



GENETIC ANALYSIS OF HEAT TOLERANCE RELATED CRITERIA IN TOMATO (*Solanum lycopersicum* L.)

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ABSTRACT: The present study aimed to assess the genetic evaluation of 5 genotypes and their 10 crosses for heat tolerance, as well as to determine the genetic behavior of heat tolerance related criteria under heat stress condition in tomato in five tomato genotypes (five parents, [P1 (s.60), P2 (HE.15.4.1), P3 (D.7.4.1), P4 (KL.3), P5 (KL.5)], and their ten F₁ hybrids) during summer season of 2014 and 2015 at The Experimental Farm At El-Kassasien, Hort. Res. Station, Ismailia, Egypt and data were analyzed by half diallel analysis. Seven characters were studied, osmotic pressure (OP), pollen fertility (PF), 50% flowering, fruit setting (FS), fruit weight (FW), total yield (TY), and total soluble solid (TSS). Positive heterosis in OP, PF, TY, FS and TSS for almost all hybrids, except (3×5) (4×5) hybrids was observed which possessed a negative heterosis in FS; Negative heterosis in 50% F, and FW for almost all hybrids, was detected except (1×4) (4×5) hybrids which possessed a positive heterosis in FW. High significant differences of additive effect (D) estimates was obtained for all studied characters except FS. Mean degree of dominance (H_1/D)^{0.5} indicated the presence of over dominance for TY, FW, PF, while the other characters, OP, 50% F, FS and TSS showed partial dominance. The deviation of b-value from zero was significant for TY, FW, 50% F, PF and FS suggesting the absence of non-allelic interaction, while it was insignificant for TSS and OP suggesting the presence of non-allelic interactions. High heritability (h^2_b) from (0.86-0.98) was obtained for all characters, indicating the little influence of the environmental conditions and subsequently, these character considered as high inherited ones. (h^2_n) from (0.32-0.96) was obtained for all characters.

Key words: Tomato, heat tolerance, heat stress.

INTRODUCTION

Tomato (*Solanum lycopersicum* L.) is one of the most important vegetables in Egypt. It is rich in natural antioxidants and bioactive compounds. The regular ingestion of an adequate amount of fresh tomatoes or processed tomato products has been inversely correlated with the development of widespread human diseases (Erdman *et al.*, 2009 ; Prakash and Kumar, 2014) and with an increase in plasma lipid peroxidation levels (Balestrieri *et al.*, 2004). This protective effect has been mainly attributed to the carotenoid constituents of the fruits, particularly lycopene and β -carotene

which act as antioxidants in detoxifying free radicals (Erdman *et al.*, 2009). So yield of tomato is to be increased several folds in a unit area. It is reported that hybrid variety of tomato resulted in increasing yield of 20 to 50%. Apart from high yield, the hybrids may have some other specific advantages of earliness, higher number of fruits per plant, fruit size, improved quality, uniformity, higher adaptation capability to adverse conditions, *etc.* It was further mentioned that exploitation of hybrid vigor in tomato is economical because each fruit contains large number of seeds as compared to other vegetables and per unit area seed requirement is also very low.

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Heat tolerance is generally defined as the ability of the plant to grow and produce economic yield under high temperatures. However, while some researchers think that night temperatures are major limiting factor others have discussed that day and night temperatures do not affect the plant independently and that the diurnal means temperature is a better interpreter of plant response to high temperature with day temperature having a secondary role (Peet and Willits, 1998).

Heat stress is the main reason for poor fruit set at high temperature in tomato. Tomato growth under high temperature is affected badly on the productive part of the flower, stigma tube elongation, poor pollen germination, poor pollen tube growth and carbohydrate. Temperature for tomato farmstead during the photoperiod is between 25°C and 30°C and during the dark period is 20°C. However, only 2-4°C rise in optimal temperature improperly influenced gamete development and prohibited the ability of pollinated flowers into seeded fruits and therefore diminished crops yield (Miller *et al.*, 2001; Firon *et al.*, 2006).

