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Estimation of Genetic Parameters in Selected Cucumber (*Cucumis sativus* L.) Hybrids.

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ABSTRACT

Cucumber breeders are dedicated to understanding the complexities of diversity to devise effective breeding strategies. The study was conducted in a greenhouse in Vegetable Research Department (VRD), Horticulture Research Institute (HRI), Agricultural Research Center, Egypt, during 2021and 2022. A half-diallel cross among five cucumber genotypes and ten hybrids was investigated to estimate several genetic parameters. Results revealed substantial variation between the investigated genotypes for all characteristics. F_1hybrids P_3XP_4, P_3XP_5 and P_4XP_5 recorded the highest heterosis effect for yield and its constituent traits compared to mid and better parent values. Mean squares for both general and specific combining ability were extremely significant for whole characters. The magnitudes of GCA were greater than those corresponding magnitudes of SCA indicating predominance of non-additive type of gene effects with regard to plant height, number of leaves/plant, early yield/plant, fruit length, fruit diameter, fruit shape index, average fruit weight, number of fruits/plant and total yield/plant traits. The findings suggested that P_4 and P_5 were the greatest combiners for all characters and considered to be promising parents. The good cross combinations for the majority of traits were recorded in the following F_1 hybrids: P_3XP_4, P_3XP_5, and P_4XP_5.Genetic analysis revealed that dominance variance (σ^2D) exceeded additive variance (σ^2A), and dominance degree was >1 for most traits except fruit length, fruit number, and total yield per plant, suggesting the importance of non-additive gene effects for such traits. Broad sense-heritability was greater than narrow sense-heritability for whole traits. These findings supported the use these genotypes to local seed production programs in Egypt.

Keywords: Cucumber- F_1hybrids- GCA- SCA- Heritability.

INTRODUCTION

Cucumber (*Cucumis sativus* L.) is a commercially important vegetable crop belonging to the family Cucurbitaceae. It has a chromosome number of 2n = 14 and is one of the most widely cultivated species within the genus Cucumis. In Egypt, approximately 21.5 thousand hectares are cultivated with cucumber, producing around 488.72 thousand tons annually (FAOSTAT, 2017).The significance of cucumber has grown in recent years due to the widespread adoption of protected cultivation techniques, which have enhanced both productivity and crop quality. With the discovery and application of hybrid vigour (heterosis), breeding programs have increasingly focused on developing high-yielding and high-quality hybrids suited to various environmental conditions. Countries such as China, Turkey, and Iran are among the leading producers, while nations like the Netherlands, England, Iceland, and Denmark achieve exceptionally high yields (FAOSTAT, 2023). In Egypt, however, cucumber production relies heavily on imported hybrid seeds, as there is currently a lack of competitive locally developed hybrids. Developing improved cucumber cultivars requires the use of diverse germplasm that exhibits superior yield, adaptability, and fruit quality. A key element in this process is understanding the genetic architecture of economically important traits. Knowledge of the inheritance patterns of such traits is critical for identifying suitable parental lines for crossing and for guiding selection decisions.

Diallel crossing systems, particularly partial diallel designs, are widely used to estimate GCA, SCA, heritability, and dominance ratios. These genetic parameters guide the selection of parents and hybrids for further evaluation. Selection based on combining ability is especially important for traits like early yield, fruit size, and total yield per plant (Fanous et al., 2024 and El-Gazzar et al., 2020).

Combining ability analysis provides a valuable tool in this context. It helps breeders determine the general combining ability (GCA) of a parent its average performance across hybrid combinations and the specific combining ability (SCA), which reflects the performance of a particular hybrid combination. These analyses also provide insight into the nature of gene action whether additive or non-additive that controls trait expression (Basbag et al., 2007, Soliman, 2022 and Borasulov et al., 2024).

Given the increasing demand for locally adapted, high-performing cucumber hybrids in Egypt by evaluating the agronomic performance of five inbred lines and their F_1 hybrids, this study aimed to: a) evaluate the agronomic performance of five inbred cucumber lines, b) Assess the extent of heterosis and general and specific combining abilities (GCA and SCA) for yield-related traits, and c) determine the relative importance of additive and non-additive gene actions in the inheritance of yield and quality traits using a partial diallel mating system, as well as heritability estimates (broad and narrow sense) for these traits, to support future hybrid development strategies.

MATERIALS AND METHODS

The experiment was conducted at the Vegetable Research Department (VRD), Horticulture Research Institute (HRI), Agricultural Research Center (ARC), Egypt, during the 2021and 2022 growing seasons. Five genetically diverse cucumber (*Cucumis sativus*, L.) inbred lines, *viz.*, P_1 (Line 1380-1); P_2 (Line 87- 674-1); P_3 (Line 99-340); P_4 (Line 99-357) and P_5 (Line 99-347), were obtained from Cornell University in 2021. These lines selected based on various agronomic traits were grown under a plastic covered greenhouse. In March 2021 and 2022 seeds were sown directly in the greenhouse. During the flowering stage, partial diallel crosses were performed following Griffing's (1956) methods to generate 10 F_1hybrids self-pollination of each parental line was also conducted to produce inbred seeds. The resulting F_1hybrids and parental lines were evaluated in the subsequent 2022 season to estimate genetic parameters **(Table 1).**

Table (1). Schema of the partial diallel mating fashion accordance to Griffing's schema model I, method II for the five parents.

	P_1	P_2	P_3	P_4	P_5
P_1		P_1 X P_2	P_1 X P_3	P_1 X P_4	P_1 X P_5
P_2			P_2 X P_3	P_2 X P_4	P_2 X P_5
P_3				P_3 X P_4	P_3 X P_5
P_4					P_4 X P_5
P_5					

The experiment used a Randomized Complete Block Design (RCBD) with three replications, based on Cochran and Cox (1957). The experimental unit was 3 m^2 consisting of two rows each measuring 3 meter in length and 1 meter in width, with a plant spacing of 0.50 meter between plants. Fertilizers, irrigation, diseases and pests management were carefully conducted to ensure a healthy crop. The following quantitative traits were measured for the 16 genotypes (5 parents, 10 F_1hybrids, plus a chick hybrid): plant height (cm), number of leaves per plant, early yield per plant (kg), fruit length (cm), fruit diameter (cm), fruit shape index (cm), average fruit weight (g), number of fruits per plant and total yield per plant (kg).

