# SELECTION AMONG SOME MELON STRAINS FOR 

 TOLERANCE TO THE TWO-SPOTTED SPIDER MITE, Tetranych usurticae kochA.A.EL- Sayed ${ }^{1}$, A.E.A Mahgoob ${ }^{2}$ and, Heba M. Emam ${ }^{2}$<br>1. Vegetables, Medicine and Aromatic Breed. Dept., Horti., Res., Inst., ARC, Giza, Egypt.<br>2. Department of Plant Protection, Faculty of Agriculture, Ain Shams University, Shoubra El-Kheima, Cairo, Egypt.


#### Abstract

This study was conducted during the period from 2016 to 2018. Seven different strains of melon (Cucumis melo L.) were tested for their response to Tetranychus urticae. Data revealed that, all plant growth parameters were affected significantly with infestation of T. urticae; leaf area which considered the main source of mite feeding was the most affected one. However, (L5) had the lowest leaf area (24.98 cm ${ }^{2}$ ) while (L7) recorded the highest leaf area ( 41.26 cm ). Also, accumulated moving stages in (L2) showed the lowest population density with an average of 1.70 individual /in ${ }^{2}$ during 4 weeks, of season 2016. During season 2017, the highest leaf area was in hybrids (L4×L1) and (L4×L2) with an average 62.93 and $61.86 \mathrm{~cm}^{2}$. All hybrids explained three levels of infestation; high level was observed in hybrids (L6×L2), (L5 522 ) and (L7×L1) and accumulated the population density of moving stages with an average of 80.70, 70.60 and 61.40 individual $/ \mathrm{in}^{2}$. While medium level was recorded in hybrids ( $L 5 \times L 1$ and $L 7 \times L 2$ ) and the third, low level of infestation was recorded in hybrids ( $L 6 \times L 1, L 4 \times L 1, L 3 \times L 2$, $L 3 \times L 1$ and L4×L2) and moving stages average were $2.70,3.30,3.70,3.90$ and 5.30 individual $/ \mathrm{in}^{2}$ so these hybrids were resistant to infestation of $T$.urticae . Regarding horticultural characters obtained data on total yield ranged from 4015.0 to 2185.0 g/plant; (L4) gave the highest value of total yield. Estimates of broad sense heritability were high for all studied traits indicating minor role of the environment. The results showed significant and highly significant mean squares for both general combining ability and specific combining ability in all studied traits, indicating the important role of both additive and non-additive gene effects in the expression of these traits. Highly significant SCA effects in all studied traits were recorded for the crosses (L3×L2), (L5 $\times$ L2), (L6 $\times L 2$ ) and (L3 $\times L 1$ ). Key words: Melon, Line $\times$ Tester, Inheritance, Spider mite, Tetranychus urticae. Heterosis, Heritability.


## INTRODUCTION

The two-spotted spider mite (TSSM) (Tetranychus urticae Koch) (Acari: Tetranychidae) is a widely distributed agricultural pest with a host range of well over 100 species of crop, ornamental, and weed plants. The active stages of this pest are sap feeders that produce irregular patterns of small light colored spots on the leaf. Yield losses in cucurbits are primarily due to feeding on the lower leaf surfaces. The TSSM damages plant cells and tissues by piercing them and sucking out their contents, leading to the collapse of the underlying mesophyll tissue and the formation of chlorotic lesions at the feeding sites, resulting in yield loss. Because the chloroplasts in leaves are gradually destroyed as the population of feeding mite's increases, photosynthesis declines, stomata close, and transpiration decreases, leading to reduced production
(Martinez-Ferrer et al 2006). In cucurbits, yield losses are due primarily to feeding on the lower leaf surface. In severe infestations, the leaves become yellow and development of necrotic regions with network of webs that cover the lower leaf surface and petiole (Scully et al 1991). The TSSM has a high fecundity rate and a short development time at high temperatures. Under favorable conditions, it can produce over 20 generations/year. Also, studied resistance to the two-spotted spider mite in muskmelon and found that, deviation of hybrid means from expected mid-parent's values were non-additive gene action contributed to the expression of resistance/susceptibility for both female density and males /immature mite numbers (Scully et al 1991). Shoorooei et al (2013) investigated the existence of antixenotic resistance to the two-spotted spider mite in 36 melons (Cucumis melo L.) genotypes using choice tests. Their results revealed significant genetic diversity for the trait, and four genotypes were resistant on the other hand another four were susceptible genotypes. These four resistant and four susceptible genotypes were used in follow-up experiments in order to assess their mechanisms of antibiosis and related enzyme activities. Combining ability is an important in plant breeding since it extends information for selection of parents and also provides information regarding nature of gene actions. In this direction, the concept of general (GCA) and specific (SCA) combining abilities helps the breeder to determine upon the choice of parents for hybridization and also gives information on gene action, which helps in understanding the nature of inheritance of the characters (Sprague and Tatum 1942). Griffing (1956) stated that GCA effects were due to additive type of gene action and SCA effects were due to non-additive (dominant or epistatic) gene action. In this context, Line $\times$ Tester mating design proposed by (Kempthrone 1957) helps the breeders by providing information on the combining ability status of genotypes (parents and hybrids) used and also on the nature of gene action involved. The results of Hussein and Selim (2014).showed significant or highly significant mean squares for both GCA and SCA in all studied traits except fruit shape index, revealing the important role of both additive and non-additive gene effects in the expression of these traits. So, the objective of this study was using different cantaloupe
inbred lines as sources of resistance to spider mite to developed new hybrids and to select the top performing melon hybrids which are spider mite resistant with an appropriate yield and good fruit quality.

MATERIALSAND METHODS
This study was conducted during the period from 2016 to 2018. Plants were maintained in the screen house of Plant Protection Dept. Fac. of Agric. Ain Shams University and Vegetable Research Departments, Horticulture Research Institute, Agricultural Research Center, Giza Governorate and Kaha Vegetable Research Farm, Qalubia Governorate Egypt. The genetic materials used in the present investigation were 7 different genotypes of melons (Cucumis melo L. Table 1).These strains collected from different sources as shown in Table (1).

Table 1. Source of Melon genotypes.

| Code No. of <br> genotype | Genotype | Source |
| :---: | :--- | :--- |
| Line1 | KAHA 1 | (Ames26809 US Carolina) |
| Line 2 | KAHA 3 | (NSL - 30032 South Carolina) |
| Line 3 | KAHA 4 | (NSL 34600 USA South Carolina) |
| Line 4 | KAHA 53 | (Deb. of vegetables breeding) |
| Line 5 | DOKKY 6 | (NGB 9999.2 Nord Gen Bank) |
| Line 6 | DOKKY 2- | (Deb. of vegetables breeding) |
| Line 7 | DOKKY 11 | (Deb. of vegetables breeding) |

Plant materials: Seven genotypes of melons (Cucumis melo L.) were investigated: Line 1, 2 and 3 were imported from USA, Whereas Line 5 was obtained from Nord Gen Bank. Lines (4-6 and7) obtained from Deb. of vegetables breeding (D V B). (Table 1). Lines (L3, L4, L5, L6 and L7) which were crossed with two tolerant Testers (L1 and L2) in Line x Tester mating design. Selfing and crosses were made manually using the standard procedure of hand emasculation and pollination in the greenhouse.

## Measured characters:

A. Main stem length (cm): main stem length was measured in centimeters from the cotyledon node to the top end.
B. Leaf area index: The leaf area was determined by the area meter (LICOR, model: LI 3050A/4, U.S.A)
C. Fruit quality: Average fruit weight (g), fruit length (cm), fruit diameter (cm), flesh thickness (cm), fruit cavity and total soluble solids (TSS) was determined in ripe fruits using a hand refractometer.
D. Yield: Total yield was weight of all fruits harvested at the yellownetted ripe.