The improvement program of tomato can be enhanced to considerable extent if some basic information relevant to the pattern and genetic variability is made available to the plant breeders. The inheritance pattern and combining ability studies are the basic themes to derive such information which can be used as guidelines in planning tomato breeding program for achieving short and long term objectives Ahmed *et al.* (2010).

Gene action refers to the mode of expression of genes in a breeding population. Mode of gene action provide guidelines in the selection of parents for utilization in hybridization program as well as choice of breeding procedures for genetic improvement of various quantitative traits of interest. Its main attributes include genetic components of variance which comprises the magnitude of combining ability variances and their relative effects. On the basis of genetic variance, gene action is being described in three different forms additive gene action, dominant gene action and epistatic gene action, respectively. The later two are collectively

termed as non-additive gene action. Different factors affect the mode of gene action which include type of genetic material utilized, mode of pollination, pattern of inheritance, sample size, sampling methods, existence of linkages and methods of derivation on gene action. Therefore, it was tried to define the inheritance pattern of some yield contributing characters of tomato which would be helpful for further breeding program (Goffar *et al.*, 2016).

Therefore the present study aimed to assess the genetic evaluation of 5 genotypes for heat tolerance, as well as determine the genetic behavior of heat tolerance related criteria under heat stress condition in tomato.

MATERIALS AND METHODS

This study carried out during summer 2014 and 2015. Hybridization and evaluation of genotypes and crosses under high temperature were carried out at El-Kassassen experimental farm during the summer season. Five tomato genotypes viz., s.60, HE.15.4.1, D.7.4.1, KL.3, KL.5, with different characters were crossed in half diallel (without reciprocal).

Evaluation of the Studied Tomato Genotypes for Heat Tolerance

Two experiments were carried out in a randomized complete block (RCB) design with three replications in 2014-2015 growing season. The experiments were designed to evaluate tomato genotypes under heat stress conditions (34°C) (Kamel *et al.*, 2010). Each replicate comprised 15 entries (five parents and their 10 F₁'s). Agricultural practices were carried out as the recommended program of the Egyptian Ministry of Agriculture for commercial tomato production. 10 plants per plot for parental and F₁ hybrids were taken for measuring the following characters:

Osmotic pressure (bar)

The osmotic pressure was estimated from transforming the total soluble solids (TSS) to osmotic pressure as air pressure (bar) and multiplied by the factor (1.013) to represent osmotic pressure (bar). The total soluble solid was determined as refraction index using Zeiss refractometer at leaf after 90 days from

transplanting at room temperature (Morgan, 1977).

- Pollen viability by staining of pollen grains with aceto carmine dye and estimation of pollen viability according to the method followed by Moreira and Gurgel (1941).
- 50% flowering, the days from transplanting to flowering 50% of plants
- Percentage of fruit set per plant was determined as the total number of fruit divided by the total flower number on clusters 2-6 of plant.
- Average fruit weight (g) was calculated by dividing total weight of fruits over total number of fruits per plant.
- Total yield/plant: it was measured from the average total weight in kilograms of harvested fruits per plant through the harvesting season.
- TSS, the total soluble solid in fruit was determined as refraction index using Zeiss refractometer at leaf after 90 days from transplanting at room temperature (Morgan, 1977).

Statistical Analysis

The experiment was laid out in randomized complete block design (RCBD) with 3 replications. Each unit plot contained 2 rows of plants (24 plants/plot). The recorded quantitative data were analyzed statistically for analysis of variance and Vr-Wr graph following Hayman (1954a) and Hayman (1954b). Components of genetic parameters were calculated following numerical approach of Jinks and Hayman (1953) based on Mather's notation (Mather and Jinks, 1982).

