



# HETEROISIS AND COMBINING ABILITY IN CUCUMBER UNDER SALT CONDITION

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## Abstract

The objective of this work was to evaluate seven parental lines of cucumber and twenty one  $F_1$ 's generated by half diallel cross, using randomized complete block design with three replications to study heterosis, potance ratio and combining ability for yield and yield component traits under salt conditions. Estimated heterosis showed that cross EGY-34×EGY-72 had the highest Better Parent (BP) heterosis in total yield. Significant general (GCA) and specific (SCA) combining ability variances were obtained in all studied traits implying that both additive and non-additive gene effects operated in the genetic expression these traits. Relative magnitude of GCA and SCA variances indicated preponderance of non-additive gene action for all traits. OZP-05 and GUAT- 85 are best general combiners while INDIA-75×GUAT- 85, OZP-05×ZAM-170, OZP-05×EGY-34, ZAM-170×GUAT- 85 and ZAM-170×EGY-34 were the best specific combiners for total yield trait.

**Key words:** *Cucumis sativus*, Heterosis, GCA, SCA, Correlation, potance ratio.

## Introduction

Cucumber (*Cucumis sativus* L.) is one of the popular and most important vegetable crops worldwide as well as in Egypt. It belongs to Cucurbitaceae family, which comprises of 117 genera and 825 species (Gopala krishnan, 2007).

Saline soil is an important problem of agricultural lands all over the world which causes great loss in crop productivity. Soluble salts accumulated in soil at harmful levels adversely affects development and productivity of plants in large areas of the world with low rainfall and as a result of great loss in crop production which leads to low economic returns and soil erosions at large scale. Unfortunately, most of the new reclaimed area in Egypt are affected by salt which lead to reducing yields and quality, also, The agriculture in Egypt depends on irrigation mainly from the river Nile and in a lot places from underground water which most of them contain a high level of salinity. (Amal, *et al.*, 2007). For this reason, it has become important to screen the germplasm of crops to isolate potential combining lines and desirable cross combinations either to exploit heterosis or to have new recombinants. so, any useful way in choosing desirable parents and crosses tolerant to salt stress will be important to breeders. Cucumber has moderate sensitivity of salinity meaning that growth and productivity is restricted by the

high saline conditions (Mather and Jink, 1982). Level of salinity more than 1.3 EC significantly influenced the growth of cucumber (Mumtaz Khan, 2013).

Recently, many efforts have been employed to produce crops in salt affected soils such as irrigating with saline water through expensive technical reclamation methods such as using the magnetic water and grow cucumber grafted on salt tolerant rootstocks, however, the most methods alternative to growing crops under salinity environments is through genetic improvement (Tiwari *et al.*, 2011). Malik *et al.*, (2010) confirmed that genotypic variation salt tolerance in cucumber has already been found. However, Tiwari *et al.*, (2011) refered that the genetics of salt tolerance in cucumber is poorly understood, Munns and Tester, (2008) showed that this due to the complexity of salt tolerance. (Maas and Poss, 1989 and Munns and Tester, 2008). Kere *et al.*, (2013) showed that it is complicated to improve salinity tolerance of cucumber through simple selection methods or pedigree breeding, this due to presence of dominance gene action, so, to concentrate desirable alleles, inter-mating of superior segregants could also be pursued. Marium *et al.*, (2019) screened 12 cucumber genotypes for salinity tolerance and found that the studied genotypes differed in its tolerant to salinity.

Choudhaury *et al.*, (1965) refer that using hybrids is

the quickest method of combining the valuable traits into one, besides the added advantages of heterotic yield. Also, understanding of gene action for expression quantitative traits is very important to decide the proper breeding method for genetic improvement. Estimation of heterosis for fruit quality and yield traits is useful to judge the best hybrid combination for exploitation of superior hybrids. Heterosis over mid parent and better parent on cucumber were reported for some characters, *i.e.*, total yield (Madhu, 2010, Airina *et al.*, 2013, Arya and Singh, 2014, Jat *et al.*, 2015, Singh *et al.*, 2015, Simi *et al.*, 2017, AL-Juboori and AL-Mashhadani, 2018, Singh and Tiwari, 2018, Ene *et al.*, 2019 and Preethi, 2019), stem length (Kere *et al.*, 2013, Simi *et al.*, 2017, Singh and Tiwari, 2018 and Abd Rabou *et al.*, 2019), fruit length (Simi *et al.*, 2017 and Abd Rabou *et al.*, 2019), early yield (AL-Juboori and AL-Mashhadani, 2018) and fruit diameter to desirable negative direction (Jat *et al.*, 2015, Singh *et al.*, 2015 and Simi *et al.*, 2017).

Several studies of combining ability for fruit quality and yield traits are available in cucumber. Dogra and Kanwar (2011) and Ene *et al.*, (2019) found significant general (GCA) and specific (SCA) combining ability variances in the characters fruit length, fruit yield and fruit diameter, total implying that both the additive and non-additive gene effects operated in the genetic expression of these characters. Tiwari *et al.*, (2011) found that values of GCA were greater than SCA which showed the preponderance of additive gene action components for inheritance of total yield under soil salinity condition on cucumber, indicating that relative magnitude of GCA and SCA variances indicated preponderance of additive gene action for these traits. Abd Rabou *et al.*, (2019) found the preponderance of non-additive and additive gene effects in stem length and fruit length traits, respectively. However, Moushumi and Sirohi (2010) and Dogra and Kanwar (2011) revealed that variance of SCA was greater than that of GCA in all studied cucumber traits. This indicates that all these traits were influenced by both

**Table 1:** Sources of used cucumber accessions in the current study.

Genotype	CODE	Source
INDIA-75	Line1	CGN
OZP-05	Line 2	CGN
ZAM-170	Line 3	CGN
GUAT- 85	Line 4	CGN
EGY-34	Line 5	HRI
EGY-17	Line 6	HRI
EGY-72	Line 7	HRI

CGN = Gene bank of Netherland and HRI = Horticultural Research Institute.

