Exploring Hybrid Vigor, Inheritance Patterns, and Genetic Progress in Tomato.

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ABSTRACT

In the present investigation, six tomato pure lines were crossed in half diallel mating design to produce 15 F_1 hybrids. Six parental genotypes and their fifteen hybrids were evaluated in open field in the two summer successive seasons 2022 and 2023. Significant differences among genotypes were observed in mean performance for all studied traits. Both parental lines BS and PE showed significant negative general combining ability effects (GCA) for days to 50% flower anthesis (DF), indicating that both lines could be considered as good combiners for developing early tomato genotype. Also, the parental line PE have significant positive general combining ability (GCA) effects for number of fruits/plant (NF), fruit length (FL), fruit flesh thickness (FSI), titratable acidity% (TA) and marketable yield/plant (MY). The parental line M-G have considerable significant positive GCA effects for fruit diameter (FD), titratable acidity% (TA) and marketable yield/plant (MY). Also, R4 have significant positive GCA effects for fruit weight (FW), fruit length (FL), fruit diameter (FD) and total soluble solids (TSS). The cross SM×M-G have significant SCA effects for earliness, (NF), (FW), (FL), (FD), number of locule (NL), (TSS), ascorbic acid (AA) and marketable yield/plant (MY) and reflected favorable significant positive MP and BP heterosis value 83.67 and 73.08% respectivelyfor (MY). The value $(H1/D)^{1/2}$ on the all traits was more than one indicating over-dominance. The parental genotypes displayed a greater prevalence of dominant alleles in their genetic makeup (KD/KR) compared to recessive alleles, indicating a higher proportion of dominant alleles across all studied traits.

Key words: Tomato, Heterosis, Combining ability, Genetic components.

INTRODUCTION

Tomato (*Solanum lycopersicum*) is one of the important Solanaceae vegetable crops grown in parts of the world. Tomato is a rich source of vitamins (A and C), minerals (Ca, P and Fe) and a antioxidant against cancer and heart diseases (Dhaliwal et al., 2003). In Egypt, the tomato crop as fresh and/or processing vegetable cultivated area reaches 409000 feddan produce 6.7 million tons fruits (Department of Agricultural Economics and Statistics, Ministry of Agriculture and Land Reclamation A. R. Egypt, 2022). Production of hybrids in tomato is possible by crossing suitable pure line parents with high specific combining ability.

The incorporation of combining ability stands as an effective technique, imparting valuable genetic insights to guide the selection of parents based on the performance of their hybrid progeny (Chezhian et al., 2000). Heterosis, or hybrid vigor, refers to a specialized genetic mechanism whereby the fusion of genotypes in a specific arrangement showcases their capability to express a remarkable shift in particular traits. The application of hybrid vigor provides an efficient approach to enhance quantitative traits in crops like tomato. Growers of tomato widely prefer hybrid varieties due to their potential for higher yields and improved quality attributes. Considering the paramount importance of tomatoes, it was decided to pursue further investigations in order to ascertain the extent to which heterosis is manifested in this particular crop. (Indu rani and Veerargavathatham, 2008). Several studies have been conducted on heterosis in F_1 hybrids of tomato for most studied quantitative traits by many researchers such as Hussien (2014) who reported that most hybrids were positive heterosis over better parent for plant height. Meanwhile, negative heterosis was detected by Ahmed et al. (2011), Hussien (2014) and

Soliman and Osman (2019) for number of days to flowering.

Kathimba et al. (2022) conducted a study on ten parental genotypes and their 45 F_1 hybrids, revealing that 89% of the hybrids exhibited a decrease in days to 50% flowering, indicating negative heterosis. All the F_1 hybrids displayed favorable heterosis in terms of fruit yield. The outcomes exhibited a substantial variation among the ten genotypes in terms of the general and specific combining ability effects (male x female) for all the traits that were assessed. The traits displayed both additive and non-additive gene actions, which are essential elements in the development of a tomato breeding program.

To develop a suitable breeding strategy for a specific crop, it is crucial to possess comprehensive knowledge regarding the genetic regulation of the crop's specific trait. The diallel method, proposed by Hayman (1954a), Hayman (1954b), Jinks (1954), and Hayman (1958) presents a potent technique for investigating the relative genetic properties of various lines. It allows for the examination of additive and dominance variations, the relative dominance properties of parental lines, and the presence or absence of non-allelic genic interaction in the inheritance of a particular trait. As a result, understanding the relative dominance properties of the parental lines and the nature and magnitude of gene action involved in the inheritance of a specific trait in a particular crop enables breeders to choose an appropriate breeding method that can effectively improve the desired trait in that crop.

The primary aim of this study was to assess the extent of heterosis, as well as general and specific combining abilities, for both yield and quality traits in a half diallel set. This investigation aimed to identify promising parents and their cross combinations that could serve as valuable genetic resources for enhancing these crucial traits. Additionally, the study aimed to pinpoint suitable materials that could be utilized in tomato breeding programs. The ultimate goal of this research is to assist tomato breeders in developing new hybrid tomato varieties with increased yield potential.

MATERIALS AND METHODS

The present study was conducted at Kaha Vegetable Research Farm, Kaliobia Governorate, Horticulture Research Institute, during 2021, 2022 and 2023. On the early summer and fall seasons of 2021 six parents were sown under unheated plastic house to obtain 15 F_1 hybrids and produce parent's seeds. On early summer seasons of 2022 and 2023, the parents and their crosses were evaluated on open field condition. Six pure lines of tomato, i.e., EL-S, SM, BS, PE, M-G, R4 developed by first author were used as parental lines in a half diallel mating design, to produce 15 F_1 hybrids. Seeds of the parents and their F_1 hybrids were sown in the nursery at 15th of January (2022-2023) and when the seedlings were forty-day-old, they were transplanted in the field at 50 cm apart on the northern side of row. Each plot consisted of three rows (5 m long × l m wide). The experimental design was a randomized complete block with three replicates. Normal cultural practices for tomato production were implemented in accordance with the guidelines provided by the Ministry of Agriculture. Data were recorded on days to 50% flower anthesis (DF), number of fruits/plant (NF), fruit weight (FW), Fruit length (FL), fruit diameter (FD), fruit shape index (FSI) which calculated as the ratio of fruit length to fruit diameter, number of locules (NL), total soluble solids (TSS) %, titratable acidity% (TA), ascorbic acid (AA) and marketable yield/plant (MY).

Statistical analysis

Means and variances were calculated for each treatment where the means were statistically compared for significant differences using New L.S.D. (Snedecor and Cochran, 1990).

