



# A STUDY OF THE GENETIC BEHAVIOUR OF SOME GENOTYPES OF MELON (*CUCUMIS MELO* L.)

Suzy M. Abdelaziz<sup>1\*</sup>, El-Eslamboly A.A.S.A.<sup>2</sup> and AbdEl-Nabi H.M.Diab<sup>1</sup>

<sup>1</sup>Cross Pollinated Vegetable Research Department, Horticulture Research Institute, ARC, Egypt.

<sup>2</sup>Vegetable Crop Production Research under Protected cultivation Department, Horticulture Research Institute, ARC, Egypt.

## Abstract

This investigation was performed during 2017-2019 in open field at Gemmezia, Gharbia government. Four parental lines of melon (*Cucumis melo* L.) were used in this study, namely: 31(P1), 111(P2), 63(P3) and 65(P4). Hybridization among the parental lines was done to obtain 6 hybrids using half diallel mating design in order to estimate the general, specific combining ability and heterosis for growth properties, flowering traits, fruit yield and related characters. The results showed high significant differences for general and specific combining ability were observed in studied traits. The ratio of GCA/SCA mean square was less than one for all the studied traits. This finding indicated that the non-additive gene action was responsible in the heritance of the studied characters. The highest positive value of GCA effects was recorded in the parental line P2 and P3 in fruit yield per plot, fruit weight and flesh thickness than all the other studied parental lines. These parental lines are considered a good general combiner in most traits and could be used them breeding programs. Furthermore, the potentiality of hybridization among previous parental lines were estimated using specific combining ability (SCA) effects of each one cross combination for all studied characters. The hybrid (P2×P3) had positive and significant SCA effects in all studied characters, except early yield. Meanwhile, the hybrid also had the highest favourable heterosis in all studied traits, except early yield, as well as had a positive potence ratio that indicated the presence of over-dominance for studied traits in the cross P2×P3 over better parental lines.

**Key words:** *Cucumis melo*, SCA, GCA, heterosis, Half diallel, Crosses, Growth properties, Fruit yield.

## Introduction

Melon (*Cucumis melo* L.) is one of the most important vegetables crops belongs to cucurbitaceous family. The species of *Cucumis melo* are a great polymorphic group including a huge number of botanical and horticultural variations (Luan *et al.*, 2010; Abdeldaym *et al.*, 2014). The fruits are highly appreciated due to their attractive flavor and sweet taste as well as their richness in vitamins, minerals, carbohydrates and fibers. Immature fruits can be directly used in salads, cooked or pickled. (Shashikumar and Pitchaimuthu, 2016). Crop improvement requires techniques for improving quality as well as inherent capacity of yield and related components. Cucurbitaceous plants may be improved through utilization of heterosis breeding (Madhu, 2012) and combining ability estimates (Zalapa *et al.*, 2006).

Genetic analysis is considered a guide line for the

\***Author for correspondence** : E-mail: Suzy\_kamel2007@yahoo.com

assessment of relative breeding potential of the parents or identifies best combiners in crops, which could be utilized either to exploit heterosis in F1 or to accumulate fixable genes to evolve new variety. Selection of parental lines on the basis of previous performance by itself does not always give the expected outcome (Golabadi *et al.*, 2015). For planned hybridization, parental selection must be by the absolute genetic information and predominance of the potential parents (Laxuman *et al.*, 2012). The select of good parents in a breeding program is considered vital factor for the producing vigor hybrids. Among the most efficient and commonly used methodologies for this purpose are diallel crossing, which offers estimates of genetic parameters, useful for the selection of genitors to be used in hybridization and in the understanding of the gene action involved in determining the characters and existence of heterosis (Cruz *et al.*, 2012). Diallel analysis is one of the fundamental methods used, this method estimates information on the general combining

ability (GCA), connected with concentration of predominantly additive genes and the specific combining ability (SCA) linked with gene on centration with non-additive effect (dominance and epistasis). Heterosis breeding plays a key role in genetic enhancement of any crop relative to yield and quality traits (Singh *et al.*, 2014). Besides, potence ratio is useful to determine the nature of dominance and its direction. The aim of this study was estimated the combinatorial and heterosis capacity displayed in experimental hybrids of melon genotypes that obtained from partial diallel cross, in order to recognize promising hybrid combinations.

## Material and Method

### Plant materials and the cultivation

This study was conducted in the open field of *Gemmezia farm*, horticulture research institute, agriculture research center during 2017 and 2019. The materials used in this experiment consist of four parental inbred lines of melon which characterized with horticultural superior and earlier was described by Daib, (2012) in his PhD thesis. They namely, 31, 111, 63 and 65. Self-pollination for the four parents was done twice to insure high degree of purity in early and late summer seasons in 2017 year. Afterward, all possible cross combinations excluded the reciprocals were done on 15<sup>th</sup> of March 2018. The ten genotypes, *i.e.* four parental lines and six single straight F1 crosses between them as well as the check variety (primal) were evaluated in March, 2019 in a randomized complete block design (RCBD) with three replications. All genotypes randomly distributed in each replicate that involve of 11 plots (four parents and six F1 hybrids and the check variety). The soil of farm was ploughed well and divided into plots. Each plot contained one row 5 m long and 5 m wide. Seedlings of melon were transplants at space 0.5 m between plants and 1 m among rows. Standard agriculture practices were followed. Therefore, each row contained 10 plants. A sample of 5 random healthy plants in each plot marked to record the following traits:

### Trait measurements

- The vegetative traits: plant length (cm), number of leaves, number of branches per plant and number of days from planting to anthesis of the first female flower.
- Yield traits: early and total yield (kg/ plot).
- Fruit characters: fruit length (cm), fruit diameter, fruit weight (g), number of fruits per plant, flesh thickness (cm) and total soluble sugar (TSS) of the mature fruits measured by handle refractometer.

### Statistical analysis

Data were subject to statistical analysis using analysis

**Table 1:** The form of the analysis of variance and the expectations of mean squares.

| S.V.             | df         | M.S.             | E.M.S  |
|------------------|------------|------------------|--|
| <b>Genotypes</b> | G-1        | M.S <sub>g</sub> | $\sigma^2 e + r \sigma^2 en$                 |
| <b>Parents</b>   | P-1        | M.S <sub>p</sub> | $\sigma^2 ep + r \sigma^2 p$                 |
| <b>Crosses</b>   | C-1        | M.S <sub>c</sub> | $\sigma^2 ec + r \sigma^2 c$                 |
| <b>Error</b>     | (r-1)(G-1) | M.S <sub>e</sub> | $\sigma^2 e$                                 |
| <b>G.C.A.</b>    | P-1        | MS <sub>g</sub>  | $\sigma^2 e + \sigma^2 s + (p+2) \sigma^2 g$ |
| <b>S.C.A.</b>    | P(P-1)/2   | MS <sub>s</sub>  | $\sigma^2 e + \sigma^2 s$                    |
| <b>Error</b>     | (r-1)(G-1) | MS <sub>e</sub>  | $\sigma^2 e$                                 |

**r:** Number of replications, **G:** Number of genotypes, **P:** Number of parents, **C:** Number of crosses, **M.S<sub>g</sub>:** mean squares of genotypes, **M.S<sub>p</sub>:** mean squares of parent, **M.S<sub>c</sub>:** mean squares of crosses, **MS<sub>g</sub>:** mean squares of GCA, **MS<sub>s</sub>:** mean squares of SCA and **M.S<sub>e</sub>:** mean squares of error.

of variance (ANOVA) with the stat soft statistical package (MSTATC) software program. The significance between means of genotypes were compared with the least significant difference L.S.D. ( $p < 0.05$ ) according to Gomez and Gomaz, (1984). The form of the analysis of variance and the expectations of mean squares are shown in (Table 1).

### Genetic analysis

General combining ability (GCA) and specific combining ability (SCA) variances and effects were assessed according to Griffing's, (1956) Method-II and Model-I (parents and F1s without reciprocal) as outlined by Singh and Chaudhary, (1985). The average degree of heterosis (ADH%) was calculated as percentage of increases of F1 performance over mid parent (M.P.) and better parent (B.P.) according to Sinha and Khanna, (1975) as the following:

$$\text{Heterosis over the Mid Parent (\%)} = (F1 - M.P. / M.P.) / 100 \quad (1)$$

$$\text{Heterosis over the better parent (\%)} = (F1 - B.P. / B.P.) / 100 \quad (2)$$

Degree of dominance (potence ratio): This parameter was determined by estimating the potence ratio value (p), according to Mather and Jinks (1982) (3)

## Results and Discussions

### Mean performance of parents and hybrids

Data presented in table 2 showed a significant differences were observed in all characters under investigation. It is clear that the parent P1 had the highly values in all traits, except flash thickness and TSS, while, the best parent was P2 in these traits compared with other parents and control. On the other hand, the parents (P2 and P4) showed the lowest values in all characters except fruit diameter, flash thickness and TSS compared

