Plant Archives Vol. 20, Supplement 2, 2020 pp. 1056-1065 **e-ISSN:2581-6063 (online), ISSN:0972-5210**

GENETIC BEHAVIOR OF SOME FRUIT CHARACTERS IN CROSSES BETWEEN TOMATO AND SOME WILD SPECIES AND AMONG WILD SPECIES

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Abstract

The present study was conducted at the Agricultural Experiment Station of the Faculty of Agriculture, Cairo University, Giza, Egypt. during 2017-2019 fall seasons under greenhouse conditions. Five wild and domestic tomato accessions were selected for this study based on their characters, especially fruit quality. Crosses were made between cv. Ace 55 VF (as female parent) and three accessions, one each *S. pimpinellifolium*, *S. cheesmaniae* and *S. lycopersicum* (Jubilee) (as males). Also, crosses were made, in both directions among the three wild accessions and were evaluated, in a completely randomized design with three replicates, for some fruit quality characters. Results indicated that low average fruit weight (AFW) was partially dominant. The minimum number of genes controlling AFW was 80 pairs in the cross Ace 55 VF × *S. pimpinellifolium* MLP 23102 and 90 pairs in the cross Ace 55 VF × *S. cheesmaniae* LA 524. Estimates of BSH for the 2 studied crosses were high and ranged from 76.4 % to 78.6%. Low fruit flesh thickness (FFT) was partially dominant in the cross Ace 55 VF × *S. pimpinellifolium* MLP 23102 and completely dominant in the cross Ace 55 VF × *S. cheesmaniae* LA 524. The minimum number of genes controlling FFT in the 2 studied crosses was one pair. Estimates of BSH for the 2 studied crosses were high and ranged from 71.3% to 88%. Low number of locules (NL) showed complete dominance in the two studied crosses. NL was controlled by one pair in the 2 studied crosses. Estimates of BSH for the 2 studied crosses were high and ranged from 80.8% to 88.6%. Ascorbic acid content (AA) showed no dominance in the cross Ace 55 VF × *S. pimpinellifolium* MLP 23102 and exhibited complete dominance of the high parent in the cross Ace 55 VF × *S. cheesmaniae* LA 524. The minimum number of genes controlling the AA content was one pair. Estimates of BSH for the 2 studied crosses were high and ranged from 93.4% to 97.9%. Low total soluble solids (TSS) content was partially dominant in the cross Ace 55 VF × *S. pimpinellifolium* MLP 23102 and high TSS content was partially dominant in the cross Ace 55 VF × *S. cheesmaniae* LA 524 and completely dominant in the cross *S. lycopersicum* var. *cerasiforme* PI 647522 × *S. cheesmaniae* LA 524. The minimum number of genes controlling TSS content in the 3 studied crosses was one pair. Estimates of BSH for the 3 studied crosses were high and ranged from 76.8 % to 81.5%. Low titratable acidity (TA) content showed complete dominance in the crosses Ace 55 VF × *S. pimpinellifolium* MLP 23102 and Ace 55 VF × *S. cheesmaniae* LA 524. The minimum number of genes controlling TA in the 2 studied crosses was one pair. Estimates of BSH for the 2 studied crosses were high and ranged from 85.5 % to 86.7%. High lycopene content (LC) was over dominant in the crosses Ace 55 VF × *S. cheesmaniae* LA 524 and Ace 55 VF × *S. lycopersicum* (Jubilee). LC was controlled by one pair of gene in the 2 studied crosses. Estimates of BSH for the 2 studied crosses were high and ranged from 94.7% to 98.7%. Low β-carotene content was partially dominant in crosses Ace 55 VF × *S. cheesmaniae* LA 524, *S. lycopersicum* var. *cerasiforme* PI 647522 × *S. cheesmaniae* LA 524, *S. pimpinellifolium* MLP 23102 × *S. cheesmaniae* LA 524 and *S. cheesmaniae* LA 524 ×*S. pimpinellifolium* MLP 23102 and over dominant in the cross Ace 55 VF ×*S. lycopersicum* (Jubilee). The minimum number of genes controlling β-carotene content in the 5 studied crosses was one pair. Estimates of BSH for the 5 studied crosses were high and ranged from 86.3% to 98.2%.

***Keywords*:** Tomato, *Solanum* spp., wild species, crosses, Fruit quality.

Introduction

Tomato (*Solanum lycopersicum* L.) is considered one of the most important vegetable crops grown in Egypt, which is one of the major tomato producing countries. Egypt's production of tomato in 2018 was 6,779,830 ton, area cultivated was 428,583 fedden, and average production was 16.6 ton/feds (Agriculture Directorates of Governorates, Economic Affairs Sector). Fruit quality is an essential factor in tomato production. Therefore, enhancement of fruit quality characters is a major goal in tomato breeding programs (Rodriguez *et al.*, 2010). The first step of plant breeding for crop improvement is evaluation of the genetic variability available in collected germplasm, which is considered as the reservoir of variability for different characters (Vavilov, 1951). Various tomato traits have been improved using wild species since the 1930s (Rick, 1986). In the case of organoleptic quality, several wild species have been used in the improvement of fruit quality (Fernie *et al.*, 2006). Fruit quality is defined as a combination of visual stimulants like size, shape and colour, and sensory properties like sweetness, acidity and taste (Bai and Lindhout, 2007).

In former studies small fruit weight was found to be partially dominant over large fruit weight (Abdel-Ati, 1985, 2000; Ibarbia and Lambeth, 1969b; Khalaf-Allah, 1970; Khalil *et al.*, 1983; 1998; Omara *et al.*, 1988; Solieman *et al.*, 2013), over dominant (Solieman *et al.*, 2013), or conversely high AFW was partially dominant (Shalaby, 2013, Solieman *et al.*, 2013). AFW was controlled by10-20 pairs (Ibarbia and Lambeth, 1969b), 5 pairs (Khalil *et al.*, 1983), 66 pairs (Abdel-Ati *et al.*, 2000), or 22-29 pairs of genes (Hazra *et al.*, 2001). Estimates of BSH for AFW were high (Aralikatti *et al.*, 2018; Ghosh *et al.*, 2010; Gillani *et al.*, 2019; Khapte and Jansirani., 2014; Kumar *et al.*, 2013; Ligade *et al.*, 2017; Mohamed *et al.*, 2012; Prajapatil *et al.*, 2015 and Shalaby ., 2013), or low (Kumar *et al.*, 2018 and Meena *et al.*, 2018). Small FFT was partially dominant (Sherpa *et al.*, 2014 and Solieman *et al.*, 2013) or over dominant (Sherpa *et al.*, 2014). Large FFT was partially dominant (Sherpa *et al.*, 2014 and Solieman *et al.*, 2013), completely dominant (Solieman *et al.*, 2013), or over dominant (Sherpa *et al.*, 2014 and Solieman *et al.*, 2013). Estimates of BSH for FFT were high (Hedau *et al.*, 2008; Khapte and Jansirani, 2014; Kumar *et al.*, 2013; Kumar *et al.*, 2018; Ligade *et al.*, 2017; Manish *et al.*, 2017; Panchbhaiya *et al.*, 2018 and Shankar *et al.*, 2013), or moderate (Aralikatti *et al.*, 2018 and Meena *et al.*, 2018). Low NL showed complete dominance (Pandiarana *et al.*, 2015), partial dominance (Pandiarana *et al.*, 2015; Solieman