GCA and SCA, with the later having a greater influence. This reflects the role of non-additive type of gene action in the expression of these traits.

High level of salinity is an important agricultural problem in old and new reclaimed soils of Egypt. Therefore, the objectives of the current study were to determine breeding lines/varieties having good combining ability effects and best cross combinations for developing promising hybrids for yield and fruit quality characters under salinity stress using diallel mating design.

## Materials and Methods

This study was carried out in research facilities of Horticulture Research Institute and private farm in Wadi El-Netroon, Behira Governorate, Egypt during the period from 2015 to 2017.

### Plant materials, treatments and cultivation

The materials used in this study consisted of seven horticultural superior and optimally divergent inbred lines of cucumber (*Cucumis sativus* L.) which illustrated in Table 1. Selfing of the seven parents was done twice to insure high degree of purity of each parent before crossing. Thereafter, half diallel crosses were made among these parents to obtain twenty one F<sub>1</sub> hybrids (excluded the reciprocals) in 2015.

### Experimental design

#### Evaluation of genotypes under greenhouse pot condition

Screening of 7 inbred lines and 21 hybrids of cucumber under greenhouse pots condition for salt tolerance was done. Seeds were sown on 29 June 2015 in 1.5 L plastic pots which filled with a 1:1 (v/v) mixture of peat and vermiculite. When the first true leaf had appear completely, the plants were subjected to salt stress with different levels of salinity like 250 (control), 2000 and 2500 ppm. Artificial saline water were produced by adding sea water to local tap (fresh) water. All seedlings were watered with salt solution every other day to pot 'field capacity' (irrigation varied from 100 to 150 ml) according to weather conditions and growth stage. All studied genotypes were grown in a complete randomized design with three replications. Five pots per replication per treatment were maintained. Five seeds of each cucumber genotype were sown in each pot. After germination, two vine was retained in each pot. The last observations on the experiment was taken after 60 days as majority of the genotypes started showing wilting symptoms. Data were collected from 10 plants for every genotype. To assess the salt tolerance of the studied genotypes some traits were assessed, *viz.*, germination

percentage, stem length, leaf area, fifth internode length and fruit length.

### Evaluation of genotypes under open field condition

Twenty one half diallel hybrids along with their 7 parental lines were grown under open field condition at Wadi El-Netroon, Behira Governorate, Egypt under salt stress (irrigated with 2900 ppm salt water) during winter season of the year 2016 and 2017 in a randomized complete block design (RCBD) with three replications. Seeding and transplanting dates were September 4<sup>th</sup> and September 24<sup>th</sup>, 2016 and September 2<sup>nd</sup> and September 22<sup>th</sup>, 2017, respectively. The dominant soil in the experiment was a sand. The area of the experiment in both two seasons was divided into 5 rows. Each plot consisted of one row with 1.5 m wide and five meter length. Plants were transplanted on both sides of the row. The distance between plants on each side of the row was 50 cm apart. Each experimental plot consisted of twenty plants. Agronomic practices were followed and plant protection measures were taken as and when required following the recommendations of Ministry of Agriculture, Egypt.

#### Trait measurements

The following reproductive characters were monitored; stem length was measured after 60 days from transplanting from the surface of the soil to the end of main stem in cm, fruit length was determined in cm using average of 10 fruits by ruler, fruit diameter was determined in cm using average of 10 fruits at the middle of the fruit by vernier caliper, early yield/plant was determined in kg of total fruits weight of the first five pickings and total yield/plant was determined in kg by weighting all produced fruits for all pickings.

#### Genetic analysis

The Performance of the  $F_1$ 's and their parents was determined according to Allard (1960). Potence ratio, *i.e.*, the relative potency of gene set (P) was used to determine the direction of dominance according to formula of Smith (1952). Heterosis (H) was calculated as the percentage of deviation from the mean parent and best parent according to Sinha and Khanna (1975) formula. Data were statistically analyzed for the study of general (GCA) and specific (SCA) combining ability according to Griffing (1956) method II, model I.

## Results and Discussion

### Evaluation of genotypes under greenhouse pot condition

Increasing salt concentration showed negative effects

on germination rate of cucumber genotypes and its characters were deteriorated under the influence of salt stress table 2. All seeds of the studied genotypes germinated under 250 ppm salt condition, however, they differed significantly, under 2000 and 2500 ppm. At 2000 ppm, some genotypes didn't germinate, *viz.*,  $P_2$  and  $P_5$ , meanwhile, the genotypes  $P_4 \times P_6$ ,  $P_1 \times P_6$  and  $P_6$  showed maximum values of germination. At 2500 ppm level, few genotypes showed good germination and the genotypes  $P_4 \times P_6$ ,  $P_1 \times P_6$  and  $P_6$  were again maintained the highest germination.

