

Combining Ability and Heterotic Patterns Using Line × Tester Analysis for Yield Under Heat Stress in Tomato (*Solanum lycopersicum* L) Abeer Abd El-Kader Soliman

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ABSTRACT

This study involved the crossing of seven pure tomato lines using a line \times tester mating design, resulting in the production of 12 F₁ hybrids. The study was conducted at the Kaha Vegetable Research Farm, Horticulture Research Institute, Kaliobia Governorate. Both parental genotypes and their twelve crosses were assessed in an open field during the two consecutive summer seasons of 2022 and 2023. The study found significant differences in mean performance across all traits examined, attributable to the different genotypes. Highly significant differences existed among genotypes for all studied traits. Lines × testers interaction was highly significant for all studied traits except number of days to 50% anthesis flowers (ND) and number of locule (NL). The estimated average degree of dominance (ADD) was higher than unity for five traits i.e., ND, fruit shape index (FSI), NL, total yield (TY) and total soluble solids (TSS), indicating that over dominance influenced the manifestation of these traits. Results from the general combining ability (GCA) effects analysis suggested that the line EL-S (P1) was a notable general combiner for fruit set % (FS), NF (number of fruit), NL and TY. The tester Saladette (P7) was a notable general combiner for FS, FW, FSI, NF and TY. The significant SCA effects for FS, NF and TY traits were obtained from the crosses $P2 \times P6$, $P2 \times P7$ and $P4 \times P5$. All crosses exhibited significant positive heterosis over better parent for TY except crosses P2 \times P5, P3 \times P5 and P3 \times P6.

Keywords: Tomato- Combining ability- Heterosis- Heat tolerance. INTRODUCTION

Tomato (*Solanum lycopersicum* L.) stands out as the vegetable crop with the highest demand and economic value worldwide. Its cultivation and trade are of utmost importance in tropical, subtropical, and temperate regions, catering to the requirements of both fresh consumption and processing sectors (Meena et al., 2017).

Tomato is influenced by some abiotic stresses that have a major impact on fruit quality and yield. The expected rise in ambient temperatures as a result of climate change is predicted to have a significant effect on plant growth and development. This is anticipated to lead to a notable decrease in crop productivity, ultimately contributing to severe famine and posing a challenge to global food security.

According to Geisenberg and Stewart (1986), the optimal daily mean temperature for tomato fruit set in standard field conditions ranges from 21 to 24 c^o.

However, the cultivation of this crop in subtropical regions results in prolonged exposure of plants to higher day and night temperatures during the reproductive growth prolonged exposure phase. This can significantly hinder fruit set. as demonstrated by the research of Peet et al. 1997, 1998, and Sato et al. 2000. The impact of heat on reproductive development and physiology in tomato is influenced by the maximum day and night temperatures, as well as the frequency and duration of exposure.

The optimum day/night temperatures for fruit set in tomato is in the range of 26-32 C° /15-20 Co (Kuo et al. ,1979).

There is a notable rise in the frequency of unpredictable weather patterns (IPCC, 2021), which highlights the necessity for developing cultivars that can adapt to harsh environmental conditions. The focus on breeding for heat tolerance has gained



considerable traction in recent years, making it an essential aim in the improvement of tomato crops.

Therefore, there was a need to produce hybrids of tomatoes that are suitable for cultivation at high temperatures and are characterized by high production under these conditions.

The efficacy of hybrids in enhancing yield and maintaining yield stability during stress conditions has been well-documented (Hernández-Leal et al., 2019 and Okada and Whitford, 2019).

Parental selection in any plant-breeding program is one of the most important decisions that breeders must make (Broem and Miranda, 2005).

The use of line × tester analysis has been identified as a highly effective method for the preliminary screening of materials to combining ability assess effects and variances. This approach enables the evaluation of a greater number of germplasm lines at once, offering insights into the combining abilities of parents and crosses, as well as information on the selection of suitable parents and breeding techniques for enhancing crop plants

In breeding programs, the information about the general combining ability (GCA) and the specific combining ability (SCA) is highly important for the selection of the right parents for hybrid development. GCA indicates the average effect that a line has on its crosses, measured as the general mean deviation, and is an expression of additive genetic effects. SCA, on the other hand, refers to deviations from anticipated behavior due to the general combining abilities of the parents, reflecting nonadditive genetic effects (Sprague and Tatum, 1942). The combining ability is an effective tool that provides useful genetic information to select parents for the development of hybrid (Chezhian et al., 2000).

Various authors have reported on the general and specific combining abilities present in different hybrid combinations of tomatoes. In their study, Shende et al. (2012) found that the parental lines 'CLN2498-D', 'CLN2762-A', and 'BCT-110' were the most proficient general combiners for fruit yield, with all hybrid combinations exhibiting high specific combining ability (SCA) for this yield trait.

The significance of both additive and non-additive gene actions in influencing characteristics tomato plant fruit is highlighted by the highly significant magnitude of variance due to general and specific combining ability effects (σ^2 GCA & σ^2 SCA) as reported by several investigators, such as Amin et al. (2001) and Sekhar et al. (2010) for plant height and total yield per plant. The same mode of inheritance of average fruit weight was also reported by Saleem et al. (2009).

Heterosis over better parent on tomato was reported by many authors i.e. Mondal et al. (2009), Saeed et al. (2014) and Khalil et al. (2015). In the context, Kumari and Sharma (2011) reported that the heterosis was maximum and significant for yield and fruit number. Moreover, Kathimba et al. (2022) mentioned that better parent heterosis for yield showed that 69% of F₁ hybrids had increased yield per plant over the better parents; while 31% had reduced yields. The high proportion of F_1 hybrids (69%) that demonstrated positive heterosis, is good news for tomato production in Kenya because it signifies high productivity per unit area, with genotypic improvement. Heterosis for yield per plant ranged from 114.39% for AVTO1429 ×AVTO1314 to -21.83% recorded in AVTO1314× Riogrande.

