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Assessment of hybrids derived from gynoecious cucumber lines

Soudeh Bahrami[1], Jamal-Ali Olfati[1]*

[1]Department of Horticultural Sciences, Faculty of Agricultural Sciences, University of Guilan, Rasht, Iran.
**Corresponding author, 0000-0002-5485-8884. Email: jamalaliolfati@guilan.ac.ir.*

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ABSTRACT

This study aimed to evaluate the general and specific combining abilities and the gene action mechanisms underlying certain traits of cucumber. The experiment was conducted using an incomplete diallel cross in a completely randomized design with three replications during the 2022-2023 growing season at the Faculty of Agriculture, University of Guilan. The results revealed significant differences across all traits except for fruit width and plant length. The mean squares for both general and specific combining abilities were significant for traits such as the number of pistillate flowers, the number of staminate flowers up to the 15th node, the number of final nodes, fruit weight, the number of fruits, and yield per plant. This indicates that both additive and non-additive gene actions are involved in the genetic control of these traits. However, the mean square for specific combining ability was not significant for ovary length, suggesting no significant variation among hybrids in terms of specific combining ability for this trait. Furthermore, based on the results, the highest significant positive and negative general combining abilities at the 1% probability level for yield per plant were associated with line 3 (0.21) and line 2 (-0.22), respectively. This indicates that line 3 contributes to increased yield, while line 2 is associated with a decrease. Therefore, line 3 could be effectively utilized in breeding programs aimed at enhancing yield. In conclusion, the findings demonstrate that additive variance plays a more prominent role in controlling these traits than non-additive variance. Consequently, the use of selected recombinant inbred lines is recommended for future breeding efforts.

Key words: Combining ability, Diallel analysis, Gynocious lines, Heterosis, Hybrid seeds.

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INTRODUCTION

Cucumber (*Cucumis sativus* L.) belongs to the Cucurbitaceae family (2n=14) and is a vegetable with a long history of cultivation (Peyvast, 2008). Native to India and China, cucumber is now widely cultivated around the world. Iran ranks fourth globally in cucumber production (FAO, 2022). Due to its high nutritional value and versatility for both fresh consumption and processing, cucumber is an important agricultural and economic crop.

One major challenge in cucumber production is low fruit yield, primarily caused by the limited number of female flowers and the excessive development of male flowers. This imbalance leads to a significant decrease in crop productivity. Female plants, which produce only female flowers, yield higher compared with other cucumber varieties. Female hybrids tend to flower earlier and produce concentrated fruiting, making this trait crucial in hybrid cultivar development (Hafeznia *et al.,* 2022).

Cucumber has the largest cultivated area among Iranian vegetables (Ghavidel, 2020). Despite its long history and high potential in Iran, a significant portion of cucumber seeds are imported (Dianati *et al.,* 2016; Najafi *et al.,* 2019). Therefore, improving local varieties and producing the required seeds domestically are essential priorities. Two key factors in cucumber breeding are enhancing yield and quality (Tatioglu, 2013).

Since yield is a quantitative trait, it is strongly influenced by environmental factors and exhibits low heritability. As a result, the most effective approach for yield improvement involves selecting related traits with higher heritability, such as plant height, the number of female flowers, the number of fruits per plant, the number of flowering nodes per branch, and the fruit set percentage (Falconer, 1996; Moradipour *et al.,* 2018).

To date, five genes responsible for sex determination in cucumber have been identified (Dhall *et al.,* 2023). The interaction and combination of these genes explain the various sexual phenotypes observed. Besides genetic control, the phytohormone ethylene plays a fundamental role in sex determination. Physiological, genetic, and biotechnological studies suggest that ethylene acts not only as a biochemical product of sex-regulating genes but also interacts with their pathways. Overall, ethylene and its related genetic pathways are critically important in the process of sex determination in cucumber flowers (Zhang *et al.,* 2021).

In a study by Hafeznia *et al.* (2022), the inheritance of floral traits in a diverging cucumber population was examined. The broad-sense heritability ranged from 71% to 92%, while narrow-sense heritability ranged from 36% to 84%. The degree of dominance was estimated between 0.12 and 1.39. These findings indicate that both additive and dominance effects can be exploited in breeding programs. The additive gene effects can be accumulated over several generations through selection, followed by crossing superior genotypes to utilize dominance effects.

The initial step in breeding high-yielding varieties with desirable traits, such as floral characteristics, is selecting suitable parents for crossing and hybrid production. The diallel analysis method involves crossing parental lines and evaluating the resulting offspring in a replicated design, with or without the parent lines. This approach enables the estimation of general and specific combining abilities, heritability, and heterosis for target traits (Farahani *et al.,* 2015).