**Table 2:** Mean performances of parent and F1 hybrids for growth, yield and related characters.

| Genotypes | Vegetative growth |               |               | No. of days   |             | Yield/plot |               | Fruit characters |               |                 |              |      |
|-----------|-------------------|---------------|---------------|---------------|-------------|------------|---------------|------------------|---------------|-----------------|--------------|------|
|           | Plant length      | No. of leaves | No. of branch | Female flower | Early yield | Total (kg) | No. of fruits | Length (cm)      | Diameter (cm) | Flash thickness | Fruit weight | TSS  |
| P1        | 146.0             | 99.3          | 3.8           | 53.5          | 89.9        | 19.6       | 35.40         | 11.0             | 11.4          | 3.1             | 552.7        | 9.6  |
| P2        | 100.4             | 72.5          | 3.7           | 43.6          | 75.8        | 18.0       | 36.13         | 10.9             | 10.4          | 3.7             | 497.6        | 11.0 |
| P3        | 131.0             | 107.7         | 3.5           | 46.3          | 83.6        | 19.5       | 38.67         | 9.6              | 9.4           | 2.9             | 504.5        | 10.4 |
| P4        | 103.7             | 88.7          | 3.4           | 40.2          | 71.0        | 16.5       | 36.93         | 9.1              | 9.7           | 3.0             | 447.9        | 10.7 |
| LSD0.05   | 6.85              | 5.63          | 0.59          | 0.26          | 1.28        | 0.45       | 0.68          | 0.27             | 0.13          | 0.19            | 4.98         | 0.52 |
| P1×P2     | 213.5             | 107.2         | 4.3           | 42.6          | 71.4        | 35.6       | 33.11         | 14.3             | 11.9          | 3.4             | 1077.4       | 10.5 |
| P1×P3     | 212.3             | 80.6          | 3.0           | 42.5          | 71.4        | 31.2       | 28.20         | 13.4             | 12.4          | 4.0             | 1108.3       | 9.3  |
| P1×P4     | 200.8             | 92.6          | 3.0           | 39.6          | 74.3        | 30.6       | 32.83         | 11.5             | 11.5          | 3.2             | 933.3        | 10.8 |
| P2×P3     | 177.0             | 92.6          | 4.0           | 34.7          | 71.1        | 46.5       | 35.73         | 13.7             | 12.9          | 4.1             | 1300.6       | 11.7 |
| P2×P4     | 96.2              | 68.4          | 3.0           | 32.2          | 66.6        | 27.6       | 30.30         | 12.3             | 11.3          | 3.4             | 910.7        | 12.4 |
| P3×P4     | 179.1             | 83.4          | 3.0           | 33.2          | 66.5        | 29.5       | 33.97         | 12.1             | 12.5          | 3.9             | 883.3        | 10.8 |
| Check     | 176.0             | 84.5          | 4.1           | 42.3          | 72.4        | 30.6       | 31.67         | 12.6             | 12.4          | 3.8             | 933.3        | 10.7 |
| LSD0.05   | 10.21             | 3.38          | 0.10          | 2.49          | 1.06        | 1.92       | 0.790         | 0.221            | 0.167         | 0.132           | 68.36        | 0.69 |

**Table 3:** Analysis of variance for genotypes, parents and crosses for growth, yield and related character.

| S.O.V.    | D.F. | M.S.              |               |               |               |             |            |               |                  |               |                 |              |       |
|-----------|------|-------------------|---------------|---------------|---------------|-------------|------------|---------------|------------------|---------------|-----------------|--------------|-------|
|           |      | Vegetative growth |               |               | No. of days   |             | Yield/plot |               | Fruit characters |               |                 |              |       |
|           |      | Plant length      | No. of leaves | No. of branch | Female flower | Early yield | Total (kg) | No. of fruits | Length (cm)      | Diameter (cm) | Flash thickness | Fruit weight | TSS   |
| Genotypes | 9    | 6526.82           | 537.483       | 0.6766        | 125.381       | 163.785     | 263.37     | 29.747        | 8.8084           | 4.1838        | 0.5389          | 272999.4     | 2.444 |
| Parents   | 3    | 1445.83           | 692.66        | 0.109         | 96.11         | 209.96      | 6.2        | 5.906         | 2.736            | 2.290         | 0.332           | 5513.2       | 1.087 |
| Crosses   | 6    | 4822.89           | 438.66        | 1.124         | 64.72         | 25.86       | 121.191    | 18.344        | 2.871            | 1.011         | 0.373           | 67728.3      | 2.840 |
| Error     | 18   | 33.880            | 7.484         | 0.048         | 2.122         | 0.791       | 1.201      | 0.241         | 0.03             | 0.0104        | 0.0095          | 1447.958     | 0.37  |

to all the other studied parents and control. Furthermore, the six straight F1 single crosses exhibited a wide range of differences in all vegetative growth, anthesis of the first female flower, yield components and fruit characters. Regarding to crosses, the F1 hybrid (P1×P2) showed a highest vegetative growth and fruit length characters than all the other F1 hybrids and control. The hybrid F1 (P2×P4) was the best one in the anthesis of the first flower and TSS of the fruits. On the other side, a significant increase was observed in the hybrid F1 (P1×P4) in the early yield compared with all the other hybrids and control. The maximum value of fruit weight, fruit diameter and flash thickness and total yield per plot were noted in the hybrid (P2×P3). These results are in agreement with Ene, *et al.*, (2019) who stated that highly significant difference in vegetative growth and yield traits were observed in

melon.

#### Analysis of variance for means and combining ability

In current study, the mean square of genotypes, parents and crosses were highly significant for all studied characters (Table 3). This showed a large diversity between the parental lines and presence of the difference among the genotypes, providing evidence for the existence of a good amount of genetic variability valid for further biometrical assessment.