RESULTS AND DISCUSSION

The behavior of F_1S regarding growth stage duration showed different interactions among seven characters (Table 1). Positive heterosis in OP, PF, TY and TSS for almost all hybrids were detected. In contrast, the behavior of F_1S regarding 50% F appeared to have negative heterosis in most hybrids. FS showed positive heterosis in almost all hybrids, except (3×5) and (4×5) hybrids, which possessed a negative heterosis. FW showed negative heterosis in

almost all hybrids, except (1×4) and (4×5) hybrids, which possessed a positive heterosis.

The analysis of variance for seven characters showed high significant difference among parents and their hybrids (Table 2). The major assumptions postulated for diallel analysis (Hayman, 1954a) were found to be valid as the t^2 value was insignificant for all characters. Another way of testing the hypothesis is through regression coefficient (b). The regression of W_r/V_r was insignificantly different from unity for all characters. The deviation of b-value from zero was significant for TY, FW, 50% F, PF and FS suggesting the absence of non-allelic interaction, while it was insignificant for TSS, OP suggesting the presence of non-allelic interactions.

Estimates of the genetic components of variation and their proportions are presented in (Table 3). High significant differences of D estimates was obtained for all studied characters Goffar *et al.* (2016) expect FS, insignificant difference of H_1 estimates was obtained for all studied characters expect TY, 50%F and PF, indicating the importance of additive and dominance gene effects in the genetic control of them. The H_2 estimate as dominance component was also insignificant expect TY, PF, 50% F and smaller than H_1 in almost all characters, expect FS. The h_2 estimate which is the measure of heterozygous loci averaged overall loci was positive and significant for TY, TSS, PF, OP, 50% F expect FW, FS. Positive and significant h_2 value indicated that dominant genes for these characters were due to heterozygosity. The results indicated the positive F value for TY, FS, PF expect FW, OP, TSS which, indicated that dominant genes were more frequent than the recessive ones among parental genotypes, Amiri *et al.* (2009) also found equal frequencies for positive and negative alleles.

Mean degree of dominance $(H_1/D)^{0.5}$ indicated the presence of over dominance for OP, FS and TSS, while the other characters, *i.e.*, PF, 50% F, FW and TY showed partial dominance. The proportion of genes with positive and negative effects in the parents $(H_2/4H_1)$ it was less than its maximum value of 0.25, indicating that the positive (\pm ve) and the negative (-ve) alleles at the loci exhibiting dominance were asymmetrically distributed in

Table 1. Mean values of osmotic pressure (OP), pollen fertility (PF), fruit setting (FS), 50% flowering (50% F), total yield (TY), fruit weight (FW), total soluble solid (TSS)

Entries	Osmotic pressure (bar)	Pollen fertility (%)	50% flowering	Fruit setting (%)	Fruit weight (g)	Total yield (kg)/ plant	TSS
P1(s.60)	6.04	19.30	68.00	42.57	125.68	0.51	4.8
P2(HE.15.4.1)	5.45	46.12	60.33	54.48	163.6	3.79	4.3
P3(D.7.4.1)	7.35	51.75	58.66	66.21	127.36	3.05	5.84
P4(KL.3)	5.85	62.29	50.33	70.05	83.83	1.85	4.65
P5(KL.5)	4.18	74.13	40.33	75.61	40.86	1.06	3.32
P1×p2	7.07	33.63	61.33	63.32	140.14	3.45	5.61
P1×p3	7.59	48.15	59.33	59.12	120.58	3.14	6.02
P1×p4	6.38	59.79	46.33	76.18	111.5	2.8	5
P1×p5	5.37	48.06	47.33	80.71	76.31	2.15	4.27
P2×p3	7.67	60.16	47.66	80.83	141.62	4.025	6.09
P2×p4	7.31	68.79	51.00	79.40	125.67	4.06	5.81
P2×p5	4.92	62.14	47.33	76.90	80.12	2.51	3.91
P3×p4	8.32	65.21	47.33	79.17	95.23	2.68	6.6
P3×p5	6.00	65.26	45.66	66.06	71.79	2.2	4.76
P4×p5	5.44	77.91	39.66	72.61	66.29	2.49	4.32