et al., 2013), or over dominance (Pandiarana *et al.*, 2015; Sherpa *et al.*, 2014). High NL was partially dominant (Pandiarana *et al.*, 2015; Solieman *et al.*, 2013), completely dominant (Pandiarana *et al.*, 2015; Sherpa *et al.*, 2014) or over dominant (Pandiarana *et al.*, 2015; Solieman *et al.*, 2013). Estimates of BSH for NL were high (Khuntia *et al.*, 2019; Ligade *et al.*, 2017; Panchbhaiya *et al.*, 2018; Shankar *et al.*, 2013), moderate (Khapte and Jansirani., 2014; Kumar *et al.*, 2018; Meena *et al.*, 2018), or low (Aralikatti *et al.*, 2018). High AA content was partially dominant (Aggour., 1999; Pandiarana *et al.*, 2015; Pujer *et al.*, 2017; Sherpa *et al.*, 2014; Solieman *et al.*, 2013), over dominant (Pujer *et al.*, 2017; Pandiarana *et al.*, 2015; Sherpa *et al.*, 2014; Solieman *et al.*, 2013), or showed no dominance (Pujer *et al.*, 2017; Hatem., 1994). Low AA content was partially dominant (Abdel-Ati 1985; Pujer *et al.*, 2017; Khalil *et al.*, 1998; Pandiarana *et al.*, 2015; Sherpa *et al.*, 2014 and Solieman *et al.*, 2013), completely dominant (Pujer *et al.*, 2017), or over dominant (Pandiarana *et al.*, 2015; Pujer *et al.*, 2017; Sherpa *et al.*, 2014). AA content was controlled by one gene pair (Khalil, 1979), 2 pairs (Aggour, 1999), or 5 pairs (Hassan *et al.*, 2000). Estimates of BSH for AA content were high (Das *et al.*,2018; Gillani *et al.*, 2019; Hedau *et al.*, 2008 Kumar *et al.*, 2013; Ligade *et al.*, 2017), moderate (Panchbhaiya *et al.*, 2018 and Prashanth *et al.*, 2007), or low (Meena *et al.*, 2018). Low TSS was partially dominant (Pujer *et al.*, 2017; Sherpa *et al.*, 2014; Solieman *et al.,* 2013), completely dominant (Khalil *et al.*, 1998; Pandiarana *et al.*, 2015; Zhou and Xu, 1990), over dominant (Pujer *et al.*, 2017; Pandiarana *et al.*, 2015; Sherpa *et al.*, 2014), or showed absence of dominance (Pujer *et al.*, 2017; Pandiarana *et al.*, 2015). High TSS was partially dominant (Monma and Kamimura., 1982; Pandiarana *et al.*, 2015; Pujer *et al.*, 2017; Solieman *et al.,* 2013), completely dominant (Pujer *et al.*, 2017), or over dominant (Pandiarana *et al.*, 2015; Pujer *et al.*, 2017; Sherpa *et al.*, 2014; Solieman *et al.,* 2013). TSS was controlled by one pair (Abdel-Ati, 1992), 2 pairs (Abdel-Ati, 1985), or 3 pairs of genes (Hassan *et al.*, 2000; Ibarbia and Lambeth, 1969a ; Khalil *et al.*, 1979). Estimates of BSH for TSS were high (Aralikatti *et al.*, 2018; Das *et al.*, 2018; Hasan *et al.*, 2016; Hedau *et al.*, 2008; Khapte and Jansirani., 2014; Khuntia *et al.*, 2019; Kumar *et al.*, 2013; Ligade *et al.*, 2017; Meena *et al.*, 2018; Panchbhaiya *et al.*, 2018; Prashanth *et al.*, 2007; Shankar *et al.*, 2013), or moderate (Kumar *et al.*, 2018). Low TA was partially dominant (Pandiarana *et al.*, 2015), completely dominant (Pandiarana *et al.*, 2015; Sherpa *et al.*, 2014), over dominant (Pandiarana *et al.*, 2015), or showed no dominance (Pandiarana *et al.*, 2015). High TA showed complete dominance (Sherpa *et al.*, 2014), or over dominance (Pandiarana *et al.*, 2015; Sherpa *et al.*, 2014). Estimates of BSH for TA were high (Das *et al.*, 2018; Panchbhaiya *et al.*, 2018; Shankar *et al.*, 2013), or low (Hedau *et al.*, 2008; Prashanth *et al.*, 2007). High LC was partially dominant (Pandiarana *et al.*, 2015; Sherpa *et al.*, 2014), over dominant (Pandiarana *et al.*, 2015; Sherpa *et al.*, 2014), or showed no dominance (Sherpa *et al.*, 2014). Low LC was partially dominant (Sherpa *et al.*, 2014), or over dominant (Pandiarana *et al.*, 2015; Sherpa *et al.*, 2014). Estimates of BSH for LC were high (Das *et al.*, 2018; Hedau *et al.*, 2008; Gillani *et al.*, 2019; Kumar *et al.*, 2013; Ligade *et al.*, 2017; Prashanth *et al.*, 2007; Panchbhaiya *et al.*, 2018; Shankar *et al.*, 2013). Estimates of BSH for β-carotene content were high (Das *et al.*, 2018; Gillani *et al.*, 2019; Ligade *et al.*, 2017; Panchbhaiya *et al.*, 2018).

This study was, therefore, conducted with the following objectives: 1) Evaluating some selected tomato genotypes for some fruit quality characters, viz., FFT, NL, pH, TA, TSS, AFW, pigments content (lycopene and β-carotene), and AA content. 2) Determining the genetic basis of the inheritance of these fruit quality characters.