For stem length trait, the genotypes  $P_4 \times P_6$  gave maximum value at 250 ppm salinity level (163.6 cm) followed by commercial hybrids Prince and Ishrak (160.5 and 157.5 cm, respectively), while the genotype  $P_3 \times P_7$  was the shortest one (70.2 cm). Stem length decreased in all studied genotypes under increasing of salinity levels. Under 2000 and 2500 ppm salinity levels, the genotype  $P_4 \times P_6$  showed higher values of stem length (154.8 and 130.4, respectively).

Same trend was observed for leaf area trait which was gradually decreased with the increased of salinity levels table 2. At 250 ppm salinity level, the genotype Ishrak achieved highest value of leaf area (274.7 cm<sup>2</sup>) as compared to rest of all genotypes followed by the genotype  $P_1 \times P_7$  (272.0 cm<sup>2</sup>) without significant differences between them. However, at 2000 ppm salinity level, maximum value was observed in Prince hybrid (224.3 cm<sup>2</sup>). At 2500 ppm salinity level, the genotypes  $P_1 \times P_6$  and  $P_6$  gave the highest values of leaf area (194.1 and 183.8 cm<sup>2</sup>, respectively) without significant differences between them.

Number of nodes/plant of all studied cucumber genotypes was affected by increasing levels of salinity table 2. Under 250 ppm salinity level, maximum number of nodes/plant was observed in the genotype  $P_4 \times P_6$  (10.6), however, minimum value was noted in the genotype  $P_5$  (6.1). At 2000 ppm salinity level, the genotypes Prince and  $P_4 \times P_6$  gave the highest values of number of nodes/plant without differences between them, meanwhile, the genotype  $P_4 \times P_6$  gave the highest value (6.7) at 2500 ppm salinity level.

Fruit length character affected by increasing of salinity levels table 2. Maximum values of fruit length were observed in the genotypes  $P_1 \times P_3$  and  $P_3 \times P_6$  at both of 250 and 2000 ppm salinity levels without significant differences between them. However, Under 2500 ppm level, genotype  $P_4 \times P_6$  exhibited highest value of fruit length (14.9 cm). Results indicated that the genotype  $P_4 \times P_6$  behaved well in all studied salinity levels as compared

**Table 2:** Mean performance of 7 cucumber inbred lines and their hybrids for studied traits under greenhouse pot condition.

Chara- cters	germination percentage (%)			Stem length (cm)			Leaf area (cm <sup>2</sup> )			fifth internode length (cm)			Fruit length (cm)		
	ppm	250	2000	2500	250	2000	2500	250	2000	2500	250	2000	2500	250	2000
P <sub>1</sub>	5.0*	4.0	3.2	102.2	91.9	66.6	236.2	188.6	168.3	7.3	4.4	3.7	20.1	15.5	13.0
P <sub>2</sub>	5.0*	0.0	0.0	115.4	0.0	0.0	224.1	0.0	0.0	8.3	0.0	0.0	17.6	0.0	0
P <sub>3</sub>	5.0*	2.6	0.0	83.8	86.2	0.0	178.8	136.3	0.0	6.5	3.5	0.0	22.0	17.9	0
P <sub>4</sub>	5.0*	3.7	1.9	118.4	110.3	62.1	178.8	124.8	104.8	8.0	5.0	4.1	16.5	12.1	9.6
P <sub>5</sub>	5.0*	0.0	0.0	75.8	0.0	0.0	0.0	157.1	0.0	6.1	0.0	0.0	13.8	0.0	0
P <sub>6</sub>	5.0*	4.6*	3.8	133.4	129.6	109.1	253.8*	203.8	183.8	9.1	6.2	5.3	21.3	16.9	14.4
P <sub>7</sub>	5.0*	1.4	0.0	77.9	89.5	0.0	241.1	190.3	0.0	6.3	3.8	0.0	15.5	11.4	0
P <sub>1</sub> ×P <sub>2</sub>	5.0*	1.2	0.0	104.3	109.7	0.0	267.6*	217.6	0.0	7.3	4.3	0.0	21.0	16.4	0
P <sub>1</sub> ×P <sub>3</sub>	5.0*	1.8	0.0	108.5	107.1	0.0	247.8	195.9	0.0	7.1	4.2	0.0	24.3*	20.2	0
P <sub>1</sub> ×P <sub>4</sub>	5.0*	3.7	2.9	140.8	139.1	113.8	226.6	174.7	151.7	9.3	6.4	5.4	18.1	13.7	11.8
P <sub>1</sub> ×P <sub>5</sub>	5.0*	1.7	0.0	99.0	88.4	0.0	223.7	173.7	0.0	7.1	3.9	0.0	17.0	13.3	0
P <sub>1</sub> ×P <sub>6</sub>	5.0*	4.7*	3.9	145.9	150.9*	109.2	268.2*	216.3	194.1	9.5	6.6	5.6	22.2	17.6	15.0
P <sub>1</sub> ×P <sub>7</sub>	5.0*	2.3	0.0	99.4	116.5	0.0	272.0*	216.3	0.0	7.0	0.0	4.1	17.7	13.0	0
P <sub>2</sub> ×P <sub>3</sub>	5.0*	0.1	0.0	102.1	36.1	0.0	199.2	47.9	0.0	7.0	1.6	0.0	20.6	5.4	0
P <sub>2</sub> ×P <sub>4</sub>	5.0*	0.9	0.0	118.5	95.9	0.0	248.6	196.5	0.0	8.0	5.1	0.0	18.3	13.9	0
P <sub>2</sub> ×P <sub>5</sub>	5.0*	0.2	0.0	91.5	31.9	0.0	213.8	51.6	0.0	6.9	1.4	0.0	16.6	4.3	0
P <sub>2</sub> ×P <sub>6</sub>	5.0*	3.2	0.0	147.1*	153.1*	0.0	251.4*	202.5	0.0	9.0	6.1	0.0	16.0	11.9	0
P <sub>2</sub> ×P <sub>7</sub>	5.0*	0.8	0.0	90.4	84.0	0.0	252.9	203.3	0.0	6.9	4.1	0.0	18.3	13.9	0
P <sub>3</sub> ×P <sub>4</sub>	5.0*	3.5	0.0	108.5	110.2	0.0	208.6	158.6	0.0	7.6	4.6	0.0	23.0*	18.6	0
P <sub>3</sub> ×P <sub>5</sub>	5.0*	1.6	0.0	90.2	85.1	0.0	186.5	134.4	0.0	6.7	3.8	0.0	17.5	13.1	0
P <sub>3</sub> ×P <sub>6</sub>	5.0*	3.2	0.0	130.2	139.6	0.0	204.2	154.2	0.0	8.4	5.7	0.0	25.0*	20.0	0
P <sub>3</sub> ×P <sub>7</sub>	5.0*	3.2	0.0	70.2	81.4	0.0	210.7	158.8	0.0	6.2	3.4	0.0	20.8	16.7	0
P <sub>4</sub> ×P <sub>5</sub>	5.0*	2.2	0.0	113.1	105.3	0.0	197.7	148.0	0.0	7.7	4.9	0.0	15.2	10.8	0
P <sub>4</sub> ×P <sub>6</sub>	5.0*	5.0*	4.4*	163.6*	154.8*	130.4	227.6	180.0	160.0	10.6*	7.7	6.7	22.0	17.6	14.9
P <sub>4</sub> ×P <sub>7</sub>	5.0*	1.8	0.0	93.8	97.8	0.0	234.5	182.6	0.0	7.4	4.8	0.0	19.8	15.4	0
P <sub>5</sub> ×P <sub>6</sub>	5.0*	2.2	0.0	121.7	90.9	0.0	224.5	175.0	0.0	7.5	4.8	0.0	22.5	17.8	0
P <sub>5</sub> ×P <sub>7</sub>	5.0*	0.9	0.0	123.8	111.6	0.0	204.5	150.5	0.0	7.5	4.7	0.0	15.8	11.7	0
P <sub>6</sub> ×P <sub>7</sub>	5.0*	2.2	0.0	136.6	125.0	0.0	256.2*	202.2	0.0	9.0	6.3	0.0	19.1	14.4	0
prince	5.0*	2.9	1.6	160.5*	131.3	100.7	269.6*	224.3	160.8	10.0*	7.8	5.1	20.2	14.9	13.0
Ishrak	5.0*	3.6	1.9	157.5*	124.2	97.7	274.7*	211.0	140.8	9.6*	7.1	4.3	17.8	12.6	11.0
LSD <sub>0.5%</sub>															