The collected findings were treated to analysis of variance (ANOVA), and a means comparison was done using the least significant difference (LSD) test (Steel and Torrie, 1980) using Co-state system software (2004).

Estimation of heterosis:

The performance of the parents and their F_1hybrids were estimated explained by Mather and Jinks, (1971), the equation to determine each heterosis as follows:

Heterosis at mid-parent (H.M.P. %) = [F_1- M.P / M.P] X 100.

Heterosis at better-Parent (H.B.P. %) = [F_1- B.P / B.P] X100.

Heterosis at check hybrid (H.C.H. %) = [F_1- C.H / C.H] X 100.

Appropriate L.S.D. values were calculated to test the significance of heterotic effects according to the following formulae:

L.S.D. for the mid-parent heterosis = t $\sqrt{3MSe/2r}$

L.S.D. for the better-parent heterosis = t $\sqrt{2MSe/r}$

L.S.D. for the superiority over the check hybrid = t $\sqrt{2MSe/r}$.

Analyses of general and specific combining abilities were performed based on Griffing (1956), the model I, method II.

GCA/SCA ratio to determine gene action was recorded according to Baker (1978).

Degree of dominance was determined accordance to the formula:

$$D.d = \sqrt{\frac{\sigma2D}{\sigma2A}}$$

D.d < 1, it means that types of gene effect are additive in nature.

D.d > 1, it means that types of gene effect are non - additive in nature.

Heritability:

Heritability broad sense percentage ($h^2_{b.s}$ %) = ($\sigma^2A + \sigma^2D / \sigma^2A + \sigma^2D + \sigma^2E$) x 100 = ($\sigma^2G / \sigma^2P$) x 100.

Heritability narrow sense percentage ($h^2_{n.s}$ %) = ($\sigma^2A / \sigma^2A + \sigma^2D + \sigma^2E$) x 100 = ($\sigma^2A / \sigma^2P$) x 100.

$\sigma^2A = 2\sigma^2g$, $\sigma^2D = \sigma^2s$, $\sigma^2E = \sigma^2e$, $\sigma^2G = \sigma^2A + \sigma^2D$, $\sigma^2P = \sigma^2G + \sigma^2E$, $\sigma^2P = \sigma^2A + \sigma^2D + \sigma^2E$.

RESULTS AND DISCUSSION

Analysis of variance:

The analysis of variance (ANOVA) and the mean squares revealed highly significant differences ($p < 0.01$) among genotypes for all measured traits **(Table 2).** This indicates the presence of substantial genetic variability among the studied genotypes (including 5 parental lines, 10 F hybrids, and a check hybrid). The findings clearly demonstrate that the genotypic mean squares were highly significant for all traits examined in this study, confirming the presence of true genetic differences among the genotypes. This significance supports the validity of subsequent analyses aimed at dissecting the nature of genetic variation and estimating heterosis for these traits. Such significant variability suggests that selection and hybrid development for improved yield and yield components are feasible. Similar findings have been reported by (Al-Araby et al., 2019, Yunusov, 2019, El-Shoura and Diab, 2022 and Bazargaliyeva et al., 2023), confirming the potential of diallel mating designs for genetic parameter estimation in cucumber.

Table (2). Analysis of variance and mean squares for some agronomic traits tested cucumber genotypes.

Traits / Parameters	df	PH (cm)	NLP	EYP (kg)	FL (cm)	FD (cm)	FShI (cm)	AFW (g)	NFP	TYP (kg)
Replicates	2	0.23^{ns}	24.42^{ns}	0.01^{ns}	0.12	0.014^{ns}	0.04^{ns}	3.63^{ns}	1.57^{ns}	0.02^{ns}
Genotypes	14	219.65**	179.00**	0.13**	1.46**	0.26**	0.65**	309.91**	50.30**	2.30**
Error	28	1.53	21.03	0.02	0.02	0.01	0.05	2.34	2.00	0.06

PH: plant height (cm), NLP: number of leaves per plant, EYP: early yield per plant (kg), FL: fruit length (cm), FD: fruit diameter (cm), FShI: fruit shape index (cm), AFW: average fruit weight (g), NFP: number of fruits per plant, TYP: total yield per plant (kg), *, **: significant at 0.05 and 0.01 levels of probability, respectively.

Mean Performance of Parents and Hybrids:

Table (3) summarizes the performance of the parental lines, F_1hybrids, and the check hybrid across the studied traits. The results indicated considerable variation among the genotypes. In terms of plant height, the hybrid P_4 X P_5 recorded the tallest plants (228.13 cm), followed by P_3 X P_5 and P_3 X P_4. Among parents, P_5 showed the greatest height (205.57 cm), while P_1 was the shortest (201.27 cm). The observed increase in plant height among hybrids likely reflects the influence of heterosis and enhanced vegetative growth, consistent with previous reports by Kulvir et al. (2016) and Naik (2018). Regarding the number of leaves per plant, P5 exhibited the highest value among the parents (56.70), while P_1 had the lowest (51.90). The hybrid P_4 X P_5 produced the most leaves (74.70), significantly surpassing all other genotypes, followed by $P_3 \times P_5$ and P_2 X P_5. For early yield per plant, P_5 again outperformed other parents (1.64 kg), while the hybrid $P_4 \times P_5$ recorded the highest early yield overall (1.99 kg), suggesting its potential for early market production. These results align with findings by Abd Rabou (2020), who emphasized the role of hybrid vigor in enhancing early productivity. Fruit length varied across genotypes, with P5 and its hybrids showing superior values. The longest fruits were observed in P_4 X P_5 (16.47 cm), whereas the shortest were in P_1 X P_2 (14.13 cm).Similarly, fruit diameter peaked in the hybrid P_4 X P_5 (3.27 cm), supporting its advantage in market-preferred fruit size. In terms of fruit shape index, P_1 X P_3 had the highest value (5.98), while P_3 X P_5 had the lowest (4.93). Variations in this trait are genetically controlled and influence consumer preference (El-Shoura and Abed, 2018 and Gad-Alla, 2019). Average fruit weight was highest in P_4 X P_5 (144.97 g), while $P_1 \times P_2$ had the lowest (113.87 g). Parental lines P_4 and P_5 consistently contributed positively to fruit weight, indicating their suitability as general combiners. Notably, the hybrids P_3 X P_5 and P_4 X P_5 also showed the highest number of fruits per plant (43.98 and 41.95, respectively), surpassing the check hybrid. Consequently, these crosses also recorded the highest total yield per plant (6.01 and 6.08 kg, respectively), confirming their superiority.

Table (3). Mean values of all genotypes (five parents, ten F_1crosses and a chick hybrid) for the studied traits in cucumber during 2021/2022 season.

Traits / Genotypes	PH (cm)	NLP	EYP (kg)	FL (cm)	FD (cm)	FShI (cm)	AFW (g)	NFP	TYP (kg)
P_1	201.27	51.9	1.37	14.06	2.53	5.56	114.6	26.7	3.06
P_2	201.63	53.87	1.14	14.53	2.47	5.9	117.47	33.7	3.72
P_3	204.83	53.07	1.56	15.13	2.37	6.41	123.5	35.5	4.4
P_4	205.07	54.33	1.6	15.5	2.43	6.37	125.47	40.1	5.02
P_5	205.57	56.7	1.64	15.57	2.53	6.15	127.87	39.4	5.03
P_1X P_2	205.17	56.03	1.35	14.13	2.43	5.81	113.87	35.6	4.05
P_1X P_3	206.1	59.93	1.42	14.33	2.4	5.98	115.47	35.6	4.06
P_1X P_4	206.43	60.6	1.44	14.5	2.63	5.53	118.37	34.5	4.08
P_1X P_5	207.57	63.1	1.45	14.47	2.5	5.79	118.78	34.3	4.07
P_2X P_3	206.53	63.23	1.45	15.1	2.73	5.53	121.87	33.5	4.09
P_2X P_4	213.07	66.5	1.66	15.63	2.67	5.86	141.63	35.8	5.07
P_2X P_5	221.27	73.77	1.55	15.57	2.63	5.91	132.93	37.9	5.03
P_3X P_4	220.76	63.3	1.73	15.47	3.13	4.94	135.03	37.6	5.7
P_3X P_5	222.67	73.67	1.83	15.6	3.17	4.93	136.67	44	6.01
P_4X P_5	228.13	74.7	1.99	16.47	3.27	5.04	144.97	42	6.08
Chick hybrid	217.6	66.23	1.77	16.06	3.13	5.13	141.93	42.3	6.01
LSD at 5 %	**2.07**	**7.67**	**0.2**	**0.24**	**0.16**	**0.39**	**2.56**	**2.36**	**0.41**
LSD at 1 %	**2.79**	**10.4**	**0.27**	**0.33**	**0.23**	**0.53**	**3.45**	**3.19**	**0.55**

PH: plant height (cm), NLP: number of leaves per plant, EYP: early yield per plant (kg), FL: fruit length (cm), FD: fruit diameter (cm), FShI: fruit shape index (cm), AFW: average fruit weight (g), NFP: number of fruits per plant, TYP: total yield per plant (kg).

Heterosis:

The success of breeding programs across various crops, including those in the commercial cucurbit sector, can largely be attributed to heterosis. While the genetic basis of hybrid vigor (heterosis) is well understood, the physiological, biochemical, and molecular mechanisms underlying this phenomenon remain largely unknown. This study provides an overview of hybrid vigor. Historically, heterosis has been associated with dominance or over dominance, but recent research has highlighted the significant roles of epistasis and linkage in this phenomenon (Leyla Cesurer et al., 2002). The results in **Table (4)** revealed that five cross combinations exhibited significantly positive heterosis for plant height relative to the check hybrid. Specifically, the crosses (P_2 X P_4, P_2 X P_5, P_3 X P_4, P_3 X P_5, and P_4 X P_5) demonstrated extremely significant positive heterosis compared to both mid and better parents, a finding consistent with those of Selim (2019) and Veera (2023). Additionally, all cross combinations exhibited positive and highly significant heterosis compared to both mid and better parents, except for the F_1hybrid P1xP2 for the number of leaves trait, as also noted by El-Gazar et al. (2020) and Naroui et al. (2023). Furthermore, all F_1hybrids demonstrated positive and highly significant heterosis over mid parents, except for the crosses (P_1 X P_3, P_1 X P_4, and P_1 X P_5). Crosses such as P_2 X P_4, P_3 X P_4, P_3 X P_5, and P_4 X P_5 showed highly significant positive heterosis compared to better parents for early yield per plant. Moreover, all crosses exhibited positive and highly significant heterosis over mid parents, except for the F_1hybrids P_1 X P_2, P_1 X P_3, P_1 X P_4, and P_1 X P_5. Notably, the F_1hybrids P_2 X P_4 and P_4 X P_5 revealed extremely significant positive heterosis relative to better parents for fruit length. For fruit diameter, all crosses exhibited positive and highly significant heterosis compared to mid and better parents, except for the F_1hybrids P_1 X P_2, P_1 X P_3, and P_1 X P_5. One F_1hybrid, P_1 X P_2, demonstrated highly significant positive heterosis for the fruit shape index trait compared to both mid and better parents. Specifically, five crosses (P_2 X P_4, P_2 X P_5, P_3 X P_4, P_3 X P_5, and P_4 X P_5) displayed highly significant positive heterosis for average fruit weight compared to both mid and better parents, a result consistent with the findings of Malav et al. (2018) Singh and Tiwari (2018) and Ene et al. (2019). Eight cross combinations showed highly significant and positive heterosis over mid parents, while the crosses P_1 X P_2, P_3 X P_5, and P_4 X P_5 exhibited positive and highly significant heterosis compared to better parents for the number of fruits per plant. Regarding total yield per plant, **Table (4)** reveals that all F_1hybrids showed positive and highly significant heterosis compared to mid parents (ranging from 0.49% for P_1 X P_5 to 27.33% for P_3 X P_5). Five hybrids exhibited significant positive heterosis over better parents (ranging from 1.00% for P_2 X P_4 to 20.68% for P_4 X P_5). However, none of the hybrids showed desirable positive and significant heterosis compared to the check hybrid for total yield per plant. These findings align with those of Simi et al. (2017) Preethi et al. (2019) and Ibrahim et al. (2024).