## Estimation of total phenolic content:

Total phenolic content in melon leaves of each treatment was determined according the methods described by Descalzo et al. (1990).
Rearing of two-spotted spider mite (TSSM), T. urticae:
A- Source of T. urticae
Two spotted spider mites were collected from infested leaves of the cucumber and melon plants grown in fields and greenhouses of Faculty of Agriculture, Ain Shams University.

## B-Mite colony:

One newly matted adult mite female was transferred by a fine camel hair brush to a sweet potato leaf ( 1 mm ), kept on a moist cotton wool pad in Petri dish and left for laying eggs. The deposited eggs were kept under laboratory conditions of $25-27^{\circ} \mathrm{C}, 60 \%$ R.H. and $16 \mathrm{~L}: 8 \mathrm{D}$ photoperiod until hatching. The female mite was mounted on a glass slide in Hoyer's, media for identification. The newly hatched larvae were then transferred singly to fresh leaves of sweet potato cutting holding about 8 leaves each was placed in glass jars containing tap water which was changed every 48 h . The sweet potato cuttings were changed weekly to provide a mite colony with a fresh leaf. (Pritam and Clare 1993).

## C- Determination of plant growth and Flowering of melon plant strains as affected by infestation with T. urticae

Seedlings of Melon plants trains were transplanted in plastic pots (14 cm . diameter) filled with a sterilized sandy-clay soil $1: 1$ (V/V). One seedling/pot, and maintained completely in separated places in the greenhouse. Three individuals of females of $T$. urticae ( $3 \mathrm{P} / \mathrm{plant}$ ) were
used to determine the sensitivity of plant strains of cantaloupe and the control (plant free of mites). There were three replicate for each plant strain. Female mites were transferred using a fine camel hair brush on cantaloupe leaves. Plants were irrigated when needed and fertilized twice a week with soluble fertilizer with N, P, and K (19.19.19). After two weeks from infestation plants and mite's parameters were recorded at weekly during for four weeks.

## Mite parameters

Three leaves from each strain and hybrid of Melon plants were collected randomly for mite counting. All mite stages (number of eggs, larvae, nymphs, adult males and females) were counted in area one $\mathrm{in}^{2}$ of plant. Counts were done using the dissecting microscope.

## Statistical analysis

All obtained data from the two seasons were subjected to the statistical analysis according to Steel and Torrie (1984). The means were compared by Duncan's Multiple Range Test (DMRT) at 5\% (1955). Genetic analysis for this study was performed according Kempthorne (1957), Heterosis based on the mid parent value was estimated according to Sinha and Khanna (1975). Broad sense heritability's (BSH) were calculated according to Allard (1960).The genetic statistical analysis for combining ability was done according to Singh and Chaudhary (1977).

## RESULTSANDDISCUSSION

Determination of plant growth and flowering of strains of melon as affected by the infestation with TSSM

Data given in Table (2) revealed that, all plant growth parameters: plant length (cm), number of leaves/plant, leaf area and flowering of all plant strains of $C$. melo were affected significantly with infestation of $T$. urticae (TSSM) comparing with control. Among all parameters, leaf area which considered the main source of mite feeding was the most affected one. Leaf area recorded highly significant differences between the inbred lines, the lowest leaf area was for strain (5) with an average of $24.98 \mathrm{~cm}^{2}$ while the highest leaf area was $41.26 \mathrm{~cm}^{2}$ in strain no. (7) Comparing with control ( 50.94 and $61.91 \mathrm{~cm}^{2}$ ) respectively. For plant length also, there were significant differences among the strains and some of them, the lowest plant length for no. (3) with an average of 14.41 cm , while the highest plant
height was 27.08 cm . in strain no. (7). Comparing with control plant (19.92 and 42.66 cm ) respectively. Also, for number of leaves, there were no significant differences among lines no. (5 and 6) with an average of 5.24 and 5.50 comparing with control ( 7.67 and 7.59 ) respectively, and they were considered the lowest in number of leaves. While the highest number of leaves was for no. (1) with an average of 13.83 comparing with control (15.92) respectively., and the lowest no. of flowers in no. (7) with an average of 3.08 , then lines ( 2,4 and 3 ) with an average of $6.66,7.16$ and 9.49 comparing with control with( $10.33,11.33$ and 17.33 ) respectively. These results are in harmony Abdel-Salam et al (1982); Masaki et al (1991) and Ibrahim (2005), who recorded that, the two-spotted spider mite, Tetranych usurticae Koch is one of the most important pests of cucurbits causing serious damage to plants.
Table 2. Vegetative growth parameters, flowering of melon, as affected with TSSM under greenhouse conditions (2016).

| Inbred lines | Vegetative growth and Flowering |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Plant length (cm) | Control | $\begin{aligned} & \text { Leaf area } \\ & \left(\mathrm{cm}^{2}\right) \end{aligned}$ | Control | No. of flowers | Control |
| Line1 | 25.08b | 31.83c | 37.49b | 55.54d | 13.83a | 15.92b |
| Line 2 | 22.83 d | 28.33e | 25.68e | 63.52a | 6.66d | 10.33d |
| Line 3 | 14.41g | 24.59f | 25.14 f | 39.60g | 9.49b | 17.33a |
| Line 4 | $17.66 f$ | 19.92g | 31.27c | 56.54c | 7.16c | 11.33c |
| Line 5 | 24.83c | 30.42d | 24.98g | 50.94e | 5.24e | 7.67e |
| Line 6 | 21.83e | 32.83b | 28.43d | 47.48f | 5.50e | 7.59e |
| Line 7 | 27.08a | 42.66a | 41.26a | 61.91b | 3.08 f | 7.75e |

Means with the same letter within each row are not significantly different from another at the $\mathbf{0 . 5 \%}$ level of probability.

Data presented in Table (3) show significant differences among the hybrids of melon in plant length the tallest plant was in hybrid no. (L5 $\times \mathrm{L} 2$ ) with an average of 185.42 cm . Comparing with control, but the lowest plant length was in hybrid no. (L6xL1) with an average of 25.94 cm . But regarding to leaf area, the highest leaf area was in hybrids (L4×L1 and $\mathrm{L} 4 \times \mathrm{L} 2)$ with an average of 62.93 and $61.86 \mathrm{~cm}^{2}$ respectively comparing with control. But the lowest leaf area in hybrid (L5×L2) with an average of $23.46 \mathrm{~cm}^{2}$ comparing with control.

Table 3. Vegetative growth parameters and flowering of melon as affected with TSSM under greenhouse conditions (2017).

| Hybrids | Vegetative growth and Flowering |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Plant length (cm) | Control | $\begin{aligned} & \text { Leaf area } \\ & \left(\mathrm{cm}^{2}\right) \end{aligned}$ | Control | No. of flowers | Control |
| L3 $\times$ L1 | 32.50 f | 192.71b | 56.53b | 84.26cd | 7.66 f | 11.68d |
| L4×L1 | 30.61g | 179.63d | 62.93a | 98.13a | $7.66 f$ | 10.93e |
| L5xL1 | 113.72d | 154.50i | 48.00 d | 85.33cd | 14.78d | 17.66b |
| L6xL1 | 25.94, | $168.85 f$ | 52.26 c | 88.53bc | 6.77 g | 9.62 g |
| L7xL1 | 97.36e | 165.46 g | $36.26 f$ | 72.53g | 11.95e | 18.50a |
| L3 $\times$ L2 | 28.50h | 176.43e | 41.60 e | 78.93ef | 6.83 g | 9.78 g |
| L4×L2 | 27.99i | 159.81h | 61.86a | 91.73b | 7.55f | 10.63f |
| L5 $\times \mathrm{L} 2$ | 185.42a | 204.75a | 23.46g | 48.00h | 18.39a | 18.42a |
| L6xL2 | 153.89c | 154.37i | 38.40ef | 74.666 fg | 16.55c | 16.58c |
| L7xL2 | 177.42b | 183.67c | 41.60 e | 83.20de | 17.45b | 17.83b |

Means with the same letter within each row are not significantly different from another at the $\mathbf{0 . 5 \%}$ level by Duncan's multiple tests (1955).