to others.

### Evaluation of genotypes under open field condition

#### Mean performance

Means estimates of parents and their hybrids under open field condition under salt stress (irrigated with 2900 ppm salt water) during winter season of the year 2016 and 2017 are given in Table 3. Differences among genotypes (parents and hybrids) for all studied characters were significant, indicating wide diversity among the parental materials used in this study, which is essential for half diallel cross design to be effective (Hayman 1954).

In general, parental lines showed narrower ranges than F<sub>1</sub>'s for all studied characters in both two seasons. Moreover, means of parental lines were less than means of F<sub>1</sub>'s for all studied characters in both two seasons.

Comparing with commercial hybrids, means of F<sub>1</sub>'s were less than means of commercial hybrids for all studied characters in both two seasons except traits early yield and total yield which were higher than the hybrid Ishrak in the second season.

Stem length trait ranged from 78.8 to 172.3 cm in the first season and from 76.9 to 172.2 cm in the second season. The cross P<sub>4</sub>×P<sub>6</sub> produced the highest significant stem length followed by the cross P<sub>2</sub>×P<sub>6</sub> without significant differences between them and with commercial hybrids except the hybrid Prince in the first season. Concerning fruit length character, data ranged from 11.5 to 21.0 cm in the first season and from 11.5 to 21.6 cm in the second season. The cross P<sub>1</sub>×P<sub>3</sub> had, significantly, the longest fruits with significant differences between it and the two commercial hybrids in the both studied

seasons. Fruit diameter ranged from 2.8 to 4.1 cm in the first season and from 2.3 to 4.1 cm in the second season. The highest value of fruit diameter was detected in fruits of the  $F_1$  hybrid  $P_3 \times P_6$  (4.1 cm in both seasons) with significant differences between it and two commercial hybrids in both seasons. Early yield per plant ranged from 0.2 to 2.1 kg/plant in the first season and from 0.3 to 2.2 kg/plant in the second season. The hybrid  $P_1 \times P_2$  produced the highest significant early yield (2.1 and 2.2 kg in the first and second seasons, respectively) followed by the cross  $P_1 \times P_4$  with significant differences between them in the second season and with significant differences

between it and commercial hybrids. Regarding total yield per plant trait, values ranged from 0.9 to 4.1 kg in the first season and from 1.2 to 4.5 kg in the second season. The cross  $P_1 \times P_2$  produced the highest total yield (4.1 and 4.5 kg in the first and second seasons, respectively) followed by the hybrid  $P_1 \times P_6$  without a significant difference between them and with significant differences with commercial hybrids in both two seasons (2.3 and 2.4 in the first season and 3.1 and 2.5 in the second season for the hybrids Prince and Ishrak, respectively).

