average fruit yield, average fruit weight, fruit cavity size and TSS.

Characters	m	d	h	i	j	l	Type of epistasis
Fruit yield (Kg plant^{-1})	-1.74 ± 0.94	1.02 ± 0.05	9.98± 2.27	3.68 ± 0.94	0.58 ± 0.29	-5.24 ± 1.36	DEDI
Fruit weight (Kg fruit^{-1})	0.59 ± 0.03	-0.10 ± 0.001	-0.80 ± 0.38	0.23 ± 0.18	0.25 ± 0.04	0.92± 0.21	DEDD
Fruit cavity size(cm)	0.47 ± 0.11	0.19 ± 0.03	1.49 ± 0.28	0.63 ± 0.10	-0.11 ± 0.04	-0.89 ± 0.19	DEDI
TSS(°Brix)	7.40 ± 0.64	-3.70 ± 0.18	-3.90 ± 1.62	1.40 ± 0.62	3.90 ± 0.26	2.80 ± 1.11	DEDD

DEDI: Duplicate epistasis between dominant increasers; DEDD: Duplicate epistasis between dominant decreasers

Table 10: Estimates of components of generation means among six generations derived from C_2 cross based on perfect fit solutions for average fruit yield, average fruit weight, fruit cavity size and TSS.

Characters	m	d	h	i	j	l	Type of epistasis
Fruit yield (Kg plant^{-1})	3.90* ± 1.73	4.25** ± 0.47	-6.46** ± 4.49	3.35 ± 1.66	-0.24 ± 0.73	11.72** ± 3.30	DEDD
Fruit weight (Kg fruit^{-1})	0.78** ± 0.18	0.18** ± 0.03	-0.14 ± 0.43	0.08 ± 0.18	0.39 ± 0.05	0.15 ± 0.26	DEDD
Fruit cavity size (cm)	0.63* ± 0.28	0.97** ± 0.03	3.63** ± 0.40	1.36** ± 0.28	0.25 ± 0.08	-1.71** ± 0.40	DEDI
TSS (°Brix)	8.09** ± 0.84	-0.90** ± 0.18	-3.54 ± 2.06	-0.19 ± 0.82	0.99 ± 0.30	3.05* ± 1.34	DEDD

DEDI: Duplicate epistasis between dominant increasers; DEDD: Duplicate epistasis between dominant decreasers

Table 11: Estimates of additive genetic effect (a) and variance (σ^2 A) and dominant genetic effect (d) and variance (σ^2D) for average fruit yield, fruit weight, fruit cavity size and TSS in C_1 and C_2 crosses.

Characters	[a]		σ^2A		[d]		σ^2D	
	C_1	C_2	C_1	C_2	C_1	C_2	C_1	C_2
Fruit yield (Kg plant^{-1})	1.02**	4.25**	0.002**	0.22	9.97	-6.46	5.14	20.16
Fruit weight (Kg fruit^{-1})	-0.10**	0.18**	0.001**	0.001**	-0.80*	-0.14	0.15	0.19
Fruit cavity size (cm)	0.19**	0.97**	0.001**	0.001**	1.49**	3.63**	0.07	0.45
TSS (°Brix)	-3.70**	-0.90**	0.03**	0.03**	-3.90**	-3.54	2.64	4.25

Our results indicating predominance of additive effects and their variances for most traits in both the crosses (C_1 and C_2) draw adequate support from theoretical expectations of greater σ^2_A than σ^2_D (Moll and Stuber 1974; Hallauer, 1985; Dudley, 1997; Bernardo, 2010; Bernardo, 2014). This is because, loci that exhibit dominance as well as epistasis also contribute to σ^2_A. This means that any segregating loci with either no

dominance or partial dominance or complete dominance or over-dominance contribute to σ^2_A (Bernardo, 2010; Bernardo, 2014).

Literature is abundant to show greater magnitude of σ^2_A than σ^2_D controlling most quantitative traits in crop plants. To quote a few, Hallauer and Miranda (1988) and Bernardo (1996) reported estimates of σ^2_A are about 67% and 200% greater than σ^2_D, respectively for grain yield in maize. Considering that dispersion of genes also reduces σ^2_A (Hanson, 1959), inter-mating in early (F_2/F_3) segregating generations not only help achieve near complete association of genes but also increases the frequency of genes that contribute to σ^2_A. Increase in σ^2_A as a result of inter mating is attributed to auto-conversion (self-conversion) of non-additive genetic variances including epistasis to σ^2_A. This conversion occurs because heterozygotes become fixed into homozygotes (Goodnight, 1988; Acquaah, 2012). The σ^2_A is the most useful component of σ^2_G in breeding as it is due to genetic effects that are transmitted from selected parents to offspring. Thus, identification and selection of best pure-lines that exploits σ^2_A in populations subjected to one or a few rounds of inter-mating is likely to be effective and expected to result in rapid genetic gains for target traits.