The analysis of general and specific combining abilities (GCA and SCA) were calculated according to Griffing (1956) method 2 model 1 also, Hayman approach was also used as followed Mather and Jinks (1982), The analysis involves assessing variance, estimating variance and covariance, constructing the Wr-Vr graph, estimating variance components, and determining various parameters, including the identification of the most prominent dominant and recessive parents. The data analysis yielded several findings. Firstly, variations attributed to the additive effect was reported, denoted as D. Additionally, the mean value of 'Fr' across the arrays was calculated, it, represented as F. 'Fr' represents the covariance between additives and non-additive effects within a single array. Furthermore, the components of variation resulting from the dominance effect of the genes was identified, It, referred to as H1. Moreover, the proportion of positive and negative genes in the parents was estimated. It denoted as

H2. The expected environmental components of variation were determined. It, represented as E. The mean degree of dominance was calculated as $(H1/D)^{1/2}$. Additionally, the proportion of genes with positive and negative effects in the parents was calculated as H2/4H1. Furthermore, the proportion of dominant and recessive genes in the parents were determined as Kd/Kr. Lastly, the heritability in narrow sense as $h^2n\%$ and the heritability in broad sense as $h^2b\%$. were calculated. Average degree of heterosis (ADH%) was estimated as the increase or decrease percent of F_1 performance over the mid-parent (MP) and better parent (BP) according Sinha and Khanna (1975).

RESULTS AND DISCUSSIONS

A-Mean performance:

Table (1) displays the data acquired from the evaluation of six pure lines and their fifteen crosses of tomato over the course of two years, specifically in 2022 and 2023. The results of this evaluation, along with their respective ranks, have been presented. Notably, significant differences were observed in all the studied characteristics during both years. However, when the data from the two seasons were combined, no significant differences were found between two seasons. Therefore, a combined analysis was performed to account for the overall performance of the genotypes and hybrids across the two seasons. For combined analysis regarding DF trait the parental values ranged from 14.17 (PE) to 32.00 (SM) days with the mean of 24.64 days. Their crosses ranged from 12.50 (EL-S×PE) to 27.50 days (EL-S×M-G) with a mean of 18.47 days. The parental value for NF trait ranged from 18.67 fruits (R4) to 29.33 fruits (SM) with a mean of 22.42 fruits. Their crosses ranged from 15.67 (PE × R4) to 35.33 fruits (SM × PE) with a mean of 25.86 fruits. The FW trait of parental genotypes ranged from 57.60 (SM) to 118.73 g (M-G) with a mean of 76.71. Their crosses ranged from 69.25 (SM × BS) to 121.88 g (M-G × R4) with a mean of 88.55 g. Regarding FL trait the parental value ranged from 4.62 (M-G) to 6.82 cm (R4) with a mean of 5.60 cm. Their crosses ranged from 4.70 (EL-S×M-G) to 7.27 cm (EL-S× BS) with a mean of 6.08 cm. Also, the parental value for FD trait ranged from 4.51 (M-G) to 5.50 cm (R4) with a mean of 5.12 cm. Their crosses ranged from 4.80 (M-G × R4) to 6.50 cm (EL-S×BS) with a mean of 5.59 cm. The FSI trait of parental genotypes ranged from 0.56 (SM) to 0.82 (PE and R4) with a mean of 0.73. Their crosses ranged from 0.6 (BS × R4) to 0.83 (PE × R4) with a mean of 0.72. Regarding NL trait the parental value ranged from 3.8 (EL-S and PE) to 5.0 (M-G) with a mean of 4.3. Their crosses ranged from 3.2 (BS×M-G) to 5.0 (SM× BS) with a mean of 4.27. Also, the parental value for TSS trait ranged from 4.17 (EL-S) to 5.25% (SM) with a mean of 4.57%. Their crosses ranged from 4.25 (EL-S × M-G) to 5.47 % (SM× M-G) with a mean of 4.96%. For TA% trait the parental value ranged from 0.60 (EL-S) to 0.87% (BS) with a mean of 0.72. Their crosses ranged from 0.52 (EL-S ×PE) to 0.95 % (BS× PE) with a mean of 0.69%. Regarding AA trait the parental value ranged from15.76 (R4) to 26.49 mg/100 fw (SM) with a mean of 20.95. Their crosses ranged from 17.96 (M-G×R4) to 33.55 mg/100 fw (EL-S × SM) with a mean of 26.27. Finally, the parental value of MY trait ranged from 1.28 (BS) to 1.93 kg/p (EL-S) with a mean of 1.66 kg/p. Their crosses ranged from 1.62 (PE×R4) to 2.95 kg/p (SM × M-G) with a mean of 2.27.

Generally, the results reflected wide range of variability among the genotypes in the general performance for all studied traits.

These results are in contrast with those obtained by Al-Aysh et al. (2012) and Hussien (2014) who reported that high genetic advance from selection as percentage over mean were observed for number of fruits per plant, average fruit weight and fruit yield per plant.

Table (1). Performances of F_1 hybrids and their parents for some vegetative and fruit traits in open field, combined across two seasons 2022, 2023.

Genotypes	DF	NF	FW (g)	FL (cm)	FD (cm)	FSI
EL-S	24.67	26.00	72.25	5.83	5.25	0.77
SM	32.00	29.33	57.60	4.65	5.45	0.56
BS	20.83	21.17	61.92	5.92	5.33	0.73
PE	14.17	26.67	65.53	5.77	4.68	0.82
M-G	25.00	12.67	118.73	4.62	4.51	0.70
R4	31.17	18.67	96.25	6.82	5.50	0.82
Mean	24.64	22.42	78.71	5.60	5.12	0.73
EL-S×SM	26.67	22.67	73.60	6.32	5.75	0.73
EL − S ×BS	19.17	28.83	73.07	7.27	6.50	0.75
EL-S×PE	12.50	34.50	79.25	6.48	5.47	0.77
EL-S × M-G	27.50	27.33	74.30	4.70	5.00	0.65
EL-S ×R4	22.67	25.17	107.98	6.90	5.93	0.78
SM×BS	15.83	28.67	69.25	6.47	5.63	0.73
SM×PE	12.50	35.33	71.20	5.73	5.20	0.70
SM× M-G	13.67	26.67	110.37	5.31	5.68	0.65
SM×R4	24.50	25.17	81.95	6.45	5.88	0.72
BS×PE	15.33	19.17	85.22	6.03	5.70	0.68
BS×M-G	15.33	28.67	74.12	5.36	4.87	0.75
BS×R4	18.17	20.83	90.95	5.21	5.82	0.60
PE× M-G	15.66	25.67	114.87	6.10	6.00	0.68
PE×R4	19.16	15.67	100.23	7.10	5.63	0.83
M-G×R4	18.33	23.5	121.88	5.81	4.80	0.76
Mean	18.47	25.86	88.55	6.08	5.59	0.72
N.L.S.D(0.05)	4.20	3.30	6.65	0.32	0.29	0.08