Table (4). Heterosis versus the mid parents, better parents of five inbred lines and their crosses for traits in cucumber.

Traits / Hybrids	PH (cm)			NLP			EYP (kg)			FL (cm)			FD (cm)		
	M.P	B.P	C.H	M.P	B.P	C.H	M.P	B.P	C.H	M.P	B.P	C.H	M.P	B.P	C.H
P_1 X P_2	1.85*	1.76*	-5.71**	5.94*	4.01	-15.40**	7.14**	-1.46**	-23.73**	-1.19**	-2.75**	-12.07**	-2.80**	-3.95**	-22.61**
P_1 X P_3	1.50*	0.62	-5.28**	14.17**	12.93**	-9.51**	-3.40**	-8.97**	-19.77**	-1.85**	-5.29**	-10.83**	-2.04**	-5.14**	-23.57**
P_1 X P_4	1.60*	0.66	-5.13**	14.08**	11.54**	-8.50**	-3.36**	-10.00**	-18.64**	-1.89**	-6.45**	-9.77**	6.05**	3.95**	-16.24**
P_1 X P_5	2.04*	0.97	-4.61**	16.31**	11.29**	-4.73	-3.97**	-11.58**	-18.08**	-2.36**	-7.06**	-9.96**	-1.19**	-1.19**	-20.38**
P_2 X P_3	0.87	0.83	-5.09**	18.25**	17.38**	-4.53	7.41**	-7.05**	-18.08**	1.82**	-0.20*	-6.04**	12.81**	10.53**	-13.06**
P_2 X P_4	4.78**	3.90**	-2.08*	22.92**	22.40**	0.41	21.17**	3.75**	-6.21**	4.06**	0.84**	-2.74**	8.98**	8.10**	-14.97**
P_2 X P_5	8.68**	7.64**	1.69*	33.42**	30.11**	11.38**	11.51**	-5.49**	-12.43**	3.46**	0	-3.11**	5.20**	3.95**	-16.24**
P_3 X P_4	7.71**	7.65**	1.45	17.88**	16.51**	-4.42	9.49**	8.13**	-2.26**	0.98**	-0.19	-3.73**	30.42**	28.81**	-0.32**
P_3 X P_5	8.51**	8.32**	2.36*	34.21**	29.93**	11.23**	14.38**	11.59**	3.39**	1.63**	0.19	-2.92**	29.39**	25.30**	0.96**
P_4 X P_5	11.11**	10.97**	4.84**	34.55**	31.75**	12.79**	22.84**	21.34**	12.43**	5.98**	5.98**	2.49**	31.85**	29.25**	4.14**

Table (4). Continue….

Traits / Hybrids	FShI (cm)			AFW (g)			NFP			TYP (kg)		
	M.P	B.P	C.H.	M.P	B.P	C.H.	M.P	B.P	C.H.	M.P	B.P	C.H.
P_1 X P_2	1.40**	-1.53**	13.25**	-1.87*	-3.06*	-19.77**	17.77**	5.61**	-15.96**	19.47**	8.87**	-33.72**
P_1 X P_3	-0.17	-6.71**	16.56**	-3.01**	-6.50**	-18.64**	14.57**	0.48	-15.87**	8.85**	-7.73**	-33.55**
P_1 X P_4	-7.37**	-13.19**	7.80**	-1.39	-5.66**	-16.60**	3.20**	-13.93**	-18.61**	0.99**	-18.73**	-33.22**
P_1 X P_5	-1.19**	-5.85**	12.87**	-2.03*	-7.11**	-16.31**	3.75**	-12.88**	-19.03**	0.49**	-19.09**	-33.39**
P_2 X P_3	-10.39**	-13.73**	7.80**	1.15	-1.32	-14.13**	-3.07**	-5.47**	-20.85**	0.74**	-7.05**	-33.06**
P_2 X P_4	-4.56**	-8.01**	14.23**	16.60**	12.88**	-0.21	-3.01**	-10.69**	-15.54**	16.02**	1.00**	-17.02**
P_2 X P_5	-1.99**	-3.69**	15.20**	8.36**	3.96**	-6.34**	3.61**	-3.84**	-10.63**	14.84**	0.00	-17.68**
P_3 X P_4	-22.69**	-22.93**	-3.70**	8.47**	7.62**	-4.86**	-0.32	-6.02**	-11.12**	21.02**	13.55**	-6.71**
P_3 X P_5	-21.50**	-23.09**	-3.90**	8.74**	6.88**	-3.71**	17.56**	11.74**	3.85**	27.47**	19.48**	-1.64**
P_4 X P_5	-19.49**	-20.88**	-1.75**	14.45**	13.37**	2.14*	5.64**	4.74**	-0.94	21.00**	20.87**	-0.65**

PH: plant height (cm), NLP: number of leaves per plant, EYP: early yield per plant (kg), FL: fruit length (cm), FD: fruit diameter (cm), FShI: fruit shape index (cm), AFW: average fruit weight (g), NFP: number of fruits per plant, TYP: total yield per plant (kg), * and **: significant at 0.05 and 0.01 levels of probability, respectively.