Third- and fourth-degree statistics-based genetics. The frequency distribution of F_2, BC_1 and BC_2 population derived from both the crosses for four quantitative traits is represented in Fig. 1-4 for C_1 cross and in Fig. 5-8 for C_2 cross. In C_1 cross, transgressive segregants are recovered for average fruit yield, average fruit weight and fruit cavity size in both F_2 and backcross population except for TSS. None of the transgressive segregants are recovered for TSS, which may be due to fact that during recombination genes controlling TSS present in both the parents are not complementing with each other (Fig. 1-4). However, in C_2 cross very few transgressive segregants are recovered for average fruit yield and also for average fruit weight, fruit cavity size and TSS (Fig. 5-8).

The frequency distribution pattern of F_2 population derived from the cross 21KGSB-258 × 21KGSB-93 was positively skewed and leptokurtic for average fruit yield, average fruit weight and fruit cavity size and similarly for expression of average fruit weight in the cross 21KGSB-218 × 21KGSB-54 which suggested the involvement of fewer number of genes involved in the expression of fruit traits viz., average fruit yield, average fruit weight and fruit cavity size (Fig. 1-4).

Positively skewed and platykurtic distribution of F_2 population derived from 21KGSB-258 × 21KGSB-93 suggested that the involvement of large number of genes with majority of them displaying complementary epistasis with decreasing effects in the expression of TSS. Similarly in the genetic background of 21KGSB-218 × 21KGSB-54, frequency distribution pattern of F_2 population was positively skewed and platykurtic for the expression of QTs *viz*., average fruit yield, fruit cavity size and TSS (Fig. 5, 6, 7 and 8). Expected genetic gain is slow with mild selection while it is rapid with intense selection for the improvement of these traits (Roy, 2000).

