

## Breeding new pickling cucumber hybrids:

### A. Morphological characterization and genetic studies

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#### ABSTRACT

Vegetable breeding is one of the most important ways to ensure food security. The current study was conducted on five inbred lines to obtain 10 F<sub>1</sub> pickling cucumber hybrids using half diallel mating design. The results indicated that high significant differences between all genotypes compared with check in all studied traits. In addition to, significant general (GCA) and specific combining ability (SCA) effects for all studied traits. The ratio GCA / SCA was less than unity, which indicates that the non-additive genetic variance component. Furthermore, some genetic parameters were revealed that two parents (P<sub>5</sub> and P<sub>2</sub>) were good general combiners for most traits. The five crosses (P<sub>1</sub> × P<sub>3</sub>), (P<sub>1</sub> × P<sub>4</sub>), (P<sub>3</sub> × P<sub>4</sub>), (P<sub>3</sub> × P<sub>5</sub>), and (P<sub>4</sub> × P<sub>5</sub>) exhibited significant desirable positive SCA in all commercial traits which effective on economic productivity. Most of these hybrids gave significant heterosis values over mid and high parents in vegetative, flowering, early, and total yield characteristics. Generally, the parent (P<sub>5</sub>) could be used as a promising progenitor for all commercial traits in addition to genetic improvements by hybridization.

**Keywords:** Cucumber, Pickling, Inbred lines, Combining ability, Heterosis.

#### INTRODUCTION

Cucumber is a member of the Cucurbitaceae family, which contains over 90 genera and 750 species. It is consumed as fresh or pickling. Egypt typically faces great challenges due to its huge population. Unfortunately, Egypt imports most of its specific needs from vegetable seeds (According to the Ministry of Agriculture Statistics, 2018). Economic statistics indicated that Egypt imports approximately 98% of the local needs of vegetable seeds. These amounts of seeds cost almost one and a half milliard pounds a year. Plant breeding represents the most essential and ancient strategy to devise adapted lines by developing promising lines suitable for the feed population. Heterosis and combining ability efficiently are practical values that sufficiently indicate the line ability to combine among each other during the hybridization where the desirable genes are typically transmitted to progeny (Kumar and Kumar, 2017). The genetic improvement values are used in most plant breeding programs to accurately determine the good parental lines provide in hybrid production (Mohanty and Mishra, 1999).

The hybrids production of cucumber are predominantly utilized in the system of many developed and developing countries for decades. Increasing cucumber yield has been the main objective of breeders (Lower and Edwards, 1986; Wehner, 1989). There are two basic cucumber types; the fresh or slicing cucumber (Wehner and Horton, 1986) and therefore the processed product termed pickling cucumber (Staub and Bacher, 1997). The foremost fruit types are the American processing and fresh market types, the Mideast Beit Alpha type, the oriental trellis (burpless) type, and also the Japanese pickling and fresh type (Shetty and Wehner, 2001). Cultivated cucumber and its wild relatives, including *Cucumis sativus* var. *hardwickii*, which is taken into account essential in pickling hybrids, exhibit large spines (size, density, and color), growth habits (vine length and branching), fruit size, sex expression, and flesh bitterness (Meglic *et al.*, 1996; Staub *et al.*, 1999.). Hybrids production with additional values such as processing efficacy is one of the essential plant breeding goals. cucumber is one of the vegetables which possesses these values. Pickling cucumbers have usually grown flat on bare ground, with machine harvest to reduce labor and other input costs (Ando and Grumet, 2006; Schultheis, 2000). Pickling lines are characterized by a large number of lateral branches and ovary length, where these traits are suitable and favorable periods for consumers (Wehner, 1998).

In Egypt, no pickling varieties were available, and all cultivated hybrids were imported. So, the interest in processing cucumber breeding takes place. Yield and quality represent a serious focus of cucumber breeders (Lower and Edwards, 1986; Tatlioglu, 1993). Velkov and Alexandrova (2010) developed three cucumber F<sub>1</sub>S on the base of two gynocious lines crossed with two monoecious lines. The results proved that the new hybrids may well be of considerable importance for pickling. De Ponti (1976) succeeded to develop parthenocarpic pickling cucumbers crosses by crossing pickling and slicing cucumbers. Genetic control of internode length, leaf width, and the number of fruits per plant was accomplished by additive effects. Significant general combining ability for fruit yield revealed that both selection and hybridization methods would typically lead to desirable genetic improvements in cucumber through the accumulation of desirable alleles from parents in the target genotype, but that hybridization would be preferred (Golabadi *et al.*, 2015).

Lalla et al. (2010) studied combining ability and heterosis of lines from Japanese cucumber type for a yield. The direct results showed that Line 7 presented the best positive values of GCA and Heterosis for many evaluated characteristics. Hybrids H1Y and H1N, with line L<sub>1</sub> showed higher values for SCA with the test populations for many of the evaluated characteristics.

In some cases, the ratio of the genetic variance was less than unity, which indicated the predominance of the non-additive gene action (Mule et al., 2012; Prashant et al., 2018). In contrast, the calculated ratio GCA/SCA was more than unity, indicates that the additive genetic variance component represents the more significant component than other specific types of genetic variance components (El-Eslamboly and Mohamed, 2018). The magnitudes of variance due to general and specific combining ability were highly significant. These results proved the importance of both additive and non-additive gene action (Pati et al., 2015; Tak et al., 2017; Dia et al., 2018; Ene et al., 2019). Over 700 gynococious cucumber hybrids were evaluated for early, total, and marketable yield. Significant differences were carefully observed among cultigens for all cultural traits accurately evaluated (Wehner et al., 2000). Furthermore, parental lines LC-1-1, GCN-20953, GCN-19533, Gyne-5, LC-15-5, and Japanese Long Green and K-75 were found superior on the basis of mean performance and general combining ability effects (Kumar et al., 2017).

The current research aimed to typically release local cucumber inbred lines and hybrids adapted to Egyptian climate conditions, in addition to their desirable commercial traits, by the final and specific combining ability and heterosis estimation. This research is going to be supported by the second essential part, which in common is the manufacturing part, to accurately determine the content validity of parents and hybrids devised for pickling.

## MATERIAL AND METHODS

### Study area:

This study was conducted during the five successive seasons of 2018, 2019, and 2020 under greenhouse conditions at Vegetable Research Departments, Horticulture Research Institute, Agriculture Research Center (A.R.C.), Dokki, Egypt.

### Plant materials:

Five genotypes were utilized in this study to produce new pickles hybrids using half diallel mating design. Self-pollination for 3 successive seasons (2018 and 2019) was done to make sure inbred lines homogeneity.