Table (1). Continued

Genotypes	NL	TSS%	TA%	AA (mg/100g. fw)	MY (kg/p)
EL-S	3.8	4.17	0.60	16.58	1.93
SM	4.5	5.25	0.80	26.49	1.72
BS	4.5	4.42	0.87	18.45	1.28
PE	3.8	4.50	0.64	25.34	1.77
M-G	5.0	4.25	0.75	23.10	1.50
R4	4.2	4.83	0.66	15.76	1.77
Mean	4.3	4.57	0.72	20.95	1.66
EL-S×SM	4.3	5.33	0.54	33.55	1.68
EL − S ×BS	3.8	4.75	0.79	27.69	2.18
EL-S×PE	4.2	5.08	0.52	30.78	2.85
EL-S × M-G	4.0	4.25	0.72	27.41	2.03
EL-S ×R4	4.8	5.17	0.54	22.06	2.65
SM×BS	5.0	5.35	0.82	30.93	1.98
SM×PE	4.2	4.97	0.67	29.31	2.63
SM× M-G	4.8	5.47	0.75	32.50	2.95
SM×R4	4.0	4.92	0.71	19.75	2.02
BS×PE	4.5	4.58	0.95	21.21	1.68
BS×M-G	3.2	4.83	0.72	19.90	2.15
BS×R4	4.0	5.33	0.62	25.60	1.90
PE× M-G	4.7	4.75	0.63	23.66	2.92
PE×R4	4.5	4.75	0.67	31.75	1.62
M-G×R4	4.0	4.91	0.72	17.96	2.86
Mean	4.27	4.96	0.69	26.27	2.27
N.L.S.D (0.05)	0.65	0.65	0.07	3.70	0.28

B- **Combining ability for the studied traits:**

Estimates of GCA effects (gi) for individual parental lines in each trait are presented in **Table (2)**. Both parental lines BS and PE showed significant negative gi effects for DF trait, indicating that both lines could be considered as good combiners for developing early tomato genotype. These findings agreed with those of Reddy et al. (2013) and Hatem and Khalil (2014).

Parental line PE had considerable significant positive gi effects for NF, FL, FSI, TA and MY traits. The parental lines M-G have considerable significant positive gi effects for FW, TA and MY traits. Also, R4 had significant positive gi effects for FW, FL, FD and TSS traits. These lines proved to be good combiners in this respect.

Similar results were found by Kumar et al., 2013 who reported that none of the parent found to be good general combiner for all the traits.

Table (2). General combining ability effects (gi) for the parental lines during season 2023.

Parents	DF	NF	FW	FL	FD	FSI	NL	TSS%	TA%	AA	MY
EL-S	6.00**	5.75**	-18.23**	0.60**	0.35**	0.10**	-0.37*	-0.39**	-0.22**	-0.002	0.17**
SM	6.00**	8.37**	-29.20**	- 0.77**	0.42**	-0.24**	0.50**	0.97**	0.07**	10.05**	0.03
BS	-6.00**	-2.12**	-31.25**	0.26**	0.33**	-0.05**	-0.12	0.10	0.27**	-3.91**	-0.90**
PE	-13.87**	3.62**	-7.50**	0.50**	-0.27**	0.13**	0.00	-0.39**	-0.06**	5.33**	0.23**
M-G	-0.25	-6.00**	50.10**	-1.92**	-1.17**	-0.08**	0.12	-0.64**	0.05**	-2.43**	0.49**
R4	8.12**	-9.62**	36.08**	1.33*	0.34**	0.14	-0.12	0.35**	-0.11**	-9.04**	-0.03
S.E(gi)	**0.77**	**0.56**	**1.15**	**0.06**	**0.05**	**0.01**	**0.12**	**0.12**	**2.61**	**0.64**	**0.03**

*and ** indicate significance at 0.05 and 0.01 probability levels, respectively.

Specific combining ability effects were listed in Table 3, the best combinations were: SM × M-G, SM × PE, EL-S × PE, M-G × R4, BS × R4, EL-S × R4 and BS × M-G (for DF trait); BS × M-G, SM × PE, EL-S × PE, M-G × R4, EL-S × BS, EL-S × M-G, EL-S × R4, PE × M-G and SM × M-G (for NF trait); SM × M-G, EL-S × R4, PE × M-G, BS × PE, M-G × R4, SM × BS, PE × R4, BS × R4, EL-S × SM and EL-S × BS (for FW trait); EL-S × BS, PE × M-G, PE × R4, SM × BS, EL-S × SM, SM × R4, SM × M-G, EL-S × R4 and EL-S × PE (for FL trait); PE × M-G, EL-S × BS, SM × M-G, SM × R 4, BS × PE, EL-S × R4 and PE × R4 (for FD trait); SM × BS, EL-S × SM, M-G × R4, BS × M-G and PE × R4 (for FSI trait); EL-S × R4, SM × M-G, BS × PE, PE × R4 and PE × M-G (for NL trait); BS × R4, EL-S × R4, EL-S × PE, SM × M-G and EL-S × SM (for TSS trait); EL-S × BS, EL-S × M-G, M-G × R4, SM × R4, EL-S × R4, EL-S × SM, BS × M-G, BS × R4 and SM × BS (for TA trait); PE × R4, SM × BS, BS × R4, SM × M-G, EL-S × SM, EL-S × BS, EL-S × PE and EL-S × M-G (for AA trait);SM × M-G,PE × M-G, M-G × R4, EL-S × PE, EL-S × R4, SM × PE, EL-S × BS, BS × M-G and BS × R 4 (for MY trait).

C- Heterosis effect:

Mid-parent (MP) and better parent (BP) heterosis of all studied traits are presented in table 4. Desirable significant negative MP heterosis for the earliness DF (days to 50% flower anthesis) was observed in twelve F_1 crosses, however, six F_1 crosses exhibited desirable significant negative BP values, i.e., SM×M-G, M-G×R4, BS×M-G, SM×BS, SM×R4 and BS×R4 with (-44.59, -27.02, -25.81, -20.97, -19.78 and -16.13% respectively).

Islam et al. (2012) and Gautam et al. (2018) have also documented instances of early flowering in hybrids. Ten out fifteen crosses showed desirable significant positive MP heterosis for the NF trait. Five F_1 crosses exhibited desirable significant positive BP values, i.e., BS×M-G, EL-S×PE, M-G×R4, SM×PE and EL-S×BS with (31.28, 24.10, 25.81, 22.41, 21.60 and 10.27 % respectively). Similar findings for higher fruits number per plant were reported by Hannan et al. (2007) and Ahmad et al. (2011).

Table (3). Estimates of specific combining ability effects (sij) for the F_1's crosses combinations during season 2023.