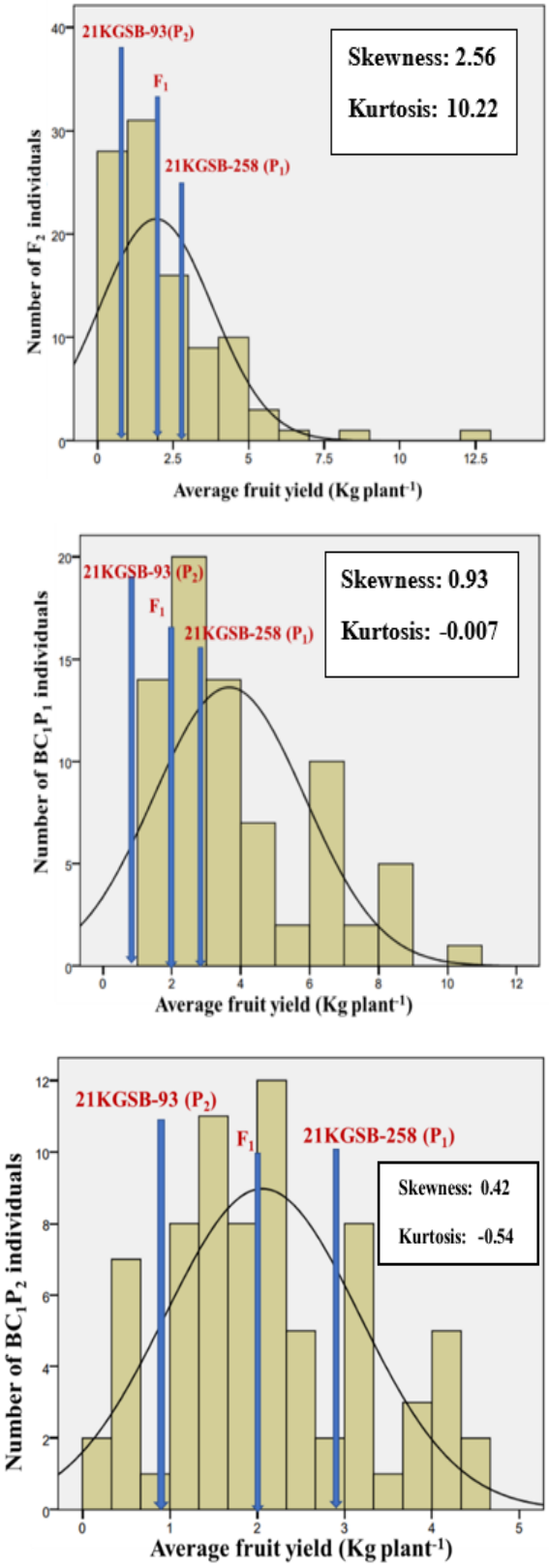


Fig. 1. Frequency distribution of average fruit yield (Kg plant^{-1}) among F_2, BC_1P_1 and BC_1P_2 individuals derived from the cross 21KGSB-258 × 21KGSB-93.

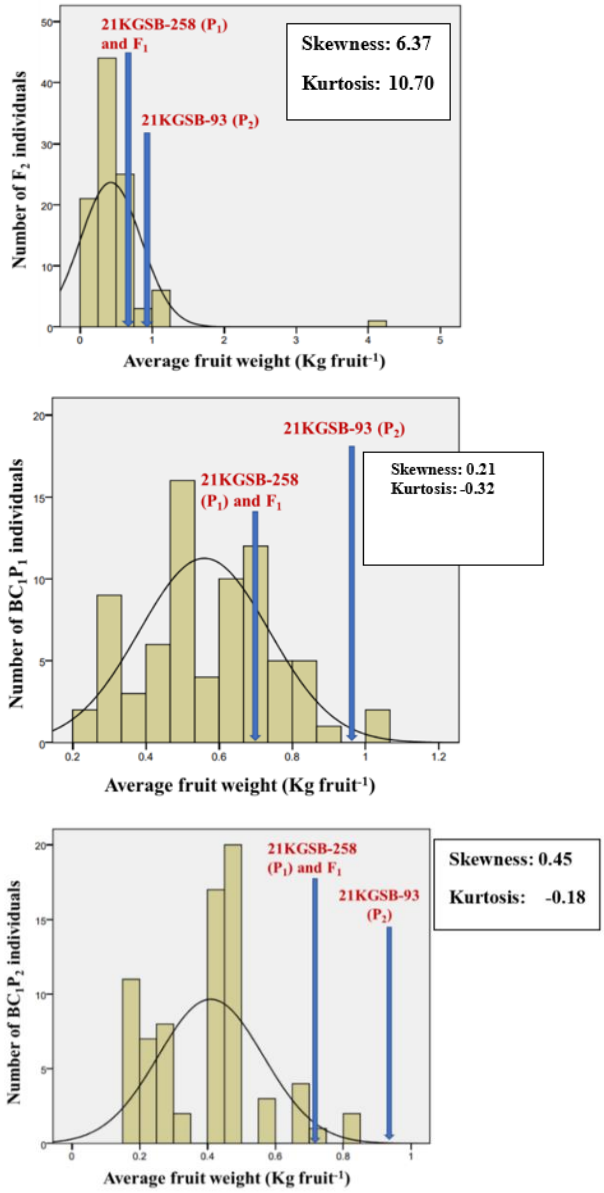
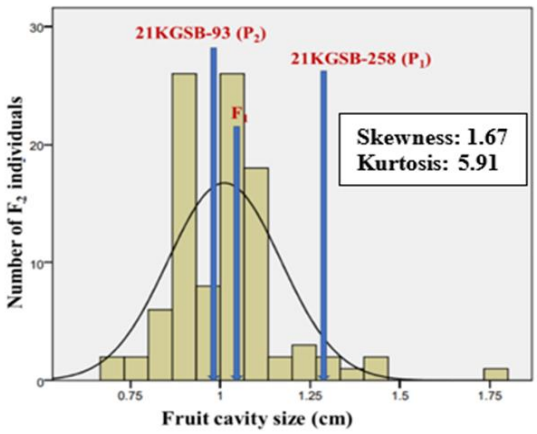


Fig. 2. Frequency distribution of average fruit weight (Kg fruit^{-1}) among F_2, BC_1P_1 and BC_1P_2 individuals derived from the cross 21KGSB-258 × 21KGSB-93.