Materials and Methods

This study was carried out during the period from 2017 to 2019 at the Agricultural Experiment Station (AES) of the Faculty of Agriculture, Cairo University, Giza, Egypt. Five wild and domestic tomato accessions (Table 1) were selected for this study based on their characters, especially fruit quality. In the first evaluation season, parental seeds were sowed in nursery on September 15, 2017 in speedling trays filled with 1:1 mixture of peatmoss and vermiculate. This mixture was enriched with macro and micro elements. Five-week-old seedlings were transplanted on October 22, 2017 in the greenhouse at AES. Plants of each accession were set 50 cm apart in one bed row 1.2 m-wide, and were subjected to the common agricultural practices. Crosses were made between cv. Ace 55 VF (as female parent) and the other 3 parents (as males), viz., *S. pimpinellifolium* MLP 23102, *S. lycopersicum* Jubilee and *S. cheesmaniae* LA 524. Also, crosses were made, in both directions among the three other accessions, viz., *S. pimpinellifolium* MLP 23102, *S. lycopersicum* var. *cerasiforme* PI 647522 and *S. cheesmaniae* LA 524. In the second season, seeds of the five parents and their F_1s were sowed in nursery on January 15, 2018 . Four-week-old seedlings were transplanted in the greenhouse in a randomized complete block design (RCBD) with three replicates. Plants were set 50 cm apart in beds 1.2 m-wide, and were subjected to the common agricultural practices. F_1 hybrids were selfed to obtain F_2 seeds and also were crossed with their parents to obtain the backcross seeds.

Table 1 : List of *Solanum* accessions evaluated.

Species	Accession
S. lycopersicum	Ace 55 VF[a]
S.pimpinellifolium	MLP 23102[b]
S. lycopersicum var. *cerasiforme*	PI 647522[a]
S.cheesmaniae	LA 524[c]
S. lycopersicum	Jubilee[a]

[a] Kindly provided by the Tomato Genetic Resources Center, University of California, Davis.

[b] Kindly received from the Institut für Pflanzengenetik und Kulturpfianzenforschung, Genebank, Gatersleben, Germany.

[c] Kindly obtained from Dr. Charles Block, Plant Introduction Station, Ames, Iowa.

The inheritance of a given character was studied in crosses between parents having high and low values of each character. These crosses were Ace 55 VF × *S. pimpinellifolium* MLP 23102 for studying AFW, NL, FFT, TSS, TA and AA content; Ace 55 VF × *S. cheesmaniae* LA 524 for studying AFW, NL, FFT, TSS, TA, and contents of AA, lycopene and β-carotene; Ace 55 VF × *S. lycopersicum* Jubilee for studying lycopene and β-carotene contents; *S. pimpinellifolium* MLP 23102 × *S. cheesmaniae* LA 524 and *S. cheesmaniae* LA 524 × *S. pimpinellifolium* MLP 23102 for studying fruit contents of β-carotene, and *S. lycopersicum* var. *cerasiforme* PI 647522 × *S. cheesmaniae* LA 524 for studying TSS and β-carotene contents.

Seeds of genetic populations of each cross, *viz.,* P_1, P_2, F_1, F_2, BCP_1 and BCP_2 were sowed on September 20, 2018 and seedlings were field-transplanted in the greenhouse on October 25 for evaluation of the fruit quality characters. Populations of each cross were planted in a RCBD with 3 replicates. Data recorded for the evaluated characters were taken on individual plants. AFW was determined as the mean weight of at least five fruits from each individual plant in the second and third pickings. NL per fruit was determined as average of at least five fruits / individual plant. FFT was determined as average of at least five fruits / individual plant. TSS was determined in at least five ripe fruits from each plant using a digital refractometer. TA was ascertained in ripe fruits using 0.1 N NaOH solution and phenolphthalein as indicator (AOAC, 1990). AA content was determined in ripe fruits using 2, 6 dichlorophenol-endophenol dye (AOAC, 1990). LC was determined in ripe fruits according to Masayasu and Ichiji (1992). β-carotene content was determined in ripe fruits according to Masayasu and Ichiji (1992). Data collected were subjected to analysis of variance of a RCBD. The T-test was used to indicate to the significant differences between the two parents for each cross according to Snedecor and Cochran (1989) and is calculating the following genetic parameters:

Potence ratio (P) as indicator of the direction of dominance and calculated according to Smith (1952) as follows:

$$P = \left(\overline{F}_1 - MP\right) / \left[1/2\left(\overline{P}_2 - \overline{P}_1\right)\right]$$

Where:

$\overline{F}_1$ = First generation mean. $\overline{P}_1$ = Mean of the smaller parent

$\overline{P}_2$ = Mean of the larger parent. MP = Mid parent value = $½\left(\overline{P}_1 + \overline{P}_2\right)$.

The absence of dominance was assumed when the difference between the parents was significant and $\overline{F}_1$ – MP was not significant. Complete dominance was assumed when potence ratio equaled to or did not differ from ± 1.0. Meanwhile, partial dominance was considered when potence ratio was between +1.0 and -1.0, but was not equal to zero. Over dominance (Heterosis) was assumed when Potance ratio exceeded ± 1.0.

The minimum number of genes was calculated using Castle-Wright equation (Castle and Wright, 1921) as follows:
$N = D^2 / 8(VF_2 - VF_1)$

Where: N = number of genes controlling the character, D = difference between parental means, VF_1 and VF_2 = variances of the F_1 and F_2 populations, respectively.

Broad sense heritability (BSH) was calculated using the equation:

BSH = (V_G / V_P) 100 where: V_G = genetic variance, which was calculated by subtracting the environmental variance (V_E) from the phenotype variance (V_P), $V_P = VF_2$ .V_E = Environmental variance, which was calculated as the geometric mean of the non-segregating populations, i.e., parents and F_1 (Allard, 1960).

Results and Discussion

Evaluation for tomato fruit quality characters

(a) Average fruit weight

Data obtained on AFW of parental, F_1, F_2 and backcross populations of the crosses between tomato accessions Ace 55 VF, as a female parent, and *S. pimpinellifolium* MLP 23102 and *S. cheesmaniae* LA 524, as male parents, are presented in Table 1. Significant differences were observed between parents of each cross. The cultivar Ace 55 VF (the female parent of the 2 crosses) produced the highest significant AFW (124.25 g) compared with the male parents, that produced fruits weighing 1.11, and 0.97g, respectively. Means of hybrids Ace 55 VF × *S. pimpinellifolium* MLP 23102 and Ace 55 VF × *S. cheesmaniae* LA 524 were very close to that of the smaller parent. In each cross, F_2 plants were widely distributed between their parents with a low tendency towards the low parent. Mean of BC to cv. Ace 55 VF of the crosses Ace 55 VF × *S. pimpinellifolium* MLP 23102 and Ace 55 VF × *S. cheesmaniae* LA 524 showed slight tendency towards the lower parent. Plants of the backcrosses to the wild parents were very close to them in AFW.