Crosses	DF	NF	FW	FL	FD	FSI	NL	TSS%	TA%	AA	MY
EL-S×SM	8.0**	-20.5**	9.8**	1.2**	0.1	0.17**	-0.3	0.7*	-0.30**	16.1**	-1.4**
EL-S×BS	-4.0	6.9**	9.6**	3.4**	2.6**	0.08	-0.6	0.1	0.20**	13.7**	0.5**
EL-S×PE	-14.1**	18.2**	5.9	0.4*	0.03	-0.01	0.2	1.1**	-0.28**	12.7**	1.8**
EL-S×M-G	16.2**	6.8**	-67.8**	-2.4**	-0.7**	-0.29**	-0.9*	-0.6	0.21**	9.3**	-1.0**
EL-S×R 4	-8.1**	6.4**	48.7**	0.8**	0.6**	-0.02*	2.4**	1.4**	-0.10*	0.5	1.5**
SM×BS	20.0**	-12.7**	22.8**	1.5**	0.2	0.32**	-0.5	0.2	-0.79**	20.1**	-0.3**
SM×PE	-15.1**	19.6**	-7.9	-0.4*	-0.8**	0.03	-0.6	-0.2	-0.12**	-2.0	1.3**
SM×M-G	-24.7**	4.2**	56.1**	0.9**	1.6**	0.04	1.2**	1.0**	0.02	16.2**	2.2**
SM×R 4	-1.1	-0.2	-14.2**	1.0**	0.9**	0.02	-1.5**	-1.0**	0.05*	-13.6**	-0.4**
BS×PE	4.9**	-21.9**	38.0**	-0.5**	0.8**	-0.25**	1.0 **	-0.9*	0.53**	-12.4**	-0.9**
BS×M-G	-7.7**	19.7**	-52.9**	-0.2	-1.0**	0.16**	-3.1**	0.4	-0.28**	-8.7**	0.5**
BS×R 4	-10.1**	0.3	12.4**	-3.8**	-0.15	-0.57**	-0.9*	1.4**	-0.38**	17.5**	0.4**
PE×M-G	1.1	4.9**	44.9**	2.0**	3.1**	-0.23**	0.7*	0.4	-0.18**	-6.0**	1.8**
PE×R 4	3.7	-21.4**	12.8**	1.6**	0.4**	0.14**	1.0**	-0.6	0.11**	25.1**	-1.7**
M-G×R 4	-13.9**	11.2**	23.8**	-0.1	-1.0**	0.16**	-1.1**	0.6	0.14**	-9.2**	1.8**
SE(Sij)	2.13	1.5	3.18	0.17	0.15	0.04	0.33	0.33	0.03	1.76	0.10

*and ** indicate significance at 0.05 and 0.01 probability levels, respectively.

For FW trait all crosses revealed desirable significant positive MP heterosis except EL-S×M-G and BS×M-G, five out fifteen crosses showed desirable significant positive BP values, i.e., BS×PE, EL-S×R4, SM×BS, EL-S×PE and SM×PE (31.06, 12.50, 11.60, 8.99 and 8.74% respectively).

These results are in agreement with those reported by Hannan et al. (2007), Rahmani et al. (2010) and Naorem et al. (2012).

For FL tait all crosses exhibited desirable significant positive MP heterosis for long fruit except five crosses, seven F_1 crosses exhibited desirable significant positive BP values for long parent, i.e., EL-S×BS, SM×M-G, EL-S×PE, EL-S×R4, SM×BS, PE×M-G and PE×R4 with (22.78, 15.00, 11.50, 8.62, 7.22, 6.94 and 2.40 % respectively). On the other hand, five F_1 crosses exhibited desirable significant negative BP values i.e., BS×R4, EL-S×M-G, M-G×R4, BS×M-G and SM×R4 with (-24.52, -18.96, -17.31, -11.11 and -6.73 % respectively).

The findings of Rahmani et al. (2010) and Hussien (2014) contradict the results presented here. Hussien studies revealed that the heterotic expression for fruit length exhibited a wide range of extreme values, ranging from -38.5% to 3.0%, for both types of heterosis. However, none of the crosses demonstrated significance in any form of heterosis. For FD trait ten out fifteen crosses revealed desirable significant positive MP, eight crosses showed desirable significant positive BP values for this trait i.e., EL-S×BS, SM×M-G, SM×R4, BS× PE, EL-S×R4, EL-S× SM and EL-S×PE with (23.12, 16.61, 7.78, 7.50, 6.00, 5.49 and 5.10 % respectively).

The outcomes of this investigation are in disagreement with those reported by Hussien (2014), as he identified a wide variation in the heterotic expression for fruit diameter, with values ranging from -25% to 7.2% for both types of heterosis. Notably, only one cross displayed MP heterosis, while none of the crosses exhibited BP heterosis.

For FSI trait only two crosses revealed significant positive MP i.e., SM×BS and EL-S×SM with (13.79 and 10.00% respectively). On the other hand, six crosses reflected significant negative BP values. For NL trait only two crosses reflected significant positive MP, only on cross showed desirable significant positive BP values i.e., EL-S×R4 with 15.38%. Seven crosses showed desirable significant positive MP for TSS trait and only one cross reflected significant positive BP values i.e., BS×R4 (15.79%).

Table (4). Relative heterosis (MP) and heteobeltiosis (BP) for studied traits of tomato during season 2023.

Crosses	DF		NF		FW		FL		FD		FSI	
	MP %	BP %	MP %	BP %	MP %	BP %	MP %	BP %	MP %	BP %	MP %	BP %
EL-S×SM	-4.19	9.59	-16.90**	-21.60**	12.73**	0.87	20.38**	8.62**	7.79**	5.49*	10.00**	-5.71
EL-S×BS	-17.04*	-9.68	19.44**	10.27*	7.71*	-0.14	24.85**	22.78**	24.29**	23.12**	0.00	-2.86
EL-S×PE	-33.91**	-9.52	27.95**	24.10*	14.84**	8.99*	11.81**	11.50**	10.74**	5.10*	-2.77	-5.40
EL-S×M-G	11.56*	12.33	39.00**	5.13	-22.67**	-37.60**	-9.90**	-18.96**	3.47	-5.10*	-10.45**	-14.28**
EL-S×R 4	-19.51**	-9.60	14.70**	0.00	27.99**	12.50**	7.85**	-0.96	9.26*	6.00*	-2.78	-5.40
SM×BS	-37.18**	-20.97*	13.00**	-1.14	16.00**	11.60**	20.62**	7.22**	4.94*	3.66	13.79**	0
SM×PE	-45.59**	-11.90	25.15**	21.60*	15.75**	8.74*	9.90**	-0.58	2.95	-4.27	3.22	-13.51**
SM×M-G	-51.19**	-44.59**	28.12**	-6.82	26.74**	-5.91*	15.41**	15.00**	16.61**	4.88*	5.26	-6.25
SM×R 4	-21.08**	-19.78**	1.37	-15.91**	8.77**	-13.10**	11.49**	-6.73**	8.76**	7.78**	3.22	-13.51**
BS×PE	-13.46	7.14**	-26.17**	-33.73**	34.34**	31.06**	2.55	0.55	14.28**	7.50**	-11.43**	-16.22**
BS×M-G	-32.35**	-25.81**	64.15**	31.82**	-17.43**	-37.10**	0.31	-11.11**	-0.34	-9.37**	1.54	0.00
BS×R 4	-32.03**	-16.13*	3.22	-3.03	15.86**	-4.57	-19.07**	-24.52**	3.36	1.20	-20.00**	-24.32**
PE×M-G	-18.96*	11.90	26.83**	-6.02	25.08**	-2.97	18.59**	6.94**	32.35**	27.66**	-10.14**	-16.22**
PE×R 4	-12.80*	38.10**	-31.91**	-42.17**	23.50**	3.77	11.81**	2.40*	9.74**	1.20	0.00	0.00
M-G×R 4	-34.54**	-27.02**	44.89**	22.41**	14.14**	3.31	-0.86	-17.31**	-2.68	-13.17**	1.45	-5.40

*and ** indicate significance at 0.05 and 0.01 probability levels, respectively.