Moradipour *et al.* (2018) investigated the general and specific combining abilities and heterosis of several fresh-eating cucumber lines using incomplete diallel analysis. The findings showed that the specific combining ability was higher than the general combining ability for traits such as the time to first female flower appearance and the number of fruits on the main branch, indicating dominance of non-additive gene effects. Conversely, traits like days to first harvest and plant length at the first fruit were primarily controlled by additive gene actions, as evidenced by their high general combining ability (Moradipour *et al.,* 2018).

Moradipour *et al.* (2017) evaluated hybrid vigor among several fresh-eating cucumber hybrids. The results revealed high genetic diversity, which could be exploited in crossbreeding programs to develop cultivars with desirable traits.

Bozorgzad and Golabadi (2019) assessed the impact of morphological traits on fruit yield in greenhouse-grown cucumber hybrids. Correlation analysis demonstrated that total fruit number and fruit diameter had positive and significant correlations with total fruit yield. Path coefficient analysis indicated that the total fruit number had the most substantial direct and positive effect on yield. Stepwise regression analysis showed that 96.30% of the variation in fruit yield could be explained by total fruit number alone. Additionally, yield and the number of end-of-season fruits contributed significantly to variations in total fruit number.

Moghbeli Hanzai *et al.* (2017) examined the combining ability, heterosis, and genetic traits of cucumber lines for morphological, biological, and yield traits using diallel crossing. The study confirmed that both additive and non-additive effects influence these traits, and the observed high genetic diversity among the hybrids suggests potential for their use in breeding programs.

Setamdideh Moslemi *et al.* (2019) evaluated progeny from crossings of selected cucumber lines with the commercial hybrid Negin. The goal was to assess their potential for improving parthenocarpy and flower quality traits. The highest percentage of female flowers was observed in progenies resulting from crossing Negin with line B10, while the lowest was in progenies from crossing Negin with line B12.

This study was conducted to evaluate several hybrids derived from gynoecious cucumber lines, with the aim of potentially introducing them for greenhouse cultivation in Iran. It also sought to assess the general combining ability of these lines for use in future breeding programs.

MATERIALS AND METHODS

In this experiment, several gynoecious lines exhibiting variation in flowering (medium-flowered, low-flowered) and response to gibberellin (positive, negative) were used to develop the desired hybrids. These lines were obtained from previous breeding programs (Dianati *et al.,* 2017) at the University of Guilan. To establish these lines, crosses were made between imported pickle lines from Taiwan, as well as existing hybrid and parthenocarpic cucumber lines available locally. Following selection and successive selfing, the progeny were stabilized over multiple generations. To accelerate the selfing process, gibberellin was applied to selected plants. In cases where the response to gibberellin was negative, kinship crosses were employed as an alternative method.

The plants were cultivated in the research greenhouse of the Faculty of Agricultural Sciences at the University of Guilan during the spring and summer of 2023. For cultivation, pots with a diameter of 29 cm were used, filled with a substrate composed of cocopeat and perlite in a 1:1 ratio (Asadian *et al.,* 2012).

For crossing and hybrid production, gibberellin at a concentration of 100 ppm was applied to induce male flower formation at the two- to four-leaf stage. Hand pollination was performed following standard procedures, with flowers bagged one day before their expected opening. On the following morning, the selected male flowers were used for pollination, after which the pollinated female flowers were re-bagged until fruit formation was confirmed (Hassani and Kordrostami, 2018). Once the fruits fully matured, seeds were harvested and stored for subsequent use.

In the next phase, 15 hybrids obtained from these crosses were grown in a completely randomized design with three replicates. Each plot contained 10 plants grown under greenhouse soil conditions. A row spacing of 0.5 meters between rows and within rows was maintained (Mamnoei, 2014). To prevent weed growth, black plastic mulch was applied, and a drip irrigation system was used for regular and uniform watering (Ahmadi and Hassannejad, 2016). The plants were evaluated for key traits according to recognized guidelines (UPOV, 2019). The measured traits included fruit length, number of fruits per plant, fruit weight, plant length, ovary length at flowering, final node number, and yield per plant.

The experimental design was a completely randomized design with three replications. Data were recorded in tables created using Excel, and statistical analysis was performed using SAS software (version 9.4) with the GLM procedure. Means were compared using Tukey's test at significance levels of 1% and 5%.

To assess heterosis and combining ability, a diallel analysis was conducted using Diallel software (version 1.1). Griffing's fourth method (fixed model for direct hybrids) was employed to estimate general and specific combining abilities of the hybrids (Griffing, 1956). Additionally, the analysis included estimation of additive and dominance variances, the degree of dominance, and narrow-sense heritability for the traits studied.