The primary objectives of this investigation were to evaluate the general and specific combining abilities, along with heterosis, for yield and quality traits in a line \times tester analysis. This study was carried out to identify promising parents and their cross combinations as genetic resources for the improvement of these important traits. Furthermore, the study aimed to pinpoint suitable materials and breeding methods for



use in tomato breeding programs targeting heat tolerance. MATERIALS AND METHODS

This study was carried out during 2021, 2022 and 2023 at Kaha Research Farm, Kaliobia Governorate under unheated plastic house (9 m \times 59 m, 4m height) and open field. The genetic materials used in this study were started by seven pure lines of tomato (Solanum lycopersicum L.) as a parental line in a line × tester analysis. Four pure lines were developed by author these pure lines were named EL-S (P1), SM (P2), M-G (P3) and R 4 (P4). Three tomato pure line were expert by Dr H. Ghobary from Asian Vegetable Research and Development center (AVRDC), Taiwan. These lines named; CLN591 (P5), CLN657 (P6) and Saladatte variety (P7) were used as male (tester).

In the summer season of 2021, the parents were planted under unheated plastic house to ensure homozygosity and seed increase of parents. In the fall season of 2021, the seven parents were planted under unheated plastic house and crossed using line \times tester meeting design, to produce F_1 seeds.

On the 15th of March of 2022 and 2023, seed of parents and their hybrids were sown in seedling trays under unheated plastic house. On May 3th 2022 and 2023, the seedling of parents and their hybrids were transplanted in open filed to evaluate.

Average of temperatures during the growing evaluation seasons of the study at Kaliobia Governorate during 2022 and 2023 (Table 1).

Table (1). Average degree of air temperature, relative humidity and soil temperature in Kaliobia Governorate.

	Air temper	ature [°C]	HC Relative humidity [%]	Soil temperature [°C]
Date/Time	max	min	avg	avg
May-2022	33.687	12.639	60.72	32.45
Jun-2022	34.56	19.558	68.12	28.38
Jul-2022	37.37	23.672	66.56	24.75
Aug-2022	36.937	23.969	71.07	19.8
Apr-2023	34.5826	9.64	62.19	32.1
May-2023	35.1842	11.49	62.6	29.5
Jun-2023	36.096	17.78	64.88	25.8
Jul-2023	37.942	21.52	68.62	22.5
Aug-2023	36.5342	21.79	67.69	18

A randomized complete block design with three replicates was used in this study. Each genotype was grown on one ridge. The seedlings were transplanted in the field at 50 cm apart. Each plot consisted of three rows (4 m long \times l m wide). The experimental design was a randomized complete block with three replicates. Each replicate contained 7 parents and their 12 F₁ crosses. According to the advice of the Egyptian Ministry of Agriculture, all agricultural techniques were implemented. Data were recorded for number of days to 50% anthesis flowers (ND), fruit set% which was calculated as the number of fruits set compared with the total number of flowers on the first 3 clusters (FS), average fruit weight (g) (FW), fruit shape index (FSI), number of fruit/ plant (NF), number of locule (NL), total yield (TY) (Ton) per feddan and total soluble solids (TSS) which was determined by a hand refractometer and ascorbic acid mg/100 fw (AA) (Ten tomato fruits at red maturity were randomly taken to determine the fruit characters).



Statistical analysis

Statistical analysis was conducted to calculate the means and variances for each treatment. The means were then compared for significant differences using the New L.S.D. method as described by Snedecor and Cochran in 1990. Average degree of heterosis (ADH%) was estimated as the increase or decrease percent of F1

RESULTS AND DISCUSSION

A- Average performance.

Table (2) presents the findings from the assessment of seven pure tomato lines and their twelve hybrids over a two-year period, specifically in 2022 and 2023. The results of this assessment, along with their corresponding rankings, are included. It is noteworthy that significant variations were detected in all examined traits during both years. However, when the data from the two years were aggregated, no significant emerged. Consequently, differences а combined analysis was conducted to evaluate the overall performance of the genotypes and hybrids across two years. For the combined analysis of ND, the parental values were found to range from 22.0 days CLN591 (P5) to 30.83 days R 4 (P4). On the other hand, the crosses ranged from 20.67 days (P3 \times P6) to 25.67 days (P1 \times P7) resulting in a mean of 24.43 days. For combined analysis regarding FS% the parental values ranged from 34.42 (SM) (P2) to 77.33 CLN591 (P5). While, their crosses ranged from 22.83 (P2 ×P6) to 84.17 % (P4×P5) with a mean of 75.08 %. The FW of parental genotypes ranged from 60.55 (SM) (P2) to 120.37 g (M-G) (P3). Their crosses ranged from 88.75 (P1 \times P5) to 126.67 g (P3 \times P6) with a mean of 103.20g. For FSI parental genotypes ranged from 0.58(SM) (P2) to 1.22 (Saladette) (P7). Their crosses ranged from 0.74 (P4 \times P5) to performance over the mid-parent (MP) and better parent (BP) according Sinha and Khanna (1975).

Combining ability effects and genetic components were estimated by using Line × Tester analysis according to Singh and Choudhary (1977).

1.26 (P3 × P6) and (P4 × P7) with a mean of 0.94. Regarding NF the parental values ranged from 14.28 (M-G) (P3) to 31.45(SM) (P2). Their crosses ranged from 14.85 (P3 × P6) to 33.75 (P1 × P5) with a mean of 23.75. For NL the parental value ranged from 3.8 (EL-S) (P1) to 5.7 CLN591 (P5). Their crosses ranged from 4.2(P4 × P7) to 5.7 (P2 × P5) with a mean of 4.8. For TY the parental value ranged from 1.72 (M-G) (P3) and CLN657 (P6) to 2.15 kg/p EL-S (P1). Their crosses ranged from 1.88 (P3 × P6) to3.18 kg/p (P1× P7) with a mean of 2.83.

Regarding TSS parental genotypes ranged from 3.83 M-G (P3) to 6.17% CLN591 (P5). Their crosses ranged from 4.92 (P1×P7) to 6.42% (P3 × P5 and P4 ×P6) with a mean of 5.39. For AA parental genotypes ranged from 16.02 EL-S (P1) to 27.12 mg/100g fw SM (P2). Their crosses ranged from 17.50 (P1 ×P5) to 28.92 mg/100g fw (P4 × P6) with mean of 22.50 mg/100g fw.