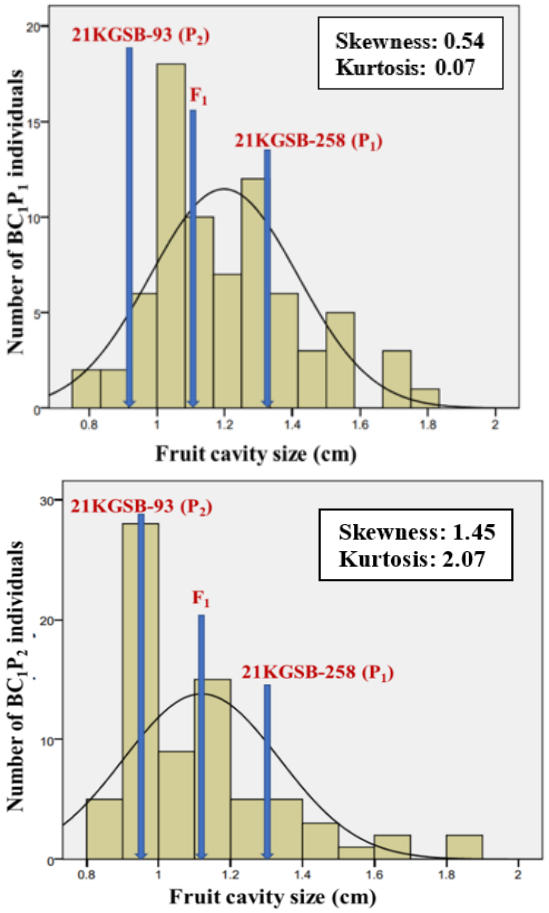
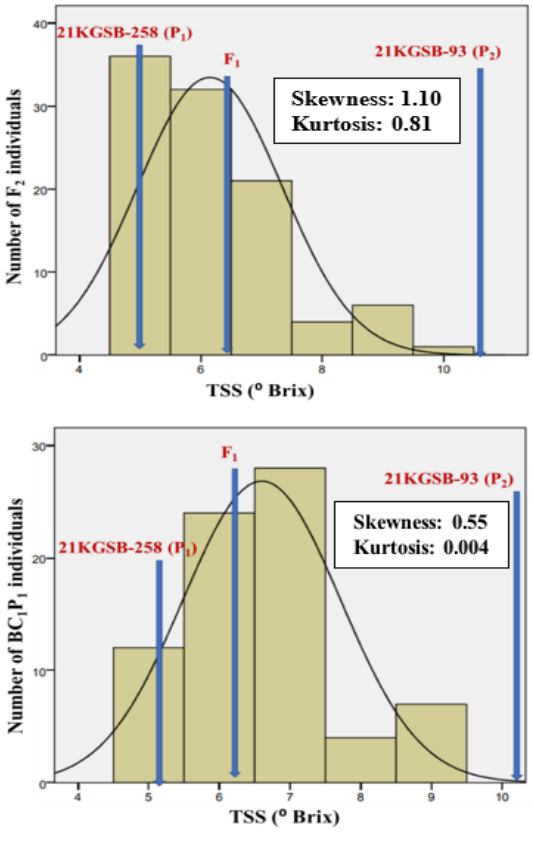


Fig. 3. Frequency distribution of fruit cavity size (cm) among F_2, BC_1P_1 and BC_1P_2 individuals derived from the cross 21KGSB-258 × 21KGSB-93.



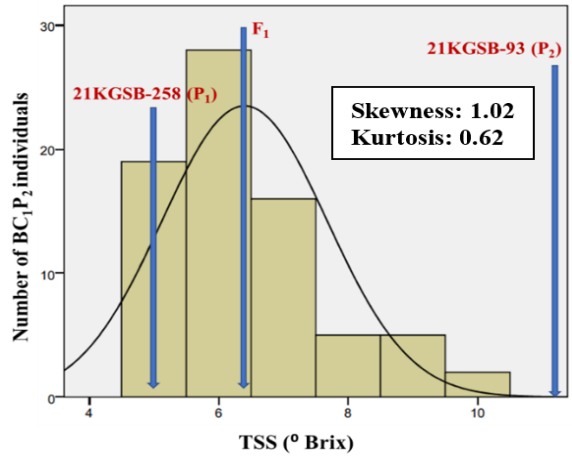


Fig. 4. Frequency distribution of TSS (°Brix) among F_2, BC_1P_1 and BC_1P_2 individuals derived from the cross 21KGSB-258 × 21KGSB-93.