But for number of flowers, no significant differences was found among hybrids ( $\mathrm{L} 4 \times \mathrm{L} 2, \mathrm{~L} 4 \times \mathrm{L} 1$ andL3 3 L 1 ) with an average of $7.55,7.66$ and 7.66 respectively. While the lowest no. of flowers was in hybrids no. ( $\mathrm{L} 6 \times \mathrm{L} 1$ and $\mathrm{L} 3 \times \mathrm{L} 2$ ) with an average of 6.77 and 6.83 respectively comparing with control ( 9.62 and 9.78 respectively). But the highest no. of flowers was in hybrid no. (L5×L2) with an average of 18.39 comparing with control.These results are in harmony with these obtained by Da Costa and Jones (1971); Gould, (1978); Metcalf and Lampman (1989) and Tallamy et al (1997)Cucurbitacins have been demonstrated to function defensively against several widespread generalist herbivores, including spider mites, several beetles, lepidopterous larvae, mice, and vertebrate. Park and Lee (2005) determined the damage caused by the two-spotted spider mite, Tetranychus urticae Koch to cucumber plants under glasshouse conditions.
Population density of TSSM mite on melon strains
Data given in Table (4) revealed that, weekly mite numbers $/ \mathrm{in}^{2}$ of Melon plants were significantly influenced by infestation of each strain. Data indicated that, strain no. (2) showed the lowest population density of accumulated moving stages with an average of 1.70 individual $/ \mathrm{in}^{2}$ during 4 weeks, then strain no. (7).

Table 4. Population density of different stages of TSSM infested melon strains under greenhouse conditions (2016).

| Average number of eggs and moving stages accumulated of mite/week |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | W1 ${ }^{\text {st }}$ |  |  | W2 ${ }^{\text {nd }}$ |  |  | W3 ${ }^{\text {rd }}$ |  |  | W4 ${ }^{\text {th }}$ |  |  | Moving Stages |  |
| lines | Egg | Imm. St. | Adu. St. | Egg | Imm. St. | Adu. St. | Egg | Imm. St. | Adu. St. | Egg | Imm. St. | Adu. St. | Total | Aver./W |
| 1 | 12.0 bc | 40.3a | 2.7 cd | 11.7a | 38.0b | 5.3 c | 29.3a | 81.0a | 10.7b | 40.3a | 87.7a | 11.3a | 277.0 | 69.3 |
| 2 | 1.7 f | 1.7 g | 0.7 f | $1.0 f$ | 1.0 g | 0.3de | 0.7 g | 0.7 g | 0.7 f | 1.0 f | 1.7 g | 0.3g | 7.0 | 1.7 |
| 3 | 7.7d | 40.0ab | 3.0c | 7.7e | 53.7a | 5.3c | 9.7 e | 62.0b | 8.3c | 13.7d | 53.3b | 9.7b | 235.3 | 58.8 |
| 4 | 13.3a | 28.0c | 16.7a | 11.3 ab | 30.3c | 7.0a | 21.0 b | 47.0c | 13.3a | 19.3b | 37.7d | 8.7d | 188.7 | 47.2 |
| 5 | 12.3b | 9.0 e | 14.3b | 7.7e | 18.0d | 0.7d | 14.3 d | 37.7d | 0.0 g | 12.3 e | 43.7c | 0.0gh | 123.3 | 30.8 |
| 6 | 7.7 d | 13.7d | 1.7e | 12.0c | 16.7e | $0.0 f$ | 16.0 c | 35.7de | 2.7 d | 14.7c | 26.7e | 2.0ef | 99.0 | 24.8 |
| 7 | 7.3e | 4.3 f | 0.71 | 9.7 d | 16.0ef | 6.3b | 5.0 f | 6.7 f | 1.0 e | 13.7d | $20.0 f$ | 2.7e | 57.7 | 14.4 |

Imm. St. = Immature stages, Adu. St. = Adult stages, Aver. $/ \mathbf{W}=$ Average/week.

The population density was 14.42 individual $/ \mathrm{in}^{2}$ for all stages. while the highest population density was in strains no. (1, 3 and 4) (69.30, 58.80 and 47.20 individual $/ \mathrm{in}^{2}$ ) respectively for all mite stages. Whereas the population density increased gradually for first week to fourth weeks and the highest average of immature moving stages was in strain (1) (87.70 individual $/ \mathrm{in}^{2}$ ) on fourth week by increasing number of adult stages with an average of 11.30 individual $/ \mathrm{in}^{2}$, but in strains ( 3 and 4)immature moving stages were reached in the third week to 62.00 and 47.00 individual $/ \mathrm{in}^{2}$ respectively, but the average number of population density of all weeks were 58.83 and 47.16 respectively for strains ( 3 and 4 ). While in strain (5) average of the population density of all mite moving stages was 30.80 individual $/ \mathrm{in}^{2}$. But the accumulated average of population moving stages density in strain (6) was 24.80 individual $/ \mathrm{in}^{2}$. In the end, total number of immature moving stages and adult stages were beginning to increase from the third week to the fourth week in all melon strains. These results are in harmony with those obtained by Mansour et al (1987), recorded the resistance of 32 melon lines to Tetranychus cinnabarinus on fourth-leaf stage, no mites were found on two lines, and on a third line very few mites were observed. All three lines also had significantly low mite counts at the fourth-leaf stage. The results suggest that there is a definite variation among melon lines in resistance to mite infestation.Data in Table (5) showed that,
all hybrid plants explained three levels of infestation, the first: high level of infestation and this was in hybrids (L6×L2, L5 $\times \mathrm{L} 2$ and $\mathrm{L} 7 \times \mathrm{L} 1$ ) and accumulated population density of total moving stages with an average of 80.70, 70.60 and 61.40individual/ $\mathrm{in}^{2}$ respectively in hybrid (L6×L2).

Table 5. Population density of different stages of T. urticae infested melon hybrids, under greenhouse conditions (2017)