The results obtained from this study appear to be consistent with those identified by Soliman (2019) found that significant differences among genotypes were observed in mean performance for all studied traits i.e., fruit set%, fruit weight (g), fruit flesh thickness (mm), fruit shape index, locule number, marketable yield.



Table	(2).	Mean	performance	of	parents	and	their	crosses	for	various	traits	in
tomato	, con	nbined a	across two seas	ons	2022, 202	23.						

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Genotypes	ND	FS%	FW(g)	FSI	NF
EL-S (P1)	23.00	46.00	77.40	0.79	27.74
SM (P2)	30.50	34.42	60.55	0.58	31.45
M-G (P3)	23.83	43.33	120.37	0.78	14.28
R 4 (P4)	30.83	51.67	99.18	0.88	19.53
CLN591 (P5)	22.00	77.33	95.35	0.87	21.83
CLN657 (P6)	25.50	55.00	118.95	1.13	14.53
Saladette (P7)	26.17	67.50	109.15	1.22	19.45
P1×P5	22.33	81.17	88.75	0.78	33.75
P1×P6	23.33	52.00	95.68	1.09	26.90
P1×P7	25.67	62.50	120.08	0.93	26.57
P2×P5	25.33	45.00	96.95	0.86	22.68
P2×P6	25.33	22.83	93.60	1.06	25.00
P2×P7	25.67	63.33	90.50	0.98	33.28
P3×P5	21.67	74.17	123.82	0.89	18.40
P3×P6	20.67	49.17	126.67	1.26	14.85
P3×P7	21.50	56.67	123.15	0.88	22.77
P4×P5	23.00	84.17	100.38	0.74	30.27
P4×P6	23.50	44.17	109.67	0.98	22.00
P4×P7	24.50	74.17	111.78	1.26	26.12
Mean	24.43	75.08	103.2	0.94	23.75
N. L. S. D (0.05	0.34	1.12	0.88	0.01	0.40
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Genotypes	nred. NL	TY	(kg/p)	TSS%	AA mg/100fw
Genotypes EL-S (P1)	<u>NL</u> 3.8	TY ((kg/p) .15	TSS% 4.17	AA mg/100fw 16.02
Genotypes EL-S (P1) SM (P2)	<u>NL</u> 3.8 4.5	TY ((kg/p) .15 .91	TSS% 4.17 5.33	AA mg/100fw 16.02 27.12
Genotypes EL-S (P1) SM (P2) M-G (P3)	NL 3.8 4.5 5.0	TY (2 1	(kg/p) 15 91 72	TSS% 4.17 5.33 3.83	AA mg/100fw 16.02 27.12 23.28
Indice (2). Continu Genotypes EL-S (P1) SM (P2) M-G (P3) R 4 (P4)	NL 3.8 4.5 5.0 5.0	TY (2 1 1 1	(kg/p) 15 91 72 94	TSS% 4.17 5.33 3.83 5.33	AA mg/100fw 16.02 27.12 23.28 24.62
Genotypes EL-S (P1) SM (P2) M-G (P3) R 4 (P4) CLN591 (P5)	NL 3.8 4.5 5.0 5.7	TY (2 1 1 1 1 2	(kg/p) 15 91 72 94 .08	TSS% 4.17 5.33 3.83 5.33 6.17	AA mg/100fw 16.02 27.12 23.28 24.62 16.43
Genotypes EL-S (P1) SM (P2) M-G (P3) R 4 (P4) CLN591 (P5) CLN657 (P6)	NL 3.8 4.5 5.0 5.0 5.7 5.5	TY (2 1) 1 1 1 2 1	(kg/p) 15 91 72 94 08 72	TSS% 4.17 5.33 3.83 5.33 6.17 4.75	AA mg/100fw 16.02 27.12 23.28 24.62 16.43 20.28
Table (2). Contin Genotypes EL-S (P1) SM (P2) M-G (P3) R 4 (P4) CLN591 (P5) CLN657 (P6) Saladette (P7)	NL 3.8 4.5 5.0 5.7 5.5 4.2	TY (2 1 1 1 1 2 2 1 2	(kg/p) 15 91 72 94 08 72 12	TSS% 4.17 5.33 3.83 5.33 6.17 4.75 4.58	AA mg/100fw 16.02 27.12 23.28 24.62 16.43 20.28 21.28
Table (2). Continu Genotypes EL-S (P1) SM (P2) M-G (P3) R 4 (P4) CLN591 (P5) CLN657 (P6) Saladette (P7) P1×P5	NL 3.8 4.5 5.0 5.7 5.5 4.2 5.5	TY(2 1 1 1 1 2 1 1 2 1 1 2 1 2 3	(kg/p) 15 91 .72 94 .08 .72 .12 .00	TSS% 4.17 5.33 3.83 5.33 6.17 4.75 4.58 6.17	AA mg/100fw 16.02 27.12 23.28 24.62 16.43 20.28 21.28 17.50
Table (2). Continu Genotypes EL-S (P1) SM (P2) M-G (P3) R 4 (P4) CLN591 (P5) CLN657 (P6) Saladette (P7) P1×P5 P1×P6	NL 3.8 4.5 5.0 5.0 5.7 5.5 4.2 5.5 5.3	TY (2 1 1 1 1 2 1 1 2 3 3 2	(kg/p) 15 91 72 94 .08 .72 12 .00 .58	TSS% 4.17 5.33 3.83 5.33 6.17 4.58 6.17 5.33	AA mg/100fw 16.02 27.12 23.28 24.62 16.43 20.28 21.28 17.50 22.20
R 4 (P4) CLN591 (P5) CLN657 (P6) Saladette (P7) P1×P5 P1×P6 P1×P7	NL 3.8 4.5 5.0 5.7 5.5 4.2 5.5 5.3 4.7	TY(2 1 1 1 1 2 2 1 1 2 3 3 2 3	(kg/p) 15 91 72 94 08 72 12 00 58 18	TSS% 4.17 5.33 3.83 5.33 6.17 4.75 4.58 6.17 5.33 4.92	AA mg/100fw 16.02 27.12 23.28 24.62 16.43 20.28 21.28 17.50 22.20 22.45
Table (2). Continu Genotypes $EL-S$ (P1) SM (P2) M-G (P3) R 4 (P4) CLN591 (P5) CLN657 (P6) Saladette (P7) P1×P5 P1×P6 P1×P7 P2×P5	NL 3.8 4.5 5.0 5.7 5.5 4.2 5.5 4.2 5.3 4.7	TY(2 1 1 1 1 1 2 1 2 3 2 3 2 3 2 2 3 1 2 3 3 2	(kg/p) 15 91 .72 .94 .08 .72 .12 .00 .58 .18 .19	TSS% 4.17 5.33 3.83 5.33 6.17 4.75 4.58 6.17 5.33 4.58 6.17 5.33 4.58 6.17 5.33 4.52	AA mg/100fw 16.02 27.12 23.28 24.62 16.43 20.28 21.28 17.50 22.20 22.45 28.37