RESULTS

The analysis of variance revealed that the effect of genotype on ovary length was significant at the 1% probability level (Table 1). According to the mean comparisons (Table 2), the shortest ovary lengths were observed in hybrids 6×3, 6×2, 5×6, and 4×5, with means of 2.45, 2.36, 2.20, and 2.15 cm, respectively. The effects of the general combining ability (GCA) for this trait were also significant, indicating differences among parents regarding GCA and suggesting the presence of additive gene effects controlling ovary length. Conversely, the effects of specific combining ability (SCA) were not significant, implying no substantial variation among hybrids for SCA in

Table 1. Analysis of variance and combinability of traits in cucumber genotypes using Griffing's method IV.

Source of variation	df	Mean of square						
		Yield per plant	Fruit number	Fruit weight	Nod number	Fruit length	Number of female flowers	Ovary length
Replication	2	0.013^{ns}	5.422^{ns}	1.204^{ns}	0.002^{ns}	0.008^{ns}	0.012^{ns}	0.037**
Genotypes	14	0.105**	25.175**	0.359**	0.056**	0.042^{ns}	2.147**	0.041**
GCA	5	0.270**	64.822**	3.482**	0.047**	-	4.759**	0.080**
SCA	9	0.014**	3.148*	7.805**	0.048**	-	0.695**	0.019^{ns}
MS_{GCA}/MS_{SCA}		19.28	20.59	0.49	1.64	-	6.84	4.21
Error	28	0.017	3.208	0.627	0.002	1.077	0.053	0.01
Coefficient of variation (%)		8.84	13.51	11.05	3.03	9.29	9.66	18.82

ns, * and **: non-significant, Significant at the 5% and 1% probability levels, respectively.

Table 2. Comparison of genotype mean values for the studied traits in cucumber.

Genotypes	Yield ($g \cdot plant^{-1}$)	Fruit number	Number of Female flowers	Fruit weight (g)	Nod number	Ovary length
2×3	541^{abc}	7.66^{ad}	12^{ad}	70^{acd}	25.66^{abd}	2.76^{abc}
2×4	263.50^{ac}	5.66^{abd}	3^{b}	46.33^{d}	33.33^{ab}	2.5^{c}
5×2	237^{c}	1.33^{b}	1^{b}	170.33^{b}	12^{cd}	2.5^{c}
6×2	285.42^{ac}	4.33^{bd}	4.16^{b}	66.41^{acd}	28.66^{abd}	2.36^{ac}
7×2	327^{abc}	6.66^{abd}	5.83^{d}	49^{ac}	28^{b}	3.65^{b}
4×3	704.51^{ab}	10.66^{ab}	13^{ad}	66.69^{acd}	28.33^{ab}	2.76^{abc}
3×5	801.81^{b}	10^{ab}	15^{ac}	80.63^{c}	26.66^{abd}	2.76^{abcd}
6×3	589.33^{abc}	9.66^{abd}	17.33^{c}	60.83^{acd}	26.33^{abd}	2.45^{ac}
7×3	917.50^{b}	13.33^{b}	12.5^{ad}	68.83^{acd}	26.66^{abd}	3.06^{abc}
4×5	351.87^{abc}	5.33^{abd}	10^{d}	66.1^{acd}	14^{c}	2.15^{c}
6×4	527.83^{abc}	6.66^{abd}	10.5^{d}	79.5^{c}	28^{abd}	2.82^{abc}
4×7	695.12^{ab}	9.33^{abd}	12.5^{ad}	74.05^{ac}	20^{c}	2.76^{abc}
5×6	426.45^{abc}	6.33^{abd}	11.83^{ad}	67.44^{acd}	14^{cd}	2.2^{ac}
5×7	448^{abc}	7.66^{ad}	11.66^{d}	59.33^{acd}	18^{acd}	2.6^{ac}
6×7	528.50^{abc}	7^{ad}	10.16^{d}	75.5^{ac}	27.33^{abd}	3.16^{ab}

Means with letters in each column are significantly different at the 5% probability level based on Tukey test.

controlling this trait (Table 1). The ratio of MS_GCA to MS_SCA was 4.21, further indicating a greater contribution of additive genes compared to non-additive genes. The highest positive GCA at the 1% level was associated with line 7 (value of 0.133), indicating its beneficial contribution to increasing ovary length in progeny. The highest negative GCA was linked to line 5 (value of -0.111), indicating its tendency to decrease this trait (Table 3). The narrow-sense heritability was estimated at 0.50, suggesting a moderate environmental influence and indicating that ovary length is likely controlled by a limited number of genes (Veena *et al.,* 2012; Kumar *et al.,* 2013). Additionally, the additive variance (σ^2A) was greater than the dominance variance (σ^2D).