The analysis of variance for combining ability of growth parameters, yield components and fruit characteristics. It showed highly significant differences in general (GCA) and specific (SCA) for all traits (Table 4). This points out the importance of both additive and non-additive genes effects as causes of the genetic

**Table 4:** Analysis of variance for general (GCA) and specific (SCA) combining ability of growth, yield and related characters.

| GC.     | D.F. | M.S.              |               |               |               |             |            |               |                  |               |                 |              |        |
|---------|------|-------------------|---------------|---------------|---------------|-------------|------------|---------------|------------------|---------------|-----------------|--------------|--------|
|         |      | Vegetative growth |               |               | No. of days   |             | Yield/plot |               | Fruit characters |               |                 |              |        |
|         |      | Plant length      | No. of leaves | No. of branch | Female flower | Early yield | Total (kg) | No. of fruits | Length (cm)      | Diameter (cm) | Flash thickness | Fruit weight | TSS    |
| GCA     | 3    | 365.05            | 31.438        | 0.0395        | 10.717        | 11.77       | 3.84       | 0.49          | 0.354            | 0.354         | 0.018           | 2852.3       | 0.2362 |
| SCA     | 6    | 2151.35           | 170.68        | 0.196         | 29.478        | 46.19       | 119.6      | 13.28         | 3.33             | 3.3296        | 0.2106          | 127219       | 0.328  |
| GCA/SCA | 3/6  | 0.17              | 0.184         | 0.21          | 0.36          | 0.255       | 0.032      | 0.04          | 0.11             | 0.035         | 0.086           | 0.02         | 0.72   |

**Table 5:** Estimates of general combining ability effects (gi) for four parental lines of growth, yield and related characters.

| Geno-<br>types | Vegetative growth |                  |                     | No. of days         |                | Yield/plot          |                    | Fruit characters |                     |                    |                 |                     |
|----------------|-------------------|------------------|---------------------|---------------------|----------------|---------------------|--------------------|------------------|---------------------|--------------------|-----------------|---------------------|
|                | Plant<br>length   | No. of<br>leaves | No. of<br>branch    | Female<br>flower    | Early<br>yield | Total<br>(kg)       | No. of<br>fruits   | Length<br>(cm)   | Diameter<br>(cm)    | Flash<br>thickness | Fruit<br>weight | TSS                 |
| P1             | 23.11**           | 5.43**           | 0.1*                | 4.58**              | 4.36**         | -0.12 <sup>ns</sup> | -0.95**            | 0.39**           | 0.3**               | -0.08**            | 19.36*          | -0.64**             |
| P2             | -15.41**          | -5.56**          | 0.21**              | -1.26**             | -1.69**        | 1.38**              | 0.13 <sup>ns</sup> | 0.51**           | 0.04 <sup>ns</sup>  | 0.14**             | 29.29**         | 0.5**               |
| P3             | 8.39**            | 4.26**           | -0.06 <sup>ns</sup> | -0.18 <sup>ns</sup> | 0.9**          | 1.49**              | 0.77**             | -0.1**           | -0.01 <sup>ns</sup> | 0.09**             | 32.17**         | -0.16 <sup>ns</sup> |
| P4             | -16.09**          | -4.13**          | -0.26**             | -3.14**             | -3.57**        | -2.75**             | 0.06 <sup>ns</sup> | -0.8**           | -0.33**             | -0.15**            | -80.81**        | 0.3*                |

variation observed. This results were in agreement with Monforte *et al.*, (2004 ) and Vianna, (2000) in melon as well as Dogra and Kanwar, (2011) and Sarkar and Sirohi, (2011) in cucumber.

However, Colombo, (2014) observed a significant effect for GCA variance in melon fruit length and diameter between all the characters studied, indicating only additive effects in the control of these morphological agronomic characteristics. On the contrary, several authors observed that the additive and non-additive components had effects in heritable variance as reported by Paris *et al.*, (2008) for fruit length, diameter and fruit yield and flash thickness and Ferreira *et al.*, (2004) for total number of fruit traits, yield and soluble solids as well as Gharib *et al.*, (2009) for number of branches and anthesis of the first female flower. The studied traits with significant variance for SCA had been confirmed to be improved by hybridization which indicated the predominance of non-additive gene effects. While, GCA has been suggestive of selection as the best improvement strategy, hence, the predominance of additive gene effects.

In the present study, GCA/SCA ratio is less than one in all vegetative growth, yield and related characters, which showed the predominance of non-additive gene effect in those traits (Table 4). The similar findings were reported by Barros *et al.*, (2013) and Costa *et al.*, (2019) who found that the GCA/SCA ratio of fruit weight, fruit length/diameter ratio, flesh thickness and fruit, flesh firmness, yield and total soluble solids in melon was less than one.

### Combining ability

General combining ability effects is successful tool

for genetic capability prediction of parental lines (Singh *et al.*, 2013). These effects compare the average of performance of each line in hybrid combinations to the other lines as well as it facilitated the selection of lines for integration in breeding populations for subsequent improvement. As shown in table 5, parental line P1 showed significantly positively GCA effect in vegetative growth parameters, early yield, fruit weight, fruit length and diameter. While, it was observed that the significant positive GCA effect for plant length, number of leaves, number of fruits, fruit weight, total yield and flesh sickness in parental line P3, as well as for number of branches, number of fruits, total yield, fruit length, flesh thickness, fruit weight and fruit TSS in the parental line P2. On the contrary, parental lines P2 had significantly negative GCA effect in number of days to flower appearances (favourable). Overall, the parental lines P2 and P3 had highly GCA effects for yield and fruit quality, where it considered a favourable general combiner in these traits than the other traits studied. This indicates those parents hold promising genes that improve fruit quantity and quality as well as can utilize them in breeding program. These similar findings were observed by Barros *et al.*, (2011) and Costa *et al.*, (2019) in melon additionally Souza *et al.*, (2013) in watermelon.