Table (2). Continu Genotypes $EL-S$ (P1) SM (P2) M-G (P3) R 4 (P4) CLN591 (P5) CLN657 (P6) Saladette (P7) P1×P5 P1×P6 P1×P7 P2×P5 P2×P6	NL 3.8 4.5 5.0 5.7 5.5 4.2 5.5 4.7 5.7 5.7	TY(2 1 1 1 2 1 1 2 1 2 3 3 2 3 3 2 2 2 2	(kg/p) 15 .91 .72 .94 .08 .72 .12 .00 .58 .18 .19 .34	TSS% 4.17 5.33 3.83 5.33 6.17 4.75 4.58 6.17 5.33 4.92 6.25 5.50	AA mg/100fw 16.02 27.12 23.28 24.62 16.43 20.28 21.28 17.50 22.20 22.45 28.37 19.93
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Table (2). Continu Genotypes $EL-S$ (P1) SM (P2) M-G (P3) R 4 (P4) CLN591 (P5) CLN657 (P6) Saladette (P7) P1×P5 P1×P6 P1×P7 P2×P5 P2×P6 P2×P7 P3×P5	$\begin{array}{r} \text{NL} \\ \hline & \text{NL} \\ \hline & 3.8 \\ \hline & 4.5 \\ \hline & 5.0 \\ \hline & 5.0 \\ \hline & 5.7 \\ \hline & 5.5 \\ \hline & 4.2 \\ \hline & 5.5 \\ \hline & 4.2 \\ \hline & 5.5 \\ \hline & 4.2 \\ \hline & 5.7 \\ \hline & 5.7 \\ \hline & 5.7 \\ \hline & 5.7 \\ \hline & 5.2 \\ \hline & 4.3 \\ \hline & 4.5 \end{array}$	TY(2 1 1 1 1 1 2 1 1 2 1 2 2 3 2 2 3 2 2 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3	(kg/p) .15 .91 .72 .94 .08 .72 .12 .00 .58 .18 .19 .34 .02 .26	TSS% 4.17 5.33 3.83 5.33 6.17 4.75 4.58 6.17 5.33 4.92 6.25 5.50 5.25 6.42	AA mg/100fw 16.02 27.12 23.28 24.62 16.43 20.28 21.28 17.50 22.20 22.45 28.37 19.93 20.98 21.02
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Table (2). Continu Genotypes EL-S (P1) SM (P2) M-G (P3) R 4 (P4) CLN591 (P5) CLN657 (P6) Saladette (P7) P1×P5 P1×P6 P1×P7 P2×P5 P2×P6 P2×P7 P3×P6 P3×P7 P4×P5	$\begin{array}{r} \text{ned.} \\ \hline \\ & \text{NL} \\ \hline \\ & 3.8 \\ \hline \\ & 4.5 \\ \hline \\ & 5.0 \\ \hline \\ & 5.0 \\ \hline \\ & 5.0 \\ \hline \\ & 5.7 \\ \hline \\ & 5.5 \\ \hline \\ & 4.2 \\ \hline \\ & 5.5 \\ \hline \\ & 5.3 \\ \hline \\ & 4.7 \\ \hline \\ & 5.7 \\ \hline \\ & 5.7 \\ \hline \\ & 5.2 \\ \hline \\ & 4.3 \\ \hline \\ & 4.5 \\ \hline \\ & 4.5 \\ \hline \\ & 4.7 \\ \hline \\ & 4.8 \end{array}$	TY(2 1 1 1 1 2 1 1 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 3 3 2 2 3	(kg/p) .15 .91 .72 .94 .08 .72 .12 .00 .58 .18 .19 .34 .02 .26 .88 .79 .07	TSS% 4.17 5.33 3.83 5.33 6.17 4.75 4.58 6.17 5.33 4.92 6.25 5.50 5.25 6.42 5.42 5.17 6.33	AA mg/100fw 16.02 27.12 23.28 24.62 16.43 20.28 21.28 17.50 22.20 22.45 28.37 19.93 20.98 21.02 22.98 21.02 22.98 22.73 24.53
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Table (2). Continue Genotypes EL-S (P1) SM (P2) M-G (P3) R 4 (P4) CLN591 (P5) CLN657 (P6) Saladette (P7) P1×P5 P1×P7 P2×P5 P2×P6 P2×P7 P3×P5 P3×P7 P4×P5 P4×P6 P4×P7	$\begin{array}{r} \text{ned.} \\ \hline \\ & \text{NL} \\ \hline \\ & 3.8 \\ \hline \\ & 4.5 \\ \hline \\ & 5.0 \\ \hline \\ & 5.7 \\ \hline \\ & 5.5 \\ \hline \\ & 4.2 \\ \hline \\ & 5.5 \\ \hline \\ & 4.2 \\ \hline \\ & 5.2 \\ \hline \\ & 4.3 \\ \hline \\ & 4.5 \\ \hline \\ & 4.5 \\ \hline \\ & 4.7 \\ \hline \\ & 4.8 \\ \hline \\ & 5.2 \\ \hline \\ & 4.2 \\ \hline \end{array}$	TY(2 1 1 1 2 1 1 2 1 1 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 3 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 3 3 3 3 2 2 3	(kg/p) 15 91 .72 .94 .08 .72 .12 .00 .58 .18 .19 .34 .02 .26 .88 .79 .07 .37 .92	TSS% 4.17 5.33 3.83 5.33 6.17 4.75 4.58 6.17 5.33 4.92 6.25 5.50 5.25 6.42 5.17 6.33 6.42 5.17	AA mg/100fw 16.02 27.12 23.28 24.62 16.43 20.28 21.28 17.50 22.20 22.45 28.37 19.93 20.98 21.02 22.98 22.73 24.53 28.92 27.10
Table (2). Continue Genotypes EL-S (P1) SM (P2) M-G (P3) R 4 (P4) CLN591 (P5) CLN657 (P6) Saladette (P7) P1×P5 P1×P7 P2×P5 P2×P6 P2×P7 P3×P6 P3×P7 P4×P5 P4×P7 Mean	NL 3.8 4.5 5.0 5.7 5.5 4.2 5.5 4.7 5.7 5.3 4.7 5.7 5.2 4.3 4.5 4.7 5.7 5.2 4.3 4.5 4.5 4.5 4.7 4.8 5.2 4.8	TY(2 1 1 1 1 2 1 1 2 3 3 2 3 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 3 2 2 3 3 3 2 2 3	(kg/p) 15 91 72 94 .08 .72 112 .00 .58 .18 .19 .34 .02 .26 .88 .79 .07 .37 .92 .83	TSS% 4.17 5.33 3.83 5.33 6.17 4.75 4.58 6.17 5.33 4.92 6.25 5.50 5.25 6.42 5.17 6.33 6.42 5.17 5.39	AA mg/100fw 16.02 27.12 23.28 24.62 16.43 20.28 21.28 17.50 22.20 22.45 28.37 19.93 20.98 21.02 22.98 22.73 24.53 28.92 27.10 22.50