**Table 1.** List of the cucumber genotypes used in the breeding program.

Genotypes	Parental lines	Scientific name	Sex expression	source	origin
1	Beit alpha	<i>C. sativus</i>	Gynococious	Variety	Egypt
2	PI 215589	<i>C. sativus</i> var. <i>hardwickii</i>	Monoecious	USDA	India
3	Ames 20089	<i>C. sativus</i>	Monoecious	USDA	Egypt
4	NSL 5739	<i>C. sativus</i>	Monoecious	USDA	USA
5	CGN21615	<i>C. sativus</i>	Monoecious	CGN	Japan

### Hybridization:

Seeds of 5 inbred lines were sown in seedling trays on 12<sup>nd</sup> August 2018. Seedlings were transplanted in a greenhouse after two weeks. The gynococious line (P<sub>1</sub>) was treated with silver nitrate to induce male flowers (Beyer, 1976). At the flowering stage, crossing using all possible combinations of a half diallel mating design, giving a total of ten crosses, were done between the five parental lines.

### Evaluation:

Seeds were extracted from mature fruits, which were cleaned and spread for drying. On February 15th, 2020, seeds of parents and their ten hybrids (15 genotypes), as well as the check (Fresh Pickles F1, from Burpee seed company), were sown. Seedlings were transplanted after twenty days into the greenhouse of 360 (940) m<sup>2</sup> in an exceedingly randomized complete block design with three replicates. Seedlings were transplanted into two rows on the bed (one 4 m in length and the other 1.0 m in width). The space between plants was 0.5 m. The standard agricultural practices for commercial cucumber production occurred. The horticultural characteristics, vegetative growth, flowering, fruits, and yield components were recorded.

### Statistical analysis:

The experiments layout was a complete randomized block design with three replicates. Data were statistically analyzed, using analyses of variance (ANOVA) with the Stat soft statistical package (MSTATC) software program (Michigan State University, East Lansing, MI, U.S.A.). Probabilities of significance among genotypes compared with the least significant difference L.S.D. (P≤0.05) according to Gomez and Gomez (1984).

### Genetic analyses:

#### Combining abilities:

The data of the parental lines and their F<sub>1</sub> hybrids were used to study the general and specific combining abilities to illustrate their relations to the type of gene action involved. The genetic analyses were based on the method proposed by Griffing (1956), Method 2, model 2 as outlined by Singh and Chaudhary (1979).

**Heterosis:**

Two types of heterosis are [relative heterosis (M.P) and heterobeltiosis (B.P)] were estimated and expressed as percentages (Mather and Jinks, 1982) as the deviation of F<sub>1</sub> mean over the mid-parents (M.P), and better parent (B.P), in each cross, respectively as follows:

a. Mid-parent heterosis (M.P) =  $[(F_1 - M.P) / M.P] \times 100$

b. better parent heterosis (B.P) =  $[(F_1 - B.P) / B.P] \times 100$

**The estimated characters**

**Vegetative characters:** Main stem length (M.S.L) (cm) : at the end of the season, Plant fresh weight (P.F.W) (gm): at the end of the season, Number of lateral branches (No. L.B) for first 50 cm, Internode length (I.L) (cm) and Leaf area (L.A) (cm<sup>2</sup>).

**Flowering characters:** Number of days until first female flower opening (No. D.F.F.O) and Number of the female flower (No. F.F) / nodes.

**Fruits characters:** Ovary length (O.L) (cm), Fruit length (F.L) (cm), Fruit weight (F.W) (g), Fruit diameter (F.D) (cm), and Ratio between fruit length and diameter (L/D. R).

**Yield characters:** Early yield (3 times weekly for four weeks from the first harvest) and Total yield (3 times weekly for ten weeks from the first harvest) was number and weight (g) of fruits.

**RESULTS****Mean performance:**

Accurate data presented in Table (2) showed significant differences among all parents and hybrids for all characters under this study. Parent 5 (P5) had the most significant values in vegetative growth (main stem length and internode length) compared with other parents and the check. However, Parent 2 (P2) was distinguished by the numerous lateral branches, which gave the highest number of lateral branches, seven for the first 50 cm from the ground surface, and the highest plant fresh weight. On the other hand, parent 1 showed the most limited values in most vegetative growth traits compared to the other parents and the check. Regarding crosses, both P3 P5 and P4 P5 F1 crosses showed a significant increase in most vegetative traits compared with the other hybrids, parents, and the check. In contrast (P1 P2), the F1 hybrid had the lowest vegetative growth values compared with all hybrids under this study and the check. In addition, flowering traits, the number of days to the first female flower antheses, were estimated to determine the earliness directly related to early and total yield. Furthermore, the P3P5 F1 hybrid produced the first female flower after 30.33 days, which is carefully considered the earliest hybrid followed by the P5 parent (33.33 days) without any statistical difference from the hybrid P2P4 (33.33 days) compared with all genotypes and check. The number of female flowers/nodes is another important flowering trait that is directly related to total yield; among all genotypes, P1 had the most female flowers/nodes, followed by the P1P3 hybrid.

**Table 2.** Mean performance for vegetative and flowering characters for five cucumber genotypes and their F1's.

Genotypes	Vegetative					Flowering	
	M.S. L	P.F. W	No. L. B	I.L	L.A	No. D.F.F. O	No. F.F
P <sub>1</sub>	207.33	244.33	2.67	4.33	241	41.67	2.67
P <sub>2</sub>	311	381.67	7	3.67	205	46.33	1
P <sub>3</sub>	374.33	338.33	4.67	7.17	382	39	1.33
P <sub>4</sub>	338	294.33	3.33	6.5	384.67	41	1
P <sub>5</sub>	407.33	352.33	2.67	7.17	352.33	33.33	1
P <sub>1</sub> ×P <sub>2</sub>	301.67	330.67	4	3.67	228	41.33	1.67
P <sub>1</sub> ×P <sub>3</sub>	388	350	5	5	368.33	36.33	2.33
P <sub>1</sub> ×P <sub>4</sub>	407	367.67	4.33	6.87	386.33	38.33	1.67
P <sub>1</sub> ×P <sub>5</sub>	357.33	315.67	3	6.5	368.33	38.33	2
P <sub>2</sub> ×P <sub>3</sub>	384	370.67	6.67	6.83	313.67	40	1.33
P <sub>2</sub> ×P <sub>4</sub>	407.67	371	3.33	7	361.67	33.33	1.67
P <sub>2</sub> ×P <sub>5</sub>	363.67	390	6.67	5.57	273.67	35.67	1.33
P <sub>3</sub> ×P <sub>4</sub>	370	318.67	7	6.067	381.33	39	1
P <sub>3</sub> ×P <sub>5</sub>	421.67	379	5	7.5	317.33	30.33	1
P <sub>4</sub> ×P <sub>5</sub>	410.33	385	3.67	8.83	375	37.67	1
Check	291.67	237	2.33	2.83	247.67	47.33	1
L.S.D 0.05%	24.13	28.44	1.304	1.206	34.42	2.28	0.80

**M.S.L:** main stem length(cm), **P.F.W:** fresh plant weight (gm), **No. L.B:** number of lateral branches

**I.L:** internode length(cm), **L.A:** leaf area(cm<sup>2</sup>), **No. D.F.F.O:** number of days to first female flowering, and **No. F.F:** number of female flowers

Data in Table (3) indicated that the highest fruit characteristics were found in the P5 parent, the F1 hybrid P4 P5 and P3 P5 compared with other genotypes and the check. P4–P5 typically had the tallest ovary, considered an extremely necessary trait for the pickling process because this stage is one of the most suitable and favourable periods for processing. In contrast, the P2 parent and the (P1P2) F1 hybrid produced the most limited values in fruit characteristics, which may be desired for another

specific type of consumer. The early and total yield, as well as number and weight, showed significant differences for all tested genotypes compared with the check. The most excellent early and total yields for parents were P5. As for F1 hybrids, P3 P5 and P4 P5 have the highest maximum productivity.