Data in table 6 shown the specific combining ability (SCA) effects of F1 cross combinations for all studied traits. In this study, all crosses combination showed highly significant positive SCA effect in fruit weight, total yield, fruit length and diameter. While, the same crosses exhibited highly significant negative SCA effect in female flower initiation (favourable), as reported by Monforte *et*

**Table 6:** Estimates of specific combining ability effects (Sij) for F1 crosses of growth, yield and related characters.

| Geno-<br>types | Vegetative growth |                  |                  | No. of days      |                | Yield/plot    |                  | Fruit characters |                  |                    |                 |          |
|----------------|-------------------|------------------|------------------|------------------|----------------|---------------|------------------|------------------|------------------|--------------------|-----------------|----------|
|                | Plant<br>length   | No. of<br>leaves | No. of<br>branch | Female<br>flower | Early<br>yield | Total<br>(kg) | No. of<br>fruits | Length<br>(cm)   | Diameter<br>(cm) | Flash<br>thickness | Fruit<br>weight | TSS      |
| P1×P2          | 49.82**           | 18.01**          | 0.51**           | -1.61**          | -5.47**        | 6.84**        | -0.2 ns          | 1.6**            | 0.21**           | -0.1**             | 207.15**        | -0.12 ns |
| P1×P3          | 24.82**           | -18.37**         | -0.51**          | -2.71**          | -8**           | 2.42**        | -5.74**          | 1.31**           | 0.78**           | 0.52**             | 235.14**        | -0.59**  |
| P1×P4          | 37.74**           | 2.03*            | -0.31**          | -2.65**          | -0.62*         | 6.03**        | -0.4**           | 0.16**           | 0.16**           | -0.08**            | 173.11**        | 0.41**   |
| P2×P3          | 28.01**           | 4.61**           | 0.37**           | -4.67**          | -2.28**        | 16.14**       | 0.71**           | 1.5**            | 1.54**           | 0.37**             | 417.53**        | 0.64**   |
| P2×P4          | -28.31**          | -11.22**         | -0.43**          | -4.25**          | -2.35**        | 1.47**        | -4.01**          | 0.8**            | 0.29**           | -0.1**             | 140.84**        | 0.91**   |
| P3×P4          | 30.76**           | -6.04**          | -0.15*           | -4.32**          | -4.97**        | 3.34**        | -0.98**          | 1.22**           | 1.51**           | 0.52**             | 110.3**         | -0.06**  |

**Table 7:** Average degree of heterosis (ADH) % based on mid- parent (MP) and better parent (BP), as well as potence ratio (P) of vegetative growth and yield.

| Genotypes | Vegetative growth |         |      |         |          |      |         |         |       | Number of days to |         |       |             |         |        | Yield/plot |         |      |               |         |       |
|-----------|-------------------|---------|------|---------|----------|------|---------|---------|-------|-------------------|---------|-------|-------------|---------|--------|------------|---------|------|---------------|---------|-------|
|           | Plant length (cm) |         |      | Number  |          |      |         |         |       | Female flower     |         |       | Early Yield |         |        | Total (kg) |         |      | No. of fruits |         |       |
|           | MP                | BP      | P    | Leaves  |          |      | Branch  |         |       | MP                | BP      | P     | MP          | BP      | P      | MP         | BP      | P    | MP            | BP      | P     |
|           |                   |         |      | MP      | BP       | P    | MP      | BP      | P     |                   |         |       |             |         |        |            |         |      |               |         |       |
| P1×P2     | 73.3**            | 46.2**  | 8235 | 24.8**  | 7.9**    | 1142 | 14.7**  | 12.2*   | 0.11  | -12.3**           | -20.4** | -118  | -13.9**     | -20.6** | -322.9 | 89.3**     | 81.7**  | 53.8 | -7.5**        | -8.4**  | -3.9  |
| P1×P3     | 53.3**            | 45.4**  | 2214 | -22.1** | -25.2**  | -385 | -18.2** | -21.7** | -0.39 | -14.8**           | -20.5** | -107  | -17.7**     | -20.6** | -193.4 | 60.02**    | 59.7**  | 2.3  | -23.9**       | -27.1** | -57.8 |
| P1×P4     | 60.8**            | 37.5**  | 6425 | -1.5 ns | -6.74**  | -30  | -17.1** | -21.7** | -0.48 | -15.4**           | -25.9** | -193  | -7.6**      | -17.4** | -232.5 | 69.7**     | 56.5**  | 77.2 | -9.2**        | -11.1** | -10.2 |
| P2×P3     | 53**              | 35.1**  | 3752 | 2.8 ns  | -14.02** | 176  | 11.6*   | 9.1 ns  | 0.16  | -22.8**           | -25.1** | -55.5 | -10.2**     | -15**   | -134.2 | 147.9**    | 138.4** | 83.3 | -4.5**        | -7.6**  | -8.5  |
| P2×P4     | -5.8 ns           | -7.3 ns | -39  | -15.1** | -22.9**  | -395 | -15.1** | -18.2** | -0.33 | -23.2**           | -26.2** | -66   | -9.4**      | -12.2** | -65.3  | 59.6**     | 53.1**  | 31.1 | -17.1**       | -18**   | -10   |
| P3×P4     | 52.6**            | 36.7**  | 3372 | -15.1** | -22.6**  | -562 | -13.1** | -14.3*  | -0.09 | -23.2**           | -28.4** | -123  | -13.9**     | -20.4** | -272.2 | 64**       | 51.6**  | 69   | -10.1**       | -12.2** | -13.3 |