Combining ability analysis:

General combining ability and specific combining ability are well-established concepts in plant breeding. It has long been recognized that the relative effectiveness of individuals within a particular group of organisms, when hybridized with a diverse tester, provides a reliable measure of general combining ability (GCA). The concept of specific combining ability (SCA) emerged to assess the performance of offspring from a particular hybrid compared to others, indicating whether a specific parental combination was notably superior or inferior. The data in **Table (5)** highlight that the mean squares for general (GCA) and specific combining ability (SCA) were highly significant for all measured traits. This finding underscores the differences in general combining ability between parents and emphasizes the importance of selecting suitable parents for hybridization, illustrating the role of additive gene action in the inheritance of these traits. Additionally, the mean squares for SCA were significant across all estimated characters, suggesting that non-additive gene action plays a crucial role in controlling these traits. The inheritance patterns for these traits were thus influenced by both additive and non-additive genetic factors. Based on the outcomes, the GCA/SCA ratio exceeded one for all traits, indicating that additive genetic effects were more dominant and primarily responsible for the inheritance of all studied traits. These results are consistent with those reported by (Sharaf, 2020, Hamdan and Al-Zubaae, 2023 and Noura and El-Shoura, 2024).

Table (5). Mean squares for all the vegetative and yield qualities, in addition the general and SCA combining ability and GCA/SCA ratio.

Parameters \ Traits	df	PH (cm)	NLP	EYP (kg)	FL (cm)	FD (cm)	FShI (cm)	AFW (g)	NFP	TYP (kg)
Genotypes	**14**	219.65	179.00	0.13	1.46	0.26	0.65	309.91	50.03	2.29
GCA	**4**	87.31**	110.74**	0.11**	1.42**	0.17**	0.33**	216.68**	41.87**	2.02**
SCA	**10**	67.58**	61.25**	0.05**	0.11**	0.09**	0.30**	57.95**	6.60**	0.26**
Error	**28**	0.51	7.01	0.01	0.01	0.003	0.02	0.78	0.67	0.02
GCA / SCA		1.29	1.81	2.20	12.911	1.88	1.10	3.73	6.33	7.76

PH: plant height (cm), NLP: number of leaves per plant, EYP: early yield per plant (kg), FL: fruit length (cm), FD: fruit diameter (cm), FShI: fruit shape index (cm), AFW: average fruit weight (g), NFP: number of fruits per plant, TYP: total yield per plant (kg), * and **: significant at 0.05 and 0.01 levels of probability, respectively.

Combining ability effects (*gi*):

For optimal breeding, high positive general combining ability (GCA) effects are desirable for most traits, while negative GCA effects can also be beneficial from a breeder's perspective. Parental lines P_1 and P_2 exhibited highly significant negative GCA effects for plant height, as shown in **Table (6)** suggesting their potential as good combiners for this trait. In contrast, parents P_3, P_4, and P_5 demonstrated positive and highly significant GCA effects. Similar findings were reported by Singh et al**.** (2019) and Hamdan and Al-Zubaae (2023). The GCA effects for the number of leaves indicated that parent P_5 was a highly significant positive combiner, making it the most desirable parent for this trait. Regarding early yield, both P_4 and P_5 exhibited highly significant positive GCA effects, suggesting that these parents are excellent combiners for this trait. Additionally, the GCA effects for fruit length revealed that parental lines P_4 and P_5 had significantly positive GCA effects, indicating their effectiveness in improving fruit length in cucumber. Similarly, for fruit diameter, P_4 and P_5 exhibited highly significant positive GCA effects, confirming them as the best general combiners for this trait. These results align with those found by Malav et al. (2018) and Ene et al. (2019). For fruit shape, parent P_2 showed highly significant positive GCA effects, indicating it is the best general combiner for this trait, as also noted by Bhutia et al. (2017) and Borasulov et al. (2024). As presented in Table (6), parental P_4 and P_5 exhibited the most substantial and desirable GCA effects for average fruit weight, identifying them as the strongest general combiners for this trait. In contrast, parental lines P_1, P_2, and P_3 showed unfavorable GCA effects for average fruit weight. These findings are consistent with those of Darrudi et al., (2018). Finally, for the number of fruits and total yield per plant, parents P_3, P_4, and P_5 displayed highly significant positive GCA effects, marking them as the best general combiners for these traits. Based on these results, P_3, P_4, and P_5 are considered excellent general combiners and should be used as donors in yield and quality improvement programs through multiple crossing strategies. These findings corroborate previous studies by Rai et al., (2018), Saeed and Adday, (2021), Abd El-Hadi et al. (2020), Mahu et al. (2022), Forhan and Adaee, (2023) and Tanveer et al. (2024), which identified the best general combiners and favorable crosses in cucumber.

Table (6). Estimates of general combining ability effects on the studied traits in five cucumber parental lines.