In general, some hybrids were taller and had wider and longer fruits than parents. Most crosses were earlier

**Table 3:** Mean performance of the 7 cucumber inbred lines and their hybrids for studied traits in 2016 and 2017.

Geno- types	Fruit diameter (cm)		Fruit length (cm)		Stem length (cm)		Early yield (kg/plant)		Total yield (kg/plant)	
	2106	2107	2106	2107	2106	2107	2106	2107	2106	2107
P <sub>1</sub>	3.1	3.3	16.2	16.2	99.7	101.8	1.0	1.1	2.8	3.0
P <sub>2</sub>	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
P <sub>3</sub>	3.7	3.9	18.6	20.1	93.9	94.0	0.3	0.3	0.9	1.2
P <sub>4</sub>	2.8	2.9	12.5	11.9	118.7	121.6	0.9	0.9	2.9	3.1
P <sub>5</sub>	3.8	3.9	11.8	12.5	78.8	76.9	0.2	0.5	1.3	1.6
P <sub>6</sub>	4.0	4.1	17.3	15.5	136.6	138.5	1.0	1.1	2.1	2.4
P <sub>7</sub>	3.2	3.3	12.1	12.6	98.3	99.5	0.2	0.5	1.2	1.6
Mean	2.9	3.1	12.6	12.7	89.4	90.3	0.5	0.6	1.6	1.8
P <sub>1</sub> ×P <sub>2</sub>	3.5	3.6	17.0	16.2	118.1	115.1	2.1	2.2	4.1	4.5
P <sub>1</sub> ×P <sub>3</sub>	3.7	3.8	21.0	20.6	114.8	117.4	1.2	1.1	2.4	2.8
P <sub>1</sub> ×P <sub>4</sub>	3.4	3.5	14.2	14.6	147.1	145.4	1.7	1.6	3.0	3.3
P <sub>1</sub> ×P <sub>5</sub>	3.1	3.1	13.9	13.4	96.2	98.4	1.3	1.2	2.1	2.4
P <sub>1</sub> ×P <sub>6</sub>	3.7	3.9	18.2	17.9	158.9	155.3	1.5	1.5	3.8	4.3
P <sub>1</sub> ×P <sub>7</sub>	3.5	3.6	13.6	13.8	107.8	111.7	1.0	1.0	3.0	3.4
P <sub>2</sub> ×P <sub>3</sub>	3.6	3.6	15.8	16.9	116.0	116.0	0.2	0.4	1.3	1.7
P <sub>2</sub> ×P <sub>4</sub>	3.2	3.3	14.4	14.7	103.7	107.6	0.9	1.0	2.7	2.9
P <sub>2</sub> ×P <sub>5</sub>	0.0	2.9	0.0	13.5	0.0	103.1	0.0	0.7	0.0	2.3
P <sub>2</sub> ×P <sub>6</sub>	3.1	3.1	12.3	13.3	161.5	163.5	1.2	1.2	2.3	2.7
P <sub>2</sub> ×P <sub>7</sub>	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
P <sub>3</sub> ×P <sub>4</sub>	3.5	3.5	19.2	19.6	118.6	114.7	0.3	0.4	2.4	2.7
P <sub>3</sub> ×P <sub>5</sub>	2.8	2.9	13.6	14.9	93.2	93.3	0.2	0.3	2.0	2.4
P <sub>3</sub> ×P <sub>6</sub>	4.1	4.1	20.6	20.2	133.9	135.9	0.9	0.8	3.2	3.5
P <sub>3</sub> ×P <sub>7</sub>	3.4	3.5	17.4	18.6	90.1	87.8	0.4	0.6	2.0	2.4
P <sub>4</sub> ×P <sub>5</sub>	2.3	2.3	11.5	12.7	113.0	115.3	1.1	1.2	2.4	2.8
P <sub>4</sub> ×P <sub>6</sub>	3.6	3.8	18.4	18.8	172.3	172.2	1.3	1.5	3.2	3.6
P <sub>4</sub> ×P <sub>7</sub>	3.8	3.8	16.0	17.1	105.5	107.7	0.3	0.4	2.5	2.8
P <sub>5</sub> ×P <sub>6</sub>	3.6	3.6	18.4	18.7	132.3	101.3	1.3	1.4	2.6	2.9
P <sub>5</sub> ×P <sub>7</sub>	3.1	3.2	12.3	13.4	118.6	116.9	0.9	1.0	2.2	2.5
P <sub>6</sub> ×P <sub>7</sub>	3.5	3.5	15.0	15.3	133.4	133.4	0.6	0.7	2.9	2.8
Mean	3.1	3.3	14.4	15.4	111.2	114.9	0.9	1.0	2.4	2.8
prince	3.3	3.3	15.0	15.9	150.5	160.5	1.3	1.4	2.3	3.1
Ishrak	3.2	3.3	15.7	16.8	157.5	157.5	0.8	1.1	2.4	2.5
LSD <sub>0.05</sub>	0.4	0.7	2.9	2.3	20.1	22.2	0.4	0.5	0.5	0.8

and had higher productively than their mid parent and higher parent.