*al.*, (2005). Overall, The cross combination (P2×P3) had highest positively SCA effect in total yield, number of fruits, fruit weight, flesh thickness, fruit length and fruit diameter than the other hybrids (Table 6). In addition, negative significant SCA effects were recorded by the same cross in female flower initiation, this indicate that this cross product flowers earlier than other having positive SCA. The Cross combination (P1×P2) exhibited maximum SCA effect in plant length, number of leaves and number of branches. While, the cross combination (P2×P4) was positively highest SCA in fruit TSS. However, the results reveal that the cross (P2×P3) is the best combination among of the six crosses evaluated in this study due to it has a good specific combiner in vegetative growth, flowering, total yield, fruit weight and fruit characteristics. This possibly because it involved to parents with good x good (Table 5), general combining ability effects which showed the attendance of additive, dominance and epistatic gene effects for controlling the traits. Therefore, the cross (P2×P3) with higher specific combining ability effects was useful to obtain high performing hybrids. On the other side, the other significant crosses with SCA effects in some studied traits could be resulted of general combiner parents with (good × poor and poor × good). Likewise, the superiority of cross combinations linking poor × poor, or good × poor general combiners as parents could be associated to the genetic

variation between parents, in the form of number of heterozygous loci of the parents contributed in the cross combinations. In some cases, parents with high GCA effects produced hybrids with low SCA effects. This possibly due to reduction in complementary gene effect. On the other side, parents with low GCA effects produced hybrids with high SCA effects which can be attributed to complementation of the parental genes. Similar findings were stated by Ene *et al.*, (2019) and Malav *et al.*, (2018) in cucumber, as well as Reddy *et al.*, (2013) in *Abelmoschus esculentus* (L.) Moench.

### Heterosis

Heterosis, the superiority of F1 over the mid parents (M.P.) or over the better parent (B.P.) is dependent on the accumulation of favourable dominant genes in the F1 population (Singh *et al.*, 2013). In table 7 and 8, the estimated amount of heterosis from MP and BP for vegetative growth showed that significant positive values for all crosses, except the cross (P2×P4). The cross (P1×P2) only gave significant positive heterosis values than MP and BP. These results suggesting dominance towards higher parent in these characters. However, all the crosses had significant negative ADH% values over MP and BP in number of days to female flower initiation. These results suggested over dominance towards the short period of flowering. Furthermore, earliness to flowering can prolong the fruit filling period of the plant which can

**Table 8:** Average degree of heterosis (ADH) % based on mid- parent (MP) and better parent (BP) and potence ratio (P) of fruit characters.

| Geno-<br>types | Fruit characters |        |     |               |        |     |                 |        |      |                  |         |         |         |         |      |
|----------------|------------------|--------|-----|---------------|--------|-----|-----------------|--------|------|------------------|---------|---------|---------|---------|------|
|                | Length (cm)      |        |     | Diameter (cm) |        |     | Flash thickness |        |      | Fruit (g) weight |         |         | TSS     |         |      |
|                | MP               | BP     | P   | MP            | BP     | P   | MP              | BP     | P    | MP               | BP      | P       | MP      | BP      | P    |
| P1×P2          | 30.5**           | 29.5** | 0.7 | 9.2**         | 4.6**  | 2   | 1ns             | -6.4** | 0    | 105.2**          | 95**    | 60858   | 1.6 ns  | -4.9 ns | 0.7  |
| P1×P3          | 29.9**           | 21.2** | 8.6 | 19.2**        | 9.1**  | 8   | 31.9**          | 27.7** | 0.4  | 109.7**          | 100.5** | 55883.1 | -6.7 ns | -10.3*  | -1.1 |
| P1×P4          | 14.6**           | 4.5**  | 5.5 | 8.9**         | 0.9 ns | 3.2 | 3.3 ns          | 1.1 ns | 0.03 | 86.6**           | 68.9**  | 90756.8 | 6.4 ns  | 0.9 ns  | 1.4  |
| P2×P3          | 34.1**           | 26.1** | 8.9 | 30.3**        | 24.0** | 6   | 23.2**          | 11**   | 1.28 | 159.6**          | 157.8** | 11033.8 | 9.4*    | 6.4 ns  | 1.2  |
| P2×P4          | 23.2**           | 13.2** | 8.3 | 12.8**        | 9**    | 1.6 | 1 ns            | -8.2** | 0.07 | 92.7**           | 83.1**  | 43532.2 | 14.6**  | 13.0**  | 1    |
| P3×P4          | 29.6**           | 26.5** | 2.6 | 30.9**        | 28.9** | 1.8 | 32.6**          | 31.1** | 0.19 | 85.5**           | 75.1**  | 46083.7 | 2.4 ns  | 0.93 ns | 0.2  |

explain to better yield.