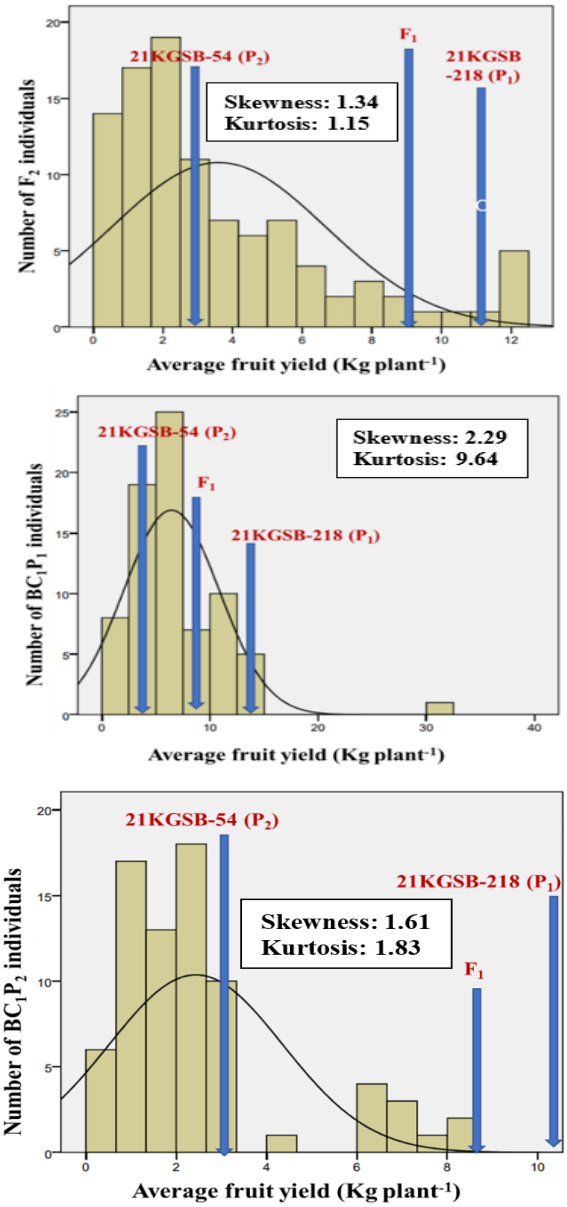


Fig. 5. Frequency distribution of average fruit yield (Kg plant^{-1}) among F_2, BC_1P_1 and BC_1P_2 individuals derived from the cross 21KGSB-218 × 21KGSB-54.

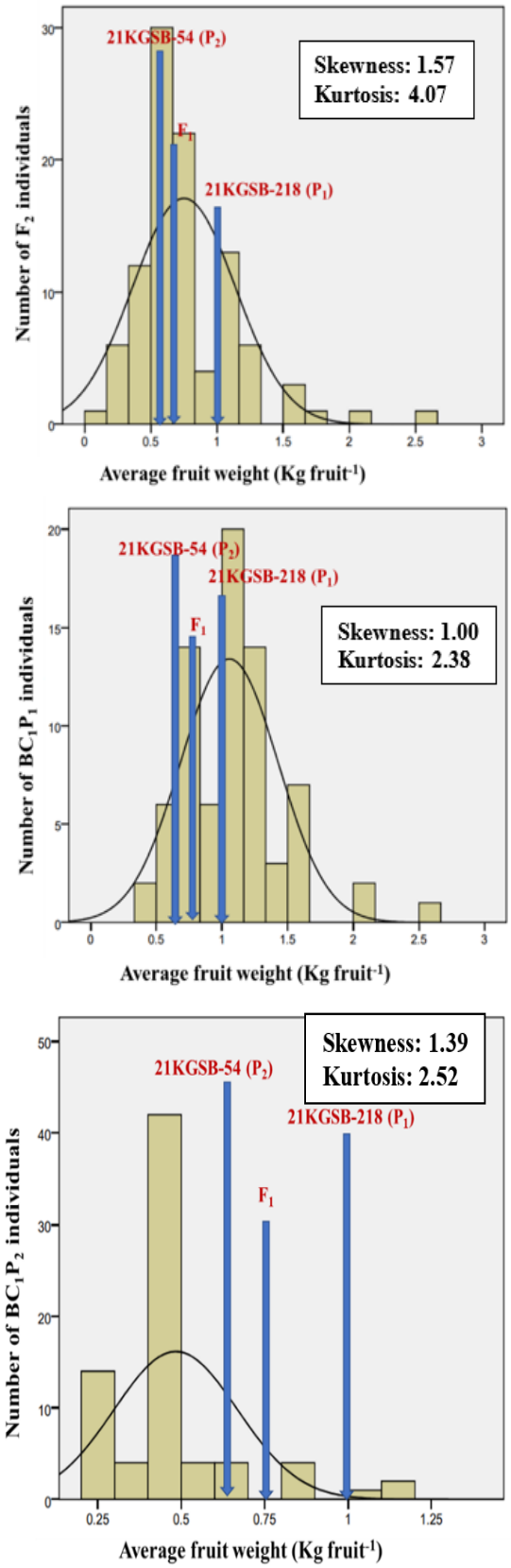


Fig. 6. Frequency distribution of average fruit weight (Kg fruit^{-1}) among F_2, BC_1P_1 and BC_1P_2 individuals derived from the cross 21KGSB-218 × 21KGSB-54.