B- Analysis of variance and components of genetic variance.

Analysis of variance for all studied traits is presented in **Table(3)**. Highly significant differences existed among genotypes (parents and their crosses) for all studied traits, revealing a large amount of variability among them, mean squares of genotypes were significant for all studied traits. The presence of adequate genetic variability is confirmed, allowing for the assessment of genetic inference as genotypes are divided into parental groups, their crosses, and the interactions that ensue. Highly significant Table (3) Analysis of variance and components of gene

differences existed among crosses for all studied traits, mean squares of crosses were further partitioned into lines (females), testers (males) and (line \times tester) interaction. Highly significant differences were obtained among lines for all studied traits except FSI, NL and TSS. The three testers differed significantly all studied in traits except ND, FW, NF and AA. However, lines \times testers interaction was highly significant for all studied traits except ND and NL. It was observed that the order of performance among the lines differed when crossed with each tester.

Table (3). Analysis of variance and components of genetic variance for some traits in tomato during 2023.											
Sources	Df	ND	FS%	FW	FSI	NF	NL	ΤY	TSS%	AA	
Genotypes	18	23.13**	653.45**	928.75**	0.01**	112.35**	0.93**	0.72**	9.44**	40.84**	
Crosses	11	10.35**	661.30**	619.55**	0.94**	97.19**	0.69*	0.56**	0.99**	35.21**	
Parents	6	37.97**	609.86**	1447.87**	0.86**	123.77**	1.52**	0.09**	1.46**	51.40**	
Parents vs Crosses	1	74.69**	828.59**	1215.27**	0.09**	210.66**	0.03	6.28**	7.34**	39.39**	
Line	3	30.63**	563.66	619.55**	0.01	189.45*	0.84	0.71**	0.23	58.95	
Tester	2	5.53	1921.53**	232.69	0.25*	84.10	1.36*	1.42**	4.40**	1.48	
Line × Tester	6	1.82	290.05**	43.43**	0.07**	55.37**	0.40	0.20**	0.23**	34.58**	
Error	36	0.94	7.51	5.76	0.001	1.12	0.25	0.01	0.08	1.78	
				Co	mponent	t of varianc	e				
σ2 G.C.A	-	0.22	0.07	0.09	0.03	0.05	0.05	0.10	0.16	0.02	
σ2 S.C.A	-	0.22	70.63	59.42	0.02	13.56	0.04	0.05	0.04	8.20	
σ2Α	-	0.44	0.15	0.17	0.06	0.10	0.10	0.19	0.32	0.04	
σ2D	-	0.22	70.63	59.42	0.02	13.56	0.04	0.05	0.04	8.20	
A. D. D	-	1.42	0.05	0.05	1.95	0.09	1.86	1.99	2.94	0.07	

The results obtained from this study appear to be consistent with those identified by Shankar et al. (2013), Saeed et al. (2014), Dagade et al. (2015), Khalil et al. (2015) and Abed El Kader (2021) in tomato crop. The estimated average degree of dominance (ADD) was higher than unity for five traits i.e., ND, FSI, NL, TY and TSS, indicating that over dominance (non-additive gene action) influenced the manifestation of these traits. As a result, the potential for improving these characters exists through the utilization of hybrid breeding methods.

The results were in conformity with Narasimhamurthy and Ramanjini (2013), along with Shankar et al. (2013), indicated that non-additive gene action was the primary factor influencing the inheritance of all traits examined in their studies.

C- Combining ability.

The exploration of general combining ability (GCA) has significantly aided in the identification of suitable parent lines. The findings regarding GCA effects, as shown in Table 4, suggest that the line EL-S was a good combiner for FS, NF, NL and TY traits. The line SM (P2) was a good combiner for NF. While, line M-G was a good combiner for earliness, FW and FSI traits. Also, the line R4 was a good combiner for FS, NF, FSI, TY, TSS and AA traits. The tester CLN591 was a good combiner for earliness, FS, NL, NF and TSS. Also, the tester CLN657 was a good combiner for FSI. Meanwhile, the tester Saladatte was a good combiner for earliness, FS, FW, FSI, NF and TY traits.

In this light, Sharma et al. (1999) and Mondal et al. (2009) performed a line x tester



analysis to estimate the combining ability of various traits in tomato, and their findings indicated that none of the parental lines was the best combiner for all evaluated traits.