The variance analysis for the number of female flowers up to the 20th node showed a significant genotype effect at the 1% probability level (Table 1). Mean comparisons (Table 2) indicated the lowest number of female flowers in hybrids 6×2, 2×4, and 5×2, with means of 4.16, 3.00, and 1.00, respectively. The highest numbers were recorded in hybrids 6×3, 3×5, 4×3, and 7×3, with means of 17.33, 15.00, 13.00, and 12.50, respectively.

Both GCA and SCA effects were significant for this trait, pointing to the involvement of additive and dominance effects. Given the higher magnitude of GCA effects, additive gene action was more influential in controlling the number of female flowers, highlighting significant differences among lines in GCA (Table 1). The ratio of MS_GCA to MS_SCA was 6.84, emphasizing the predominance of additive effects. The highest positive GCA at the 1% level was associated with line 3 (value of 0.779), indicating a favorable contribution to increasing this trait, while the lowest negative GCA was related to line 2 (value of -1.142),

Table 3. General combining ability of lines and specific combining ability of hybrids for ovary length trait in cucumber genotypes using Griffing's method IV.

Parent	G_1	G_2	G_3	G_4	G_5	G_6
G_2	0.030^{ns}	-0.005^{ns}	-0.046^{ns}	0.032^{ns}	-0.096^{ns}	0.116*
G_3		0.009^{ns}	0.040^{ns}	0.043^{ns}	-0.049^{ns}	-0.029^{ns}
G_4			0.026^{ns}	-0.2**	0.113*	-0.086^{ns}
G_5				0.111**	-0.010^{ns}	-0.044^{ns}
G_6					-0.036^{ns}	0.043^{ns}
G_7						0.133**

ns, * and **: non-significant, Significant at the 5% and 1% probability levels, respectively.
SE[gca(i)] = 0.026, *SE[gca(i) - gca(j)]* = 0.041, *SE[sca(I,j)]* = 0.045, *SE[sca(i,j) - sca(i,k)]* = 0.071, *SE[sca(i,j) - sca(k,l)]* = 0.058.

Table 4. General combining ability of lines and specific combining ability of hybrids for number of female flowers in cucumber genotypes using Griffing's method IV.

Parent	G_2	G_3	G_4	G_5	G_6	G_7
G_2	-1.142**	0.779**	-0.226*	-0.844**	-0.004^{ns}	0.296*
G_3		0.779**	-0.262*	0.099^{ns}	-0.113^{ns}	-0.503**
G_4			0.055^{ns}	0.250*	0.020^{ns}	0.217^{ns}
G_5				-0.039^{ns}	0.302*	0.192^{ns}
G_6					0.127^{ns}	-0.203^{ns}
G_7						0.219*

ns, * and **: non-significant, Significant at the 5% and 1% probability levels, respectively.
SE[gca(i)] = 0.060, *SE[gca(i) - gca(j)]* = 0.093, *SE[sca(I,j)]* = 0.102, *SE[sca(i,j) - sca(i,k)]* = 0.162, *SE[sca(i,j) - sca(k,l)]* = 0.132.

Table 5. General combining ability of lines and specific combining ability of hybrids for number of nods in cucumber genotypes using Griffing's method IV.

Parent	G_2	G_3	G_4	G_5	G_6	G_7
G_2	0.063**	-0.114**	0.122**	-0.050**	0.008ns	0.051**
G_3		0.090**	0.092**	0.098**	-0.071**	0.004ns
G_4			-0.029**	-0.067**	0.078**	-0.255**
G_5				-0.123**	0.070**	0.098**
G_6					0.388**	0.071**
G_7						-0.035**

ns, * and **: non-significant, Significant at the 5% and 1% probability levels, respectively.
SE[gca(i)] = 0.010, *SE[gca(i) - gca(j)]* = 0.016, *SE[sca(I,j)]* = 0.018, *SE[sca(i,j) - sca(i,k)]* = 0.029, *SE[sca(i,j) - sca(k,l)]* = 0.023.

indicating a decreasing effect (Table 4). The narrow-sense heritability was high at 0.92, indicating effective selection potential for this trait, with additive variance (σ^2A) exceeding dominance variance (σ^2D).

The analysis of variance showed that the effect of genotype on the number of nodes was significant at the 1% probability level (Table 1). Based on the mean comparisons (Table 2), the lowest number of nodes was observed in hybrids 2×3 and 6×3, with means of 25.66 and 26.33, respectively.