Geno. \ Traits	PH. (cm)	NLP	EYP (kg)	FL (cm)	FD (cm)	FShI (cm)	AFW (g)	NFP	TYP (kg)
P_1	-4.95^{**}	-3.77^{**}	-0.12^{**}	-0.69^{**}	-0.13^{**}	-0.01	-8.53^{**}	-3.56^{**}	-0.77^{**}
P_2	-1.87^{**}	-0.37	-0.14^{**}	-0.13^{**}	-0.08^{**}	0.10^{**}	-1.45^{**}	-1.18^{**}	-0.30^{**}
P_3	0.47^{**}	-0.52	0.04^{*}	0.05^{*}	0.03^{**}	-0.01	0.09	0.47^{**}	0.12^{**}
P_4	2.30^{**}	0.56	0.11^{**}	0.38^{**}	0.09^{**}	-0.02	5.08^{**}	1.65^{**}	0.45^{**}
P_5	4.05^{**}	4.11^{**}	0.12^{**}	0.40^{**}	0.10^{**}	-0.05^{*}	4.81^{**}	2.62^{**}	0.50^{**}
SE(gi)	0.24	0.89	0.03	0.03	0.01	0.04	0.29	0.27	0.04
SE(gi – gj)	0.38	1.41	0.05	0.05	0.02	0.07	0.47	0.43	0.07

PH: plant height (cm), NLP: number of leaves per plant, EYP: early yield per plant (kg), FL: fruit length (cm), FD: fruit diameter (cm), FShI: fruit shape index (cm), AFW: average fruit weight (g), NFP: number of fruits per plant, TYP: total yield per plant (kg), * and **: significant at 0.05 and 0.01 levels of probability, respectively.

Specific combining ability effects (*Sij)*:

The most desirable cross combinations were those exhibiting the highest and significantly positive specific combining ability (SCA) effects across most of the measured characters. **Table (7)** presents the SCA effects for ten F hybrids. Among them, six hybrids (P_1 X P_2, P_2 X P_4, P_2 X P_5, P_3 X P_4, P_3 X P_5, and P_4 X P_5) showed highly significant and positive SCA effects, indicating their superiority for improving plant height. Regarding the number of leaves, seven crosses (P_1 X P_3, P_1 X P_4, P_2 X P_3, P_2 X P_4, P_2 X P_5, P_3 X P_5, and P_4 X P_5) demonstrated extremely significant and positive SCA effects, suggesting these hybrids as the most promising for this trait. For early yield per plant, two hybrids (P_2 X P_4 and P_4 X P_5) exhibited significantly positive SCA effects, highlighting them as the best candidates for improving early yield. In terms of fruit length, three hybrids (P_2 X P_4, P_2 X P_5, and P_4 X P_5) recorded significantly positive SCA effects, affirming their potential for enhancing this trait. A majority of the crosses (four out of ten) exhibited highly significant and positive SCA effects for fruit diameter, indicating their effectiveness for fruit size improvement. Meanwhile, one hybrid (P_1 X P_3) recorded a significantly positive SCA effect for fruit shape index, suggesting its suitability for this specific trait. Additionally, five hybrids (P_2 X P_4, P_2 X P_5, P_3 X P_4, P_3 X P_5, and P_4 X P_5) showed highly significant and favorable SCA effects for average fruit weight (AFW), as reported in **Table (7),** implying their value in enhancing this yield component. Four hybrids (P_1 X P_2, P_1 X P_3, P_3 X P_5, and P_4 X P_5) also displayed significantly positive SCA effects for the number of fruits per plant, indicating their potential for increasing fruit count. Finally, six hybrids (P_1 X P_2, P_2 X P_4, P_2 X P_5, P_3 X P_4, P_3 X P_5, and P_4 X P_5) exhibited significantly positive and desirable SCA effects for total yield per plant, demonstrating their potential in maximizing productivity. The significant SCA effects reflect the contribution of non-additive gene action including dominance, dominance × dominance, and additive × dominance interactions which is often positively correlated with heterosis. Based on **Table (7),** all crosses, with the exception of four (P_1 X P_3, P_3 X P_4, P_3 X P_5, and P_4 X P_5), showed strongly positive SCA effects for total yield per plant, identifying them as the most effective hybrids for enhancing overall yield. These results are in agreement with those reported in cucumber by Golabadi et al. (2015) and Borasulov et al. (2024).

Table (7). Estimates of specific combining ability effects (*SCA*) on agronomic traits of ten F_1 hybrids, derived from all possible combinations of the five cucumber parental lines.

Traits / Genotypes	PH (cm)	NLP	EYP (kg)	FL (cm)	FD (cm)	FShI (cm)	AFW (g)	NFP	TYP (kg)
P_1X P_2	1.58**	-1.47**	0.07*	-0.11*	-0.01	0.01	-2.05**	3.93**	0.49**
P_1X P_3	0.17	2.58**	-0.04	-0.09*	-0.16**	0.28**	-2.01**	2.32**	0.08*
P_1X P_4	-1.32**	2.17**	-0.09**	-0.25**	0.02	-0.15*	-4.07**	-0.01	-0.23**
P_1X P_5	-1.94**	1.12	-0.09**	-0.31**	-0.12**	0.13*	-3.40**	-1.17**	-0.28**
P_2X P_3	-2.47**	2.48**	0.002	0.11*	0.12**	-0.26**	-2.67**	-2.17**	-0.37**
P_2X P_4	2.24**	4.67**	0.15**	0.32**	-4.40**	0.08*	12.11**	-1.10**	0.28**
P_2X P_5	8.69**	8.39**	0.03	0.23**	-0.04*	0.15*	3.67**	0.01	0.21**
P_3X P_4	7.58**	1.61*	0.04	-0.03	0.36**	-0.74**	3.97**	-0.88*	0.49**
P_3X P_5	7.74**	8.43**	0.12*	0.08*	0.38**	-0.73**	5.86**	4.48**	0.76**
P_4X P_5	11.38**	8.39**	0.22**	0.62**	0.42**	-0.60**	9.17**	1.27**	0.50**
SE(S_{ij})	0.31	1.15	0.04	0.04	0.02	0.06	0.38	0.35	0.06
SE(S_{ij}-S_{ik})	**0.93**	**3.46**	**0.13**	**0.13**	**0.07**	**0.18**	**1.16**	**1.07**	**0.18**
SE(S_{ij}-S_{kl})	**0.85**	**3.16**	**0.11**	**0.11**	**0.06**	**0.16**	**1.05**	**0.97**	**0.16**

PH: plant height (cm), NLP: number of leaves per plant, EYP: early yield per plant (kg), FL: fruit length (cm), FD: fruit diameter (cm), FShI: fruit shape index (cm), AFW: average fruit weight (g), NFP: number of fruits per plant, TYP: total yield per plant (kg), * and **: significant at 0.05 and 0.01 levels of probability, respectively.