Table (4). Continued

Crosses	NL		TSS		TA		AA		MY	
	MP %	BP %	MP %	BP %	MP %	BP %	MP %	BP %	MP %	BP %
EL-S×SM	0.00	-7.14	12.28*	0.00	-21.60**	-31.56**	56.03**	25.43**	-8.10*	-13.56**
EL-S×BS	-7.70	-14.28*	9.43	3.57	6.97*	-9.50**	61.13**	50.81**	24.50**	3.39
EL-S×PE	8.33	8.33	13.21*	7.14	-17.46**	-20.41**	47.04**	20.01**	47.83**	44.07**
EL-S×M-G	-11.11*	-20.00**	4.00	4.00	5.85	-4.82	37.73**	17.12**	14.28**	1.69
EL-S×R 4	20.00**	15.38*	18.52**	10.34	-11.29*	-15.07**	38.68**	35.83**	39.82**	33.90**
SM×BS	7.14	7.14	10.00*	3.12	-3.35	-6.84	36.48**	15.80**	31.87**	15.38**
SM×PE	0.00	-7.14	0.00	-6.25	-9.09*	-18.03**	11.80**	9.63*	46.30**	41.07**
SM×M-G	3.45	0.00	12.28*	0.00	-4.24	-7.38	31.19**	22.49**	83.67**	73.08**
SM×R 4	-11.11*	-14.28*	-1.64	-6.25	-3.84	-12.70**	-2.03	-22.47**	11.32**	9.26*
BS×PE	7.69	0.00	-3.57	-3.57	24.62**	8.74*	-4.11	-17.29**	-1.05	-16.07**
BS×M-G	-31.03**	-33.33**	9.43	3.57	-12.02**	-17.87**	-4.77	-14.12**	50.59**	39.13**
BS×R 4	-11.11*	-14.28*	15.79**	13.79**	-17.75**	-27.76**	54.16**	41.53**	24.73**	7.41
PE×M-G	3.70	-6.67	5.66	0.00	-8.96*	-15.35**	-3.69**	-8.39	72.55**	57.14**
PE×R 4	12.00*	7.69	-1.75	-3.45	3.80	3.01	54.81**	24.34**	-12.72**	-14.28**
M-G×R 4	-14.28**	-20.00**	11.11*	3.45	3.04	-3.51	-6.87*	-22.15**	72.00**	59.26**

*and ** indicate significance at 0.05 and 0.01 probability levels, respectively.

For TA trait only two crosses revealed significant positive MP i.e., BS × PE and EL-S × BS with (24.62 and 6.97% respectively). On the other hand, only one cross reflected significant positive BP values i.e., BS ×PE (8.74 %). For AA ten out fifteen crosses reflected significant positive MP and BP values for this trait. For MY trait twelve out fifteen crosses reflected significant positive MP values, nine out fifteen crosses reflected significant positive BP values i.e., SM×M-G, M-G × R4, PE × M-G, EL-S × PE, SM× PE, BS × M-G, EL-S × R4, SM × BS and SM × R4 with (73.08, 59.26, 57.14, 44.07, 41.07, 39.13, 33.90, 15.38 and 9.26% respectively).

D- Genetic parameters:

Genetic analysis was performed on the obtained data using the half diallel method described by Hayman (1954) and (Singh &Chaudhary, 1979). In order to expand our knowledge regarding the genetic behavior of the traits investigated in our study (Table 5), it is essential to gather more information. The influence of additives (D) was significantly different for all the observed traits except NL and MY. The influence of the dominant (H1) was also significantly different for all the observed traits. The dominance genetic variations H1 and H2 were significant for all studied traits except H2 for FSI and TA traits, indicating the importance of dominance effects in the inheritance of these traits.

The evaluation of the ratio of positive genes can be deduced by examining the disparity between the values of H1 and H2. In the event that H1 surpasses H2, it signifies a greater

abundance of positive genes. Conversely, if H1 is lower than H2, it implies a higher prevalence of negative genes. Genes involved more heavily in determining the all studied traits were positive genes reflected in the value of H1 > H2.

According to a study conducted by Tasisa et al. (2018), the mean degrees of dominance $(H1/D)^{1/2}$ for titratable acidity were found to be greater than 1, suggesting the presence of over dominance effects. On the other hand, the $(H1/D)^{1/2}$ for shape index was less than 1, indicating that the dominance was not complete. The proportion of positive and negative genes (H2/4H1) was estimated to be 0.13 for shape index and 0.14 for titratable acidity, which differs from the expected value of 0.25.

The magnitude of dominance effects becomes apparent when considering the value $(H1/D)^{1/2}$. Across all traits, this value exceeded one, indicating the prevalence of over-dominance. Regarding (F) values in Table 5, it is apparent that all studied traits were not significant and this might indicate that there is symmetric gene distribution or the equality in the relative frequencies of dominant and recessive genes in the parents.

Broad sense heritability h^2b was found to be high for all studied traits. However, h^2n values were high (65 and 67%) for FW and TA traits respectively, moderate (50, 45, 44%) for FSI, DF and FL traits respectively. However, the estimates of narrow sense heritability were low and valued 0.06% (NL trait). According to the findings of Kumar et al. (2013), the heritability of total soluble solids (TSS) was controlled by non-additive genetic factors.

Theses finding agree with Mohamed et al. (2012) who found that the highest heritability was recorded on fruit weight (92.0%) with an expected genetic advance over percentage of mean of 92.9%, days to 50% flowering (69.0%) with an expected genetic advance over percentage of mean of 9.4%, while the lowest heritability was that of fruit yield per plant (43.0%) with an expected genetic advance over percentage of mean of 33.9%

In the genetic constitution of the parents, the ratio of dominant to recessive alleles (KD/KR) surpassed unity, indicating the predominance of dominant alleles in the parental genotypes for all traits under examination.