Both GCA and SCA effects were significant for this trait, indicating the involvement of additive and dominance effects. The higher GCA value suggested a greater contribution of additive genes in controlling the number of nodes. The highest positive GCA at the 1% level was associated with line 3 (value of 0.09), indicating its progenies tend to increase this trait, while the highest negative GCA was linked to line 5 (value of -0.123), indicating a tendency to decrease this trait (Table 5). The ratio of MS_GCA to MS_SCA was 1.64, indicating a low environmental influence and suggesting that this trait is likely controlled by a limited number of genes. The narrow-sense heritability was estimated at 0.75, implying effective potential for selection. Additionally, the additive variance (σ^2A)

Table 6. General Combining Ability of Lines and Specific Combining Ability of Hybrids for fruit weight in cucumber genotypes using Griffing's method IV.

Parent	G_2	G_3	G_4	G_5	G_6	G_7
G_2	0.049^{ns}	-1.026*	-1.252*	3.566**	-0.316^{ns}	-0.970*
G_3		0.398^{ns}	0.505^{ns}	0.058^{ns}	0.138^{ns}	0.717^{ns}
G_4			-0.326^{ns}	-0.964*	0.899*	0.811*
G_5				1.081*	-1.215*	-1.329**
G_6					-0.001^{ns}	0.770*
G_7						-0.404^{ns}

ns, * and **: non-significant, Significant at the 5% and 1% probability levels, respectively.
SE[gca(i)] = 0.28, *SE[gca(i) - gca(j)]* = 0.323, *SE[sca(i,j)]* = 0.354, *SE[sca(i,j) - sca(i,k)]* = 0.559, *SE[sca(i,j) - sca(k,l)]* = 0.459.

Table 7. General Combining Ability of Lines and Specific Combining Ability of Hybrids for number of fruits in cucumber genotypes using Griffing's method IV.

Parent	G_2	G_3	G_4	G_5	G_6	G_7
G_2	-2.88**	-0.41^{ns}	1.00^{ns}	-1.58*	0.58^{ns}	0.41^{ns}
G_3		3.52**	-0.41^{ns}	0.66^{ns}	-0.50^{ns}	0.66^{ns}
G_4			0.11^{ns}	-0.58^{ns}	0.08^{ns}	0.08^{ns}
G_5				-1.63**	1.33^{ns}	0.16^{ns}
G_6					-0.8^{ns}	-1.33^{ns}
G_7						1.69**

ns, * and **: non-significant, Significant at the 5% and 1% probability levels, respectively.
SE[gca(i)] = 0.47, *SE[gca(i) - gca(j)]* = 0.73, *SE[sca(i,j)]* = 0.80, *SE[sca(i,j) - sca(i,k)]* = 1.26, *SE[sca(i,j) - sca(k,l)]* = 1.03.

exceeded the dominance variance (σ^2D).

The effect of genotype on fruit length was not significant, so diallel analysis was not performed for this trait. However, for fruit weight, the variance analysis indicated a significant genotype effect at the 1% level (Table 1). Mean comparisons (Table 2) showed that the lowest average fruit weights were in hybrids 5×7, 7×2, and 2×4, with means of 59.33, 49.00, and 46.33 grams, respectively. Both GCA and SCA effects were significant, indicating the presence of additive and dominance effects (Table 6). The highest positive SCA was observed in hybrid 5×2 (value of 3.566), while the highest negative was in hybrid 5×7 (value of -1.329). Notably, the contribution of non-additive variance (σ^2D) was greater than that of additive variance.

The analysis of variance for the number of fruits per plant revealed a significant effect of genotype at the 1% level (Table 1). The lowest average was in hybrids 5×2, 4×5, and 4×2, with means of 1.33, 5.33, and 4.66, respectively; the highest was in hybrids 2×3, 7×3, and 4×3, with means of 11.66, 13.00, and 11.00 (Table 7). The effects of both GCA and SCA were significant, emphasizing the role of additive and dominance effects. The higher GCA effects indicated a greater contribution of additive genes. The ratio of MS_GCA to MS_SCA was 3.15, confirming the predominance of additive effects. The highest positive GCA at the 1% level was associated with line 3 (value of 0.572), signifying its favorable influence, while the lowest negative GCA was linked to line 5 (value of -0.561) (Table 8). The narrow-sense heritability was 0.74, indicating that direct selection would be efficient, with additive variance (σ^2A) surpassing dominance variance (Table 9).