**Table 3.** Mean performance for fruits and yield characters for 5 cucumber genotypes and their F1's.

Genotypes	Fruit					Yield			
	O. L	F. L	F.W	F. D	L/D. R	EY (F. No)	EY (F.W)	TY (F. No)	TY (F.W)
P <sub>1</sub>	2.5	11.6	76	2.767	4.207	11.667	888.67	26	1972
P <sub>2</sub>	1.7	9.83	78.67	3.133	3.137	19	1497.33	45.33	3577.667
P <sub>3</sub>	3.63	27.5	118.33	3.367	8.263	10	1180	23.33	2763.333
P <sub>4</sub>	2.93	18.167	133	3.233	5.62	16.667	2288.67	36	4807
P <sub>5</sub>	4.37	29.3	135.67	2.967	9.913	24	3259.33	46	6229.67
P <sub>1</sub> ×P <sub>2</sub>	2.1	10.43	77.33	3.033	3.433	20	1548.67	48	3715
P <sub>1</sub> ×P <sub>3</sub>	4.17	27.33	127.7	3.5	7.84	23.333	2980	49.3	6303
P <sub>1</sub> ×P <sub>4</sub>	3.57	19.23	96	2.8	6.86	25.66	2470	52.3	5032.67
P <sub>1</sub> ×P <sub>5</sub>	2.6	17.77	106.3	2.833	6.3	20.33	2159	39.3	4166
P <sub>2</sub> ×P <sub>3</sub>	4.03	19	108.6	3	6.32	15	1632	41.3	4491.33
P <sub>2</sub> ×P <sub>4</sub>	3.8	25	112.3	2.8	9.04	19	2135.67	39.7	4464
P <sub>2</sub> ×P <sub>5</sub>	2.9	18.067	101	2.67	6.8	23.333	2371	52.6	5328.33
P <sub>3</sub> ×P <sub>4</sub>	2.9	15.867	114	2.9	5.423	23.667	2716.67	53.3	6073
P <sub>3</sub> ×P <sub>5</sub>	3.9	28.1	117.7	3.067	9.19	28	3291.33	63.3	7445.33
P <sub>4</sub> ×P <sub>5</sub>	4.33	27.5	120	3.367	8.16	24.7	2935	50.7	6081
Check	2.43	13.5	91	3	4.5	25	2271.67	51.3	4678.33
L.S.D 0.05%	0.69	2.43	13.296	0.33	1.34	2.92	441.007	5.23	750.039

O. L: ovary length (cm), F.L: fruit length (cm), F.W: fruit weight(gm), F.D: fruit diameter(cm), L/D. R: the ratio between fruit length and diameter, EY (F. No): early yield as fruit number, EY (F.W): early yield as fruit weight, T.Y. (F. No): total yield as fruit number, T.Y. (F.W): total yield as fruit weight.

#### 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. In Table (4), The estimated amount of heterosis over M.P. for main stem length showed significant positive values for all hybrids except P2P5 and P3P4. However, the amount of heterosis over B. P was significant positive values for P1P4 and P2P4 for the identical character. In terms of plant fresh weight, P1P4 and P4P5 have significant positive heterosis over mid and high parent. Internode length has a significant positive heterosis value over B.P for the P4–P5 hybrid. These findings point to a preference for middle and better-off parents in these characters. However, all crosses had significant negative ADH% values over B.P for leaf area. These findings indicated a preference for the smallest leaf area.

**Table 4.** Average degree of heterosis (ADH) % based on mid- parent (M.P) and better parent (B.P) of vegetative growth.

Genotypes	Vegetative characters									
	M.S. L		P.F. W		No. L. B		I.L		L.A	
	M.P	B. P	M.P	B. P	M.P	B. P	M.P	B. P	M.P	B. P
P <sub>1</sub> ×P <sub>2</sub>	16.4**	-3 <sup>ns</sup>	5.64 <sup>ns</sup>	-13.36**	-17.24 <sup>ns</sup>	-42.86**	-8.33 <sup>ns</sup>	-15.38 <sup>ns</sup>	2.24 <sup>ns</sup>	-5.39 <sup>ns</sup>
P <sub>1</sub> ×P <sub>3</sub>	33.41**	3.65 <sup>ns</sup>	20.14**	3.45 <sup>ns</sup>	36.36*	7.14 <sup>ns</sup>	-13.04 <sup>ns</sup>	-30.23**	18.25**	-3.58 <sup>ns</sup>
P <sub>1</sub> ×P <sub>4</sub>	49.27**	20.41**	36.51**	24.92**	44.44*	30 <sup>ns</sup>	26.77*	5.64 <sup>ns</sup>	23.49**	0.43 <sup>ns</sup>
P <sub>1</sub> ×P <sub>5</sub>	16.27**	-12.27**	5.81 <sup>ns</sup>	-10.41*	12.5 <sup>ns</sup>	12.5 <sup>ns</sup>	13.04 <sup>ns</sup>	-9.3 <sup>ns</sup>	24.16**	4.54 <sup>ns</sup>
P <sub>2</sub> ×P <sub>3</sub>	12.06**	2.58 <sup>ns</sup>	2.96 <sup>ns</sup>	-2.88 <sup>ns</sup>	14.29 <sup>ns</sup>	-4.76 <sup>ns</sup>	26.15*	-4.65 <sup>ns</sup>	6.87 <sup>ns</sup>	-17.89**
P <sub>2</sub> ×P <sub>4</sub>	25.63**	20.61**	9.76**	-2.79 <sup>ns</sup>	-35.48**	-52.38**	37.7**	7.69 <sup>ns</sup>	22.67**	-5.98 <sup>ns</sup>
P <sub>2</sub> ×P <sub>5</sub>	1.25 <sup>ns</sup>	-10.72**	6.27 <sup>ns</sup>	2.18 <sup>ns</sup>	37.93**	-4.76 <sup>ns</sup>	2.77 <sup>ns</sup>	-22.33*	-1.79 <sup>ns</sup>	-22.33**
P <sub>3</sub> ×P <sub>4</sub>	3.88 <sup>ns</sup>	-1.16 <sup>ns</sup>	0.74 <sup>ns</sup>	-5.81 <sup>ns</sup>	75**	50**	-11.22 <sup>ns</sup>	-15.35 <sup>ns</sup>	-0.52 <sup>ns</sup>	-0.87 <sup>ns</sup>
P <sub>3</sub> ×P <sub>5</sub>	7.89**	3.52 <sup>ns</sup>	9.75**	7.57 <sup>ns</sup>	36.36*	7.14 <sup>ns</sup>	4.65 <sup>ns</sup>	4.65 <sup>ns</sup>	-13.57**	-16.93**
P <sub>4</sub> ×P <sub>5</sub>	10.11**	0.74 <sup>ns</sup>	19.07**	9.27*	22.22 <sup>ns</sup>	10 <sup>ns</sup>	29.27**	23.26*	1.76 <sup>ns</sup>	-2.51 <sup>ns</sup>