Gene action and Heritability:

Understanding gene effects is essential for selecting appropriate breeding strategies aimed at improving specific quantitative traits. Therefore, before implementing a targeted breeding program, plant breeders must first assess the nature of gene action influencing the expression of these traits. To this end, various genetic parameters were estimated through the analysis of general (GCA) and specific combining ability (SCA), and the results are summarized in

Table (8). Upon examination, the ratio of σ^2g to σ^2s was less than one for all traits except fruit length and total yield per plant, indicating the predominance of non-additive gene action in most traits, particularly the dominance effect in their inheritance; such findings support the suitability of hybrid breeding strategies. Comparable results were reported by Darrudi et al. (2018), Gad-Alla, (2019) and Soliman Abeer (2022). For most traits, the dominance genetic variance (σ^2D) exceeded the additive genetic variance (σ^2A), except for fruit length, number of fruits per plant, and total yield per plant, suggesting that dominance effects played a key role in trait inheritance. This conclusion is consistent with findings by Saeed and Adday, (2021) and Zhiyan and Mohammed, (2024). The dominance degree (D.d) exceeded unity for all traits except for fruit length, number of fruits per plant, and total yield per plant, further confirming the significant role of non-additive gene action in controlling these traits. Among the evaluated traits, broad-sense heritability ranged from 85.71% for early yield per plant to 99.30% for plant height, while narrow-sense heritability varied from 2.60% for fruit shape index to 77.55% for fruit length. Moreover, the broad-sense heritability ($h^2_{b.s}$) exceeded 99.30% and was markedly higher than its corresponding narrow-sense heritability ($h^2_{n.s}$), as reported by Abd El-Hadi et al. (2020) and Noura and El-Shoura, (2024). High estimates of broad-sense heritability indicate minimal environmental influence on the expression of these traits. Accordingly, Bartaula et al. (2019) emphasized that heritability reflects the efficiency of genotype selection based on phenotypic variability. High heritability suggests a strong potential for selection response, whereas low heritability may result from a substantial environmental contribution to trait variability. These findings are consistent with those reported by (Rai et al., 2018, Forhan and Adaee, 2023, Siavash et al., 2023 and Tanveer et al., 2024).

Table (8). The relative magnitude of various genetic parameters for all the studied traits.

Traits / Parameters	PH (cm)	NLP	EYP (kg)	FL (cm)	FD (cm)	FShI (cm)	AFW (g)	NFP	TYP (kg)
σ^2g / σ^2s	0.04	0.13	0.25	1.90	0.11	0.01	0.40	0.85	1.04
σ^2A	5.64	14.14	0.02	0.38	0.02	0.008	45.36	10.08	0.50
σ^2D	67.07	54.24	0.04	0.10	0.09	0.28	57.17	5.93	0.24
D.d	3.45	1.96	1.41	0.51	2.12	5.92	1.12	0.77	0.69
h^2_{bs} %	99.30	90.70	85.71	97.96	97.35	93.51	99.24	95.98	97.37
h^2_{ns} %	7.70	18.76	28.57	77.55	17.70	2.60	43.91	60.43	65.79

PH: plant height (cm), NLP: number of leaves per plant, EYP: early yield per plant (kg), FL: fruit length (cm), FD: fruit diameter (cm), FShI: fruit shape index (cm), AFW: average fruit weight (g), NFP: number of fruits per plant, TYP: total yield per plant (kg), * and **: significant at 0.05 and 0.01 levels of probability, respectively.

From the present study, to estimate the most important criteria, it was necessary to compare the performance of the hybrids on the basis of average performance, heterosis (over mid and better parent) and SCA along with GCA effects for concerned parents, it can be concluded that cucumber lines P_3, P_4 and P_5, are a good general combiner and could be utilized in multiple crossing program to produce high yield and quality cucumber hybrids **(Table, 9 and Fig.1)**. Parent (P5) a parent-rated above as the best general combiner for all analyzed traits expect for fruit shape index and average fruit weight, produced the first best hybrid. Therefore, in genetic advancement, this parent (P5) may serve as a promising predecessor for the aforementioned traits. In addition, P_4 X P_5 recorded the largest average of early yield, total yield, and created from high x high general combiner parents for yield per plant. Additionally, it revealed highly significant desirable SCA impacts for three crucial traits: plant height (PH cm), early yield (EY kg) and average fruit weight (AFWg). This F1hybrid can be considered as the discernible hybrid. The second best hybrid, P_3 X P_5, had high mean for total yield and highly significant SCA effects for most traits and also, formed from high x high general combiner parents, referring to exploitation of heterosis breeding to obtain superior cross combinations with regard to yield and its constituent characteristics with a favorable strategy for development and improvement of new hybrids in cucumber.

Table (9). Selected F Hybrid for High Fresh Fruit Yield Based on Average Performance, Heterosis (Over Mid- and Better-Parent), SCA, and GCA Effects of the Respective Parents.