For the yield per plant, the ANOVA revealed a significant effect of genotype at the 1% probability level (Table 1). Mean comparisons (Table 2) showed the lowest yields in hybrids 5×2 and 4×2, with averages of 237.00 g and 263.00 g, respectively. The highest positive GCA was associated with line 3 (value of 6.88), indicating its potential to increase yield, while the highest negative GCA was linked to line 5 (value of -6.20). The cross 4×3 exhibited the highest specific combining ability (10.24), suggesting a strong hybrid effect for increased yield, whereas the 6×3 cross had the lowest (−4.30), indicating limited combining ability in that pairing. The ratio of MS_GCA to MS_SCA was 3.30, further emphasizing the importance of additive genetic factors. The narrow-sense heritability was 0.54.

Table 8. General Combining Ability of Lines and Specific Combining Ability of Hybrids for yield per plant in cucumber genotypes using Griffing's method IV.

Parent	G_2	G_3	G_4	G_5	G_6	G_7
G_2	-0.22**	-0.057^{ns}	-0.029^{ns}	-0.03^{ns}	0.014^{ns}	-0.011^{ns}
G_3		0.21**	-0.045^{ns}	0.39^{ns}	-0.1^{ns}	-0.004^{ns}
G_4			0.012^{ns}	-0.052^{ns}	0.057^{ns}	-0.07^{ns}
G_5				-0.07^{ns}	-0.035^{ns}	-0.046^{ns}
G_6					-0.01^{ns}	-0.007^{ns}
G_7						-0.085^{ns}

ns, * and **: non-significant, Significant at the 5% and 1% probability levels, respectively.

SE[gca(i)] = 0.034, *SE[gca(i) - gca(j)]* = 0.052, *SE[sca(i,,j)]* = 0.058, *SE[sca(i,j) - sca(i,k)]* = 0.091, *SE[sca(i,j) - sca(k,l)]* = 0.074.

Table 9. Estimation of additive and dominance variances and degree of dominance in cucumber genotypes using Griffing's method IV.

Source of variation	Yield per plant	Fruit number	Fruit weight	Nod number	Number of female flowers	Ovary length
Additive variance (σ^2_A)	0.128	30.83	1.98	0.12	0.902	0.03
Dominant variance (σ^2_D)	0.009	3.148	7.6	0.04	0.678	0.016
σ^2_A/ σ^2_D	0.07	0.102	3.83	0.33	0.751	0.533

DISCUSSION

The hybrids 7×2, 6×4, and 7×3 exhibited the longest ovary lengths, with means of 3.65, 3.16, and 3.06 cm, respectively. Organ size in cucumbers results from a combination of cell number and size, with the developing ovary serving as the foundation for fruit size and shape (Grumet *et al.,* 2023).

The highest number of nodes was observed in hybrids 4×3 and 2×4, with averages of 33.66 and 33.33, respectively. The number of nodes per plant is a key genetic trait influenced by environmental factors such as temperature, humidity, and light intensity, which reflect the growth potential of the plant and its capacity to produce flowers and fruits (Subedi *et al.,* 2024).

The hybrids 5×2, 3×5, and 6×4 showed the highest average fruit weights, at 170.33, 80.16, and 79.50 grams, respectively. Fruit weight is negatively correlated with the number of fruits, as increasing fruit number tends to decrease the size and dry weight of each individual fruit. Conversely, a higher ratio of fruit length to diameter is positively associated with fruit weight (Mashayekhi and Mousavizadeh, 2009). The higher general contribution of specific combining ability indicates that non-additive genetic effects play a greater role in controlling fruit weight and that there are significant variations among hybrids in their combining abilities. These findings align with studies by Manggoel *et al.* (2021).

Genetic variance component analysis suggests that both additive and dominance effects influence fruit weight, but the additive effect is more prominent, consistent with previous reports (Moghbeli Hanzaei *et al.,* 2017). However, El-Rimali *et al.* (2021) found higher GCA than SCA for fruit weight, indicating primarily additive gene control, a result that is not aligned with this study. The MS_{GCA}/MS_{SCA} ratio was 0.49, implying a greater role for dominance effects and high environmental influence on this trait. The low narrow-sense heritability further supports the significant environmental impact on fruit weight, suggesting that heritability is affected by genotype, environment, and crossing type (Strefler and Wehner, 1989).

Since cucumber fruits are harvested during the immature stage, their size significantly affects total yield. Generally, larger fruits contribute more to overall yield, whereas smaller fruits tend to lower yield output (Golabadi *et al.,* 2015; Moghbeli Henzaei *et al.,* 2017). Consequently, the number of fruits per plant is a critical trait for yield evaluation and improvement. Both GCA and SCA effects were significant, indicating that additive and dominance gene actions influence this trait. The higher GCA effect suggests that additive genes predominantly control fruit number, consistent with findings by Lopez *et al.* (2002) and Golabadi *et al.* (2015). The dominance effects observed support heterosis as a pathway to achieve higher yields, as noted by Sarkar and Sirohi (2011). However, Manggoel *et al.* (2021) reported dominance effects as more influential than additive effects for this trait, which may be due to varying environmental conditions and maternal influences across different studies.