| Average number of eggs and moving stages accumulated of mite/week |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Hybrids | W1 ${ }^{\text {st }}$ |  |  | W $2^{\text {nd }}$ |  |  | W3 ${ }^{\text {rd }}$ |  |  | $W 4^{\text {th }}$ |  |  | Moving Stages |  |
|  | Egg | $\begin{gathered} \text { Imm. } \\ \text { St. } \end{gathered}$ | $\begin{gathered} \text { Adu. } \\ \text { St. } \\ \hline \end{gathered}$ | Egg | $\begin{gathered} \text { Imm. } \\ \text { St. } \end{gathered}$ | Adu. St. | Egg | $\begin{gathered} \text { Imm. } \\ \text { St. } \end{gathered}$ | Adu. St. | Egg | $\begin{gathered} \text { Imm. } \\ \text { St. } \end{gathered}$ | $\begin{array}{\|c} \hline \text { Adu. } \\ \text { St. } \end{array}$ | Total | Aver./W |
| $\mathbf{L} 3 \times$ L1 | 0.7g | 1.0h | 0.7fg | 3.0gh | 4.7 fg | 1.0fg | 3.3f | 4.7 g | 0.7i | 2.0 fg | 2.7 f | 0.3gh | 15.7 | 3.9 |
| L4 $\times$ L1 | 0.0h | 1.0h | 0.0hi | 3.3g | 4.0fgh | 1.0 fg | 2.7 g | 4.3gh | 1.0gh | 1.0hi | 2.0gh | 0.0hi | 13.3 | 3.3 |
| L5 $\times$ L1 | 11.0b | 19.3b | 4.3b | 14.7d | 48.7c | 8.7e | 19.7d | 15.0e | 6.3e | 22.7d | 45.7d | 24.3bc | 172.3 | 43.1 |
| L6 $\times$ L1 | 0.7g | 1.3 fg | 1.0ef | 2.0 i | 2.0ij | 0.7gh | 2.0gh | 1.7j | 1.0gh | 1.3 gh | 2.3fg | 0.7g | 10.7 | 2.7 |
| L7xL1 | 9.3c | 15.0c | 3.7bcd | 18.0b | 26.7d | 30.3a | 34.7c | 50.3c | 23.7b | 64.7a | 71.3a | 24.7b | 245.7 | 61.4 |
| L3 $\times$ L2 | 0.0h | 1.7f | 1.0ef | 1.7ij | 3.0hi | 0.7gh | 3.3 f | 3.7hi | 1.3fg | 1.0hi | 2.7 f | 0.7g | 14.7 | 3.7 |
| L4×L2 | 1.3 f | 1.3 fg | 0.3fgh | 4.7 f | 5.7f | 1.3 f | 3.3 f | 6.3 f | 2.0 f | 2.7 f | 2.7 f | 1.3 f | 21.0 | 5.3 |
| L5 $\times$ L2 | 4.0de | 6.7e | 4.0bc | 10.7e | 24.3e | 12.7d | 86.3a | 89.3a | 41.7a | 40.0 c | 65.3b | 38.3a | 282.3 | 70.6 |
| L6xL2 | 23.0 a | 27.0a | 9.7 a | 16.3 c | 84.7a | 22.7b | 49.3b | 75.3b | 18.3c | 46.0 b | 64.0bc | 21.0d | 322.7 | 80.7 |
| L7xL2 | 4.3d | 10.7d | 1.7e | 31.3a | 67.3b | 14.0c | 11.3e | 32.7d | 10.0d | 9.7e | 19.3e | 5.0e | 160.7 | 40.2 |

Imm. St. $=$ Immature stages, Adu. St. $=$ Adult stages, Aver. $/ \mathbf{W}=$ Average/week.
Means with the same letter within each row are not significantly different from another at the $\mathbf{0 . 5 \%}$ level by Duncan's multiple tests (1955).

Average number of eggs was increased in $2^{\text {nd }}$ and $3^{\text {rd }}$ week with an average of 16.30 and $49.30 \mathrm{egg} / \mathrm{in}^{2}$, then decreased slightly in $4^{\text {th }}$ week ( 46.00 egg $/ \mathrm{in}^{2}$ ) while, average number of immature stages in $2^{\text {nd }}$ week reached 84.70individual $/ \mathrm{in}^{2}$ and also decreased in $3^{\text {rd }}$ and $4^{\text {th }}$ week ( 75.30 and 64.00 individual $/ \mathrm{in}^{2}$ ) and average number of adult stages was increased in $2^{\text {nd }}$ week comparing with other weeks with an average of 22.70 individual/in ${ }^{2}$. But in hybrid (L5 $\times$ L2) average number of egg, moving stage and adult stage of mites was increased in $3^{\text {rd }}$ week with an average of 86.30 egg $/ \mathrm{in}^{2}, 89.30$ and 41.70 individual $/ \mathrm{in}^{2}$, respectively and these stages were decreased in $4^{\text {th }}$ week, thus could be due to the severe damage to melon leaves. On the other hand, average numbers of egg, immature stages and adult stages was suddenly increased gradually in $4^{\text {th }}$ week in hybrid no. (L7×L1) which recorded $64.70 \mathrm{egg} / \mathrm{in}^{2}, 71.30$ and 24.70 individual $/ \mathrm{in}^{2}$,
respectively. The second: medium level of infestation was in hybrids (L5 $\times \mathrm{L} 1$ and $\mathrm{L} 7 \times \mathrm{L} 2$ ) and accumulated population density of total moving stages with an average of 43.10 and 40.20 individual $/ \mathrm{in}^{2}$ in hybrid no. (L5 5 L 1 ). Average number of eggs, immature stages and adult stages were increased in $4^{\text {th }}$ week with an average of 22.70 egg $/ \mathrm{in}^{2}, 45.70$ and 24.30 individual $/ \mathrm{in}^{2}$, respectively. While in hybrid no. (L7×L2) average numbers of eggs, immature stages and adult stages were increased in $2^{\text {nd }}$ week with an average of $31.30 \mathrm{egg} / \mathrm{in}^{2}, 67.30$ and 14.00 individual $/ \mathrm{in}^{2}$ respectively. The third: low level of infestation was in hybrids (L6xL1, L4×L1, L3×L2, $\mathrm{L} 3 \times \mathrm{L} 1$ and $\mathrm{L} 4 \times \mathrm{L} 2$ ) with accumulated population density of total moving stages with an average of $2.70,3.30,3.70,3.90$ and 5.30 individual $/ \mathrm{in}^{2}$ in hybrid (L6×L1) numbers of immature moving stages slightly stable in $1^{\text {st }}$, $2^{\text {nd }}, 3^{\text {rd }}$ and $4^{\text {th }}$ week with an average $1.30,2.00,1.70$ and 2.30 individual $/ \mathrm{in}^{2}$ respectively.In hybrid no. (L3×L1 and L4×L2) the immature moving stages had highly appeared comparing with all stages of mite. In hybrid (L3×L1) recoded immature moving stages 4.70 individual $/$ in $^{2}$ in $2{ }^{\text {nd }}$ and $3^{\text {rd }}$ week, but hybrid no. (L4×L2) recoded average immature moving stages of 5.70 individual/ $\mathrm{in}^{2}$ in $2^{\text {nd }}$ week while in $4^{\text {th }}$ week recorded 6.30 individual $/ \mathrm{in}^{2}$. While in hybrids ( $\mathrm{L} 4 \times \mathrm{L} 1$ and $\mathrm{L} 3 \times \mathrm{L} 2$ ) average number of moving stages was still low in all weeks but increased slightly in $2^{\text {nd }}$ and $3^{\text {rd }}$ week with an average of 4.00 and 4.30 individual $/ \mathrm{in}^{2}$ and 3.00 and 3.70 individual $/ \mathrm{in}^{2}$, respectively, and the lowest population density of all stages of mite was recorded in hybrid no. (L6 $\times \mathrm{L} 1$ ) during all weeks. Therefore, the population density in hybrids ( $\mathrm{L} 6 \times \mathrm{L} 1, \mathrm{~L} 4 \times \mathrm{L} 1, \mathrm{~L} 3 \times \mathrm{L} 2, \mathrm{~L} 3 \times \mathrm{L} 1$ and $\mathrm{L} 4 \times \mathrm{L} 2$ ) was decreased clearly, so these hybrids were considered resistant to infestation of T. urticae. This is due to the host plant characteristics and chemical contents and they are considered important factors when exploring integrated pest management for the two spotted spider mites, T. urticae. Shoorooei et al (2013) reported that, the number of eggs laid by each female per day showed significant differences between genotypes and the lowest number of eggs was laid on 'Darunghermez' and 'Dastanbu 1', while the highest number of eggs was laid on 'Garmsari' and 'Zard-khareji. The activities of both peroxidase and polyphenol oxidase increased in response to infestation by T. urticaein the resistant genotypes ('Dastanbu 1' and 'Darunghermez').The resistant melon genotypes identified in this study may
provide new sources of resistance against $T$. urticaein breeding programmes. Negin et al (2013) studied The effect of Tetranychus urticae on two host plant species including eight genotypes of melon and four genotypes of cucumber, and found that, the highest mortality percentage of immature stages of T.urticae was recorded on Ananasi and the lowest was recorded on Super sultan. Comparison of the data collected in their study revealed that the mites had considerably better performance on cucumber genotypes than melon genotypes, so they assumed that cucumber is the preferable host species for T. urticae. The use of preferable and resistant host plants is helpful in crop rotation and it will be one of the beneficial strategies to integrated pest management programmes.