M.S.L: main stem length(cm), P.F.W: plant fresh weight (gm), No. L.B: number of lateral branches, I.L: internode length(cm), L.A: leaf area(cm<sup>2</sup>). M.P: mid-parent, H.P: high-parent, S.P: standard- parent.

As for the flowering traits in Table (5), For most hybrids, the estimated heterosis from M.P. and B.P for the number of days to the first female flower anthesis refers to significant negative values. This direct result suggested over dominance towards the short period of flowering, indicating earliness in all hybrids. Moreover, all hybrids do not have any significant heterosis values over mid-parent heterosis in the number of female flowers/nodes for most hybrids.

**Table 5.** Average degree of heterosis (ADH)% based on mid- parent (M. P) and better parent (B.P) of flowering characters

Genotypes	Flowering characters			
	No. D.F.F. O		No. F. F	
	M.P	B. P	M.P	B. P
P <sub>1</sub> ×P <sub>2</sub>	-6.06**	-10.79**	-9.09 <sup>ns</sup>	-37.5*
P <sub>1</sub> ×P <sub>3</sub>	-9.92**	-12.8**	16.67 <sup>ns</sup>	-12.5 <sup>ns</sup>
P <sub>1</sub> ×P <sub>4</sub>	-7.26**	-8**	-9.09 <sup>ns</sup>	-37.5*
P <sub>1</sub> ×P <sub>5</sub>	2.22 <sup>ns</sup>	-8**	9.09 <sup>ns</sup>	-25 <sup>ns</sup>
P <sub>2</sub> ×P <sub>3</sub>	-6.25**	-13.67**	14.29 <sup>ns</sup>	0 <sup>ns</sup>
P <sub>2</sub> ×P <sub>4</sub>	-23.66**	-28.06**	66.67 <sup>ns</sup>	66.67 <sup>ns</sup>
P <sub>2</sub> ×P <sub>5</sub>	-10.46**	-23.02**	33.33 <sup>ns</sup>	33.33 <sup>ns</sup>
P <sub>3</sub> ×P <sub>4</sub>	-2.5 <sup>ns</sup>	-4.88 <sup>ns</sup>	-14.29 <sup>ns</sup>	-25 <sup>ns</sup>
P <sub>3</sub> ×P <sub>5</sub>	-16.13**	-22.22**	-14.29 <sup>ns</sup>	-25 <sup>ns</sup>
P <sub>4</sub> ×P <sub>5</sub>	1.35 <sup>ns</sup>	-8.13**	0 <sup>ns</sup>	0 <sup>ns</sup>

**N.D.F.F.O:** number of days to first female flowering and **No. F.F:** number of female flowers **M.P:** mid-parent and **B.P:** better-parent. Moreover, **Table (6)**, accurately reported that five hybrids typically gave positive heterosis values for mid parent and only one hybrid gave the positive heterosis over better parent for ovary length. The estimated amount of heterosis over M.P., and B.P for ovary length, fruit length, and the proper ratio between fruit length and diameter were significant positive values for (P<sub>2</sub>×P<sub>4</sub>). Heterosis values were negative values in all crosses except the cross (P<sub>1</sub>×P<sub>3</sub>). These results indicated that hybrids P<sub>1</sub>×P<sub>3</sub>, P<sub>1</sub>×P<sub>4</sub>, P<sub>2</sub>×P<sub>3</sub>, P<sub>2</sub>×P<sub>4</sub>, and P<sub>4</sub>×P<sub>5</sub> gave the positive heterosis from M.P for the ovary and fruit length.

**Table 6.** Average degree of heterosis (ADH)% based on mid- parent (M. P) and better parent (B.P) and of fruits characters.

Genotypes	Fruits characters									
	O. L		F. L		F.W		F. D		L/D. R	
	M.P	B. P	M.P	B. P	M.P	B. P	M. P	B. P	M.P	B. P
P <sub>1</sub> ×P <sub>2</sub>	0 <sup>ns</sup>	-16 <sup>ns</sup>	-2.64 <sup>ns</sup>	-10.06 <sup>ns</sup>	0 <sup>ns</sup>	-1.69 <sup>ns</sup>	2.82 <sup>ns</sup>	-3.19 <sup>ns</sup>	-6.49 <sup>ns</sup>	-18.38 <sup>ns</sup>
P <sub>1</sub> ×P <sub>3</sub>	35.87**	14.68 <sup>ns</sup>	39.81**	-0.61 <sup>ns</sup>	31.39**	7.89 <sup>ns</sup>	14.13**	3.96 <sup>ns</sup>	25.74**	-5.12 <sup>ns</sup>
P <sub>1</sub> ×P <sub>4</sub>	31.29**	21.59 <sup>ns</sup>	29.23**	5.87 <sup>ns</sup>	-8.13 <sup>ns</sup>	-27.82**	-6.67 <sup>ns</sup>	-13.4*	39.62**	22.06 <sup>ns</sup>
P <sub>1</sub> ×P <sub>5</sub>	-24.27**	-40.46**	-13.12*	-39.36**	0.47 <sup>ns</sup>	-21.62**	-1.16 <sup>ns</sup>	-4.49 <sup>ns</sup>	-10.76 <sup>ns</sup>	-36.45**
P <sub>2</sub> ×P <sub>3</sub>	51.25**	11.01 <sup>ns</sup>	1.79 <sup>ns</sup>	-30.91**	10.32 <sup>ns</sup>	-8.17 <sup>ns</sup>	-7.69 <sup>ns</sup>	-10.89*	10.88 <sup>ns</sup>	-23.52**
P <sub>2</sub> ×P <sub>4</sub>	64.03**	29.55*	78.57**	37.61**	6.14 <sup>ns</sup>	-15.54**	-12.04*	-13.4*	106.4**	60.79**
P <sub>2</sub> ×P <sub>5</sub>	-4.4 <sup>ns</sup>	-33.59**	-7.67 <sup>ns</sup>	-38.34**	-5.75 <sup>ns</sup>	-25.55**	-12.57*	-14.89**	4.93 <sup>ns</sup>	-30.93**
P <sub>3</sub> ×P <sub>4</sub>	-11.68 <sup>ns</sup>	-20.18*	-30.51**	-42.3**	-9.28 <sup>ns</sup>	-14.29**	-12.12**	-13.86**	-21.87*	-34.37**
P <sub>3</sub> ×P <sub>5</sub>	-2.5 <sup>ns</sup>	-10.69 <sup>ns</sup>	-1.06 <sup>ns</sup>	-4.1 <sup>ns</sup>	-7.35 <sup>ns</sup>	-13.27*	-3.16 <sup>ns</sup>	-8.91 <sup>ns</sup>	1.16 <sup>ns</sup>	-7.26 <sup>ns</sup>
P <sub>4</sub> ×P <sub>5</sub>	18.72*	-0.76 <sup>ns</sup>	15.87**	-6.14 <sup>ns</sup>	-10.67*	-11.55*	8.6 <sup>ns</sup>	4.12 <sup>ns</sup>	5.06 <sup>ns</sup>	-17.69*