Negative heterosis in number of days to flower appearance had been stated in bitter gourd Laxuman *et al.*, (2012). Moreover, all crosses gave negative heterosis values in early yield. The findings were in accordance with the results of Munshi *et al.*, (2005) who also observed negative heterosis in days to first fruit harvest. The estimated amount of heterosis from MP and BP in total yield, fruit weight and fruit length and diameter show that, heterosis values were positive in all crosses except the cross (P1×P4) in fruit diameter towards the BP was not significant. These results indicated that there are over dominance towards the BP in these characters (Singh *et al.*, 2013). The improvement of melon yield could be mainly associated to high fruit weight and length as reported by Munshi and Verma, (1997) in muskmelon and Chaubey and Ram, (2004) in bitter gourd and Sarkar, (2003) and Ene *et al.*, (2019) in cucumber.

The similar trends were observed in the crosses (P1×P3), (P2×P3) and (P3×P4) in flesh thickness as well as the cross (P2×P4) in TSS, as observed by Costa *et al.*, (2019). Overall, the crosses were P2×P3 followed by P1×P2 giving the highest positive heterosis values than mid-parent (MP) and better parent (BP) in terms of total yield /plot. These results indicated that over dominance of previous crosses was higher than the high parent in this character (total yield) as well as the positive value of potence ratio (p) confirmed this result (p= 83.25 and 53.76 respectively). (Shashikumar and Pitchaimuthu, 2016).

## Conclusions

The obtained results from the current study confirmed that the best general combiners in yield and some studied traits for parental lines P2 and P3 might be promising in future breeding programmers. At the same time, the existence of predominantly large amount of non-additive gene action for yield and its components as noted in the present study, requires the maintenance of the heterozygosity in the population. The significant amount of heterosis was detected in desired direction of fruit yield and related components.

## References

Abdeldaym, E.A., F. Erriquens, N. Sasanelli, F.G. Ceglie, C. Zaccone, T. Miano and C. Coccozza (2014). Effects of several amendments on organic melon growth and production, *Meloidogyne incognita* population and soil properties. *Sci. Hort.*, **180**: 156-160.

Barros, A., G.H. Nunes, M.A. Queiróz, E.W. Pereira and J.H. Filho (2011). *Crop Breed Appl Biot.*, **11**: 313-319.

Chaubey, A.K. and H.H. Ram (2004). Heterosis for fruit yield

and its components in bitter gourd (*Momordica charantia* L.). *Veg. Sci.*, **31(1)**: 51-3.

Colombo, G.A., A. Vaz de Melo, M. Taubing, R.C. Tavares and R.R. Silva (2014). Diallel analysis for resistance to southern rust in corn at different levels of phosphorus fertilization. *Bragantia.*, **73**: 65-71.

Costa, Í.J.N.1, R.N. Valadares, D.A. Nóbrega, A.Q. Mendes, F.S. Silva and D. Menezes (2011). Diallel analysis of yield and quality traits of melon fruits. *Crop Breed Appl Biot.*, **11**: 313-319.

Cruz, C.D., A.J. Regazzi and P.C.S. Carneiro (2012). Biometric models applied to genetic improvement. 4<sup>th</sup> edn. Viçosa: UFV.

Diab, A.H.M. (2012). Enhanced production of Haploid plants through parthenogenesis technique in some genotypes of melon. Ph.D thesis, faculty of agriculture, Kafrelsheikh University. 119.

Dogra, B.S. and M.S. Kanwar (2011). Selecting parents for developing superior hybrids in cucumber (*Cucumis sativus* L.). *Adv. Hort. Sci.*, **25(4)**: 239-44.

Ene, C.O., P.E. Ogbonna, C.U. Agbo and U.P. Chukwudi (2019). Heterosis and combining ability in cucumber (*Cucumis sativus* L.). *Information Processing In Agriculture.*, **6**: 150-157.

Ferreira, F.M, J.I. Ribeiro Júnior, C.A.P. Pacheco, C.H.O. Silva and F.S. Martins (2004). Genetic components of combining ability in a complete diallel. *Crop Breed Appl Biot.*, **4**: 338-343.

Gharib, A.A., Y.M. Ahmed, Y.T. EL-Lithy and S.M. Kamel (2009). General and specific combining ability for some genotypes of sweet melon. Egypt. *J. Plant Breed.*, **13**: 173-182.