## Evaluation of some horticultural characters of melon strains: Vegetative growth

Data obtained on seven melon strains evaluated during 2016 and 2017 summer seasons are presented in Table (6). Main stem length of the cultivated genotypes ranged from 427.83 to 158.33 cm . The line (7) gave the highest value of plant length. but line (4) gave the lowest value of main stem length and there was no significant differences between it and line (4) in the two seasons. Concerning, leaf area, it ranged from 172.54 to $32.16 \mathrm{~cm}^{2}$ data showed that, line (5) gave the highest leaf area. On the contrary line (2) gave the lowest leaf area and there was no significant differences between it and lines (1-3-4-6).These results are in agreement with Hussein and Selim (2014)

## Fruit quality and total yield

Table (6) showed significant differences among the inbred lines for some fruit characters, which are very important for breeders to produce hybrids with high quality. Fruit weight ranged from 1381.7 to 768.3 g. Data showed that, line (4) gave the highest value of fruit weight on the other hand inbred (6) gave the lowest value with no significant differences between it and lines (2-7).Concerning fruit length, there were significant differences among melon lines. line (3) gave the highest value while, line (1) gave the lowest value. Fruit diameter, data in Table (5) showed that, there were significant differences among lines. Line (4) gave the highest value of fruit diameter but line (2) gave the lowest value.

Table 6. Plant length, leaf area, fruit weight, fruit length, fruit diameter, flesh thickness, fruit cavity, TSS and total yield of some melon inbred lines evaluated (data are combined across 2016-2017 seasons).

| Inbred lines | Plant length (cm) | Leaf area ( $\mathrm{cm}^{2}$ ) | Fruit weight <br> (g) | Fruit length (cm) | Fruit diameter | Flesh thickness | Fruit cavity (cm) | TSS | Total yield g/plant |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| L1 | 325.00c | 37.69bc | 968.3 bc | 11.36ef | 9.66e | 3.00b | 4.03e | 8.20c | 2875.0c |
| L2 | 210.67e | 32.16c | 921.0bcd | 11.93e | 11.96b | 3.03b | 3.10f | 9.10a | 2741.0cd |
| L3 | 309.00d | 39.85bc | 1083.3b | 15.80a | 10.90d | 3.03b | 5.20c | 6.10d | 3116.7b |
| L4 | 158.33f | 40.42bc | 1381.7a | 15.06b | 13.76a | 3.50a | 6.00b | 6.10d | 4015.0a |
| L5 | 358.67b | 172.54a | 1103.7b | 13.90c | 13.90a | 3.46a | 7.10a | 9.10a | 3103.3b |
| L6 | 319.00c | 34.18bc | 768.3de | 13.90c | 11.10 cd | 3.10b | 4.10e | 6.10d | 2218.3e |
| L7 | 427.83a | 49.15b | 881.7cd | 13.06d | 11.36c | 3.50a | 4.80d | 9.00 ab | 2565.0d |

Means with the same letter within each row are not significantly different from another at the $\mathbf{0 . 5 \%}$ level by Duncan's multiple tests (1955).

Regarding flesh thickness, it was found that inbred (4) gave the highest value while line (1) gave the lowest value with no significant differences between it and line (2) during the two seasons. Fruit diameter ranged from ( 13.90 to 9.66 cm ). It was found that line (5) gave the highest value and there was not significant differences between it and line (5) across the two seasons. Regarding flesh thickness which is very important for researchers and growers in selection of melon inbred lines where they are looking for the highest value, inbred (4) gave the highest value and there were no significant differences between it and lines $(5,7)$. While, line (1) gave the lowest value with no significant differences between it and lines ( 2 , 3, 6). Concerning, fruit cavity this character is very important for researchers to select genotypes of melon which has low value of fruit cavity. Fruit cavity ranged from 7.10 to 3.10 cm showing significant differences among lines. Line (5) gave the highest value but, line (2) gave the lowest values. Total soluble solids (TSS) was ranged from $9.10 \%$ to $6.10 \%$ showing significant differences among lines were line (2) gave the highest value with no significant differences between it and lines $(5,7)$ while, inbred (3) gave the lowest value with no significant differences between it and lines (4 and 6). Total yield is the most important character for breeders and growers to produce and select melon genotypes. Total yield ranged from 4015.0 to 2218.3 kg . Line (4) gave the highest value of total yield. On the
contrary, inbred (6) gave the lowest value across the two seasons. These results are in agreement with those reported by Hussein and Selim (2014)
Evaluation of some horticultural characters of hybrids Vegetative growth

Table (7) show significant differences among the hybrids for some characters, Main stem length of the cultivated hybrids ranged from 425.33 to 215.83 cm . Data showed that hybrid (L7×L2) gave the highest value compared with the control but hybrid (L7xL1) gave the lowest value. Regarding leaf area ranged from 529.86 to 119.28 showing significant differences among the hybrids, where hybrid (L7×L2) gave the highest leaf area while, hybrid (L3×L2) gave the lowest value compared with the control.

Table 7. plant length, leaf area, fruit weight, fruit length, fruit diameter, flesh thickness, fruit cavity, tss and total yield of some melon hybrids evaluated during (data are combined across 2017-2018 seasons).

| Hybrids | Plant length (cm) | Leaf area ( $\mathrm{cm}^{2}$ ) | Fruit weight (g) | Fruit length (cm) | Fruit <br> diameter <br> $(\mathrm{cm})$ | Flesh thickness $(\mathrm{cm})$ | Fruit cavity (cm) | TSS | Total yield kg/fed |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| L3 $\times$ | 320.67e | 153.46 i | 1160.0ef | 12.74e | 11.80abcd | 3.83c | 5.54c | 6.43e | 13140de |
| L4×L1 | 425.33a | 254.46 f | 1618.0c | 15.11cd | 15.45ab | 4.16 | 7.42a | 11.93a | 18605.2bc |
| L5 $\times$ L1 | 317.50e | 485.39 b | 77 | 14.32d | 10.48d | 3.30 d | 3.10e | 9.53 b | g |
| L6xL1 | 376 | 192.16 g | 1120.7 | 15. | 13.16a | 3.7 | 5.80bc | 8.06cd | 1361 |
| L7 | 23 | 42 | 985.0fg | 15 | 10. | 3.06 | 6. | 9.20 bc | 12006.8ef |
| L3 $\times$ | 215.83g | 11 | 610 | 13.10e | 9.33 cd | 3.10de | 3.16e | 6.33 e | 7160.8h |
| $\mathrm{L} 4 \times \mathrm{L} 2$ | 319.00e | 187.50 h | 1244.0de | 18.12b | 14.12abc | 3.76c | 5.81bc | 11.81 a | 13200.2d |
| $\mathbf{L 5 \times L} 2$ | 370.00c | 353.18 e | 2423.3a | 19.11 | 16.33a | 4.46a | 7.11a | 8.40bcd | 21000a |
| L6xL2 | 318.50e | 421.99 c | 1417.7cd | 18.11b | 13.44abc | 4.43a | 5.10d | 9.26b | 17334cd |
| $\mathbf{L} 7 \times$ L2 | 346.19d | 529.86 a | 1993.3b | 17.75b | 15.46ab | 4.46a | 6.11b | 7.40de | 18973.2ab |
| Control <br> (Galia) | 370.33c | 187.50 h | 800.0 d | 13.70d | 10.85d | 3.11b | 5.98b | 8.33b | 12950.3e |

Means with the same letter within each row are not significantly different from another at the $\mathbf{0 . 5 \%}$ level by Duncan's multiple tests (1955).