**O.L:** ovary length (cm), **F.L:** fruit length (cm), **F.W:** fruit weight(gm), **F.D:** fruit diameter(cm), **L/D. R:** the ratio between fruit length and diameter, **M.P:** mid-parent and **B.P:** better-parent.

Furthermore, the estimated amount of heterosis was over mid and better parent for early and total yield/plant and demonstrated significant positive values for (P<sub>1</sub>×P<sub>3</sub>, P<sub>1</sub>×P<sub>4</sub>, P<sub>3</sub>×P<sub>4</sub>, and P<sub>3</sub>×P<sub>5</sub>) crosses in **Table (7)**. Furthermore, the most considerable value was for the P<sub>1</sub>×P<sub>3</sub> cross, followed by P<sub>1</sub>×P<sub>4</sub>. The initial results accurately indicate that (P<sub>1</sub>×P<sub>3</sub>, P<sub>3</sub>×P<sub>4</sub>, and P<sub>3</sub>×P<sub>5</sub>) F<sub>1</sub> crosses exceeded their better parent for early and total yield/plant. In this specific case, the non-additive gene effects refer to the dominance that appeared by heterosis values, which means the characters controlled by a non-additive gene refer to one allele being expressed stronger than another allele. In contrast, mid-parent (M.P) heterosis values were positive in all crosses except two crosses (P<sub>1</sub>×P<sub>5</sub> and P<sub>2</sub>×P<sub>5</sub>).

**Table 7.** Average degree of heterosis (ADH)% based on mid- parent (M. P) and better parent (B.P) of yield characters.

Genotypes	Yield characters							
	EY (F. No)		EY (F.W)		TY (F. No)		TY (F.W)	
	M.P	B. P	M.P	B. P	M.P	B. P	M.P	B. P
P <sub>1</sub> ×P <sub>2</sub>	30.43**	5.26 <sup>ns</sup>	29.81 <sup>ns</sup>	3.43 <sup>ns</sup>	34.58**	5.88 <sup>ns</sup>	33.88**	3.84 <sup>ns</sup>
P <sub>1</sub> ×P <sub>3</sub>	115.38**	100**	188.11**	152.54**	100**	89.74**	166.21**	128.09**
P <sub>1</sub> ×P <sub>4</sub>	81.18**	54**	55.48**	7.92 <sup>ns</sup>	68.82**	45.37**	48.48**	4.69 <sup>ns</sup>
P <sub>1</sub> ×P <sub>5</sub>	14.02 <sup>ns</sup>	-15.28*	4.1 <sup>ns</sup>	-33.76**	9.26 <sup>ns</sup>	-14.49*	1.59 <sup>ns</sup>	-33.13**
P <sub>2</sub> ×P <sub>3</sub>	3.45 <sup>ns</sup>	-21.05**	21.91 <sup>ns</sup>	8.99 <sup>ns</sup>	20.39**	-8.82 <sup>ns</sup>	41.66**	25.54*
P <sub>2</sub> ×P <sub>4</sub>	6.54 <sup>ns</sup>	0 <sup>ns</sup>	12.82 <sup>ns</sup>	-6.69 <sup>ns</sup>	-2.46 <sup>ns</sup>	-12.5*	6.48 <sup>ns</sup>	-7.14 <sup>ns</sup>
P <sub>2</sub> ×P <sub>5</sub>	8.53 <sup>ns</sup>	-2.78 <sup>ns</sup>	-0.31 <sup>ns</sup>	-27.26**	15.33**	14.49*	8.66 <sup>ns</sup>	-14.47*
P <sub>3</sub> ×P <sub>4</sub>	77.5**	42**	56.64**	18.7 <sup>ns</sup>	79.78**	48.15**	60.44**	26.34**
P <sub>3</sub> ×P <sub>5</sub>	64.71**	16.67**	48.28**	0.98 <sup>ns</sup>	82.69**	37.68**	65.58**	19.51**
P <sub>4</sub> ×P <sub>5</sub>	21.31**	2.78 <sup>ns</sup>	5.8 <sup>ns</sup>	-9.95 <sup>ns</sup>	23.58**	10.14 <sup>ns</sup>	10.2 <sup>ns</sup>	-2.39 <sup>ns</sup>

**EY (F. No):** early yield as fruit number, **EY (F.W):** early yield as fruit weight, **T.Y. (F. No):** total yield as fruit number, **T.Y. (F.W):** total yield as

fruit weight, **M.P**: mid-parent, **B.P**: better-parent.

**Analysis of variance:**

In this study, the mean square of genotypes, parents, and crosses was extremely significant for all studied characters except fruit diameter **Table (8)**. These results demonstrated the most extensive diversity between the parental lines. They referred to the difference among the genotypes, providing evidence for the existence of a good amount of genetic variability valid for further biometrical assessment and a big amount of considerable variability between produced hybrids that fit consumers' acceptance.

**Table 8.** Analysis of variance for genotypes, parents and crosses for growth, flowering, fruits and yield characters.

S.O.V.	D.F.	M.S.															
		Vegetative					Flowering			Fruits				Yield			
		M.S.L	P.F.W	N.L.B	I.L	L.A	N.D.F.F.O	N.F.F	O.L	F.L	F.W	F.D	L/D.R	EY(F.No)	EY(F.W)	TY(F.No)	TY(F.W)
Genotypes	14	9466.4**	4830.8**	7.5**	6.5**	10856.3**	47.1**	0.8**	2.1**	136.7**	1113.6**	0.2**	12.98**	80.6**	1679326.98**	334.3**	6494815.5**
Parent	4	17541.9**	8658.2**	10.1**	8.2**	18285.8**	66.7**	1.6**	3.04**	238.1**	2535.8**	0.16ns	23.8**	95.9**	2754288.9**	334.0**	8518927.2**
Crosses	9	3744.8**	2255.6**	6.5**	6.1**	8412.4**	31.9**	0.6*	1.7**	104.2**	605.2**	0.2**	9.1**	42.2**	986645.5**	164.0**	4012749.8**
Error	28	206.5	285.6	0.6	0.6	623.5	1.6	0.2	0.2	2.1	66.4	0.04	0.6	3.1	74107.12	9.4	184842.3

**M.S.L**: main stem length(cm), **P.F.W**: plant fresh weight (gm), **No. L.B**: number of lateral branches, **I.L**: internode length(cm), **L.A**: leaf area(cm<sup>2</sup>). **No. D.F.F.O**: number of days to first female flowering and **No. F.F**: number of female flowers **O.L**: ovary length (cm), **F.L**: fruit length (cm), **F.W**: fruit weight(gm), **F.D**: fruit diameter(cm), **L/D. R**: the ratio between fruit length and diameter, **EY (F. No)**: early yield as fruit number, **EY (F.W)**: early yield as fruit weight, **T.Y. (F. No)**: total yield as fruit number, **T.Y. (F.W)**: total yield as fruit weight, \*, and \*\* indicates significance at 5% and 1% level respectively.