S=sensitive M=moderate T=tolerant

Table 2. Analysis of variance, t^2 -values, regression coefficients and their test of significant for the studied characters

MSS								
Source of variation	df	Osmotic pressure (bar)	Pollen fertility (%)	50% flowering	Fruit setting (%)	Fruit weight (g)	Total yield (kg)/plant	TSS fruit
Replication	2	0.001	0.187**	0.156	13.045	64.469	0.004	0.001
Genotypes	14	4.155**	715.531**	204.279**	366.780**	3504.160**	3.098**	2.615**
Error	28	0.093	28.774	32.727	42.529	165.911	0.025	0.059
t^2		4.089	0.640	2.050	1.368	0.000	0.341	4.470
b		0.517	0.874	0.851	1.098	0.983	0.948	0.517
\pm S.E(b)		0.222	0.162	0.122	0.151	0.132	0.100	0.214
H_0 : b =0		2.332	5.404*	6.993**	7.250**	7.445**	9.515**	2.416
H_0 : b =1		2.177	0.776	1.226	-0.644	0.127	0.526	2.253

*,** Significant at 5% and 1% level of probability, respectively

Table 3. Estimates of components of genetic variation and their proportions of the studied characters

	Osmotic pressure (bar)	Pollen fertility (%)	50% flowering	Fruit setting (%)	Fruit weight (g)	Total yield(kg)/plant	TSS
D±SE (D)	1.182 ^{**} ±0.196	422.75 ^{**} ±17.13	111.66 ^{**} ±5.11	230.583±26.145	2113.96 ^{**} ±38.25	1.774 ^{**} ±0.048	0.74 ^{**} ±0.12
F±SE (F)	-1.032±0.490	41.01±42.81	13.75±12.78	149.772±65.310	-82.90±95.57	0.735 ^{**} ±0.121	-0.66±0.31
H1±SE (H1)	1.424±0.530	171.02 [*] ±46.28	73.39 [*] ±13.82	249.186±35.304	212.10±103.32	1.349 ^{**} ±0.131	0.82±0.33
H2±SE (H2)	1.153±0.481	144.19 [*] ±41.97	70.59 [*] ±12.53	55.985±64.042	170.12±93.71	1.118 ^{**} ±0.119	0.67±0.30
H±SE (h)	1.774 [*] ±0.324	171.75 ^{**} ±28.34	99.54 ^{**} ±8.46	11.377±43.238	10.28±63.27	2.019 ^{**} ±0.080	1.06 [*] ±0.20
E±SE (E)	0.029±0.080	8.95±6.99	10.27 [*] ±2.09	14.176±10.674	45.16±15.61	0.081 [*] ±0.020	0.01±0.05
H₁/D^{0.5}	1.098	0.636	0.681	1.439	0.317	0.872	1.049
H₂/4H₁	0.202	0.211	0.240	0.220	0.201	0.207	0.205
h²/H₂	1.539	1.191	1.410	1.084	0.060	1.807	1.574
R	-0.066	-0.606	0.895	-0.985	0.943	-0.605	-0.083
r²	0.004	0.368	0.802	0.970	0.890	0.366	0.007
KD/KR	0.431	1.165	1.164	1.789	0.883	1.623	0.405
h²(b.s)	0.98	0.96	0.86	0.88	0.96	0.91	0.98
h²(n.s)	0.771	0.850	0.740	0.321	0.963	0.638	0.757

the studied parents. If the coefficient (r) between them is negative it means that parents may contain the most increasing genes having lowest values of $W_{ri}+V_{ri}$ and thus containing most dominant genes. Correlation will be positive if the case is reversed. Thus, one can conclude whether or not the increasing or decreasing genes are the dominant ones (Singh and Chaudhary, 1977). The value KD/KR which reflects the proportion of dominant and recessive genes in the parents (Dom./rec.) had little than one for FW, OP and TSS showing more recessive genes than dominant in the parents. Another way (KD/KR) showed that proportion of dominant genes is greater than recessive in parents in TY, 50% F, PF and FS.