## Fruit quality and total yield

The results in Table (7) cleared the differences between the hybrids. Concerning fruit weight, it ranged from 2423.3 to 610.0 g . The hybrid
(L5 5 L2) gave the highest value compared with the control but hybrid ( $\mathrm{L} 3 \times \mathrm{L} 2$ ) gave the lowest value across the two seasons. Regarding fruit length, it was found that hybrid ( $\mathrm{L} 5 \times \mathrm{L} 2$ ) gave the highest value but hybrid (L3×L2) gave the lowest value compared with the control. Fruit diameter ranged from 16.33 to 9.33 cm , there were significant differences among hybrids where hybrid (L5×L2) gave the highest value but hybrid (L3×L2) gave the lowest value. There were significant differences among the hybrids for flesh thickness where hybrid (L7×L2) gave the highest value with no significant differences between it and hybrids (L5×L2 andL6×L2) while, hybrid (L7×L1) gave the lowest value with no significant differences between it and hybrid (L3×L2). Concerning fruit cavity which is very important character in melon, it ranged from 7.42 to 3.10 cm there were significant differences among hybrids where hybrid (L4×L1) gave the highest value while hybrid ( $\mathrm{L} 5 \times \mathrm{L} 1$ ) gave the lowest value with no significant differences between it and hybrid (L3×L2). TSS ranged from $11.93 \%$ to $6.33 \%$ showing significant differences among the hybrids the hybrid (1) gave the highest value with no significant differences between it and hybrid (L4×L1) while hybrid (L3×L2) gave the lowest value with no significant between it and hybrid (L3×L1). Our results showed that the hybrid (L5 $\times$ L2) gave the greatest total yield with no significant differences between it and hybrid ( $\mathrm{L} 7 \times \mathrm{L} 2$ ). On the contrary, hybrid (L3 $\times \mathrm{L} 2$ ) gave the lowest value. These results are in partial agreement with Hussein and Selim (2014)

## Genetic studies

## Estimates of heterosis over mid-parents

Data obtained on heterosis over mid-parent are presented in Table (8). Hybrid ( $\mathrm{L} 4 \times \mathrm{L} 1$ ) gave the highest positive percentage of heterosis over mid-parent for the character plant length. All hybrids gave highly positive percentage of heterosis value over mid-parent for leaf area. Concerning fruit weight, Hybrid (L5 $\times \mathrm{L} 2$ ) gave the highest positive percentage of heterosis value over mid-parent which means partial dominance for this character towards the high parent but hybrid (L4×L2) gave the lowest value. heterosis over mid-parent for flesh thickness ranged from $44.54 \%$ to $2.16 \%$ where hybrid (L6×L2) gave the highest positive percentage of heterosis value over
mid-parent which means partial dominance for this character towards the high parent while, hybrid ( $\mathrm{L} 5 \times \mathrm{L} 1$ ) gave the lowest value.
Table 8. Estimates of heterosis (\%) for some characters in melon.

| Crosses | Plant length (cm) | Leaf area | Fruit weight | Flesh thickness | Total yield | No. of mite eggs | No of mite immature stages | No. of mite adult. stage |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| L3×L1 | 19.72* | 339.39* | 22.79 NS | 27.03* | 367.9** | -90.3* | -94* | -94.3 ${ }^{\text {NS }}$ |
| L4×L1 | 75.99** | 551.54** | $37.70{ }^{\text {NS }}$ | 28.00* | 440.1** | $-96.6{ }^{\text {NS }}$ | -96.8 ${ }^{\text {NS }}$ | $-100{ }^{\text {NS }}$ |
| $\mathbf{L 5 \times L 1}$ | -7.11* | 361.77* | $-24.93{ }^{\text {NS }}$ | 2.16* | 213.8** | -13.9* | -30.5* | 329.1* |
| L6xL1 | 16.87* | 434.74** | $29.06{ }^{\text {NS }}$ | 23.28** | 434.5** | -95.2* | -95.9* | -90.1* |
| L7×L1 | -37.21* | 870.88** | 6.48* | -5.85* | 341.4** | 139.5* | 32.52* | $252.2{ }^{\text {NS }}$ |
| $\mathbf{L} 3 \times \mathrm{L} 2$ | -16.93* | 231.28* | $-39.13{ }^{\text {NS }}$ | 2.31* | 144.5** | -86.4* | -90.3* | -86.6* |
| L4×L2 | 36.52* | 367.17** | $0.93{ }^{\text {NS }}$ | 15.16* | 270.2** | -83.8* | -94.1* | -85.4* |
| $\mathbf{L 5 \times L 2}$ | 10.83* | 232.57* | 121.60** | 37.44* | 575.2** | 207.7** | $34.71{ }^{\text {NS }}$ | $693.0{ }^{\text {NS }}$ |
| L6×L2 | 1.43* | 1040.05** | 53.13** | 44.54* | 549.8** | 224.6** | 60.00* | 259.9* |
| L7×L2 | -6.03* | 1090.69** | 102.88** | 36.60* | 567.9** | -29.3 ${ }^{\text {NS }}$ | $-47.3^{\text {NS }}$ | $-19.00^{\text {NS }}$ |

NS and *: insignificant and significant at 0.05 level of probability, respectively.

Similar results were reported by several investigators for several characters (Feyzianet al 2009 and Fernandez-Silva et al 2009 and Hatem et al 2014). Total yield heterosis value over mid-parent ranged from $567.9 \%$ to $144.5 \%$ Hybrid (L7×L2) gave the highest positive percentage of heterosis value over mid-parent meanwhile, hybrid (L3×L2) gave the lowest value. These results are in agreement with Hussein and Selim (2014), who found that, all crosses ( $10 \mathrm{~F}_{1}$ 's), significantly exceeded their respective MP values, suggesting the presence of dominance towards high parent in total yield. Heterosis over mid-parent for number of spider mite eggs ranged from 224.6 \% to -13.9 Hybrid (L6×L2) gave the highest positive percentage of heterosis value over mid-parent on the other hand hybrid (L5 $\times$ L1) gave the lowest negative value which considered the best. Concerning, number immature stages Hybrid (L6×L2) gave the highest positive percentage of heterosis value over mid-parent meanwhile, hybrid (L4×L1) gave the lowest value. Heterosis over mid-parent for adult stages ranged from $693.0 \%$ to 100 Hybrid (L5×L2) gave the highest positive percentage of heterosis value over mid-parent meanwhile, hybrid (L4×L1) gave the lowest negative value which considered the best.

## Analysis of variance and mean squares for the mating design Line $\times$ Tester:

Table (9) shows significant mean squares due to genotypes for all studied traits except, flesh thickness of testers were not significant. These results are in agreement with Hussein and Selim (2014) who found significant or highly significant mean squares due to genotypes in all studied traits except, fruit shape index also Hatem et al 2014 who found that, the analysis of variance showed significant variation in most studied characters, indicating a wide range of variability among the studied genotypes.