**Analysis of variance for combining ability:**

In **Table (9)**, the statistical analysis of variance for combining ability demonstrates extremely significant differences in GCA and SCA for all traits. The studied characteristics with significant variance for SCA had been confirmed to be progressively improved by hybridization, which sufficiently indicated the predominance of non-additive gene effects. Regarding, GCA/SCA ratio represents a smaller amount than unity all told vegetative growth except leaf area, flowering, fruits trait except fruit weight and yield characters, which typically showed the predominance of non-additive gene effect in a very majority of these traits. They found that the calculated ratio general combining ability/specific ability was over unity.

**Table 9.** Analysis of variance for combining ability for different characters in cucumber.

Sources of variations	Vegetative					Flowering			Fruits				Yield			
	M.S.L	P.F.W	N.L.B	I.L	L.A	N.D.F.F.O	N.F.F	O.L	F.L	F.W	F.D	L/D.R	EY(F.No)	EY(F.W)	TY(F.No)	TY(F.W)
GCA	848.01	416.6	0.67	0.72	1474.03	3.57	0.11	0.16	14.19	138.3	0.006	1.25	3.895	153088.06	8.9	484631.6
SCA	1946.85	954.4	1.3	0.76	1229.6	11.23	-0.01	0.47	23.12	101.6	0.05	2.25	25.22	320457.28	126.7	1587699.1
GCA: SCA	0.44	0.44	0.5	0.95	1.19	0.32	-8.2	0.33	0.62	1.4	0.118	0.56	0.154	0.48	0.07	0.30

**M.S.L**: main stem length(cm), **P.F.W**: plant fresh weight (gm), **No. L.B**: number of lateral branches, **I.L**: internode length(cm), **L.A**: leaf area(cm<sup>2</sup>). **No. D.F.F.O**: number of days to first female flowering and **No. F.F**: number of female flowers **O.L**: ovary length (cm), **F.L**: fruit length (cm), **F.W**: fruit weight(gm), **F.D**: fruit diameter(cm), **L/D. R**: the ratio between fruit length and diameter, **EY (F. No)**: early yield as fruit number, **EY (F.W)**: early yield as fruit weight, **T.Y. (F. No)**: total yield as fruit number, **T.Y. (F.W)**: total yield as fruit weight, \*, and \*\* indicates significance at 5% and 1% level respectively.

**Combining ability:**

In **Tables (10 and 11)**, GCA effects of individual parental genotypes were typically found to be significant or highly significant for the most studied traits. In this proper regard, P<sub>5</sub> typically showed the highest GCA value, followed by P<sub>2</sub> and P<sub>4</sub> for most studied traits. These parents were recognized to be a good general combiner for the most critical considered characters. Parent P<sub>5</sub> exhibited the highest significant GCA effects in the desired direction in most crosses for plant vigor, flowering, fruits in addition to yield traits. Therefore, this parent could be typically selected as a potential donor for vegetative growth, fruits, and yield traits. These results are in agreement with (Golabadi *et al.*, 2015; Lalla *et al.*, 2010.) on Japanese cucumber. Regarding P<sub>1</sub>(Beit alpha) was not a good combiner, this disagrees with (Ene *et al.*, 2019), who indicated Beit alpha as a good combiner.

**Table 10.** General combining ability estimates of some quantitative traits in the cucumber parents used for the study.

Genotypes	Vegetative					Flowering	
	M.S. L	P.F. W	No. L. B	I.L	L.A	No. D.F.F. O	No. F. F
P <sub>1</sub>	-44.44**	-31.87**	-0.85**	-0.91**	-20.35**	1.29**	0.6**
P <sub>2</sub>	-14.39**	21.42**	1.01**	-0.95**	-55.5**	2.05**	-0.11 <sup>ns</sup>
P <sub>3</sub>	18.94**	2.75 <sup>ns</sup>	0.77**	0.38*	24.17**	-0.71**	-0.07 <sup>ns</sup>
P <sub>4</sub>	13.04**	-6.39 <sup>ns</sup>	-0.37*	0.67**	42.6**	0.24 <sup>ns</sup>	-0.21*
P <sub>5</sub>	26.85**	14.09**	-0.56**	0.81**	9.08*	-2.86**	-0.21*

**M.S.L**: main stem length(cm), **P.F.W**: plant fresh weight (gm), **No. L.B**: number of lateral branches, **I.L**: internode length(cm), **L.A**: leaf area(cm<sup>2</sup>). **No. D.F.F.O**: number of days to first female flowering and **No. F.F**: number of female flowers.

**Table 11.** General combining ability estimates of some quantitative traits in the cucumber parents used for the study.

Genotypes	Fruit					Yield			
	O. L	F. L	F. W	F. D	L/D. R	EY (F.No)	EY (F.W)	TY (F.No)	TY (F.W)
P <sub>1</sub>	-0.33**	-3.42**	-12.82**	-0.07 <sup>ns</sup>	-1.05**	-1.3**	-343.76**	-3.67**	-831.29**
P <sub>2</sub>	-0.51**	-4.24**	-13.2**	-0.06 <sup>ns</sup>	-1.19**	-0.91*	-379.9**	0.81 <sup>ns</sup>	-546.53**
P <sub>3</sub>	0.36**	3.35**	7.94**	0.15**	0.73**	-1.68**	-51.62 <sup>ns</sup>	-1.81**	122.8 <sup>ns</sup>
P <sub>4</sub>	0.10 <sup>ns</sup>	0.29 <sup>ns</sup>	8.47**	0.02 <sup>ns</sup>	0.07 <sup>ns</sup>	0.66 <sup>ns</sup>	213.33**	0.19 <sup>ns</sup>	326.42**
P <sub>5</sub>	0.38**	4.02**	9.61**	-0.04 <sup>ns</sup>	1.44**	3.23**	561.95**	4.48**	928.61**

O. L: ovary length (cm), F. L: fruit length (cm), F. W: fruit weight(gm), F. D: fruit diameter(cm), L/D. R: the ratio between fruit length and diameter, EY (F. No): early yield as fruit number, EY (F.W): early yield as fruit weight, T.Y. (F. No): total yield as fruit number, T.Y. (F.W): total yield as fruit weight.