High heritability estimates in broad-sense (h^2_b) [0.86-0.98] was obtained for all characters, indicating the little influence of the environmental conditions and subsequently, these character considered high inherited ones. In addition, intermediate to high heritability estimates in narrow sense (h^2_n) [0.32-0.96] was obtained for all characters. These findings suggested that early generation selection for these characters would be effective in improving characters in the studied material, as they are

governed more by additive than dominance genes.

The F₁ graphic analysis for the seven studied characters is shown in Figs. 1, 2, 3, 4, 5, 6 and 7. The regression line passed above the point for FW. These results are in agreement with the findings of Bhatt *et al.* (2001) who also reported that the non-additive geneaction for the trait., TY, 50% F and PF, suggesting partial dominance. The regression line of FS passed below the point of origin, OP.T.S.S suggesting over dominance with the findings of Bhatt *et al.* (2001). If the regression line touches parabola limit, it indicate no-dominance therefore, the between parabola limit and regression line determine the dominance volume and subsequently additive effects. Regarding tailoring period, the regression line almost touched the parabola limit and the array points of the parents also was near regression line, suggesting that additive gene effects play an important role in the genetic control of this trait, the order of the array points along the regression line showed that S.60 had most recessive genes for PF, FS, TY, 50% F and OP, as well as an excess of dominant genes for FW and TSS p2 had most recessive genes for PF, TSS, OP and FW, an excess of dominant genes for TY, 50% F and FS.

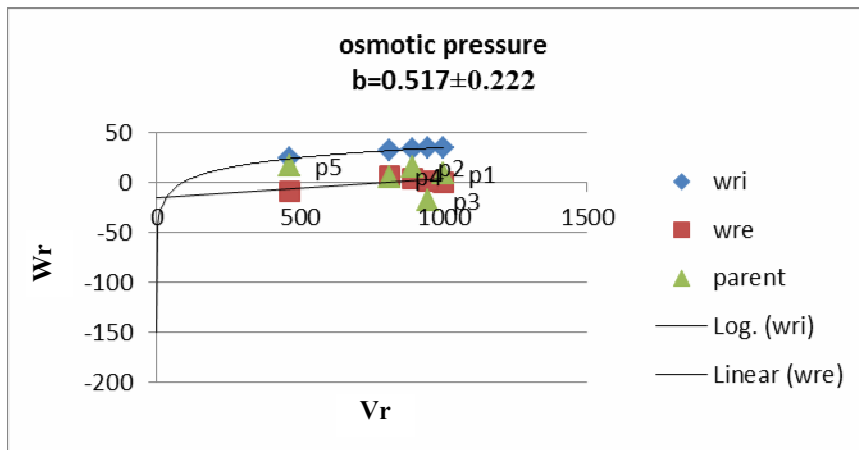


Fig. 1. The relationship between Vr and Wr for osmotic pressure under heat stress