Table 9. Analysis of variance and mean squares for some melon characters infected by TSSM.

| SOV | df | Mean sum of squares |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Plant length (cm) | Fruit weight | Flesh thickness | Total yield | No. of mite eggs | No. of <br> mite <br> immature <br> stages | No. of mite adult Stages |
| Genotypes | 16 | 16664.05* | 638517.43* | 0.90* | 3677505.98* | 1078.92* | 711.21* | 367.30* |
| Lines | 4 | 12388.19* | 723549.53* | 1.16* | 4457996.62* | 1645.47* | 1080.22* | 628.12* |
| Testers | 1 | 44175.38* | 216580.03* | $0.15{ }^{\text {NS }}$ | 1138411.20* | 974.70* | 270.53* | 43.20* |
| $\mathbf{L} \times \mathrm{T}$ | 4 | 767910.69* | 12588325.47* | 110.74* | 96777566.22* | 846.93* | 450.68* | 290.72* |
| Error | 32 | 5.87 | 5163.23 | 0.02 | 80643.14 | 43.33 | 84.61 | 91.51 |

NS and *: insignificant and significant at 0.05 level of probability, respectively.

## Components of variance, broad sense heritability, components of genetic variance and proportional contribution

Table (10) presents genotypic and phenotypic variance ( $\sigma^{2} \mathrm{~g}$ and $\sigma^{2}$ prespectively), broad sense heritability (BSH), genotypic and phenotypic coefficient of variance (G.C.V. \% and P.C.V. \%) and the ratio of G.C.V. /P.C.V. $\sigma^{2} \mathrm{~g}$ and $\sigma^{2} \mathrm{p}$ for all the studied traits show high values except $\sigma^{2} g$ and $\sigma^{2}$ p for flesh thickness show low values. All the studied traits show low values of difference between phenotypic and genotypic variance. Also, the G.C.V./P.C.V. ratios for the studied traits show high values (close to unity). Estimates of BSH were high for all studied traits indicating minor effect of the environment on these characters while; BSH for number of adult was medium which indicated that, the environment and genetics had equal effect on this character.

Table 10.Components of variance, heritability, (BSH\%), components of genetic variance and proportional contribution for some melon characters infected by TSSM.

| SOV | Plant length (cm) | Fruit weight | Flesh thickness | Total yield | No. of mite eggs | No. of mite immature stages | No. of mite <br> adult <br> stages |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Components of variance |  |  |  |  |  |  |  |
| $\sigma^{2} \mathrm{~g}$ | 5553.63 | 211438.33 | 0.29 | 1198954.28 | 348.04 | 260.73 | 91.93 |
| $\sigma^{2} \mathrm{p}$ | 5556.79 | 216601.55 | 0.31 | 1279597.42 | 391.37 | 322.66 | 183.44 |
| BSH | 99.94 | 97.62 | 94.66 | 93.70 | 88.93 | 96.97 | 50.12 |
| G.C.V.\% | 8.25 | 15.19 | 5.60 | 12.38 | 36.48 | 26.34 | 57.36 |
| P.C.V.\% | 8.25 | 15.38 | 5.76 | 12.79 | 38.68 | 29.30 | 81.03 |
| G.C.V./P.C.V. | 1.00 | 0.99 | 0.97 | 0.97 | 0.94 | 0.90 | 0.71 |
| Components of genetic variance |  |  |  |  |  |  |  |
| $\sigma^{2}$ Lines (L) | 50455.39 | 1971165.21 | 18.26 | 15459887.66 | 107.42 | 129.91 | 56.23 |
| $\sigma^{2}$ Testers(T) | 120773.39 | 822316.77 | 7.37 | 6404340.83 | -1.25 | -12.88 | -16.50 |
| $\sigma^{2} \mathrm{GCA}$ (average) | 19240.84 | 305860.09 | 2.82 | 2395397.01 | 13.13 | 15.00 | 5.65 |
| $\boldsymbol{\sigma}^{\mathbf{2}} \mathrm{SCA}(\mathrm{L} \times$ T) | 256393.00 | 4181490.80 | 36.91 | 1064620.89 | 320.52 | 141.62 | 66.40 |
| $\sigma^{2} \mathbf{G C A} / \sigma^{2} \mathrm{SCA}$ | 0.034 | 0.043 | 0.033 | 0.033 | 0.018 | 0.05 | 0.037 |
| Proportional contribution (\%) |  |  |  |  |  |  |  |
| Lines (L) | 18.51 | 28.25 | 32.36 | 29.67 | 37.91 | 46.152 | 42.75 |
| Tester (T) | 16.68 | 2.10 | 1.025 | 1.84 | 5.66 | 2.688 | 0.73 |
| (L x T) | 64.81 | 69.65 | 66.61 | 68.49 | 56.43 | 51.16 | 56.52 |

Data obtained in Table 9 show that, lines gave variances higher than testers for all the studied traits except Plant length variances testers were higher than lines. The results in Table 10 indicated that, GCA and SCA variances showed a wide range of variation for all studied characters. In all studied traits, SCA variances were greater than GCA variances and the ratio of $\sigma^{2} \mathrm{GCA} / \sigma^{2} \mathrm{SCA}$ were found less than unity except plant length equal unity. The higher magnitude of SCA variances indicates the preponderance of non-additive gene action over the additive on for these characters. Several researchers reported the importance of both additive and non-additive effects in the genetic control of yield components in melon (Barros et al 2011, Dehghani et al 2012). The results in Table (10) cleared that, testers had lower proportional contribution than lines and the interaction lines x testers for all studied traits which revealed predominance influence for these traits.

However, the contribution interaction (Line x Tester) played higher role than the individual contribution for all traits.
General combining ability (GCA) effects
It is well known that GCA is a function of additive gene effect and the additive portions of epistatic variance, while SCA is the function due to non- additive gene effects and the remainder of epistatic variance (Matzinger et al 1959). Estimation of GCA effects of lines and testers represented that some of single line was exhibited good general combining ability for all the traits (Table 11).

Table 11. Estimation of parental general combining ability (GCA) effects for some melon characters infected by TSSM.

| Genotypes | Plant <br> length <br> (cm) | Fruit weight | Flesh thickness | Total yield | No. of mite eggs | No. of mite immature stages | No. of mite adult stages |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Lines (Females) |  |  |  |  |  |  |  |
| L3 | -5.83* | -132.63* | -0.03 ${ }^{\text {NS }}$ | -415.97** | -16.67* | -17.20* | -10.63* |
| L4 | -47.91** | -453.30** | -0.66* | -1023.30** | 24.67** | 25.07** | 12.53** |
| L5 | -34.74** | 180.37** | -0.08 ${ }^{\text {NS }}$ | 218.70** | $1.33{ }^{\text {NS }}$ | $-2.43{ }^{\text {NS }}$ | 8.03* |
| L6 | 24.14** | -65.47* | 0.27* | $-67.13{ }^{\text {NS }}$ | $4.50{ }^{\text {NS }}$ | 5.23* | $-0.80{ }^{\text {NS }}$ |
| L7 | 64.34* | 471.03** | 0.50* | 1287.70* | -13.83* | -11.27* | -9.13* |
| S.E. ( $\hat{\mathrm{g} i}-\hat{\mathrm{g} j}$ ) | 1.40 | 41.49 | 0.09 | 167.32 | 3.80 | 4.15 | 5.52 |
| Testers (Males) |  |  |  |  |  |  |  |
| L1 | -38.37** | -84.63** | -0.07* | -190.63** | $5.73{ }^{\text {NS }}$ | $2.87{ }^{\text {NS }}$ | $-1.20{ }^{\text {NS }}$ |
| L2 | 38.37** | 84.63** | 0.07* | 190.63* | -5.73 NS | $-2.87{ }^{\text {NS }}$ | $1.20{ }^{\text {NS }}$ |
| S.E. ( g i - $\hat{\mathrm{g}} \mathbf{j}$ ) | 1.08 | 2.94 | 0.06 | 129.61 | 2.94 | 3.21 | 4.28 |

NS, *, **: insignificant, significant and highly significant at $0.05 \%$ probability level.