Regarding specific combining ability effects (SCA), data are presented in Table (5) for the various studied traits. The highly significant SCA effects were manifested by the crosses $P1 \times P5$ for earliness, FS and NF (-0.97, 5.00,3.76, respectively); cross P1× P7 for FW and AA (13.93 and 1.59, respectively); cross P2×P5 for FW, FSI, NL and AA (7.68, 0.005, 0.36 and 5.63, respectively): cross $P2\times$ P6 for FS, NF and TY (5.14, 1.28 and 0.17, respectively); cross P2×P7 for FS, NF and TY (9.31, 9.39 and 0.18, respectively); cross P3×P5 for FS and FW (3.33 and 3.67, respectively); cross P3×P6 for FSI (0.38)); cross P3×P7 for NF, NL and TY (2.11, 0.47 and 0.14, respectively); cross P4×P5 for FS, NF and TY (6.11,3.27 and 0.33, respectively);

cross P4×P6 for FW, TSS and AA (3.06, 0.46 and 2.02, respectively); cross P4×P7 for FS and FSI (3.19 and 0.23, respectively), These may be regarded as the optimal combinations for each trait. The combinations did not exhibit simultaneous significant SCA effects that were beneficial for all traits; nonetheless, there were occasions where certain combinations displayed favorable outcomes.

The presence of high SCA values in any variable suggests that hybridization is the most effective means of optimizing the use of that variable. By taking advantage of genetic variance, one can utilize dominance or epistatic effects more efficiently. In this regard, Peña et al. (1998) state that a high SCA indicates that both parental lines are strong candidates for producing families, populations, or lines in a breeding program, with the intention of achieving specific targets.

Table (4). Estimates of general combining ability effects (\widehat{gi}) of each line and tester for all studied traits during 2023.

Parents	ND	FS	FW	FSI	NF	NL	ΤY	TSS	AA
Lines									
EL-S (P1)	0.39	4.58**	-5.42**	-0.04**	3.94**	0.36**	0.29**	-0.18**	-2.40**
SM (P2)	1.94**	-10.97**	-13.58**	-0.01	1.74**	0.14	-0.13**	-0.01	-0.08
M-G (P3)	-2.50**	-0.42	18.13**	0.03**	-6.61**	-0.31**	-0.33**	-0.01	-1.08**
R 4 (P4)	0.17	6.81**	0.87	0.02**	0.93**	-0.19	0.17**	0.21**	3.56**
Testers									
CLN591 (P5)	-0.47**	10.56**	-4.21**	-0.16**	1.02**	0.31**	0.001	0.58**	-0.36
CLN657 (P6)	-0.31	-14.03**	-0.37	0.12**	-3.01**	0.06	-0.34**	0.04	0.34
Saladette (P7)	0.78**	3.47**	4.58**	0.04**	1.99**	-0.36**	0.35**	-0.63**	0.03
S.E (\widehat{gl}) line	0.32	0.91	0.80	0.01	0.12	0.17	0.03	0.09	0.44
S.E $(\widehat{\boldsymbol{gl}})$ tester	0.28	0.79	0.69	0.01	0.09	0.15	0.03	0.08	0.39
Table (5). Es	timates of sj	pecific comb	ining ability	y effects ($\widehat{S\iota}$	j) of crosse	s for all stu	died traits o	during 2023	•
Crossesz	ND	FS	FW	FSI	NF	NL	ΤY	TSS	AA
P1×P5	-0.97**	5.00**	-8.55**	0.01	3.76**	0.14	0.08	0.14	-2.68**
P1×P6	-0.14	1.25	-5.38**	0.03	0.68	0.06	0.001	-0.15	1.09
P1×P7	1.11**	-6.25**	13.93**	-0.04	-4.44**	-0.19	-0.08	0.01	1.59**
P2×P5	0.47	-14.44**	7.68**	0.05**	-5.68**	0.36**	-0.35**	-0.03	5.63**
P2×P6	0.31	5.14**	-0.22	-0.03	1.28**	-0.06	0.17**	-0.15	-3.50**
P2×P7	-0.78	9.31**	-7.47**	-0.02	4.39**	-0.31	0.18**	0.18	-2.13**
P3×P5	0.58	3.33**	3.67**	0.04	-1.35**	-0.19	-0.06	0.14	-0.77
P3×P6	-0.86	-25.14**	1.79	0.38**	-6.77**	-0.17	-0.76**	-0.07	1.07
P3×P7	-0.33	-6.25**	-6.21**	-0.17**	2.11**	0.47**	0.14**	0.01	0.37
P4×P5	-0.08	6.11**	-2.81**	-0.10**	3.27**	-0.31	0.33**	-0.25	-2.18**
P4×P6	0.08	-9.31**	3.06**	-0.14**	-1.21**	0.28	-0.09**	0.46**	2.02**
P4×P7	0.01	3.19**	-0.26	0.23**	-2.06**	0.03	-0.24**	-0.21	0.16
S.E.(Sij)	0.56	1.58	1.39	0.03	0.61	0.29	0.05	0.16	0.77

Z: EL-S (P1), SM (P2), M-G (P3), R 4 (P4), CLN591 (P5), CLN657 (P6) and Saladatte (P7).



These results are in agreement with the finding of Soliman (2019) found that favorable crosses (P 1 × P 3, P 1 × P 5 and P $3 \times P 5$) combined highly significant and positive SCA effects for average fruit weight, marketable yield. It was also noticed that, these three crosses included three out of the five parents used. Besides, each of the three parents was common to two of the three F1 hybrids.

D- Heterosis degree.

Data presented in **Table (6)** showed that, enviable significant negative MP heterosis for the earliness ND (days to 50% flower anthesis) was observed in seven crosses, two crosses recorded enviable significant negative BP values, i.e. $P3 \times P6$ and $P3 \times P7$ (-14.01and -9.86%, respectively).

For FS six out of the twelve evaluated crosses exhibited significant positive heterosis over MP. Only one cross enviable significant positive heterosis over BP i.e., P4 \times P5 (10.87%).

For average fruit weight, data obtained in table 6 showed that from twelve F1's studied, only one cross exhibited dominance toward the small fruits, where they give insignificant negative heterosis values relative to their MP. However, seven crosses exhibited dominance toward the heavy fruits, since they have significant positive heterosis values based on MP. From these crosses, two ones reflected over dominance toward the BP, indicating hybrid vigour for FW with values 10.01% in the cross P1×P7 and 5.45% in the cross P3×P6.