Table (5). Estimation of genetic parameters of some yield components of tomato using the diallel analysis of the Hayman Method during season 2023.

Traits	Genetic components					Derived parameters				
	D	H1	H2	F	E	$(H1/D)^{1/2}$	H2/4H1	h^2n	h^2b	KD/KR
DF	39.14±* 9.17	76.98* ±23.28	68.73* ±20.79	15.88 ±22.40	1.92 ±3.47	1.40	0.223	0.45	0.93	1.34
NF	34.49* ±8.96	103.24** ±22.75	87.67* ±20.32	28.73 ±21.89	1.26 ±3.39	1.73	0.21	0.31	0.97	1.63
FW	564.07** ±97.11	649.39* ±246.52	574.94* ±220.23	95.30* ±37.24	4.35 ±36.70	1.07	0.22	0.65	0.99	1.17
FL	0.75* ±0.22	1.67* ±0.56	1.47* ±0.50	0.35 ±0.54	0.01 ±0.08	1.49	0.22	0.44	0.98	1.37
FD	0.21* ±0.09	0.82* ±0.24	0.78* ±0.21	0.08 ±0.23	0.01 ±0.04	1.97	0.24	0.29	0.96	1.21
FSI	0.02** ±0.00	0.03* ±0.01	0.02 ±0.01	0.02 ±0.01	0.0 ±0.0	1.22	0.17	0.50	1.00	2.38
NL	0.11 ±0.14	0.94* ±0.35	0.77* ±0.32	0.25 ±0.34	0.05 0.05±	2.92	0.20	0.06	0.88	2.27
TSS	0.15** ±0.03	0.29* ±0.09	0.27* ±0.08	0.02 ±0.08	0.05 ±0.01	1.39	0.23	0.39	0.72	1.10
TA	0.01** ±0.00	0.03* ±0.01	0.02 ±0.01	0.00 ±0.01	0.00 ±0.00	1.73	0.17	0.67	1.00	1.00
AA	22.57** ±4.40	101.46** ±11.16	82.54** ±6.71	13.29 ±10.74	1.35 ±1.66	2.12	0.22	0.33	0.96	1.32
MY	0.05 ±0.08	1.02** ±0.21	0.91** ±0.19	0.02 ±0.20	0.00 ±0.03	4.52	0.22	0.23	1.00	1.09

*and ** indicate significance at 0.05 and 0.01 probability

E-Graphical analysis:

To assess the adequacy of the additive-dominance mode of gene action, graphical analysis was conducted on the data obtained from the diallel table for each trait. The regression line intercepted the Wr axis above the origin in FW, FL, FD, NL, TSS, TA and MY traits (Fig. 3, 4, 5, 7, 8, 9 and 11, respectively) that showcased evidence demonstrates a precise case of partial dominance. Nevertheless, the

regression line intersects the Wr axis below the origin in NF, FSI and AA traits (Fig. 2, 6 and 10) indicating over-dominance in these traits. Conversely, complete dominance had a significant impact on the regulation of the DF trait (Fig.1). The Vr/Wr graph provides insights into the distribution of array points, indicating that the parental genotypes (BS) exhibit a high prevalence of dominant alleles for DF, FW and MY traits, (EL-S) for NF, FW and NL traits. Nevertheless, the genetic composition of the parental tomato genotype (EL-S) exhibited a nearly equal distribution of both dominant and recessive alleles for DF, FSI, TA, and MY traits.

In light of this, it is evident that the parental genotypes exhibit a considerable level of genetic diversity. This implies that breeders can effectively employ these genetic materials to produce tomato cultivars with a high potential for yield. The determination of this potential is based on the study of physiological traits.