### Potence ratio and heterosis

High positive P values indicating over dominance towards high parent were found in all crosses for stem length, fruit diameter and fruit length traits. For early yield trait, different types of dominance were observed. High Positive P values were estimated indicating over dominance of the high parent in 12 crosses and partial dominance towards the high parent in four crosses, meanwhile, negative P values were observed indicating partial dominance towards the low parent in two crosses, complete dominance towards low parent were found in two crosses and over dominance towards low parent was found in one cross. Regarding to total yield trait, different types of dominance were observed. High Positive P values were estimated indicating over dominance of the high yielding parent in 12 crosses and partial dominance towards the high parent in six crosses, however, negative P values were estimated indicating over dominance of the low parent in one cross and complete dominance of the low parent in two crosses. These results partially confirm previous report of Tiwary *et al.*, (2011) and Kere *et al.*, (2013) who observed over dominance and partial dominance towards the high parent in studied crosses under salt condition.

Heterosis estimates over mid parent and high parent are given in table 4. For the fresh consumption, less fruit diameter is preferred (Arya and Singh, 2014). Three out of the 21 evaluated hybrids showed significant negative heterosis over its mid parent for fruit diameter

trait. Concerning high parent heterosis, 6 out of the 21 evaluated hybrids showed significant positive heterosis over its higher parent ranging from -1.00% to -0.02%. For fruit length trait, 10 hybrids gave mid parent heterosis. With regard to high parent heterosis, 5 crosses showed significant positive heterosis. Concerning stem length trait, 7 hybrids showed significant heterosis over mid parent. Meanwhile, 5 hybrids gave positive high parent heterosis. For early yield trait, 11 out of the 21 evaluated hybrids exhibited significant positive heterosis over mid parent. All the hybrids that involved P<sub>1</sub> as a common parent had positive heterosis over mid parent. With regard to high parent heterosis, 5 out of the 21 evaluated hybrids exhibited significant positive heterosis ranging from 0.05% for the hybrid P<sub>2</sub>×P<sub>4</sub> to 3.45% for the hybrid P<sub>6</sub>×P<sub>7</sub>. Three out of these 5 crosses had P<sub>1</sub> as a common parent. Fifteen out of the 21 evaluated hybrids exhibited significant positive heterosis over mid parent for total yield trait, meanwhile, 9 evaluated hybrids exhibited significant positive heterosis over its higher parent ranging from 0.10% for the hybrids P<sub>1</sub>×P<sub>7</sub> and P<sub>4</sub>×P<sub>6</sub> to 0.58% for the hybrid P<sub>3</sub>×P<sub>7</sub>. These results are in agreement with those of Kere *et al.*, (2013), Jat *et al.*, (2015), Singh *et al.*, (2015), Simi *et al.*, (2017), AL-Juboori and AL Mashhadani (2018), Singh and Tiwari (2018), Abd Rabou *et al.*, (2019), Ene *et al.*, (2019) and

Preethi, (2019) who estimated mid and better parent heterosis values for cucumber traits in some crosses.

**Combining ability**

Combining ability analysis table 5 showed significant mean squares due to both general and specific combining abilities for all studied traits, indicating that both additive and non- additive gene action existed except for NFF trait, which was controlled by additive gene action only. Concerning GCA/ SCA ratio, it was indicated that all studied traits exhibited low GCA/ SCA ratio which less than unity, revealing the predominance of non- additive gene effects in inheritance of these characters. These results agree with those of Dogra and Kanwar (2011), Ene *et al.*, (2019) and Abd Rabou *et al.*, (2019) who found that mean squares due to GCA and SCA were

**Table 5:** Mean squares for general (GCA) and specific (SCA) combining ability from ANOVA for 21 F<sub>1</sub>'s and their parents for studied characters in cucumber.

Character	GCA	SCA	GCA/SCA
Stem length	684.9**	1031.7	0.7
Fruit length	11.1	11.9	0.9
Fruit diameter	0.4	0.7	0.5
Early yield/plant	0.1	0.2	0.6
Total yield/plant	0.3	0.6	0.6

**Table 4:** Potence ratio (P), heterosis over mid parent (MP) and over high parent (HP) of 21 F<sub>1</sub>'s for studied traits of cucumber in season 2015.