Genetic parameters obtained for AFW in the crosses Ace 55 VF × *S. pimpinellifolium* MLP 23102 and Ace 55 VF × *S. cheesmaniae* LA 524 are presented in Table 2. Low AFW was partially dominant in the two crosses. These results agree with those of Ibarbia and Lambeth (1969b), Khalaf-Allah (1970), Khalil *et al.* (1983 & 1998), Abdel-Ati (1985 & 2000), Omara *et al.*(1988) and Solieman *et al.* (2013) who reported that small fruit weight was found to be partially dominant over large fruit weight. In accordance, Solieman *et al.* (2013) reported over dominance of the low parent. On the contrary, high AFW was partially dominant as found by Shalaby (2013) and Solieman *et al.* (2013).

The minimum number of genes controlling AFW in the 2 studied crosses was 80 pairs in the cross Ace 55 VF × *S. pimpinellifolium* MLP 23102 and 90 pairs in the cross Ace 55 VF × *S. cheesmaniae* LA 524. Generally, AFW of the studied crosses was quantitatively inherited. These results are in agreement with those of Khalil *et al.* (1983), Ibarbia and Lambeth (1969b), Hazra, *et al.* (2001) and Abdel-Ati, (2000) who, respectively, estimated it as 5, 10-20, 22-29 and 66 pairs.

Estimates of BSH for the 2 studied crosses were high and ranged from 76.4 % to 78.6%. These results agree with those of Ghosh *et al.* (2010), Mohamed *et al.* (2012), Kumar *et al.* (2013), Shalaby (2013), Khapte and Jansirani (2014), Prajapatil *et al.* (2015), Ligade *et al.*(2017), Aralikatti *et al.* (2018) and Gillani *et al.* (2019) who reported that BSH for AFW were high. On the contrary, BSH for AFW were low as estimated by Meena *et al.* (2018) and Kumar *et al.* (2018).

(b) Fruit flesh thickness (FFT)

Data obtained on FFT of parental, F_1, F_2, and backcross populations of the crosses between tomato accession Ace 55 VF, as a female parent, and *S. pimpinellifolium* MLP 23102 and *S. cheesmaniae* LA 524, as male parents, are presented in Table 3. Significant differences were observed between parents of each cross. The cultivar Ace 55 VF (the female parent of the 2 crosses) produced the highest significant FFT (5.4 mm) compared with the male parents, that produced FFT of 1.86 and 1.93mm, respectively. In each cross, F_1 mean was

intermediate between its two parents with a tendency towards the low parent. In each cross, F_2 plants were widely distributed between their parents with a low tendency towards the low parent in the crosses Ace 55 VF × *S. pimpinellifolium* MLP 23102 and Ace 55 VF × *S. cheesmaniae* LA 524. The mean of BC to cv. Ace 55 VF of the crosses Ace 55 VF × *S. pimpinellifolium* MLP 23102 and Ace 55 VF × *S. cheesmaniae* LA 524 showed slight tendency towards the lower parent. Plants of the backcrosses to the wild parents were very close to them in FFT.

Genetic parameters obtained for FFT in the crosses Ace 55 VF × *S. pimpinellifolium* MLP 23102 and Ace 55 VF × *S. cheesmaniae* LA 524 are presented in Table 4. Low FFT was partially dominant in the cross Ace 55 VF × *S. pimpinellifolium* MLP 23102 and completely dominant in the cross Ace 55 VF × *S. cheesmaniae* LA 524. These results agree with those of Solieman *et al.* (2013) and Sherpa *et al.* (2014) who reported that low FFT was partially dominant over the high FFT. In accordance, Sherpa *et al*. (2014) reported over dominance of the low parent. On the contrary, high FFT was partially dominant as detected by Solieman *et al.* (2013) and Sherpa *et al.* (2014), completely dominant as found by Solieman *et al.* (2013) and over dominant (Sherpa *et al.*, 2014 and Solieman *et al.*, 2013).

The minimum number of genes controlling FFT trait in the 2 studied crosses ranged from 1 to 4 pairs.

Estimates of BSH for the 2 studied crosses were high and ranged from 71.3% to 88%. These results agree with those of Hedau *et al.* (2008), Kumar *et al.* (2013), Shankar *et al.* (2013), Khapte and Jansirani (2014), Ligade *et al.* (2017), Manish *et al.* (2017), Kumar *et al.* (2018) and Panchbhaiya *et al.* (2018) who reported high BSH estimates for this trait. On the contrary, BSH for FFT were moderate as estimated by Meena *et al.* (2018) and Aralikatti *et al.* (2018).

(c) Number of locules

Data obtained on NL of parental, F_1, F_2, and backcross populations of the crosses between tomato accession Ace 55 VF, as a female parent, and *S. pimpinellifolium* MLP 23102 and *S. cheesmaniae* LA 524, as male parents, are presented in Table 5. Significant differences were observed between parents of each cross. The cultivar Ace 55 VF (the female parent of the 3 crosses) produced the highest significant NL (3.46) compared with the male parents, that produced number of locules 2.13 and 2.06 respectively. The means of two hybrids Ace 55 VF × *S. pimpinellifolium* MLP 23102 and Ace 55 VF × *S. cheesmaniae* LA 524 were close to that of the smaller parent. F_2 plants were widely distributed between their parents with a low tendency towards the high parent in the hybrids Ace 55 VF × *S. pimpinellifolium* MLP 23102 and Ace 55 VF × *S. cheesmaniae* LA 524. The mean of BC to cv. Ace 55 VF of the cross Ace 55 VF × *S. pimpinellifolium* MLP 23102 showed high tendency towards the higher parent, but it was very close the mid-parent value in the cross Ace 55 VF × *S. cheesmaniae* LA 524. Plants of the backcross to the wild parents were very close to them it in the crosses Ace 55 VF × *S. pimpinellifolium* MLP 23102 and Ace 55 VF × *S. cheesmaniae* LA 524.

Genetic parameters obtained for NL in the crosses Ace 55 VF × *S. pimpinellifolium* MLP 23102 and Ace 55 VF × *S. cheesmaniae* LA 524 are presented in Table 6. Low NL showed complete dominance in the two studied crosses. These results agree with those of Pandiarana *et al.* (2015) who reported that low NL exhibited complete dominance over the high NL. In accordance, low NL showed partial dominance (Pandiarana *et al.*, 2015; Solieman *et al.*, 2013) or over dominance (Pandiarana *et al.*, 2015; Sherpa *et al.*, 2014). On the contrary, high NL was partially dominant (Pandiarana *et al.*, 2015; Solieman *et al.*, 2013), completely dominant (Pandiarana *et al.*, 2015; Sherpa *et al.*, 2014) or showed over dominance (Pandiarana *et al.*, 2015; Solieman *et al.*, 2013).