Hybrids 7×3, 2×3, 4×3, and 5×3 produced the highest yields, with respective averages of 893.50, 795.00, 752.48, and 728.51 grams. Both GCA and SCA effects significantly contributed to yield, with higher GCA effects indicating that additive gene action is the primary factor controlling this trait. This aligns with findings by Moghbeli Hanzai *et al.* (2017). Strefler and Wehner (1989) reported broad heritability estimates for cucumber yield, ranging from 0.02 to 0.88, depending on crossing methods and populations. They highlighted that high narrow-sense heritability and additive effects make selection an effective strategy for yield improvement. Golabadi *et al.* (2015) also proposed that crossbreeding, combining favorable alleles, would be optimal for genetic enhancement in cucumber, with a preference for crossbreeding techniques. The additive variance component (σ^2A) exceeded the dominance component (σ^2D), supporting the conclusion that additive genetic effects are critical for yield improvement in this context.

CONCLUSION

This study identified superior cucumber lines and hybrids based on evaluated traits. Significant differences were found among lines for all traits except fruit length, and genotype significantly affected most traits. Both additive and dominance genetic effects influenced the number of female flowers, fruit weight, fruit number, and yield per plant, with additive gene effects having a greater contribution. However, fruit weight was more influenced by non-additive gene effects, with significant differences observed among hybrids. Hybrid 7×3 demonstrated superior overall performance and is now commercially produced by a knowledge-based company at the Growth Center of the University of Guilan; it has also been submitted for official variety registration. These results indicate that selection methods can effectively improve desirable traits and increase cucumber yields, and that high-yielding hybrids from the breeding population can be introduced.

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REFERENCES

Ahmadi A., and Hassannejad S. (2016). Effects of different types of mulch on cucumber yield and some weed characteristics. *Journal of Agricultural Knowledge and Sustainable Production*, 26(3): 73-84.

Asadian A., Mostafazadehfard B., Mousavi F., Khoshgoftarmanesh A., and Landi A. (2012). The effect of different irrigation levels and substrate type on cucumber plant yield. M.Sc. Thesisi, Isfahan University of Technology, Faculty of Agriculture and Natural Resources.

Bozorgzad G., and Golabadi M. (2019). Determining the contribution and importance of morphological traits on fruit yield of greenhouse cucumber hybrid cultivars. *Iranian Scientific Journal of Agriculture and Plant Breeding*, 15(2): 19-34.

Dhall R. K., Kaur H., Manchanda P., and Eshanee (2023). Genetics and marker-assisted breeding for sex expression in cucumber. *Frontiers in Genetics*, 14: 1180083. DOI: https://doi.org/10.3389/fgene.2023.1180083.

Dianati M., Olfati J. A., and Hamidoghli Y. (2017). Crossing of commercial cultivar Ailar with selected parental lines of cucumber and evaluation of their progeny. *Journal of Horticultural Sciences*, 32(3): 451-458.

El-Remaly E. B., El-Hakim A., Ismail H., Smuda S. S., and Abedelmaksoud T. G. (2021). Breeding new pickling cucumber hybrids: A. Morphological characterization and genetic studies. *Egyptian Journal of Agricultural Research*, 99(4): 464-474.

Falconer D. S. (1996). Introduction to quantitative genetics. Longman, London, pp. 448.

FAO. (2022). FAOSTAT agricultural database. Available at: http://apps.fao.org.

Farahani A., Azizinia Sh., Lotfi M., Karimifar H., and Armion A. (2015). Study of the combining ability of some morphological traits of cucumber. In: Proceedings of the 9th Congress of Horticultural Sciences, Shahid Chamran University of Ahvaz (20-22 February).

Golabadi M., Golkar P., and Eghtedary A. (2015). Combining ability analysis of fruit yield and morphological traits in greenhouse cucumber (*Cucumis sativus* L.). *Canadian Journal of Plant Science*, 95(2): 377-385.

Griffing B. (1956). Concept of general and specific combining ability in relation to diallel crossing systems. *Australian Journal of Biological Sciences*, 9(4): 463-493.

Grumet R., Lin Y. C., Rett-Cadman S., and Malik A. (2023). Morphological and genetic diversity of cucumber (*Cucumis sativus* L.) fruit development. *Plants*, 12(1): 23. DOI: https://doi.org/10.3390/plants12010023.