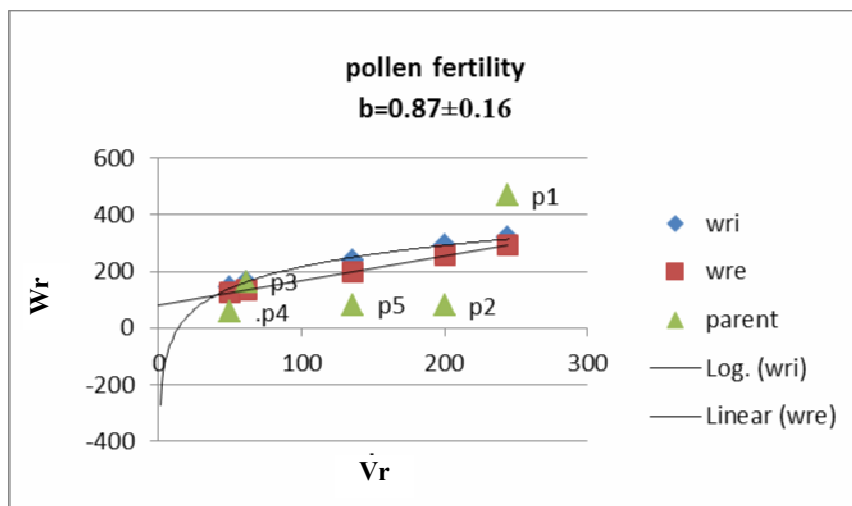


Fig. 2. The relationship between Vr and Wr for Pollen fertility under heat stress