Golabadi, M., P. Golkar and A.R. Eghtedary (2015). Combining ability analysis of fruit yield and morphological traits in greenhouse cucumber (*Cucumis sativus* L.). *Can. J. Plant Sci.*, **95(2)**: 377-85.

Gomez, K. and A. Gomez (1984). Statistical procedures for agricultural research (2<sup>nd</sup> Ed) John Wiley & Sons, New York, 680.

Griffing, B. (1956). Concept of general and specific combining ability in relation to diallel crossing system. *Aust. J. Biol. Sci.*, **9**: 463-93.

Laxuman, S.A., P.M. Patil, P.R. Salimath, A.S. Dharmatti and B. Nirmalayanagi (2012). Heterosis and combining ability analysis for productivity traits in bitter gourd (*Momordica charantia* L.). *Karnataka J. Agric. Sci.*, **25(1)**: 9-13.

Lopez-Sese, A.L. and J. Staub (2002). Combining ability analysis of yield components in cucumber J. *Americ. Socie. Hort. Sci.*, **127**: 931-7.

Luan, F., Y. Sheng, Y. Wang and J.E. Staub (2010). Performance of melon hybrids derived from parents of diverse geographic origins. *Euphytica.*, **173**: 1-16.

Madhu, S. (2010). Gene action and heterosis studies involving

- gynoecious lines in cucumber (*Cucumis sativus* L.) Doctor Thesis. Palampur, India: Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya.
- Mather, K. and J.L. Jinks (1982). Biometrical genetics. 3<sup>rd</sup> Ed Champan and Hall, London.
- Monforte, A.J., I. Eduardo, S. Abad and P. Arus (2005). Inheritance mode of fruit traits in melon heterosis for fruit shape and its correlation with genetic distance. *Euphytica.*, **144**: 31-38.
- Monforte, A.J., M. Oliver, M.J. Gonzalo, J.M. Alvarez and R. DolcetSanjuan (2004). Identification of quantitative trait loci involved. in fruit quality traits in melon (*Cucumis melo* L.). *Theor Appl Genet.*, **108**: 750-758.
- Munshi, A.D., R. Kumar and B. Panda (2005). Heterosis for yield and its components in cucumber (*Cucumis sativus* L.). *Veg. Sci.*, **32(2)**: 133-5.
- Munshi, A.D. and V.K. Verma (1997). Studies on heterosis in muskmelon (*Cucumis melo* L.). *Veg. Sci.*, **21(2)**:103-6.
- Olfati, J.A., H. Samizadeh, B. Rabiei, G. Peyvast and S. Griffing (2012). methods of comparison for general and specific ability in cucumber. *Sci. World J.*, **3**: 1-4.
- Paris, M.K., J.E. Zalapa, J.D. McCreight and J.E. Staub (2008). Genetic dissection of fruit quality components in melon (*Cucumis melo* L.) using a RIL population derived from exotic x elite US Western Shipping germplasm. *Mol Breed.*, **22**: 405- 419.
- Reddy, M.T., K.H. Babu, M. Ganesh, H. Begum, J. Dilipbabu and R.S.K. Reddy. Gene action and combining ability of yield and its components for late kharif season in okra (*Abelmoschus esculentus* L. Moench). *Chilean JAR.*, **73(1)**: 9-16.
- Sarkar, M. (2003). Genetical studies in cucumber (*Cucumis sativus* L.) Doctor Thesis. New Delhi, India: IARI.
- Sarkar, M. and P.S. Sirohi (2011). Diallel analysis of quantitative characters in cucumber (*Cucumis sativus* L.). *Veg. Sci.*, **38**: 73-5.
- Shashikumar, K.T. and M. Pitchaimuthu (2016). Heterosis and combining ability analysis of quantitative and qualitative traits in muskmelon (*Cucumis Melo* L.). *Int. J. Agric. Res.*, **6,2**: 341-348.
- Singh, A.K., R.S. Pan and P. Bhavana (2013). Heterosis combining ability analysis in bitter gourd (*Momordica charantia* L.). *Bioscan.*, **8(4)**: 1533-6.
- Singh, R.K. and B.D. Chaudhary (1985). Biometrical methods in quantitative genetic analysis. New Delhi-Ludhiana, India: Kalyani Publishers. 39-78.
- Singh, S., S.V. Singh and J.P. Srivastava (2014). Heterosis and inbreeding depression for yield and its component traits in cucumber. *Agriways.*, **2(1)**: 47-51.
- Sinha, S.K. and R. Khanna (1975). Physiological, biochemical and genetic basis of heterosis. *Adv. Agron.*, **27**: 123-174.
- Souza, F.F., R.C.S. Dias and M.A. Queiróz (2013). Combining ability of advanced lines and marketable cultivars of watermelon. *Hortic. Bras.*, **31**: 595-601.
- Vianna, J.M.S. (2000). The parametric retrictions of the Griffing diallel analysis model: combining ability analysis. *Genet. Mol. Biol.*, **23**: 877-881.
- Zalapa, J.E., J.E. Staub and J.D. McCreight (2006). Generation means analysis of plant architectural traits and fruit yield in melon. *Plant Breed.*, **125**: 482-487.