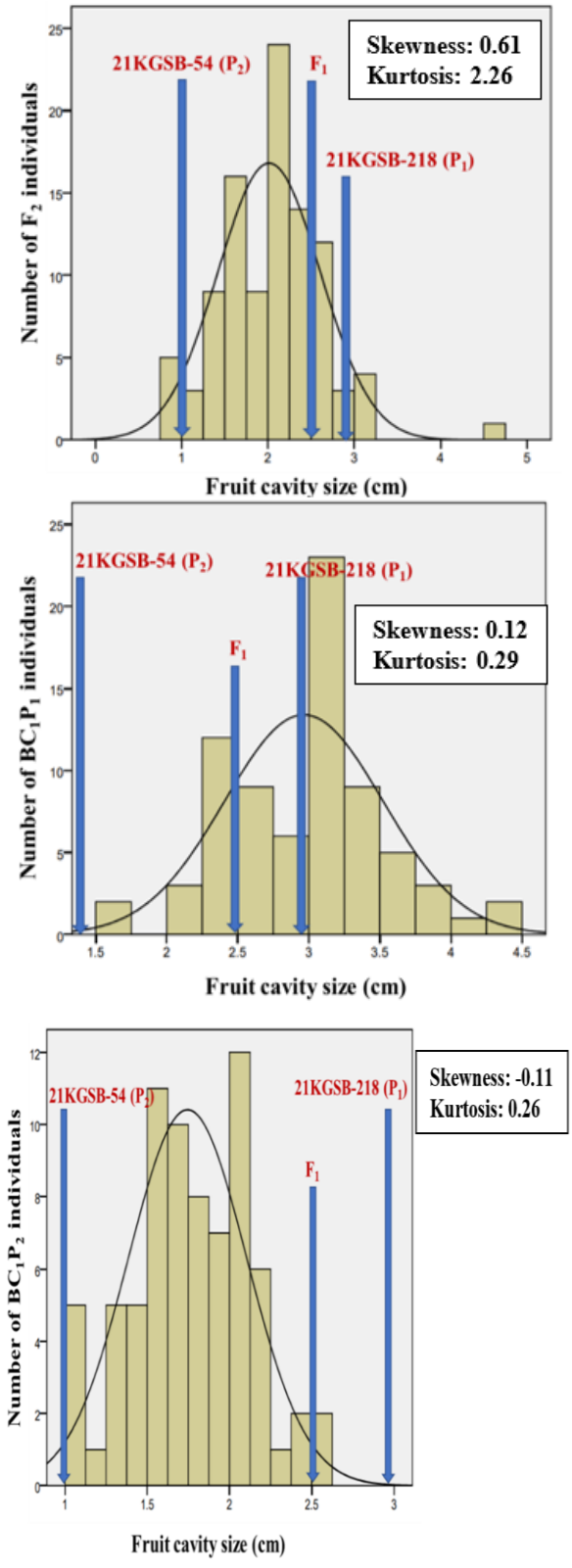


Fig. 7. Frequency distribution of fruit cavity size (cm) among F_2, BC_1P_1 and BC_1P_2 individuals derived from the cross 21KGSB-218 × 21KGSB-54.