Cross	Yield	Heterosis		SCA	GCA		Favorable significant SCA for other characters
		M.P	B.P		1st parent	2nd parent	
P_4 X P_5	6.08	21.00**	20.87**	0.50**	0.45**	0.50**	PH (cm), EYP (kg), FL (cm) and FD (cm)
P_3 X P_5	6.01	27.47**	19.48**	0.76**	0.12**	0.50**	NLP, NFP and TYP(kg)

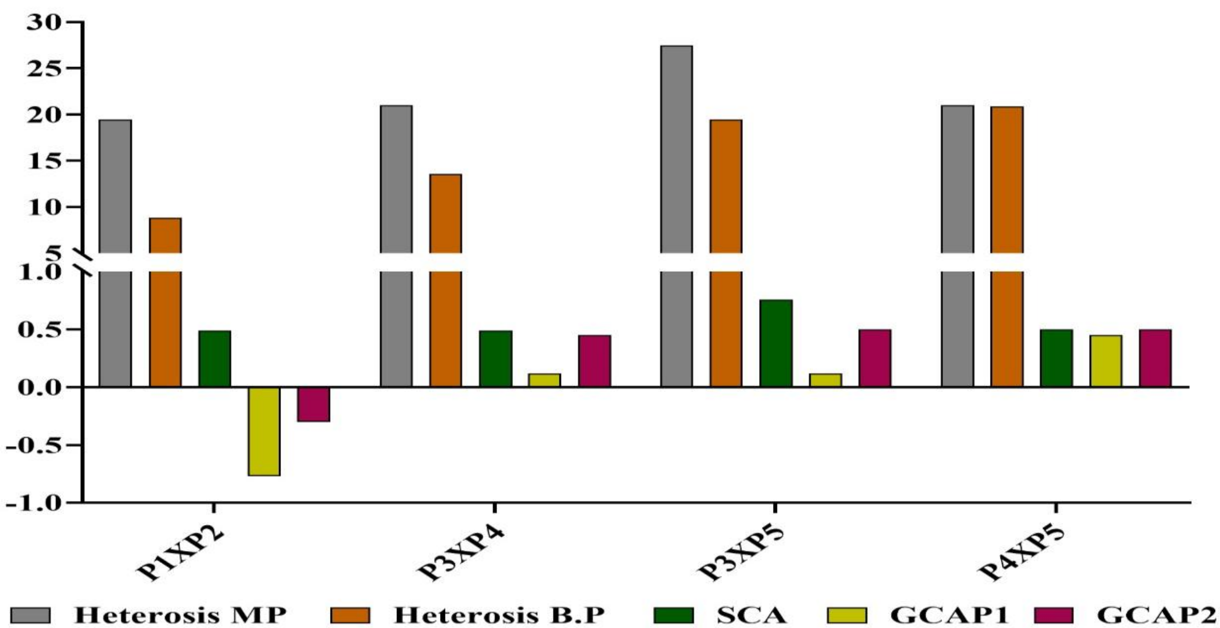

Fig.1: The best F_1hybrid chosen for total yield based on mean performance, Heterosis (versus mid and better parent) and SCA in addition GCA effects for concerned parents.

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الملخص العربى

تقدير القياسات الوراثية في هجن الخيار المنتخبة

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يكرس مربو الخيار جهودهم لفهم تعقيدات التنوع الوراثى من أجل وضع إستراتيجيات تربية فعالة لذلك أجريت تجربة حقلية بالصوب الخاصة بقسم بحوث الخضر - معهد بحوث البساتين – مركز البحوث الزراعية - مصر خلال موسمى 2021، 2022 وقد استخدمت فى هذه الدراسة خمسة سلالات من الخيار وقد أجرى التهجين بين هذه السلالات بنظام التهجين النصف دائرى وذلك فى قطاعات كاملة العشوائية فى ثلاث مكررات للحصول على 10 هجن بهدف تقدير العديد من المعايير الوراثية الهامة للخيار. وقد أشارت نتائج تحليل التباين للأباء والهجن الي وجود إختلافات معنوية عالية لجميع الصفات. لا يوجد هجين ذات قيمة عالية لجميع الصفات. كانت أعلي قيم معنويه مرغوبه لقوه الهجين مقارنه بمتوسط الأبوين وأعلى الآباء للهجن (P_3XP_4, P_3XP_5 , P_4XP_5) لمعظم الصفات. كما أشارت النتائج الى وجود إختلافات معنوية عالية لكلاً من تباين القدرة العامة والخاصة على التآلف لكل الصفات محل الدراسة مما يؤكد على أهمية الفعل الجينى الإضافى والغير إضافى فى وراثة تلك الصفات. وأن القدرة العامة على التآلف كانت أعلي من القدرة الخاصة على التآلف لجميع الصفات تحت الدراسة مما يؤكد على أهمية الفعل الجينى الإضافى فى وراثة تلك الصفات . كما أظهرت سلالات الآباء أن الأب الرابع والخامس ذو قوة تآلف عامة عالية لمعظم الصفات. كما أشارت تقديرات القدرة الخاصة على التآلف للهجن الناتجة أن أفضل التوليفات لصفة المحصول الكلى والصفات المرتبطة به كان للهجن P_3XP_4, P_3XP_5 , P_4XP_5 حيث أظهرت تأثيرات معنوية عالية لمعظم الصفات تحت الدراسة . كما أظهرت النتائج أن معامل درجة السيادى كان أكبر من الوحدة لجميع الصفات باستثناء صفتى طول الثمرة وعدد الثمار المحصول الكلى للنبات مما يشير الى أهمية الفعل الجينى الغير إضافى فى تحسين مختلف الصفات عبر التربية بالتهجين. كما سجلت النتائج أيضا أن القيم المقدرة لمعامل التوريث فى المدى الواسع كانت أكبر من نظيرتها فى المدى الضيق. مما يشير إلى التأثيرات الكبيرة للتباين الجيني على التعبير عن هذه الصفات. وارتفاع قيم معامل التوريث فى المدى الواسع تشير إلى التأثير القليل من البيئة على هذه الصفات في الخيار وتراوحت قيم معامل التوريث فى المدى الواسع من 85.71 إلى 99.30٪ لصفتى المحصول المبكر للنبات طول النبات ، فى حين تراوحت قيم معامل التوريث فى المدى الضيق من 2.60 الى 77.55 % لصفتى سمك اللحم وطول الثمرة. لذلك يمكن التوصية باستخدام هذه التراكيب الوراثية لإنتاج التقاوى من الخيار فى مصر.