On the other hand, the potentiality of crossing between specific parents was detected by estimating the specific combining ability (SCA) effects of each F<sub>1</sub> cross combination for all studied traits shown in Tables (12 and 13). Six of ten hybrids (P<sub>1</sub>P<sub>3</sub>, P<sub>1</sub>P<sub>4</sub>, P<sub>1</sub>P<sub>5</sub>, P<sub>2</sub>P<sub>3</sub>, P<sub>2</sub>P<sub>4</sub>, and P<sub>3</sub>P<sub>5</sub>) showed significant positive SCA effects for main stem length/plant. The majority of the same crosses exhibited significant and desirable positive SCA for other vegetative growth. P<sub>1</sub>P<sub>3</sub>, P<sub>1</sub>P<sub>4</sub>, P<sub>3</sub>P<sub>4</sub>, and P<sub>3</sub>P<sub>5</sub> combinations exhibited significant positive SCA for yield components/plant. Finally, five crosses, namely: (P<sub>1</sub> x P<sub>3</sub>), (P<sub>1</sub> x P<sub>4</sub>), (P<sub>3</sub> x P<sub>4</sub>), (P<sub>3</sub> x P<sub>5</sub>), and (P<sub>4</sub> x P<sub>5</sub>), exhibited significant and desirable positive SCA for all commercial traits, which were effective in the final productivity. These results were in line with Kaur and Dhall (2017); Malav et al. (2018); Lalla et al. (2010); and EL-Shawaf and Baker (1981). Because of the importance of GCA effects, the obtained results in breeding programmes for traditional breeding programmes for a yield or some of its essential components through selection in the segregating generations to exploit a fixable additive gene action.

**Table 12.** Specific combining ability effects of some vegetative and flowering traits of ten cucumber F<sub>1</sub>'s hybrids.

Genotypes	Vegetative					Flowering	
	M.S. L	P.F. W	N.L. B	I.L	L.A	N.D.F.F. O	N.F.F
P <sub>1</sub> ×P <sub>2</sub>	-2.79 <sup>ns</sup>	-4.84 <sup>ns</sup>	-0.76**	-0.65**	-25.4**	-0.11 <sup>ns</sup>	-0.29*
P <sub>1</sub> ×P <sub>3</sub>	50.21**	33.16**	0.48*	-0.65**	35.27**	-2.35**	0.33*
P <sub>1</sub> ×P <sub>4</sub>	75.11**	59.97**	0.95**	0.93**	34.84**	-1.3**	-0.19 <sup>ns</sup>
P <sub>1</sub> ×P <sub>5</sub>	11.63**	-12.51**	-0.19 <sup>ns</sup>	0.42*	50.37**	1.79**	0.14 <sup>ns</sup>
P <sub>2</sub> ×P <sub>3</sub>	16.16**	0.54 <sup>ns</sup>	0.29 <sup>ns</sup>	1.23**	15.75**	0.56 <sup>ns</sup>	0.05 <sup>ns</sup>
P <sub>2</sub> ×P <sub>4</sub>	45.73**	10.02*	-1.9**	1.1**	45.32**	-7.06**	0.52**
P <sub>2</sub> ×P <sub>5</sub>	-12.08**	8.54 <sup>ns</sup>	1.62**	-0.47*	-9.16 <sup>ns</sup>	-1.63**	0.19 <sup>ns</sup>
P <sub>3</sub> ×P <sub>4</sub>	-25.27**	-23.65**	2**	-1.16**	-14.68**	1.37**	-0.19 <sup>ns</sup>
P <sub>3</sub> ×P <sub>5</sub>	12.59**	16.21**	0.19 <sup>ns</sup>	0.13 <sup>ns</sup>	-45.16**	-4.21**	-0.19 <sup>ns</sup>
P <sub>4</sub> ×P <sub>5</sub>	7.16 <sup>ns</sup>	31.35**	0 <sup>ns</sup>	1.17**	-5.92 <sup>ns</sup>	2.17**	-0.05 <sup>ns</sup>

M.S.L: main stem length(cm), P.F.W: plant fresh weight (gm), No. L.B: number of lateral branches, I.L: internode length(cm), L.A: leaf area(cm<sup>2</sup>). No. D.F.F.O: number of days to first female flowering and No. F.F: number of female flowers.

**Table 13.** Specific combining ability values for fruits and yield component of ten cucumber F<sub>1</sub>'s hybrids.

Genotypes	Fruit					Yield			
	O. L	F. L	F.W	F. D	L/D. R	EY (F. No)	EY (F.W)	TY (F. No)	TY (F.W)
P <sub>1</sub> ×P <sub>2</sub>	-0.36**	-2.22**	-4.83*	0.13*	-1.03**	1.92**	48.78 <sup>ns</sup>	6.41**	262.87*
P <sub>1</sub> ×P <sub>3</sub>	0.85**	7.09**	24.37**	0.39**	1.46**	6.02**	1151.83**	10.37**	2181.54**
P <sub>1</sub> ×P <sub>4</sub>	0.51**	2.04**	-7.83**	-0.18**	1.14**	6.02**	376.87**	11.37**	707.59**
P <sub>1</sub> ×P <sub>5</sub>	-0.75**	-3.15**	1.37 <sup>ns</sup>	-0.08 <sup>ns</sup>	-0.79**	-1.89**	-282.75**	-5.92**	-761.27**
P <sub>2</sub> ×P <sub>3</sub>	0.89**	-0.41 <sup>ns</sup>	5.75**	-0.12*	0.08 <sup>ns</sup>	-2.7**	-160.03*	-2.11*	85.11 <sup>ns</sup>
P <sub>2</sub> ×P <sub>4</sub>	0.91**	8.64**	8.89**	-0.19**	3.45**	-1.03*	78.68 <sup>ns</sup>	-5.78**	-145.84 <sup>ns</sup>
P <sub>2</sub> ×P <sub>5</sub>	-0.27*	-2.02**	-3.59 <sup>ns</sup>	-0.26**	-0.11 <sup>ns</sup>	0.73 <sup>ns</sup>	-34.6 <sup>ns</sup>	2.94**	116.3 <sup>ns</sup>
P <sub>3</sub> ×P <sub>4</sub>	-0.85**	-8.09**	-10.59**	-0.3**	-2.08**	4.4**	331.4**	10.51**	793.82**
P <sub>3</sub> ×P <sub>5</sub>	-0.14 <sup>ns</sup>	0.42 <sup>ns</sup>	-8.06**	-0.07 <sup>ns</sup>	0.32 <sup>ns</sup>	6.16**	557.44**	16.22**	1563.97**
P <sub>4</sub> ×P <sub>5</sub>	0.55**	2.87**	-6.25**	0.36**	-0.06 <sup>ns</sup>	0.49 <sup>ns</sup>	-63.84 <sup>ns</sup>	1.56 <sup>ns</sup>	-3.98 <sup>ns</sup>

O. L: ovary length (cm), F. L: fruit length (cm), F. W: fruit weight(gm), F. D: fruit diameter(cm), L/D. R: the ratio between fruit length and diameter, EY (F. No): early yield as fruit number, EY (F.W): early yield as fruit weight, T.Y. (F. No): total yield as fruit number, T.Y. (F.W): total yield as fruit weight.