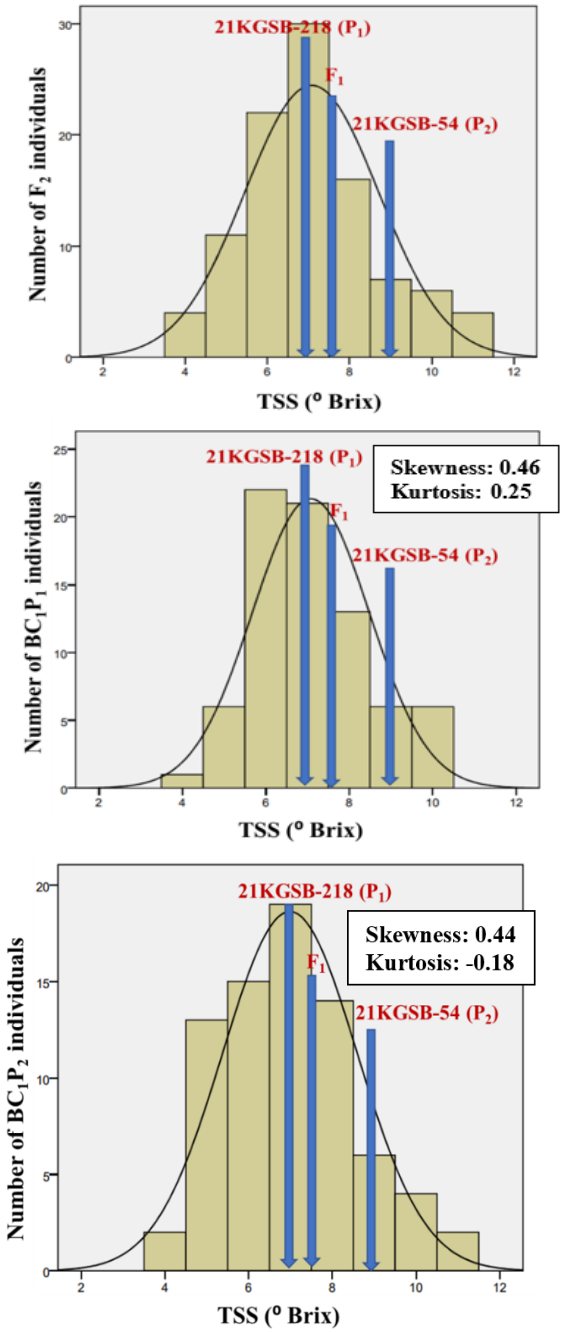


Fig. 8. Frequency distribution of TSS (^{0} Brix) among F_2, BC_1P_1 and BC_1P_2 individuals derived from the cross 21KGSB-218 × 21KGSB-54.

CONCLUSIONS

The first, second, third and fourth degree statistics based genetic models served as valuable tools and provided comprehensive and mutually complementary information on the nature and magnitude of gene action in controlling commercially important fruit traits in muskmelon.

FUTURE SCOPE

The efficiency of breeding efforts to develop crop cultivars could be enhanced by maximizing genetic gains per selection cycle and per unit time using the knowledge on the mode of action of genes controlling the target traits such as fruit yield, fruit weight, fruit cavity size and TSS in relation to working germplasm or breeding material. The genetic information obtained from the present study could be used in employing appropriate breeding strategies to develop melon cultivars.

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Conflict of interest. None.

REFERENCES

Acquaah, G. (2012). Principles of plant genetics and breeding. Second edition. John Wiley and Sons, Ltd. Pp 63-75.

Ahmed, O. K., 2009, Evaluation of objective maturity indices for muskmelon (*Cucumis melo* L.) cv. Galia. *Journal of King Abdulaziz University*.

Bernardo, R. (1996). Best linear unbiased prediction of maize single cross performance. *Crop Sci., 36*, 50-56.

Bernardo, R. (2010). Breeding for quantitative traits in plants. Stemma Press, Woodbury, Minnesota.

Bernardo, R. (2014). Essentials of plant breeding. Stemma Press, Woodbury, Minnesota.

Bernardo, R. (2020). Breeding for quantitative traits in plants. Stemma Press, Minnesota, USA.

Chakrabarti, A. K. (2001). Importance of vegetables. In Textbook of vegetables, Tuber crops and spices. Eds. *Indian Council of Agric. Res.,* New Delhi, pp. 4.

Dudley, J. W. (1997). Quantitative genetics and plant breeding. *Adv. Agron., 59*, 1-23.

Dudley, J. W. (1982). Theory for transfer of alleles. *Crop Sci*., *22*, 631–637.

Dudley, J. W. (1984). A method of identifying lines for use in improving parents of a single cross. *Crop Sci*., *24*, 355-357.

Fergany, M., Kaur, B., Monforte, A. J., Pitrat, M., Lecoq, C. H., Dhillon, N. P. S. And Dhaliwal, S. S. (2011). Variation in melon (*Cucumis melo*) landraces adapted to the humid tropics of southern India. *Genet. Resour. Crop Evol*., *55*, 225–243.

Feyzian, E., Dehghani, H., Rezai, A. M., And Jalali, M. (2009). Correlation and sequential path model for some yield-related traits in melon (*Cucumis melo* L.). *J. Agric. Sci. Technol*., *11*, 341-353.