The minimum number of genes controlling the NL trait in the 2 studied crosses was one pair.

Estimates of BSH for the 2 studied crosses were high and ranged from 80.8% to 88.6%. These results agree with those of Shankar *et al.* (2013), Ligade *et al.* (2017), Panchbhaiya *et al.* (2018) and Khuntia *et al.* (2019) who reported that BSH for NL was high. On the contrary, BSH estimates for NL were moderate (Khapte and Jansirani., 2014; Kumar *et al.*, 2018; Meena *et al.*, 2018), or low (Aralikatti *et al.*, 2018).

(d) Ascorbic acid content

Data obtained on AA content of parental, F_1, F_2, and backcross populations of the crosses between tomato accession Ace 55 VF, as a female parent, and *S. pimpinellifolium* MLP 23102 and *S. cheesmaniae* LA 524, as male parents, are presented in Table 7. Significant differences were observed between parents of each cross. The cultivar Ace 55 VF (the female parent of the 2 crosses), produced the least significant AA content (14.48 mg/100 g fresh fruit weight) compared with the male parents, that produced AA content of 31.21, and 31.29 mg/100g, respectively. In each cross, F_1 mean was intermediate between its two parents with a high tendency towards the mid-parent in the cross Ace 55 VF × *S. pimpinellifolium* MLP 23102 and high tendency towards the high parent in the cross Ace 55 VF × *S. cheesmaniae* LA 524. In each cross, F_2 plants were widely distributed between their parents with a low tendency towards the low parent in the crosses Ace 55 VF × *S. pimpinellifolium* MLP 23102 and Ace 55 VF × *S. cheesmaniae* LA 524. The mean of BC to cv. Ace 55 VF in each cross was very close to this backcross parent. Plants of the backcrosses to the wild parents surpassed them in their AA content.

Genetic parameters obtained for AA content in the crosses Ace 55 VF × *S. pimpinellifolium* MLP 23102 and Ace 55 VF × *S. cheesmaniae* LA 524 are presented in Table 8. Ascorbic acid content showed no dominance in the cross Ace 55 VF × *S. pimpinellifolium* MLP 23102 and exhibited complete dominance of the high parent in the cross Ace 55 VF × *S. cheesmaniae* LA 524. These results agree with those of Hatem (1994) and Pujer (2017) who reported no dominance for AA content. On the contrary, AA content showed partial dominance of the high parent (Aggour, 1999; Pandiarana *et al.*, 2015; Pujer, 2017; Sherpa *et al.*, 2014 and Solieman *et al.*, 2013), partial dominance of the low parent (Abdel-Ati 1985; Khalil *et al.*, 1988; Pandiarana *et al.*, 2015; Pujer 2017; Sherpa *et al.*, 2014 and Solieman *et al.*, 2013), complete dominance of the low parent (Pujer, 2017), over dominance of the low parent (Pandiarana *et al.*, 2015; Pujer, 2017; Sherpa *et al.*, 2014), or over dominance of the high parent (Pandiarana *et al.*, 2015; Pujer, 2017; Sherpa *et al.*, 2014; Solieman *et al.*, 2013)

The minimum number of genes controlling the AA trait in the 2 studied crosses was one pair. These results agree with those of Khalil (1979) who reported one pair of genes controlled AA content. On the contrary, AA content was controlled by 2 genes or 5 genes as estimated by Aggour (1999) and Hassan *et al.* (2000), respectively.

Estimates of BSH for the 2 studied crosses were high and ranged from 93.4% to 97.9%. These results agree with those of Hedau *et al.* (2008), Kumar *et al.* (2013), Ligade *et al.* (2017), Das *et al.* (2018) and Gillani *et al.* (2019) who reported that BSH for AA content were high. On the contrary, BSH estimates for AA content were moderate (Panchbhaiya *et al.*, 2018 and Prashanth *et al.*, 2007), or low (Meena *et al.*, 2018).

(e) Total soluble solids

Data obtained on TSS content of parental, F_1, F_2, and backcross populations of the crosses Ace 55 VF × *S. pimpinellifolium* MLP 23102, Ace 55 VF × *S. cheesmaniae* LA 524 and *S. lycopersicum* var. *cerasiforme* PI 647522 × *S. cheesmaniae* LA 524 are presented in Table 9. Significant differences were observed between parents of each cross. The cultivar Ace 55 VF (the female parent of the 2 crosses), produced the least significant TSS content (5.5%) compared with the male parents whose TSS content valued 8.9% and 9.3%, respectively. In the first two crosses, F_1 mean was intermediate between its two parents with a tendency towards the low parent in the cross Ace 55 VF × *S. pimpinellifolium* MLP 23102, but it tended more towards the high parent in the crosses Ace 55 VF × *S. cheesmaniae* LA 524 and *S. lycopersicum* var. *cerasiforme* PI 647522 × *S. cheesmaniae* LA 524. In each cross, F_2 plants were widely distributed between their parents with a high tendency towards the high parent in the three crosses. Means of BCs to cv. Ace 55 VF in the crosses Ace 55 VF × *S. pimpinellifolium* MLP 23102 and Ace 55 VF × *S. cheesmaniae* LA 524 were close to the backcross parent. BC to a given parent were very close to this In the cross *S. lycopersicum* var. *cerasiforme* PI 647522 × *S. cheesmaniae* LA 524, plants of the backcross to *S. cheesmaniae* LA 524 surpassed this parent in TSS content.

Genetic parameters obtained for TSS content in the crosses Ace 55 VF × *S. pimpinellifolium* MLP 23102, Ace 55 VF × *S. cheesmaniae* LA 524 and *S. lycopersicum* var. *cerasiforme* PI 647522 × *S. cheesmaniae* LA 524 are presented in Table 10. Low TSS content was partially dominant over the high one in the cross Ace 55 VF × *S. pimpinellifolium* MLP 23102 and high TSS content was partially dominant in the cross Ace 55 VF × *S. cheesmaniae* LA 524, and completely dominant in the cross *S. lycopersicum* var. *cerasiforme* PI 647522 × *S. cheesmaniae* LA 524. These results agree with results of previous studies that reported partial dominance of the low TSS content (Pujer, 2017, Sherpa *et al.*, 2014; Solieman *et al.*, 2013); partial dominance of the high TSS content (Monma and Kamimura, 1982, Pandiarana *et al.*, 2015; Pujer, 2017; Solieman *et al.*, 2013), and complete dominance of the high TSS content (Pujer, 2017).