Seven crosses exhibited enviable significant positive MP heterosis for FSI, only one cross exhibited significant positive heterosis over BP i.e., $P3 \times P6$ (11.47%).

Regarding NF nine out twelve crosses exhibited enviable significant positive MP heterosis, four crosses exhibited significant positive heterosis over BP i.e., P3×P7, P1×P5, P4×P7 and P4×P5 with (18.78, 22.89, 31.99 and 38.64%, respectively).

None of evaluated crosses exhibited enviable significant positive MP heterosis for NL, only one cross i.e., P3×P6 exhibited significant negative BP heterosis value (-23.53%) indicated over dominance towards low NL parent.

All crosses showed enviable significant positive MP heterosis for TY except two crosses i.e., P2×P5 and P3×P6, all crosses showed enviable significant positive heterosis over BP except three crosses i.e., P2×P5, P3×P6 and P3×P5. BP heterosis values ranged from 12.06 (P2×P6) to 50.00% (P4×P5)

Pertaining to the TSS, the data outlined in Table 6 indicate that none of any crosses demonstrated characteristics of no dominance or a preference for lower TSS, as shown by their heterosis values, which were either insignificant or significantly negative in relation to the MP. Seven out twelve exhibited enviable crosses significant positive MP heterosis for TSS trait. Three out twelve crosses exhibited enviable significant positive BP for higher TSS i.e., P4×P6, P3×P6 and P3×P7 with (18.18,17.24 and 10.71%, respectively).

Similar to these results, the findings of Shalaby (2012) who found three and two crosses from eight ones had positive with significant values from heterosis over MP and BP, respectively for TSS.

For AA six out twelve crosses exhibited enviable significant positive MP heterosis, only one cross exhibited enviable significant positive exhibited enviable significant positive BP i.e., $P4 \times P6$ with (16.16%) indicated dominance or a preference for high AA content.



Table (6). Relative heterosis mid-parent	t (MP) and	better parent ((BP) for	studied traits of
tomato during season 2023.				

Crassar	ND		F	TS	F	W	FSI		
Crosses	MP %	BP %	MP %	BP %	MP %	BP %	MP %	BP %	
P1 × P5	0.75	3.08	33.15**	6.52	2.68	-6.65**	-5.43	-9.61**	
P1 × P6	-2.78	2.94	5.96	-2.44	-2.62	-19.43**	13.70**	-3.523	
P1 × P7	5.48	13.23**	11.60**	-6.172	28.41**	10.01**	-7.28**	-23.70**	
P2 × P5	-2.56	16.92**	-16.81**	-39.13**	24.44**	1.82	18.16**	-1.15	
P2× P6	-8.98**	0.00	-7.61	-23.78**	3.43	-21.95**	23.49**	-6.47**	
P2 × P7	-10.06**	-2.56	22.94**	-6.172	6.69**	-17.05**	8.49**	-19.90**	
P3 × P5	-7.35	-3.08	25.00**	-2.17	15.45**	3.26	7.69**	2.31	
P3 × P6	-17.00**	-14.01**	2.04	-8.534	6.24**	5.45**	32.05**	11.47**	
P3× P7	-14.09**	-9.86**	5.26	-13.58**	7.47**	2.35	-12.48**	-28.34**	
P4 × P5	-12.10**	6.15	32.47**	10.87**	3.54	1.20	-15.64**	-16.29**	
P4 × P6	-16.67**	-7.89	-15.36**	-17.68**	1.14	-7.06**	-2.65	-13.53**	
P4 × P7	-14.12**	-6.41	25.87**	11.11	7.45**	2.78	19.81**	3.00	

^Z: EL-S (P1), SM (P2), M-G (P3), R 4 (P4), CLN591 (P5), CLN657 (P6) and Saladatte (P7).

Table (6). Continued.

NF		NL		Т	Y	TS	SS	AA	
MP %	BP %	MP %	BP %	MP %	BP %	MP %	BP %	MP %	BP %
36.91**	22.89**	17.24	0.00	41.40**	39.23**	22.58**	2.70	9.295	8.08
27.59**	-2.77	10.34	-5.88	33.16**	19.54**	22.22**	13.79	21.52**	8.43
14.31**	-3.25	16.67	16.67	50.00**	47.69**	13.21**	7.14	17.70**	1.81
-16.49**	-29.14**	9.67	0.00	7.88	3.17	8.57	2.70	30.68**	5.17
9.84**	-19.85**	-3.22	-11.76	29.30**	12.06**	9.68**	3.03	-15.88**	-25.98**
31.67**	5.81	0.00	-7.14	51.87**	45.24**	4.92**	-3.03	-14.17**	-22.04**
0.82	-16.67**	-12.50	-17.65	17.08**	7.143	21.87**	5.40	5.560	-9.97**
3.23	2.76	-18.75	-23.53**	9.61	8.99	21.43	17.24**	4.32	-1.99
35.78**	18.78**	3.70	-6.67	45.71**	33.33**	12.73	10.71**	-0.66	-3.41
45.93**	38.64**	-15.15	-17.65	54.54**	50.00**	8.57	2.70	16.73**	-3.31
28.28**	11.11	-9.09	-11.76	28.83**	20.57**	25.81**	18.18**	27.79**	16.18**
34.13**	31.99**	-7.14	-18.75	43.58**	39.36**	1.64	-6.06	14.47**	7.56
	MP % 36.91** 27.59** 14.31** -16.49** 9.84** 31.67** 0.82 3.23 35.78** 45.93** 28.28** 34.13**	NF MP % BP % 36.91** 22.89** 27.59** -2.77 14.31** -3.25 -16.49** -29.14** 9.84** -19.85** 31.67** 5.81 0.82 -16.67** 3.23 2.76 35.78** 18.78** 45.93** 38.64** 28.28** 11.11 34.13** 31.99**	NF MP % 36.91** 22.89** 17.24 27.59** -2.77 10.34 14.31** -3.25 16.67 -16.49** -29.14** 9.67 9.84** -19.85** -3.22 31.67** 5.81 0.00 0.82 -16.67** -12.50 3.23 2.76 -18.75 35.78** 18.78** 3.70 45.93** 38.64** -15.15 28.28** 11.11 -9.09 34.13** 31.99** -7.14	$\begin{array}{c c c c c c c } NF & NL \\ \hline MP \% & BP \% & MP \% & BP \% \\ \hline 36.91^{**} & 22.89^{**} & 17.24 & 0.00 \\ \hline 27.59^{**} & -2.77 & 10.34 & -5.88 \\ \hline 14.31^{**} & -3.25 & 16.67 & 16.67 \\ \hline -16.49^{**} & -29.14^{**} & 9.67 & 0.00 \\ \hline 9.84^{**} & -19.85^{**} & -3.22 & -11.76 \\ \hline 31.67^{**} & 5.81 & 0.00 & -7.14 \\ \hline 0.82 & -16.67^{**} & -12.50 & -17.65 \\ \hline 3.23 & 2.76 & -18.75 & -23.53^{**} \\ \hline 35.78^{**} & 18.78^{**} & 3.70 & -6.67 \\ \hline 45.93^{**} & 38.64^{**} & -15.15 & -17.65 \\ \hline 28.28^{**} & 11.11 & -9.09 & -11.76 \\ \hline 34.13^{**} & 31.99^{**} & -7.14 & -18.75 \\ \hline \end{array}$	$\begin{array}{c c c c c c c c c c c c c c c c c c c $	$\begin{array}{c c c c c c c c c c c c c c c c c c c $	$\begin{array}{c c c c c c c c c c c c c c c c c c c $	$\begin{array}{c c c c c c c c c c c c c c c c c c c $	$\begin{array}{c c c c c c c c c c c c c c c c c c c $