Gaikwad, S. D., Musmade, A. M., Patil, R. S. And Shete, M. B. (2016). Correlation coefficient analysis in F_5 and F_6 progenies of muskmelon (*Cucumis melo*). *Int. J. Agric. Sci*., *8*(59), 3326–3328.

Goodnight, C. J. (1998). Epistasis and the effect of founder events on the additive genetic variance. *Evolution,42*, 441-454.

Hallauer, A. R. (1985). Compendium of recurrent selection methods and their application. *Critical Rev. Plant Sci.,3*, 1-10.

Hallauer, A. R. and Miranda, F. O. (1988). Quantitative genetics in maize breeding. 2nd edition, Iowa state Univ. press Ames., pp.119.

Hanson, W. D. (1959). The break-up of initial linkage blocks under selected mating system. *Genetics*., *44*, 857-868.

Hayman, B. I. (1958). Separation of epistasis from additive and dominance variation in generation means. *Heredity, 12*, 371-391.

Ibrahim, E. M. (2012). Variability, heritability and genetic advance in Egyptian sweet melon (*Cucumis melo* var. *aezyptiacus* L.) under water stress condition. *Int. J. Pl. Breed. Genet., 6*(4), 236–244.

Javanmard, T., Soltani Saleh-Abadi, F. And Bihamta, M. R. (2018). Estimation of some genetic parameters through generation mean analysis in melon. *Indian J. Agric. Res*., *52*(6), 619-624

Jinks, J. L. and Jones, R. M. (1958). Estimation of components of heterosis. *Genetics, 43*, 223-234.

Kearsey, M. J. and Pooni, H. S. (1996). The genetic analysis of quantitative traits. Chapman and Hall, London, UK.

Mather, K. and Jinks, J. L. (1971). Biometrical genetics, Chapman and hall, London.

Mather, K. and Jinks. I. L. (1982). Biometrical Genetics. Third Edition. Champan and Hall, London.

Melchinger, A. E. (1987). Expectation of means and variances of testcrosses produced from F_2 and backcross individuals and their selfed progenies. *Heredity, 59*, 105–115.

Metwally, E. I., Ahmed, M. E. M., Al-Ballat, I. A., Al-Abbasy, U. K. and Konsowa, A. M. (2015). Gene action and heritability of fruit yield and it's components on melon (*Cucumis melo* L.). *Egypt. J. Plant Breed*., *19*(3), 37-55.

Mishra, S., Sharma, A. K. And Sharma, V. (2017). Genetic variability studies in response to drought under different water regimes in muskmelon (*Cucumis melo* L.). *Journal of Applied and Natural Science*, *9*(3), 1744 -1750.

Moll, R. and Stubber, C. W. (1974). Quantitative genetics – empirical results relevant to plant breeding. *Adv. Agron*., *26*, 277-313.

Nunes, G. H. S., Santos Júnior, J. J., Andrade, F. V., Bezerra, Neto, F., Menezes, J. B. And Pereira, E. W. L., (2005). Desempenho de híbridos do grupo inodorus em Mossoró. *Horticultura Brasileira*, *23*, 90-94.

Paris, M. K., Zalapa, J. E., Mccreight, J. D. and Staub, J. E. (2008). Genetic dissection of fruit quality components in melon (*Cucumis melo* L.) using a RIL population derived from exotic 9 elite US Western Shipping germplasm. *Mol. Breeding*., *22*, 405-419.

Rodriguez, J. C., Shaw, N. And Cantliffe, D. (2002). High tunnel cantaloupe and specialty melon cultivar evaluation, production of galia type muskmelon using a passive ventilated greenhouse and soilless culture. *Cucurbitaceae*, 365-372.

Roy, D. (2000). Plant breeding: The analysis and exploitation of variability. PB: Narosa Publishing House. New Delhi, India. Pp. 198.

Saha, K., Mishra, S., Choudhary, H. and Mahapatra, S. (2018). Estimates of Genetic Component of Variation in Muskmelon (*Cucumis melo* L.). *Int. J. Curr. Microbiol. App. Sci*., *7*(7), 1144-1151.

Snedecor, G.W. and Cochran, W. G. (1974). Statistical Methods. 6th ed., Oxford and IBH Pub. Co., New delhi (India).

Stepansky, A., Kovalski, I. And Perl-Treves, R. (1999). Intraspecific classification of melons (*Cucumis melo* L.) in view of their phenotypic and molecular variation. *Plant Syst. Evol., 217*, 313–332.

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