The minimum number of genes controlling TSS content in the 3 studied crosses was one pair. These results agree with those reported by Abdel-Ati, (1992) who estimated that one pair of genes governed this trait. Other reported estimates were 2 pairs of genes (Abdel-Ati, 1985) or 3 pairs of genes (Hassan *et al.*, 2000; Ibarbia and Lambeth, 1969a and Khalil *et al.*, 1979).

Estimates of BSH for the 3 studied crosses were high and ranged from 76.8 % to 81.5%. These results agree with those of Prashanth *et al.* (2007), Hedau *et al.* (2008), Kumar *et al.* (2013), Shankar *et al.* (2013), Khapte and Jansirani. (2014), Hasan *et al.* (2016), Ligade *et al.* (2017), Meena *et al.* (2017), Aralikatti *et al.* (2018) Das *et al.* (2018), Panchbhaiya *et al.* (2018) and Khuntia *et al.* (2019) who reported that BSH for TSS were high. On the contrary, BSH for TSS was moderate as reported by Kumar *et al.* (2018).

(f) Titratable acidity

Data obtained on fruit TA of parental, F_1, F_2, and backcross populations of the crosses between tomato accession Ace 55 VF, as a female parent, and *S. pimpinellifolium* MLP 23102 and *S. cheesmaniae* LA 524, as male parents, are presented in Table 11. Significant differences were observed between parents of each cross. The cultivar Ace 55 VF (the female parent of the 2 crosses) produced the least significant value of TA (0.60 mg citric acid/100 g fresh fruit weight) compared with the male parents, that produced TA of 1.16 and 0.99, respectively. In each cross, F_1 mean was intermediate between its two parents with a low tendency towards the low parent. In each cross, F_2 plants were widely distributed between their parents with a high tendency towards the high parent in the crosses Ace 55 VF × *S. pimpinellifolium* MLP 23102 and Ace 55 VF × *S. cheesmaniae* LA 524. The mean of BC to cv. Ace 55 VF in the cross Ace 55 VF × *S. pimpinellifolium* MLP 23102 showed slight tendency towards the lower parent. Plants of the backcrosses to the wild parents surpassed these parents in the crosses Ace 55 VF ×*S. pimpinellifolium* MLP 23102 and Ace 55 VF × *S. cheesmaniae* LA 524.

Genetic parameters obtained for fruit TA in the crosses Ace 55 VF × *S. pimpinellifolium* MLP 23102 and Ace 55 VF × *S. cheesmaniae* LA 524 are presented in Tables 12. Titratable acidity content showed complete dominance of the low parent in the crosses Ace 55 VF × *S. pimpinellifolium* MLP 23102 and Ace 55 VF × *S. cheesmaniae* LA 524. These results agree with those reported as complete dominance of the low TA (Pandiarana *et al.*, 2015, Sherpa *et al.*, 2014). On the contrary, other studies reported complete dominance of the high parent (Sherpa *et al.*, 2014) and over dominance of the high parent (Pandiarana *et al.*, 2015; Sherpa *et al.*, 2014), no dominance (Pandiarana *et al.*, 2015), partial dominance of low TA (Pandiarana *et al.*, 2015), and over dominance of the low parent (Pandiarana *et al.*, 2015).

The minimum number of genes controlling TA trait in the 2 studied crosses was one pair.

Estimates of BSH for the 2 studied crosses were high and ranged from 85.5 % to 86.7%. These results agree with those of Shankar *et al.* (2013), Das *et al.* (2018) and Panchbhaiya *et al.* (2018) who reported that BSH for TA was high. On the contrary, BSH for TA was low as estimated by Prashanth *et al.* (2007) and Hedau *et al.* (2008).

(g) Lycopene content

Data obtained on LC of parental, F_1, F_2, and backcross populations of the crosses Ace 55 VF × *S. cheesmaniae* LA 524, and Ace 55 VF ×*S. lycopersicum* (Jubilee) are presented in Tables 13. Significant differences were observed between parents of each cross. In each cross, F_1 mean surpassed its

high parent in the crosses Ace 55 VF × *S. cheesmaniae* LA 524 and Ace 55 VF × *S. lycopersicum* (Jubilee). In each cross, F_2 plants were widely distributed between their parents and surpassed them in their LC. The mean of BCP_1 and BCP_2 of the crosses Ace 55 VF × *S. cheesmaniae* LA 524 was high and surpassed the two parents of each cross.

Genetic parameters obtained for LC content in the crosses Ace 55 VF × *S. cheesmaniae* LA 524 and Ace 55 VF ×*S. lycopersicum* (Jubilee), are presented in Tables 14. High LC content was over dominant in the crosses Ace 55 VF × *S. cheesmaniae* LA 524, Ace 55 VF ×*S. lycopersicum* (Jubilee), These results agree with those of Sherpa *et al.* (2014) and Pandiarana *et al.* (2015) who reported that high LC was found to be partially dominant or over dominant. On the contrary, in other studies low LC showed partial dominance (Sherpa *et al.*, 2014), over dominance (Pandiarana *et al.*, 2015; Sherpa *et al.*, 2014) or no dominance (Sherpa *et al.*, 2014).

The minimum number of genes controlling the LC trait in the 2 studied crosses was one pair.

Estimates of BSH for the 2 studied crosses were high and ranged from 94.7% to 98.7%. These results agree with those of Prashanth *et al.* (2007), Hedau *et al.* (2008), Kumar *et al.* (2013), Shankar *et al.* (2013), Ligade *et al.* (2017), Das *et al.* (2018), Panchbhaiya *et al.* (2018) and Gillani *et al.* (2019) who reported that BSH for LC were high.

(h) β-carotene content

Data obtained on β-carotene content of parental, F_1, F_2, and backcross populations of the crosses Ace 55 VF × *S. cheesmaniae* LA 524, Ace 55 VF ×*S. lycopersicum* (Jubilee), *S. lycopersicum* var. *cerasiforme* PI 647522 × *S. cheesmaniae* LA 524, *S. pimpinellifolium* MLP 23102 × *S. cheesmaniae* LA 524 and its reciprocal cross are presented in Table 15. Significant differences were observed between parents of each cross. In each cross, F_1 mean showed slight tendency towards the lower parent. And F_2 plants were widely distributed between their parents with slight tendency towards the high parent in the cross Ace 55 VF × *S. cheesmaniae* LA 524 and *S. cheesmaniae* LA 524 × *S. pimpinellifolium* MLP 23102, slight tendency towards the low parent in the cross *S. lycopersicum* var. *cerasiforme* PI 647522 × *S. cheesmaniae* LA 524 and surpassed the two parents in the crosses Ace 55 VF ×*S. lycopersicum* (Jubilee) and *S. pimpinellifolium* MLP 23102 × *S. cheesmaniae* LA 524. In the crosses Ace 55 VF × *S. cheesmaniae* LA 524, *S. lycopersicum* var. *cerasiforme* PI 647522 × *S. cheesmaniae* LA 524, BCP_1 means tended more towards the low parent. Also, plants of the backcrosses to the wild parent *S. cheesmaniae* LA 524 showed slight tendency towards it in the cross *S. lycopersicum* var. *cerasiforme* PI 647522 × *S. cheesmaniae* LA 524, but surpassed it in the cross Ace 55 VF × *S. cheesmaniae* LA 524.