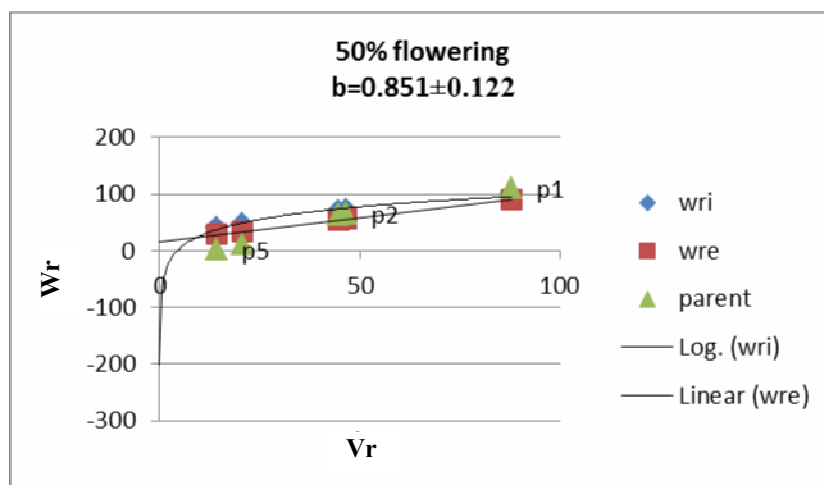


Fig. 3. The relationship between Vr and Wr for 50% flowering under heat stress

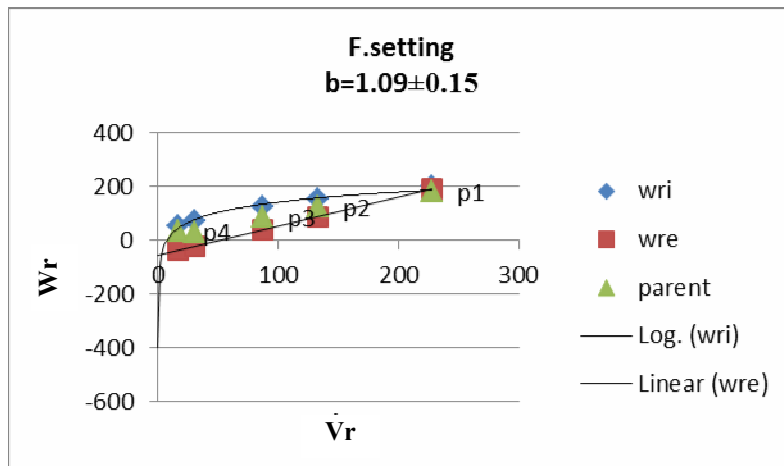


Fig. 4. The relationship between V_r and W_r for fruit setting under heat stress

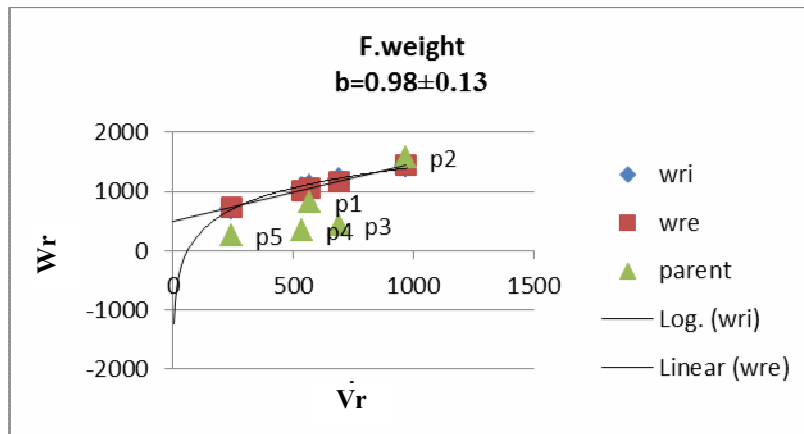


Fig. 5. The relationship between V_r and W_r for fruit weight under heat stress

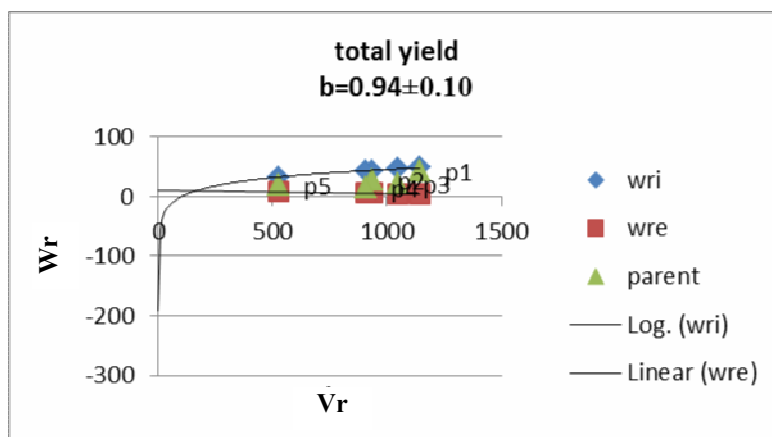


Fig. 6. The relationship between V_r and W_r for total yield under heat stress

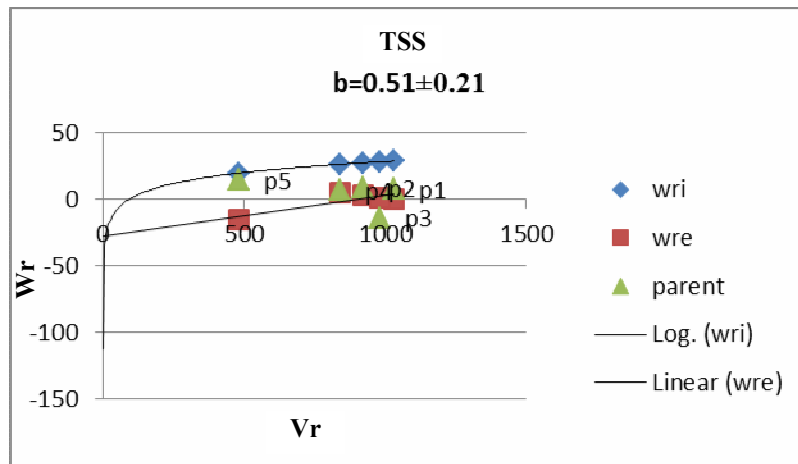


Fig. 7. The relationship between Vr and Wr for TSS under heat stress

P3 had most dominant genes for PF, FS, TSS, 50% F, FW and TY, as well as an excess recessive genes for OP. P4 had most dominant genes for PF, FS, 50% F, FW and TY, as well as an excess recessive genes for TSS and OP. P5 had most dominant genes for PF, FS, TSS, FW, 50% F, OP and TY.

Based on these information it may be concluded that the importance of both additive and non-additive genetic parameters suggests the use of integrated breeding strategies for tomato improvement. The use of hybrid breeding accompanied with recurrent selection may provide example opportunities for novel recombination and accumulation of genes of interest.