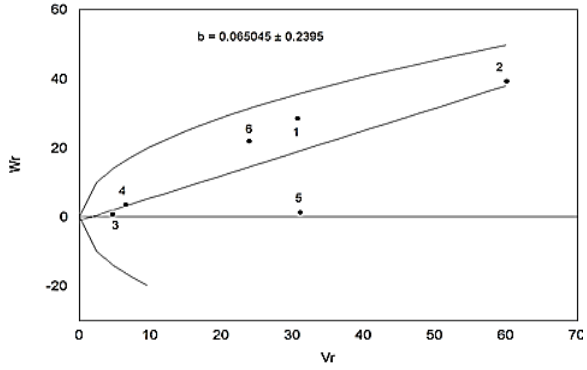

Fig.1: Vr/Wr graph for DF

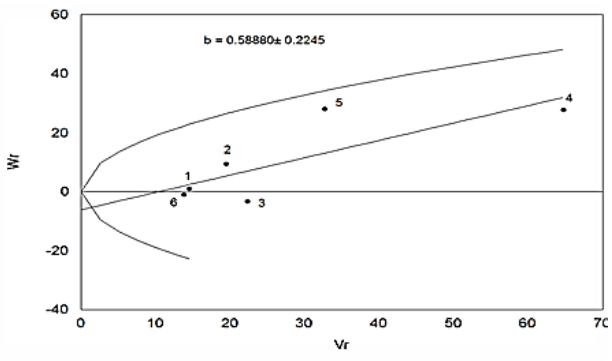

Fig.2: Vr/6Wr graph for NF

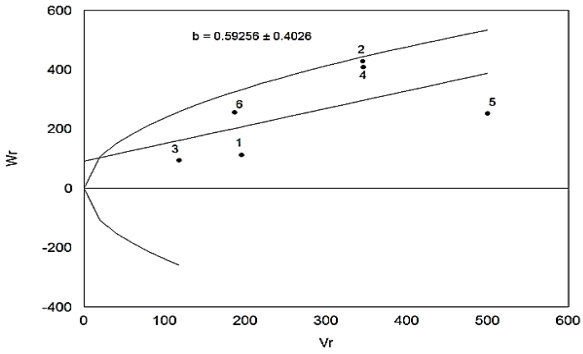

Fig.3: Vr /Wr graph for FW

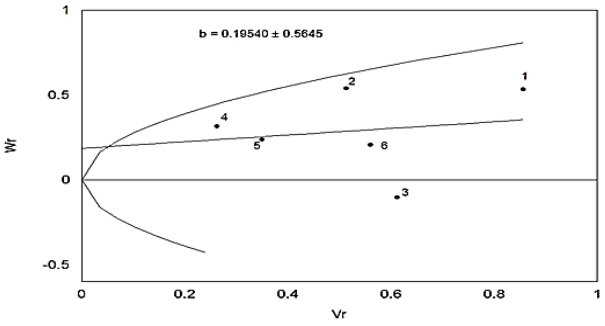

Fig.4: Vr/Wr graph for FL

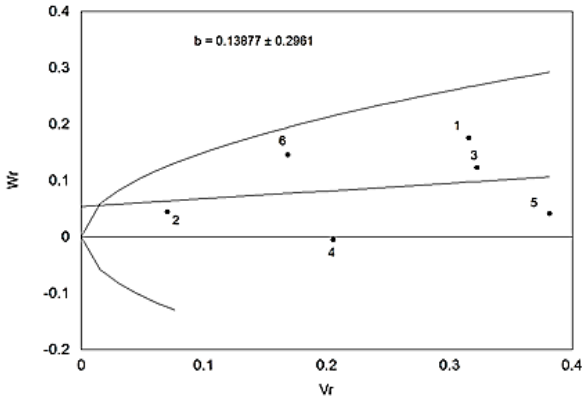

Fig.5: Vr/Wr graph for FD

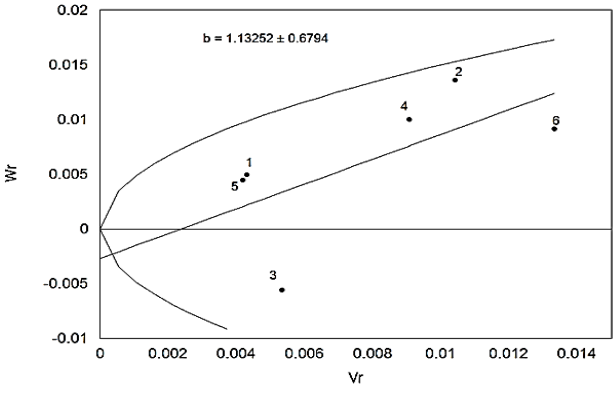

Fig.6: Vr/Wr graph for FSI

1=EL-S, 2=SM, 3-BS, 4=PE, 5=M-G, 6=R 4

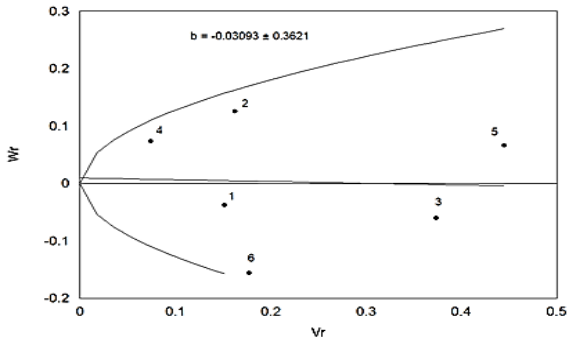

Fig.7 Vr/Wr graph for NL

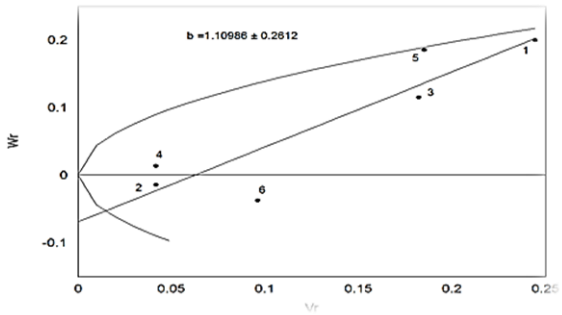

Fig.8: Vr/Wr graph for TSS

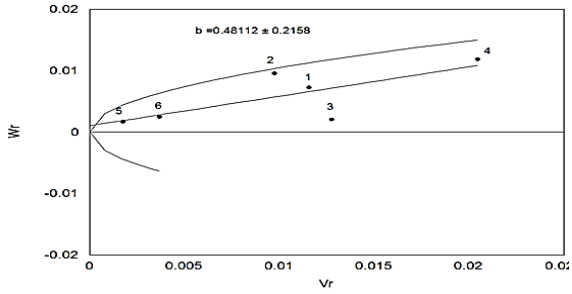

Fig.9: Vr/Wr graph for TA

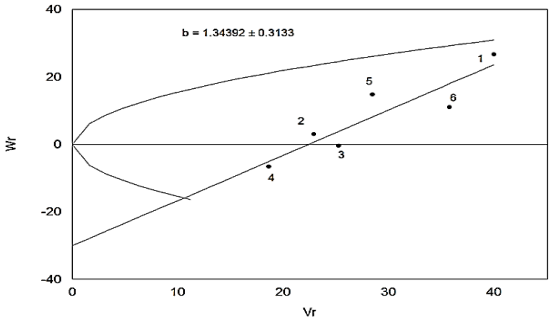

Fig.10: Vr/Wr graph for AA

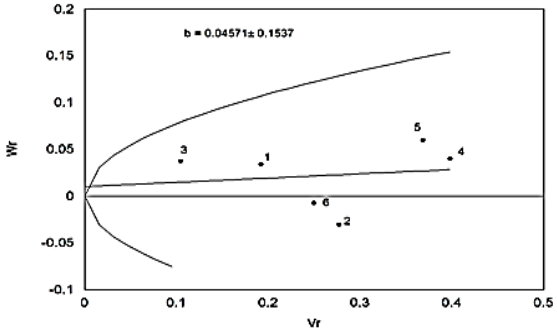

Fig.11: Vr/Wr graph for MY

1=EL-S, 2=SM, 3-BS, 4=PE, 5=M-G, 6=R 4

Conclusion:

The aim of our study is to explore the magnitude of heterosis, general and specific combining abilities, and genetic resources for improving yield and quality traits in tomato (*Solanum lycopersicum* L). The study utilized a half diallel mating design to produce 15 F_1 hybrids and evaluated six parental genotypes and their hybrids over two summer seasons. Significant differences were observed among genotypes for traits like days to flower, number of fruits per plant, fruit weight, acidity, and marketable yield. The study revealed the importance of hybrid vigor and combining ability in developing new hybrid varieties of tomato. The results also indicated the presence of over-dominance, the proportion of dominant alleles, and the significance of genetic components in controlling various traits. The conclusions highlight the potential for using these genetic resources in breeding programs for developing high-yielding tomato varieties.

REFERNCES

Ahmad, S., A. K. M. Quamruzzaman and M. R. Islam (2011). Estimate of heterosis in tomato (*Solanum lycopersicum* L.) Bangladesh J. Agri. Res., 36(3): 521-527.

Al-Aysh, F., M. Al-Serhan, A. Al-Shareef, M. Al-Nasser and H. Kutma (2012). Study of genetic parameters and character interrelationship of yield and some yield components in tomato (*Solanum lycopersicum* L.) International J. of Genet., 2(2): 29-33.

Chezhian, P., S. Babu and J. Ganesan (2000). Combining ability studies in Eggplant (*Solarium melongena* L.). Tropical Agricultural Research , 12 :394-397.

Dhaliwal, M. S., S. Singh and D. S. Cheema (2003). Line × tester analysis for yield and processing attributes in tomato. J. Res., 40: 49-53.

Gautam, N., M. Kumar, A. Vikram, S. Kumar and S. Sharma (2018). Heterosis studies for yield and its components in tomato (*Solanum lycopersicum* L.) under North Western Himalayan Region, India, International Journal of Current Microbiology and Applied Sciences, 7(02):1949-1957.