Genetic parameters obtained for fruit β-carotene content in the studied crosses are presented in Table 16. Low β-carotene content was partially dominant in crosses Ace 55 VF × *S. cheesmaniae* LA 524, *S. lycopersicum* var. *cerasiforme* PI 647522 × *S. cheesmaniae* LA 524, *S. pimpinellifolium* MLP 23102 × *S. cheesmaniae* LA 524 and *S. cheesmaniae* LA 524 × *S. pimpinellifolium* MLP 23102 and over dominant in the cross Ace 55 VF ×*S. lycopersicum* (Jubilee).

The minimum number of genes controlling β-carotene content in the 5 studied crosses was one pair.

Estimates of BSH for the 5 studied crosses were high and ranged from 86.3% to 98.2%. These results agree with those of Ligade *et al.* (2017), Panchbhaiya *et al.* (2018), Das *et al.*(2018) and Gillani *et al.* (2019) who reported that BSH estimates for β-carotene content were high.

Table 1 : Mean performance, variance and coefficient of variation for average fruit weigh(g) in two tomato crosses.

***S.chees*. LA 524 × Ace 55 VF**				***S.pimp*. MLP 23102 × Ace 55 VF**				**Population**
CV	**V**	**Mean**	**Total no. of plants**	**CV**	**V**	**Mean**	**Total no. of plants**	
3.10	14.93	124.25	15	3.10	14.93	124.25	15	P_1
9.49	0.008	0.97	15	11.72	0.02	1.11	15	P_2
16.91	0.43	3.87	15	11.45	1.20	9.57	15	F_1
65.25	21.67	7.13	89	74.46	25.15	6.73	85	F_2
17.04	13.74	21.75	39	14.61	11.79	23.48	35	BCP_1
24.96	0.25	2.02	21	23.29	0.21	1.98	17	BCP_2

V= Variance, **CV**= Coefficient of variation

Table 2 : Quantitative genetic parameters obtained for average fruit weigh in two tomato crosses.

BSH	**No. of genes**	**Potence ratio**	**Cross**
78.60	79.16	-0.86	*S. pimp*. MLP 23102 × Ace 55 VF
76.37	89.66	-0.95	*S. chees*. LA 524 × Ace 55 VF

Table 3 : Mean performance, variance and coefficient of variation for flesh thickness in two tomato crosses.

***S. chees*. LA 524 × Ace 55 VF**				***S. pimp*. MLP 23102 × Ace 55 VF**				**Population**
CV	**V**	**Mean**	**Total no. of plants**	**CV**	**V**	**Mean**	**Total no. of plants**	
9.39	0.25	5.40	15	9.39	0.25	5.40	15	P_1
13.35	0.06	1.93	15	18.84	0.12	1.86	15	P_2
16.49	0.12	2.13	15	18.81	0.17	2.20	15	F_1
26.58	0.52	2.71	89	37.78	1.75	2.31	85	F_2
10.49	0.10	3.05	39	21.69	0.52	3.34	35	BCP_1
14.35	0.09	2.09	21	18.05	0.15	2.17	17	BCP_2

V= Variance, **CV**= Coefficient of variation

Table 4 : Quantitative genetic parameters obtained for flesh thickness in two tomato crosses.

BSH	No. of genes	Potence ratio	Cross
88	0.99	-0.81	*S. pimp*. MLP 23102 × Ace 55 VF
71.34	3.77	-0.88	*S. chees*. LA 524 × Ace 55 VF

Table 5 : Mean performance, variance and coefficient of variation for number of locules in two tomato crosses.

***S. chees*. LA 524 × Ace 55 VF**				***S. pimp*. MLP 23102 × Ace 55 VF**				**Population**
CV	**V**	**Mean**	**Total no. of plants**	**CV**	**V**	**Mean**	**Total no. of plants**	
14.89	0.26	3.46	15	14.89	0.26	3.46	15	P_1
12.49	0.06	2.06	15	16.49	0.12	2.13	15	P_2
16.49	0.12	2.13	15	18.81	0.17	2.2	15	F_1
36.25	1.33	3.19	89	43.29	1.55	2.88	85	F_2
25.25	0.47	2.71	39	20.45	0.47	3.37	35	BCP_1
20.70	0.23	2.33	21	20.47	0.22	2.29	17	BCP_2

V= Variance, **CV**= Coefficient of variation

Table 6 : Quantitative genetic parameters obtained for number of locules in two tomato crosses.

BSH	No. of genes	Potence ratio	Cross
80.76	0.16	-0.90	*S. pimp*. MLP 23102 × Ace 55 VF
88.65	0.20	-0.89	*S. chees*. LA 524 × Ace 55 VF

Table 7 : Mean performance, variance and coefficient of variation for vitamin C content (mg /100 g fresh fruit weight) in two tomato crosses.

***S. chees*. LA 524 × Ace 55 VF**				***S. pimp*. MLP 23102 × Ace 55 VF**				**Population**
CV	**V**	**Mean**	**Total no. of plants**	**CV**	**V**	**Mean**	**Total no. of plants**	
12.01	3.02	14.48	15	12.01	3.02	14.48	15	P_1
8.27	6.71	31.29	15	3.75	1.37	31.21	15	P_2
7.38	4.97	30.19	15	3.47	0.63	22.92	15	F_1
38.30	74.26	22.49	89	40.55	82.69	22.42	85	F_2
27.37	17.51	15.28	39	22.52	13.12	16.08	35	BCP_1
13.30	21.80	35.1	21	18.08	32.84	31.69	17	BCP_2

V= Variance, **CV**= Coefficient of variation

Table 8 : Quantitative genetic parameters obtained for vitamin C content in two tomato crosses.

BSH	No. of genes	Potence ratio	Cross
97.97	0.43	0.01	*S. pimp*. MLP 23102 × Ace 55 VF
93.39	0.51	0.86	*S. chees*. LA 524 × Ace 55 VF

Table 9 : Mean performance, variance and coefficient of variation for total soluble solids in three tomato crosses.