Among the lines, in this concern, lines 7 and 2 was good general combiners which gave significant and positive GCA value for plant length, fruit weight, total yield while gave negative GCA for number of eggs, immature stages and adult stage. Regarding line 3 was good general combiner for number of eggs, immature stages and adult stage. But not good general combiner for the rest characters. Line 4 was not good general combiner for all studied traits. These results are in agreement with Hussein and Selim (2014) who estimated GCA effects of individual parental genotypes in the $F^{\prime}{ }_{1 S}$ generation and found them significant or highly
significant for most studied traits and Hatem et al 2014 who found that significant and positive GCA values are desirable for most of studied characters on melon.
Specific combining ability effect
The potentiality of crossing between specific parents were detected by estimating specific combining ability (SCA) effects of each $\mathrm{F}_{1}$ cross combination for all studied traits (Table 12).

Table 12. Estimation of specific combining ability (SCA) effects of melon hybrids infected by TSSM for some traits.

| Crosses | Plant <br> length <br> (cm) | Fruit weight | Flesh thickness | Total yield | No. of mite eggs | No. of mite immature stages | No. of mite adult Stages |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| L3 $\times$ L1 | -38.21** | -126.63** | $-0.04{ }^{\text {NS }}$ | $-203.47{ }^{\text {NS }}$ | $5.40{ }^{\text {NS }}$ | 9.89* | $-1.37{ }^{\text {NS }}$ |
| L4×L1 | 1.63* | -272.30** | -0.22* | -519.13** | 1.23 NS | -7.61* | $-3.20{ }^{\text {NS }}$ |
| L5xL1 | 4.21* | -188.30** | $0.05{ }^{\text {NS }}$ | -510.97** | -15.27* | $5.89{ }^{\text {NS }}$ | -1.53 NS |
| L6xL1 | -8.51* | -233.13** | -0.40* | -658.30** | -16.77* | -25.28 | -11.20* |
| L7×L1 | -4.21* | 188.30** | -0.05 ${ }^{\text {NS }}$ | 510.97** | 15.27* | -5.89 NS | $1.53{ }^{\text {NS }}$ |
| L3 $\times$ L2 | -40.88** | -820.37** | -0.61* | -1891.87** | -25.40** | -17.13** | -17.30** |
| L4×L2 | 38.21** | 126.63** | $0.04{ }^{\text {NS }}$ | $203.47{ }^{\text {NS }}$ | $-5.40 \mathrm{NS}$ | -9.89* | $1.37{ }^{\text {NS }}$ |
| $\mathbf{L 5} \times \mathrm{L} 2$ | 40.88** | 820.37** | 0.61* | 1891.87** | 25.40** | 17.13** | 17.30* |
| L6xL2 | 8.51* | 233.13** | 0.40* | 658.30** | 16.77* | 25.28** | 11.20* |
| L7×L2 | -1.63* | 272.30** | $0.22{ }^{\text {NS }}$ | 519.13** | -1.23 NS | 7.61* | $3.20{ }^{\text {NS }}$ |
| S.E. (Sij-Sik) | 1.45 | 70.11 | 0.31 | 236.63 | 6.42 | 7.45 | 9.33 |
| SE (Sij-Skl) | 1.02 | 58.67 | 0.22 | 167.32 | 3.80 | 5.87 | 7.77 |

NS,*, **: insignificant and significant at 0.05 and $0.01 \%$ probability levels respectively.

It is noticed that the most of good combinations which showed highly positive and significant SCA effects in plant length, fruit weight, total yield were resulted from the crossing (L5×L2 and L6 $\times \mathrm{L} 2$ ) while not good for number of eggs, immature stages and adult stage. Obtained data showed that the $\mathrm{F}_{1}$ crosses (L6×L1 and L3×L2) achieved good combinations which gave negative SCA effects for number of eggs, immature stages and adult stage but not good for plant length, fruit weight, total yield which gave negative SCA effects which means this combination were good in resistance
or spider mite tolerant. Similar findings were reported with Hussein and Selim (2014) who stated that all the studied crosses exhibited significant positive (SCA) effect for total yield and Hatem et al 2014 on melon.
6- Estimates of total phenols in leaves of the melon genotypes $(\mathbf{m g} / \mathrm{g})$ :
Data in Figure (1) showed the difference among melon lines in total phenols in leaves where, phenols is one of the main methods used by the plant to resist spider mite infection. It was found that L2 gave the highest value of total phenols content and there were not significant differences between it and L3 so, we can say that, the high level of total phenols in this inbred line may reflect its resistance to the spider mite infection; on the other hand L7 gave the lowest value of total phenols content.


Fig. 1. Estimates of total phenols in leaves of the melon genotypes ( $\mathrm{mg} / \mathrm{g}$ ).

## CONCLUSION

It is concluded from the present study that, the cross (L6xL2) was the best combination for most of studied characters also their SCA effects were related to GCA effects of their parents. Moreover, this cross included both of their parents with high GCA effects for almost all the studied characters. Therefore, these genotypes of high significant GCA and SCA effects might be exploited in future breeding program.

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## الانتخاب بين بعض سلالات الثمام لمقاومة العنكبوت الأحمر ذو البقعتين

## Tetrany chusurticae Koch

> عمرو أحمد السيد أحمد ؛ أحمد عيد عبد المجيد محجوب‘ و هبه محمد إمام محمد سليمانَ ا. قسم تربية الخضر والنباتات الطبية معهد بحوث البساتين .الدقي. الجيزة.
> r. ب. قس وقاية النبات، كلية الزراعة، جامعة عين شمس.

 النتائـج إلبي أن كل قياسات النمو للنبات تأثرت معنويا بالإصابة بالأكاروس وكانت مساحة الورقة هي الأكثر تأثرا









 وأخيرا المستوي الثالث ( منخفض الإصابة) حيث سجل في الهجن رقم (L6×L1)، (L4×L1, (L3×L2)، (L3×L1) و (L4×L2) وكان متوسط الكثافة العدلدية التركمية للأطوار المتحركة ،
 أعتبرت مقاومة للإصابة بأكاروس العنكبوت الأحمر ني البقعتين. بلالنسبه للصغات البستانية أظهرت النتائـج أن (المحصول الكلى ترلوح بين 4015.0, 2185.0 جم/النبات واعطت السلالة ؛ أعلي محصول. كما ظهت قوة (الهجين في كل الصفات تحت اللدرسة.أيضاكفاءة التوربيث علي النطاق العريض أظهرت قيما عالية مدا بيل علبي الأثر القليل للبيئة في توريث هذه الصفات. كان التباين لكل من القدرة العامة والخاصة على الائتلاف معنويا لكل (الصفات المدروسة مدا يؤكن على أهمية كل من الفعل المضيف وغير المضيف للجبينات في وراثة هذه الصفات, أظهرت حسابات تأثيرات الثدرة الخاصة على الائتلاف للهجن المختلفة أن أفضل الإتحادات للصغات المدروسة كان في الهجن الآتية: LL5×L2) و (L6×L2 حيث أظهرت تأثبيرا معنوية في صفات طول النبات ومتوسط وزن (الثمرة والمحصول الكلي بينما الهجن (L6×L1 and L3×L2) كانت أفضل في تحمل الاصابة بالاكاروس ولهغا يكن الاستفادة بها في برامج التربية لتصسين الشمام.