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التحليل الوراثي للصفات المرتبطة بتحمل الحرارة في الطماطم

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تهدف هذه الدراسة إلى تقييم وراثي ل ٥ أنواع من التراكيب الوراثية مع ١٠ تهجينات من أجل تحمل الحرارة، وكذلك تحديد السلوك الوراثي لمعايير التحمل الحراري ذات الصلة تحت ظروف الإجهاد الحراري في الطماطم، تم إجراء الدراسة في مزرعة التجارب البحثية، محطة بحوث البساتين بالقصاصين، مركز البحوث الزراعية، محافظة الإسماعيلية صيف ٢٠١٤ و ٢٠١٥، تم استخدام خمسة تراكيب وراثية من الطماطم في هذه الدراسة هي HE.15.4.1، D.7.4.1، KL.3، KL.5، والعشرة هجن الناتجة عنها في الموسم الصيفي ٢٠١٤ و ٢٠١٥ تم زراعة التراكيب الأبوية والتهجين بينهم للحصول على هجن الجيل الأول وفي الموسم الصيفي ٢٠١٥-٢٠١٦ تم دراسة السلوك الوراثي لسبعة صفات تحت ظروف الحرارة المرتفعة وكانت هذه الصفات هي الضغط الاسموزي، حيوية حبوب اللقاح، نسبة الثمار إلى عدد الأزهار في العنقود الزهري، ٥٠% من الأزهار، وزن الثمرة، المحصول الكلي، نسبة المواد الصلبة الذائبة في الثمار وتم تحليل النتائج المتحصل عليها باستخدام تحليل الداي الليل وتقدير مكونات التباين الوراثي والمكافئ الوراثي للصفات، أظهرت صفات الضغط الاسموزي، حيوية حبوب اللقاح، المحصول الكلي، نسبة الإنبات، ونسبة المواد الصلبة في الثمار إيجابية في جميع الهجن ماعدا الهجن (٣ × ٥) (٤ × ٥) لصفة نسبة الثمار إلى عدد الأزهار بينما صفات وزن الثمرة و ٥٠% أزهار أظهرت سلبية في جميع الهجن ماعدا الهجن (٤ × ٤) (١ × ٥) لصفه وزن الثمرة، أظهرت قيم (D) فروق عالية المعنوية لكل الهجن ماعدا نسبة الثمار إلى عدد الأزهار، كما أن قيم (H₂) أظهرت عدم وجود معنوية في الصفات ماعدا حيوية حبوب اللقاح والمحصول الكلي و 50% أزهار كذلك أظهرت قيم اصغر من قيم (H₁) في جميع الصفات ماعدا نسبة الثمار إلى عدد الأزهار، نسبة (H₁/D)^{0.5} كانت اقل من الواحد الصحيح في إشارة إلى وجود سيادة جزئية متحكممة في الصفات التالية حيوية حبوب اللقاح، ٥٠% إزهار، وزن الثمرة، المحصول الكلي بينما كانت أعلى من الواحد الصحيح في إشارة إلى وجود سيادة متحكممة في الصفات التالية الضغط الاسموزي نسبة الثمار إلى عدد الأزهار، نسبة المواد الصلبة في الثمار، كانت تقديرات المكافئ الوراثي بالمفهوم الضيق عالية لجميع الصفات ماعدا صفة نسبة الثمار إلى عدد الأزهار مما يشير إلى الانتخاب المبكر لهذه الصفات سيكون فعال في حين الانتخاب لصفة نسبة الثمار إلى عدد الأزهار يكون في الأجيال المتأخرة، أظهرت النتائج (W_T-V_T) أن خط الانحدار يقطع محور W_T أعلى نقطة الأصل لصفات حيوية حبوب اللقاح، ٥٠% أزهار، وزن الثمرة، المحصول الكلي أي أن تلك الصفات محكومة بسيادة جزئية بينما الصفات الأخرى محكومة بسيادة فائقة لان خط الانحدار يقطع محور W_T أسفل نقطة الأصل.

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