***S.lyc.* var. *ceras*. PI 647522 ×*S. chees.* LA 524**				***S. chees*. LA 524 × Ace 55 VF**				***S. pimp*. MLP 23102 × Ace 55 VF**				**Population**
CV	**V**	**Mean**	**Total no. of plants**	**CV**	**V**	**Mean**	**Total no. of plants**	**CV**	**V**	**Mean**	**Total no. of plants**	
5.22	0.12	6.73	15	10.43	0.33	5.55	15	10.43	0.33	5.55	15	P_1
9.82	0.84	9.37	15	9.82	0.84	9.37	15	8.17	0.53	8.90	15	P_2
6.98	0.43	9.40	15	10.03	0.79	8.60	15	9.95	0.47	6.90	15	F_1
17.54	2.01	8.09	90	23.14	3.46	8.03	89	20.91	2.41	7.43	85	F_2
8.81	0.40	7.20	35	16.17	0.95	6.03	39	12.56	0.50	5.62	35	BCP_1
10.87	1.06	9.50	17	9.20	1.07	11.27	21	11.03	1.12	9.59	17	BCP_2

V= Variance, **CV**= Coefficient of variation

Table 10 : Quantitative genetic parameters obtained for total soluble solids in three tomato crosses.

BSH	No. of genes	Potence ratio	Cross
81.55	0.72	-0.20	*S. pimp*. MLP 23102 × Ace 55 VF
81.41	0.67	0.59	*S. chees*. LA 524 × Ace 55 VF
76.80	0.55	1.02	*S.lyc.* var. *ceras*. PI 647522 ×*S. chees.* LA 524

Table 11 : Mean performance, variance and coefficient of variation for titratable acidity (mg citric acid /100g fresh fruit weight) in three tomato crosses.

***S. chees*. LA 524 × Ace 55 VF**				***S. pimp*. MLP 23102 × Ace 55 VF**				**Population**
CV	**V**	**Mean**	**Total no. of plants**	**CV**	**V**	**Mean**	**Total no. of plants**	
16.81	0.01	0.60	15	16.81	0.01	0.60	15	P1
9.85	0.009	0.99	15	8.05	0.008	1.16	15	P2
19.97	0.01	0.64	15	23.84	0.02	0.64	15	F1
33.39	0.08	0.87	89	31.39	0.10	1.05	85	F2
26.68	0.02	0.57	39	19.82	0.02	0.72	35	BCP1
14.58	0.02	1.05	21	14.96	0.04	1.35	17	BCP2

V= Variance, **CV**= Coefficient of variation

Table 12 : Quantitative genetic parameters obtained for titratable acidity (mg citric acid /100g fresh fruit weight) in two tomato crosses.

BSH	**No. of genes**	**Potence ratio**	**Cross**
86.77	0.46	-0.86	*S. pimp*. MLP 23102 × Ace 55 VF
85.53	0.26	-0.79	*S. chees*. LA 524 × Ace 55 VF

Table 13 : Mean performance, variance and coefficient of variation for lycopene content (mg /100g fresh fruit weight) in three tomato crosses.

Ace 55 VF ×Jubilee				***S. chees*. LA 524 × Ace 55 VF**				**Population**
CV	**V**	**Mean**	**Total no. of plants**	**CV**	**V**	**Mean**	**Total no. of plants**	
17.73	0.013	0.65	15	17.73	0.01	0.65	15	P_1
23.57	0.0002	0.071	15	8.42	0.009	1.15	15	P_2
16.53	0.02	0.99	15	6.54	0.008	1.44	15	F_1
56.32	0.25	0.89	59	65.18	0.82	1.39	89	F_2
				39.84	0.19	1.12	39	BCP_1
				34.28	0.43	1.91	21	BCP_2

V= Variance, **CV**= Coefficient of variation

Table 14 : Quantitative genetic parameters obtained for lycopene content in three tomato crosses.

BSH	**No. of genes**	**Potence ratio**	**Cross**
98.71	0.038	2.18	***S. chees*. LA 524 × Ace 55 VF**
94.71	0.18	2.15	**Ace 55 VF ×Jubilee**

Table 15 : Mean performance, variance and coefficient of variation for β-carotene content (mg /100g fresh fruit weight) in five tomato crosses.

***S. lyc.* var. *ceras.* PI 647522 ×*S. chess*. LA 524**				**Ace 55 VF ×Jubilee**				***S. chees*. LA 524 × Ace 55 VF**				**Population**
CV	**V**	**Mean**	**Total no. of plants**	**CV**	**V**	**Mean**	**Total no. of plants**	**CV**	**V**	**Mean**	**Total no. of plants**	
28.04	0.0026	0.18	15	48.34	0.006	0.16	15	48.34	0.006	0.16	15	**P_1**
11.23	0.01	0.92	15	19.01	0.01	0.63	15	11.23	0.01	0.92	15	**P_2**
27.78	0.02	0.52	15	33.29	0.00041	0.061	15	19.90	0.009	0.49	15	**F_1**
77.19	0.17	0.53	90	74.66	0.28	0.720	59	103.56	0.40	0.61	89	**F_2**
56.08	0.05	0.43	35					52.03	0.01	0.26	39	**BCP_1**
42.51	0.07	0.66	17					21.83	0.18	1.98	21	**BCP_2**

continued

Table 15. continued.

S. pimp.* MLP 23102 ×LA 524. *S. chees				**LA 524 *S. chees*. ×MLP 23102 *S. pimp.***				**Population**
CV	**V**	**Mean**	**Total no. of plants**	**CV**	**V**	**Mean**	**Total no. of plants**	
11.23	0.01	0.92	15	29.82	0.01	0.38	15	P_1
29.82	0.01	0.38	15	11.23	0.01	0.92	15	P_2
24.31	0.013	0.48	15	16.94	0.006	0.47	15	F_1
35.02	0.09	0.86	37	67.74	0.56	1.11	90	F_2

V= Variance, **CV**= Coefficient of variation

Table 16 : Quantitative genetic parameters obtained for β -carotene content in five tomato crosses.

BSH	No. of genes	Potence ratio	Cross
97.79	0.18	-0.11	***S. chees*. LA 524 × Ace 55 VF**
97.53	0.098	-1.43	**Ace 55 VF ×Jubilee**
93.33	0.45	-0.087	***S. lyc.* var. *ceras*. PI 647522 ×*S. chess*. LA 524**
98.22	0.064	-0.65	**LA 524 *S. chees*. ×MLP 23102 *S. pimp.***
86.26	0.47	-0.63	***S. pimp.* MLP 23102 ×LA 524. *S. chees***

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