Hybrids	Frit diameter			Fruit length			Stem length			Early yield			Total yield		
	P	MP	HP	P	MP	HP	P	MP	HP	P	MP	HP	P	MP	HP
P <sub>1</sub> ×P <sub>2</sub>	1.6	1.22*	1.22	8.1	1.10*	0.05	49.8	1.37*	0.19	3.02	3.02*	1.01*	1.9	1.93*	0.47*
P <sub>1</sub> ×P <sub>3</sub>	3.4	0.87	0.08*	17.4	0.20*	0.13*	96.8	0.19	0.15	1.44	0.87*	0.17	0.7	0.34*	-0.12
P <sub>1</sub> ×P <sub>4</sub>	3.0	2.42*	0.15*	14.4	-0.01	-0.12	109.2	0.35*	0.24*	10.11	0.79*	0.66*	2.9	0.05	0.03
P <sub>1</sub> ×P <sub>5</sub>	3.5	-1.12	-0.11	14.0	-0.01	-0.14*	88.7	0.08	-0.03	1.61	1.14*	0.25	0.1	0.04	-0.23*
P <sub>1</sub> ×P <sub>6</sub>	3.6	0.34	0.04	16.8	0.09	0.05	118.1	0.35*	0.16*	16.76	0.47*	0.43*	4.1	0.56*	0.37*
P <sub>1</sub> ×P <sub>7</sub>	3.1	46.20	0.12	14.2	-0.04	-0.16	99.0	0.09	0.08	0.95	0.65*	-0.02	1.4	0.51*	0.1*
P <sub>2</sub> ×P <sub>3</sub>	1.9	0.93*	0.93	9.3	0.70*	-0.15*	47.0	1.47*	0.24*	0.67	0.67	-0.17*	1.8	1.83*	0.42
P <sub>2</sub> ×P <sub>4</sub>	1.4	1.28*	1.28*	6.3	1.29*	0.15*	59.4	0.75*	-0.13	1.10	1.10*	0.05*	0.8	0.85*	-0.08*
P <sub>2</sub> ×P <sub>5</sub>	1.9	-1.00*	-1.00*	5.9	-1.00*	-1.00*	38.9	-1.00*	-1.00*	-1.00	-1.00	-1.00	-1.0	-1*	-1*
P <sub>2</sub> ×P <sub>6</sub>	2.0	0.56*	0.56	8.7	0.42*	-0.29*	68.3	1.36*	0.18*	1.36	1.36*	0.18	1.2	1.19*	0.1
P <sub>2</sub> ×P <sub>7</sub>	1.6	-1.00*	-1.00*	6.1	-1.00*	-1.00*	49.1	-1.00*	-1.00*	-1.00	-1.00	-1.00	-1.0	-1*	-1*
P <sub>3</sub> ×P <sub>4</sub>	3.3	-0.50	0.07*	15.6	0.23*	0.03*	106.3	0.12	0.00	-0.72	-0.40	-0.61*	0.5	0.26	-0.17*
P <sub>3</sub> ×P <sub>5</sub>	3.8	27.90*	-0.25*	15.2	-0.11	-0.27*	85.9	0.09	-0.01	-1.24	-0.24	-0.36	-4.2	0.81*	0.51*
P <sub>3</sub> ×P <sub>6</sub>	3.9	2.17	0.07	18.0	0.15*	0.11*	115.3	0.16	-0.02	0.77	0.45	-0.08	2.9	1.17*	0.54*
P <sub>3</sub> ×P <sub>7</sub>	3.4	0.25	-0.02	15.4	0.13	-0.06*	96.1	-0.06	-0.08	5.40	0.79	0.56	5.0	0.85*	0.58*
P <sub>4</sub> ×P <sub>5</sub>	3.3	1.94*	-0.31*	12.2	-0.05	-0.08	98.3	0.15	-0.05	1.47	0.98*	0.19	0.4	0.15	-0.16*
P <sub>4</sub> ×P <sub>6</sub>	3.4	0.46	0.08	14.9	0.23*	0.06	127.7	0.35*	0.26*	7.50	0.37	0.31	1.7	0.27*	0.1*
P <sub>4</sub> ×P <sub>7</sub>	3.0	-4.29*	0.28*	12.3	0.30*	0.28*	108.5	-0.03	-0.11	-0.61	-0.39	-0.63*	0.5	0.21*	0.91
P <sub>5</sub> ×P <sub>6</sub>	3.9	-3.28	-0.07	14.6	0.26*	0.06	107.2	-0.08	-0.28*	1.83	1.27*	0.34	2.4	0.55*	0.26*
P <sub>5</sub> ×P <sub>7</sub>	3.5	-1.02	-0.10	12.0	0.03	0.01	88.0	0.35*	0.21*	81.00	3.65*	3.45*	30.1	0.71*	0.67*
P <sub>6</sub> ×P <sub>7</sub>	3.6	-0.18	-0.02*	14.7	0.02	-0.13*	117.4	0.14	-0.02	0.04	0.03	-0.39	1.7	0.43*	0.14

\*indicate significance at 0.05 probability level.

highly significant for most cucumber traits. Meanwhile, Moushumi and Sirohi (2010) and Dogra and Kanwar (2011) revealed that variance of SCA was greater than that of GCA in all studied cucumber traits, indicating that all these traits were influenced by both GCA and SCA, with the later having a greater influence.

Estimates of GCA effects for individual parents are presented in table 6. The GCA effects differed significantly in most traits. Data showed that the parental genotypes  $P_1$ ,  $P_4$  and  $P_6$  had considerable significant positive GCA effects for all studied traits, indicating that these genotypes proved to be good combiners in this respect for developing these traits. However, parental genotypes  $P_2$ ,  $P_5$  and  $P_7$  exhibited negative GCA effects for all studied traits, indicating that these parents appeared to be poor general combiners for these traits. Meanwhile, genotype  $P_3$  showed significant positive GCA effects for stem length, fruit length and fruit diameter trait and significant negative GCA effects for the characters early yield and total yield.