Griffing, B. (1956). Concept of general and specific combining ability in relation to diallel crossing system. Aust . Jour. Biol. Sci., 9: 463-493.

Hannan, MM., MB. Ahmed, UK. Roy, MA. Razvy, A. Haydar, MA. Rahman, MA. Islam and R. Islam (2007). Heterosis, combining ability and genetics for brix% days to first fruit ripening and yield in tomato (*Lycopersicon esculentum* Mill). Middle east J. Sci. Res., 2:128-131.

Hatem, M.K. and Mona R. Khalil (2014). Genetic studies on some important characters in tomato. 2- Estimates of combining ability for yield components and some fruit characters. Minufiya J. Agric. Res., 39 (2): 299 -307.

Hayman, BI (1954 a). The analysis of variance of diallel tables. Biometrics, 10:235–244.

Hayman, BI (1954b). The theory and analysis of diallel crosses. Genetics, 39:789–809.

Hayman, BI (1958). The theory and analysis of diallel crosses: II. Genetics, 43:63–85 11.

Hayman, BI (1960). The theory and analysis of diallel crosses: III. Genetics, 45:155–172

Hussien, A. H. (2014). Combining ability, heterosis and path coefficient analysis for yield and its components in tomato. Egypt. J. Plant Breed, 18(4):737 – 753.

Indu rani, C and D. Veerargavathatham (2008). Studies on heterosis in root knot nematod. (*Meloidogyne incognita*) resistant hybrids in tomato (*Lycopersicom esculentum* Mill.) the Asian J. of Hort., 3(1) :40-44.

Islam, M.R., S. Ahmad and M.M Rahman (2012). Heterosis and qualitative attributes in winter tomato (*Solanum lycopersicum* L.) hybrids, Bangladesh Journal of Agricultural Research., 37(1):39-48.

Jinks, JL (1954). The analysis of continuous variation in a diallel cross of Nicotianarustica varieties. Genetics, 39:767–788.

Kathimba, F.K., P.M. Kimani, R.D. Narla and L.M. Kiriika (2022).Heterosis and combining ability for related traits in tomato. African Crop Science Journal, 30 109-125.

Kumar, R., K. Srivastava, N.P. Singh, N. K. Vasistha, R. K. Singh and M. K. Singh (2013). Combining ability analysis for yield and quality traits in tomato (Solanum lycopersicum, L.). J. of Agr. Sci., l. 5 (2): 213-218.

Mather, K. and J. L. Jinks (1982). Biometrical Genetics.3rd Chapman and Hall Ltd., London.

Mohamed, S.M., E. E. Ali, T.Y. Mohamed (2012). Study of Heritability and Genetic Variability among Different Plant and Fruit Characters of Tomato (*Solanum lycopersicom* L.) International Journal of Scientific & Technology Research,1(2):55-58.

Naorem, B. S., H. W. Shabir, A. Haribhushan and N. Rita (2012). Heterosis studies for yield and its components in tomato (*Solanum lycopersicum* L.) under valley conditions of Manipur. Vegetos, 25 (2): 257-265.

Rahmani, G., U.R. Hidayat, H. K. Iftikhar, M. A. S. Syed and Abdul Ghafoo (2010). Heterosis for flower and fruit traits in tomato (Lycopersicom esculentum Mill.). African J. of Biotechnology, 9 (27):4144-4151.

Reddy, B. R., D. S. Reddy, K. Reddaiah, N. Sunil (2013). Studies on genetic variability, heritability and genetic advance for yield and quality traits in tomato (*Solanum lycopersicum* L). Int. J. Curr. Microbiol. App. Sci., 2(9): 238-244.

Singh, R. K, R. D Chaudhary (1979).Biometrical methods in quantitative genetic analysis. New Delhi: Kalyani Publ.

Sinha, S.K. and R. Khanna (1975). Physiological, biochemical and genetic basis of heterosis. Advan. Agron., 27: 123-174.

Snedecor, G. W. and W. G. Cochran (1990). Statistical Method. 7th ed. The Iowa State Univ. Ames. USA.

Soliman- Abeer, A. El. K. and A. A. Osman (2019). Nature of gene action and heterotic performance for yield, yield components and nematode resistance in tomato. Egypt. J. of Appl. Sci., 34 (3): 1-20.

Tasisa, J., W. Mohamed, S. Hussien and V. Kumar (2018). Genetic control of inheritance of fruit quality attributes in tomato (*Solanum lycopersicon* L.). Agri. Res., (7):120-128.

استكشاف قوة الهجين وأنماط الوراثة والتقدم الوراثي في الطماطم

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استخدمت فى هذة الدراسة ستة اباء نقية من الطماطم في تصميم هجن نصف دائرية لانتاج 15 هجينا. تم إجراء التجربة في مزرعة بحوث الخضر فى قها ، معهد بحوث البساتين ، محافظة القليوبية. تم تقييم ستة أنماط وراثية أبوية وخمسة عشر هجينا في حقل مفتوح في الموسمين الصيفيين المتتاليين 2022 و 2023. لوحظت اختلافات معنوية في متوسط الأداء لجميع الصفات المدروسة. وفى تحليل القدرة العامة على التالف اظهرا الابوين BSوPE معنوية سالبة كبيرة لعدد الأيام اللازمة لازهار 50٪ من النباتات، مشيرا إلى أن كلا الابوين يمكن اعتبارها مصدرجيد لصفة التبكير فى الطماطم أيضا يعتبر الاب PE من الافضل الاباء فى القدرة العامة على التالف فى صفات عدد الثمار/نبات وطول الثمرة وسمك اللحم والحموضة المعايرة واخيرا المحصول القابل للتسويق اما الاب M-Gفكان من افضل الاباء من حيث القدرة العامة على التالف فى صفات قطر الثمرة و الحموضة المعايرة و المحصول القابل للتسويق اما الاب R4 فكان من افضل الاباء من حيث القدرة العامة على التالف فى صفات وزن الثمرة و طول وقطر الثمرة والمواد الصلبة الذائبة الكلية.

اما من حيث القدرة الخاصة على التالف فالهجين SM×M-G يعتبر من افضل الهجن في الصفات التالية: عدد الثمار/ نبات طول ووزن وقطر الثمرة وعدد الحجرات والمواد الصلبة الذائبة الكلية وحمض الاسكوربيك واخيرا المحصول القابل للتسويق كما اظهر هذا الهجين قوة هجين تراوحت من 83.76%بالنسبة لمتوسط الابوين و73.08% بالنسبة للاب الاعلى فى صفة المحصول القابل للتسويق. دلت مؤشرات التباين على أهمية الدور الذي يلعبة الفعل الجينى السيادى لكل الصفات المدروسة مما يدل على امكانية استغلال قوة الهجين فى تحسين هذة الصفات.