## DISCUSSION

Highly significant mean performance differences were observed among all parents and hybrids for all characters which agreed with Wehner *et al.* (2000) and Kumar *et al.* (2017). Furthermore, the obtained results proved that the Japanese cucumber was the promising parental line due to its desirable traits, growth, earliness, yield, and its components (Kumar *et al.*, 2017; Gruetze *et al.*, 2016). In this study, the mean square of genotypes, parents, and crosses was highly significant for all measured traits. These results demonstrated the most extensive diversity between the parental lines.

The difference among the genotypes, providing evidence for the existence of an adequate amount of genetic variability valid for further biometrical assessment and a vast amount of variability between produced hybrids. As for, heterosis the superiority of  $F_1$  over the mid-parents (M.P.) or over the better parent (B.P.) is dependent on the accumulation of favorable dominant genes in the  $F_1$  population. Significant positive values of heterosis over mid and better parent for early and total yield/plant were found (Kamooh *et al.*, 2000; Munshi *et al.*, 2007; Lalla, *et al.*, 2010; Mule *et al.*, 2012; Malav *et al.*, 2018). In this case, the non-additive gene effects refer to the dominance that appeared by heterosis values, which means the characters controlled by a non-additive gene with one allele being expressed stronger than another allele. Here, it is interesting to note that hybrid combinations produced from gynocious  $\times$  monoecious crosses are more heterotic than produced from monoecious  $\times$  monoecious parental lines. Regarding, GCA/SCA ratio was less than unity which prove that the predominance of non-additive gene effect in the majority of measured traits (Golabadi *et al.*, 2015; Prashant *et al.*, 2018).

However, Ene *et al.* (2019); Mule *et al.* (2012); El-Eslamboly and Mohamed, (2018) found that the GCA/SCA calculated ratio over than unity. In Combining ability analysis correctly is an imperative method to recognize the genetic potential of parental lines and their hybrids. GCA represents the average performance of a line in a series of crosses, which is governed by additive gene action and is fixable. Five crosses, namely: ( $P_1 \times P_3$ ), ( $P_1 \times P_4$ ), ( $P_3 \times P_4$ ), ( $P_3 \times P_5$ ), and ( $P_4 \times P_5$ ) exhibited significant desirable positive SCA for all commercial traits which effective in the final productivity. these results were in line with Kaur and Dhall, (2017); Malav *et al.*, (2018); Lalla, *et al.*, (2010) and EL-Shawaf and Baker (1981).

Because of the importance of GCA effects, the obtained results in breeding programmes for traditional breeding programmes for a yield or some of its essential components through selection in the segregating generations to exploit a fixable additive gene action. combining ability (SCA) is the performance of these parental lines in specific crosses, which is due to the action of the non-additive gene and is not repairable. It is good to mention that Japanese cucumber (P5) typically exhibited the highest significant GCA effects in the desired direction in most crosses. Therefore, this parent could be selected as a potential donor for all traits. These results are in agreement with Lalla *et al.*, (2010) and Golabadi *et al.* (2015) on Japanese cucumber. While these results disagreed with Ene *et al.* (2019). Finally, five crosses exhibited significant desirable positive SCA for all commercial traits which were effective in the final productivity (Kaur and Dhall, 2017; Malav *et al.*, 2018; EL-Shawaf and Baker, 1981).

## CONCLUSION

The research contributed to the intermixing of some desirable inbred lines to elicit promising hybrids suitable for picking pickled cucumbers. These lines, characterized by significant differences, served as a broad genetic basis for breeders and varied between long and short fruit varieties and multi-lateral branch varieties. Furthermore, these inbred lines and hybrids are subjected to additional research to demonstrate their suitability for manufacturing process packaging. Scientifically based on the key findings that indicate the non-additional effects of specific genes, these parents should typically be included in hybridization programs directly. The non-additive effects of the genes (the effect of dominance) are non-inherited but transmitted by mating, in contrast to the additive effects of the genes, which are inherited and transmitted through generations, so the best way, in this case, represents the selection.

Therefore, the research typically recommends using these parents in hybridization programs, especially the Japanese line (P5), which is accurately characterized by the highest fruit length and productivity, and *C. sativus* var. *hardwickii* (P2), which is typically characterized by the numerous lateral branches that equally affect the economic productivity to take advantage of the dominance effects of the specific genes typically controlling these essential traits. The future plan for this research will be complemented by a preceding part to carefully study the pickling quality of produced hybrids.

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## تربية هجن خيار تـخليل جديدة

### أ. التوصيف المورفولوجي والدراسات الوراثية

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### الملخص العربي

تعتبر تربية الخضر واحدة من أهم الوسائل لتحقيق الأمن الغذائي . تمت الدراسة الحالية علي خمس من سلالات الخيار النقية للحصول علي عشرة هجن بطريقة التلقيح النصف دائري. أشارت النتائج الي إختلافات معنوية عالية بين كل التراكيب الوراثية مقارنةً بالصنف المقارن في كل الصفات المدروسة. بالإضافة الي التأثيرات المعنوية للقدرة العامة والخاصة علي الإتلاف. بينما قلت النسبة بين القدرة العامة الي القدرة الخاصة علي الإتلاف عن الواحد الصحيح وهو مايشير الي أن مكون التباين الوراثي غير الاضافي هو الأعلي. علاوة علي ما أظهرته النتائج من تفوق الأبوين (الأب الثاني P<sub>2</sub>) و (الأب الخامس P<sub>5</sub>) كمانح عام جيد في كل الصفات. حققت الهجن الخمسة (P<sub>1</sub>×P<sub>3</sub>)، (P<sub>1</sub>×P<sub>4</sub>)، (P<sub>3</sub>×P<sub>4</sub>) ، (P<sub>3</sub>×P<sub>5</sub>) و (P<sub>4</sub>×P<sub>5</sub>) معنوية موجبة في القدرة الخاصة علي الإتلاف من بين الهجن المختبرة بالنسبة للصفات المرتبطة بالإنتاجية. حققت معظم هذه الهجن قوة هجين أعلي من متوسط الابوين وأعلي من الاب الاعلي لصفات النمو الخضري ، الزهري و المحصول المبكر والكلي. عموماً فإن الاب (P<sub>5</sub>) يجب أن يدخل كأب واعد في برامج التحسين الوراثي بالتهجين. الكلمات المفتاحية: الخيار، التخليل، السلالات المرباة داخليا، القدرة علي الإتلاف و قوة الهجين