^Z: EL-S (P1), SM (P2), M-G (P3), R 4 (P4), CLN591 (P5), CLN657 (P6) and Saladatte (P7).

Conclusion:

The establishment of heat-tolerant tomato varieties is critical for enhancing the production window and adapting to the anticipated rise in temperatures. This study focused on the potential of hybridization to create heat-resistant hybrids, aimed to understand the genetic effects that control heat tolerance traits, and sought to identify heterotic patterns. the line EL-S (P1) was a good combiner for FS, NF, NL and TY traits. Line M-G was a good combiner for ND, FW and FSI traits. Also, the line R4 was a good combiner for FS, NF, FSI, TY, TSS and AA traits. The tester CLN591 was a good combiner for earliness, FS, NL, NF and TSS. Meanwhile, the tester Saladatte was a good combiner for ND, FS, FW, FSI, NF and TY. The significant SCA effects for FS, NF and TY traits were obtained from the crosses P2 × P6, P2 × P7 and P4× P5. For TY, TSS and AA traits the cross P4 × P6 showed significant heterosis based on MP and BP for these traits. Meanwhile, the cross P1 × P7 showed significant heterosis based on MP and BP for FW and TY traits.



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الملخص العربى

القدرة على التآلف وقوة الهجين بإستخدام التهجين القمي تحت ظروف الحرارة العالية لمحصول الطماطم علي القدرة على الت

قسم بحوث تربيه الخضر - معهد بحوث البساتين- مركز البحوث الزراعية –الجيزه

أجريت هذه الدراسة خلال أعوام 2021 و 2022 و 2023 منزرعة بحوث الخضر بقها بمحافظة القليوبية. تضمنت الدراسة تهجين سبعة آباء نقية من الطماطم بإستخدام نظام التهجين القمى ، مما أدى إلى إنتاج 12 هجين. تم تقييم كل من وأصحت النتائج والهجن الناتجة عنها في حقل مغتوح خلال موسمي الصيف المتاخر المتتاليين لعامي 2022 و2023. و2023 و2023 و2023 والعرحت الطرز الوراثية الأبوية و الهجن الناتجة عنها في حقل مغتوح خلال موسمي الصيف المتاخر المتتاليين لعامي 2022 و2023 و2023 وأوضحت النتائج وجود اختلافات معنوية في متوسط الأداء في جميع الصفات المدروسة، والتي تعزى إلى الأنماط الجينية أوضحت النتائج وجود اختلافات معنوية في متوسط الأداء في جميع الصفات المدروسة، والتي تعزى إلى الأنماط الجينية المختلفة. كما اظهرت النتائج بأنه يوجد فروق معنوية عالية بين التراكيب الوراثية لجميع الصفات المدروسة. كان التقاعل بين لوحظ ان متوسط درجة السيادة المقدرة (ADD) أعلى من الواحد لخمس صفات، وهي عدد الأيام حتى 50% من الأز هار وعدد الحجرات. كما معامل شكل الثمرة ،عدد الحجرات/ ثمرة ، المحصول الكلي/ نبات والمواد الصلبة الذائبة الكلية مما يشير إلى أن السيادة الفائقة لوحظ ان متوسط درجة السيادة المقدرة (ADD) أعلى من الواحد لخمس صفات، وهي عدد الأيام حتى 50% من الأز هار ، معامل شكل الثمرة ،عدد الحجرات/ ثمرة ، المحصول الكلي/ نبات والمواد الصلبة الذائبة الكلية مما يشير إلى أن السيادة الفائقة التحكم فى هذة الصفات. كما أشارت نتائج تحليل تأثيرات القدرة العامة على التالف (GCA) إلى والدول (P1) المواد (P1) ألمرة و معامل شكل الأمرة و عدد الحرات. كما أن من يتحكم فى هذة الصفات. كما أشارت نتائج تحليل تأثيرات القدرة العامة على التالف (GCA) من من الول (P1) الحصول الكلي/ نبات والمواد الحرات/ثمرة والمحسول الكلى/نبات. كان الاب عائمة و عدد الثمار على النار على النار على والى التها علي و من من عد صفات من و ومتوسط وزن الثمرة و معامل شكل الأمرة و عدد الثمار على التالف عالية من حيث صفات نسبة العقد و متوسط وزن الثمرة و معامل شكل من متفوقا فى مجموعة الصفات التالي العلى مالغمان ، عدد الثمار م و الحمول الكلى/نبات. كان الاب عان متفوقا فى مجموعة الصفات التالي قائمة على النام ، عدد الثمار م على النارم و ومعد المامة على النام ، عدد الثمار على النبات والمحصول الكلى من الهجن 96 × 92 و 27 × 92 و 75 × 92