Concerning to SCA, data obtained in table 7 showed that the  $F_1$  hybrids  $P_1 \times P_2$ ,  $P_2 \times P_4$ ,  $P_2 \times P_6$  and  $P_5 \times P_7$  achieved significant positive SCA effects for all studied traits. Eleven crosses showed significant SCA effects for stem length trait. For long fruits, ten crosses achieved significant positive SCA effects. In respect to fruit diameter character, the crosses  $P_2 \times P_5$ ,  $P_2 \times P_7$ ,  $P_3 \times P_4$ ,  $P_3 \times P_5$ ,  $P_3 \times P_7$  and  $P_4 \times P_5$  showed the lowest SCA effects for narrowest fruit, however, Eight hybrids, viz.,  $P_1 \times P_2$ ,  $P_1 \times P_7$ ,  $P_2 \times P_3$ ,  $P_2 \times P_4$ ,  $P_2 \times P_6$ ,  $P_4 \times P_7$ ,  $P_5 \times P_6$  and  $P_5 \times P_7$  exhibited significant positive SCA effects. Significant positive SCA effects were observed in eleven crosses for early yield trait. For total yield character, SCA effects for hybrids  $P_1 \times P_2$ ,  $P_1 \times P_7$ ,  $P_2 \times P_3$ ,  $P_2 \times P_4$ ,  $P_2 \times P_6$ ,  $P_3 \times P_5$ ,  $P_3 \times P_6$ ,  $P_4 \times P_5$ ,  $P_4 \times P_7$ ,  $P_5 \times P_6$  and  $P_5 \times P_7$  were significant and positive.

### Correlation

Correlation data for five studied characters were computed presented in table 8. Total yield trait showed significant positive correlation with all studied characters, viz., stem length, fruit length, fruit diameter and early yield traits. On the other hand, there were not any significant correlation between the studied characters.

### Conclusion

Results showed that the parental lines  $P_2$  and  $P_4$  were good general combiners and the crosses  $P_1 \times P_4$ ,  $P_2 \times P_3$ ,  $P_2 \times P_5$ ,  $P_3 \times P_4$  and  $P_3 \times P_5$  were the best and promising hybrids under salt stress condition. However, the results also point at the potential of certain crosses as source for

**Table 6:** Estimates of general combining ability effect ( $\hat{g}_i$ ) of studied cucumber parents.

Parents	Stem length	Fruit length	Fruit diameter	Early yield/plant	Total yield/plant
$P_1$	14.02**	2.03**	0.32**	0.52**	0.74**
$P_2$	-35.21**	-5.82**	-1.22**	-0.21**	-0.78**
$P_3$	4.26*	3.68**	0.47**	-0.28**	-0.26**
$P_4$	20.17**	0.77**	0.11**	0.13**	0.49**
$P_5$	-31.20**	-2.05**	-0.19**	-0.14**	-0.38**
$P_6$	35.12**	2.86**	0.59**	0.27**	0.49**
$P_7$	-7.15**	-1.47**	-0.08**	-0.30**	-0.30**
S.E. ( $\hat{g}_i$ )	2.24	0.21	0.03	0.03	0.03
S.E. ( $\hat{g}_i - \hat{g}_j$ )	4.28	0.40	0.06	0.05	0.07

**Table 7:** Estimates of specific combining ability effect ( $s_{ij}$ ) of  $F_1$ s among seven cucumber parents.

Crosses	Stem length	Fruit length	Fruit diameter	Early yield/plant	Total yield/plant
$P_1 \times P_2$	37.30**	6.80**	1.35**	1.00**	1.94**
$P_1 \times P_3$	-5.47	1.28**	-0.13	0.19**	-0.20**
$P_1 \times P_4$	10.92*	-2.55**	-0.07	0.29**	-0.43**
$P_1 \times P_5$	11.35*	-0.10	-0.07	0.14*	-0.40**
$P_1 \times P_6$	7.77*	-0.68*	-0.25	-0.09*	0.41
$P_1 \times P_7$	-1.09	-0.98*	0.25**	0.02	0.44**
$P_2 \times P_3$	44.96**	3.96**	1.30**	-0.08*	0.13*
$P_2 \times P_4$	16.67**	5.44**	1.23**	0.23**	0.78**
$P_2 \times P_5$	-35.62**	-6.11**	-1.63**	-0.44**	-1.00**
$P_2 \times P_6$	59.59**	1.28**	0.69**	0.31**	0.43**
$P_2 \times P_7$	-59.67**	-6.69	-1.74**	-0.28**	-1.08
$P_3 \times P_4$	-7.83*	0.77*	-0.13*	-0.29**	-0.04
$P_3 \times P_5$	18.07**	-1.98**	-0.48*	-0.20**	0.44**
$P_3 \times P_6$	-7.48*	0.11	0.01	0.12*	0.84**
$P_3 \times P_7$	-9.05*	-16.18**	-3.44**	-0.21**	-1.60**
$P_4 \times P_5$	22.02**	-1.17**	-0.67**	0.28**	0.12*
$P_4 \times P_6$	14.99**	0.75*	-0.09	0.10*	0.00
$P_4 \times P_7$	-9.51*	2.72**	0.71**	-0.29**	0.14*
$P_5 \times P_6$	-6.97*	3.63**	0.18**	0.40**	0.36**
$P_5 \times P_7$	54.88**	1.84**	0.38**	0.51**	0.70**
$P_6 \times P_7$	3.37	-0.34	-0.06	-0.16**	0.05
S.E. ( $S_{ij}$ )	6.53	0.61	0.08	0.07	0.10
S.E. ( $S_{ij} - S_{ik}$ )	12.45	1.17	0.16	0.14	0.19

**Table 8:** Correlation coefficients among total yield/plant and other related characters in cucumber.

	Early yield	Fruit length	Stem length	Fruit diameter
Fruit length	0.45*			
Stem length	0.62	0.75		
Fruit diameter	0.43	0.92	0.78	
Total yield	0.69	0.76	0.83	0.77

selecting high yielding lines in their segregating generations because additive gene effects were responsible for their performance.

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