Hafeznia M., Olfati J. A., and Rabiei B. (2018). Genetic evaluation of floral traits in cucumber using the generation mean analysis method. *Journal of Plant Production Research*, 29(3): 1-15.

Hosseini M., and Kord Rostami M. (2018). Principles of plant breeding. Jihad Daneshgahi Publications, Isfahan Industrial Branch.

Kumar S., Kumar D., Kumar R., Thakur K. S., and Dogra B. S. (2013). Estimation of genetic variability and divergence for fruit yield and quality traits in cucumber (*Cucumis sativus* L.) in North-Western Himalayas. *Universal Journal of Plant Science*, 1(2): 27-36.

López-Sesé A. I., and Staub J. (2002). Combining ability analysis of yield components in cucumber. *Journal of the American Society for Horticultural Science*, 127(6): 931-937.

Mamnouei A., Dolatkhahi A., and Esfandiari B. (2014). The effect of different density levels on yield and quantitative characteristics of two greenhouse cucumber cultivars. *Greenhouse Crop Sciences and Techniques*, 5(18): 123-130.

Manggoel W., Uguru M. I., Ogbonna P. E., and Dasbak M. A. (2021). Exploiting combining ability in a diallel cross between native and elite cucumber (*Cucumis sativus* L.) varieties. *Journal of Plant Breeding and Crop Science*, 13(3): 136-143.

Mashayekhi K., and Mousavizadeh S. (2009). The investigation of leaf number, leaf area and plants dry weight in three cucumber cultivars (*Cucumis sativus* L.). *Journal of Horticultural Science*, 23(1): 57-68.

Moghbali Henzaei A. (2017). Comparison of combining ability, heterosis rate and genetic characteristics of cucumber lines for morphological, biological and yield traits using diallel crossing. Master's Thesis, Ferdowsi University of Mashhad. (In Persian)

Moradipour F., Olfati J. A., Hamidoghli Y., Zahedi B., and Sabouri A. (2017). Investigation of general, specific and heterosis combining of vegetative traits of some cucumber lines. *Horticultural Sciences*, 31(1): 131-140.

Moradipour F., Olfati J. A., Hamidoghli Y., Zahedi B., and Sabouri A. (2018). Investigation of general, specific and heterosis combining of some fresh-eating cucumber lines by incomplete diallel analysis. *Plant Production Technology*, 18(2): 107-120.

Najafi A., Karbasi A. R., and Mohammadzadeh S. H. (2019). Factors affecting vegetable seeds imports to Iran and selected countries. *Journal of Agricultural Economics and Development*, 33(2): 165-176.

Peyvast G. A. (2009). Vegetable cultivation. Daneshpazir Publications, pp. 578.

Qavidel Farouj M. (2017). Investigation of the quantitative and qualitative characteristics of three commercial greenhouse cucumber cultivars and the populations resulting from their crossing. Master's Thesis, Shahrood University of Technology.

Sarkar M., and Sirohi P. S. (2011). Diallel analysis of quantitative characters in cucumber (*Cucumis sativus* L.). *Vegetable Science*, 38: 73-75.

Setamdideh Moslemmi F. (2017). Transfer of the parthenocarpy trait to a selected cucumber line through crossing with parthenocarpy cucumber (*Cucumis sativus* L). Master's Thesis, University of Guilan.

Strefeler M. S., and Wehner T. C. (1989). Effect of gynoecious expression on yield and earliness of a fresh market cucumber hybrid. *Journal of the American Society for Horticultural Science*, 110: 464-466.

Subedi S., Bhandari N., Basnet M., Pradhan N. G., and Gautam I. P. (2024). Evaluation of cucumber genotypes under plastic house and open field conditions in Lalitpur, Nepal. *Cogent Food & Agriculture*, 10(1): 229-531.

Tatlioglu T. (1993). Cucumber: *Cucumis sativus* L. In: Kalloo G., and Bergh B. O. (Eds.), Genetic improvement of vegetable crops (pp. 197-234), Pergamon Press, Ltd., Tarrytown, NY.

Veena R., Sidhu A. S., Pitchaimuthu M., and Souravi K. (2012). Genetic evaluation of cucumber (*Cucumis sativus* L.) genotypes for some yield and related traits. *Electronic Journal of Plant Breeding*, 3(3): 945-948.

Wehner T. C. (1989). Breeding for improved yield in cucumber. *Plant Breeding Reviews*, 6: 323-359.

Zhang H., Li S., Yang L., Cai G., et al. (2021). Gain-of-function of the 1-aminocyclopropane-1-carboxylate synthase gene ACS1G induces female flower development in cucumber gynoecy. *The Plant Cell*, 33(2): 306-321. DOI: https://doi.org/10.1093/plcell/koaa018.