

SABRAO Journal of Breeding and Genetics
 56 (4) 1367-1376, 2024
<http://doi.org/10.54910/sabrao2024.56.4.4>
<http://sabraojournal.org/>
 pISSN 1029-7073; eISSN 2224-8978



COMBINING ABILITY ANALYSIS OF ECONOMICALLY IMPORTANT TRAITS IN THE DIALLEL CROSSES OF CUCUMBER

**A.M. BORASULOV^{1*}, J.M. TURSAGATOV¹, X.K. RUZIMOVA¹, I.X. MAXMATKULOV¹,
 G.A. MENGLIYEV¹, O.R. KUCHCHIYEV¹, SH.N. KODIROVA¹, Z.U. RUZIKULOVA¹,
 M.R. XASHIMOVA¹, SH.X. XALILOV², S.YU. TOSHTMIROV³, D.D. BORASULOVA⁴,
 F.M. CHORSHANBIYEV⁵ and R.A. NIZOMOV⁶**

¹Biotechnology, Ecology, and Forestry Division, Samarkand State University of Veterinary Medicine, Animal Husbandry and Biotechnology, Tashkent Branch, Tashkent, Uzbekistan

²Faculty of Uzbek-English Translation, Tashkent State University of Uzbek Language and Literature, Tashkent, Uzbekistan

³Faculty of Philology and Teaching Languages, Renaissance University, Tashkent, Uzbekistan

⁴Faculty of Applied Translation, Uzbekistan State University of World Languages, Tashkent, Uzbekistan

⁵Forestry Division, Tashkent State Agrarian University, Tashkent, Uzbekistan

⁶Vegetable growing division, Vegetable, melon crops and potato research institute, Tashkent, Uzbekistan

*Corresponding author's email: bioinformatics-genetics@mail.ru

Email addresses of co-authors: tursagatovjahongir@gmail.com, kholida1986@mail.ru, Iskandar.maxmatkulov@mail.ru, drgayrat2@mail.ru, kuchchievoxunjon@gmail.com, shahri19721103@gmail.com, rz960913@gmail.com, madinamadi993@gmail.com, xalilovshokir3@gmail.com, sanjarbektoshtemirov02@gmail.com, translatordilnozauzswlu@mail.ru, farkhodch@gmail.com, bioritim@mail.ru

SUMMARY

The article evaluated the genetics of six cucumbers (*Cucumis sativus* L.) cultivars and 30 hybrids based on morpho-yield traits. The dominant and epistatic gene effects managed the fruit weight in three cucumber hybrids (C-25/1, A-6, and A-9), while additive gene effects in three other hybrids were supreme. For productivity per plant, dominant genes with epistatic effects controlled these in three accessions, while additive effects played a special role in manifesting the trait in three other hybrid (C-25/1, A-6, and A-9) genes. Likewise, dominant genes with epistatic effects controlled the yield per plant trait in three accessions, while additive effects influenced the attribute in three other hybrids (C-25/1, A-6, and A-9). According to these traits, the promising hybrids were C-25/1 x C-25/2, C-26 x C-25/2, C-26 x C25/1, A-9 x C-26, and A-6 x C-25/1. The cucumber F₁ hybrids C-26 x C-29, A-9 x A-6, and A-9 x C-25/2 showed characteristics of large fruits weighing 108.2 to 113.1 g. In the accessions, C-25/1, A-6, and A-9, the additive gene effects dominated the studied trait ($\sigma_2^2 > \sigma_2^2$). The superior-in-yield hybrid combinations were C-26 x C-29, A-9 x A-6, and A-6 x A-9, with a total fruit yield of 691 to 769 g per plant.

Communicating Editor: Dr. Himmah Rustiami

Manuscript received: December 15, 2023; Accepted: April 25, 2024.

© Society for the Advancement of Breeding Research in Asia and Oceania (SABRAO) 2024

Citation: Borasulov AM, Tursagatov JM, Ruzimova XK, Maxmatkulov IX, Mengliyev GA, Kuchchiyev OR, Kodirova SHN, Ruzikulova ZU, Xashimova MR, Xalilov SHX, Toshtemirov SYU, Borasulova DD, Chorshanbiyev FM, Nizomov RA (2024) Combining ability analysis of economically important traits in the diallel crosses of cucumber. *SABRAO J. Breed. Genet.* 56(4): 1367-1376. <http://doi.org/10.54910/sabrao2024.56.4>.

Keywords: Cucumber (*Cucumis sativus* L.), diallel crosses, general and specific combining ability, female flowering, fruits, physiological maturity, productivity

Key findings: The study enunciated that in cucumber (*C. sativus* L.), the average fruit weight bore control from dominant genes with epistatic effects in three accessions (C-25/1, A-6, and A-9), and additive gene effects were vital in three other accessions. The fruit productivity per plant also had dominant and epistatic gene effects managing the trait in three accessions, while in three others (C-25/1, A-6, and A-9), the additive gene effects manifested most in the trait. The promising hybrids, viz., C-26 x C-29, A-9 x A-6, and A-6 x A-9, performing best were choices to serve as source material for further selection.

INTRODUCTION

Cucumber (*Cucumis sativus* L.) is one of Earth's most common vegetables, planted on 2.118 million hectares yearly. The gross yield was 71.366 million tons, while the average yield was 33.6 t ha⁻¹. Worldwide, the cucumber-leading producers are China (54,363 million tons), Turkey (1,755 million tons), and Iran (1,570 million tons). Other countries giving remarkably high yields were the Netherlands (666.6 t ha⁻¹), England (536.1 t ha⁻¹), Iceland (445.2 t ha⁻¹), Denmark (349.0 t ha⁻¹), and Sweden (279.0 t ha⁻¹). In the Russian Federation in 2017–2021, cucumber cultivation occurred on 67,267 hectares, obtaining 1,068,000 tons of gross harvest, while the average productivity was 15.8 t ha⁻¹ (FAOSTAT, 2023).

Cucumber is an essential vegetable crop cultivated worldwide. Currently, cucumber genetic and genomic resources, especially molecular markers, are lacking, impeding breeding efforts on cucumbers (Cavagnaro *et al.*, 2010). Cucumber cultivation has existed for about 3000 years in India, and soon after, its dissemination proceeded to the south and east of the Himalayas. From India, the transfer of cucumber continued to Greece, Italy, and later, China. Historical records have confirmed cucumber cultivation in France and the Great Moravian Empire in central Europe (Jeffrey, 1990). Advanced research work to ensure food safety progressed to develop exportable, high-yielding cucumber cultivars and F₁ hybrids suitable for soil and climate conditions in various regions (Mamedov, 2015; FAOSTAT, 2020). In particular, an increase in air

temperature above +32°C degrees in cucumber crops causes a decrease in female flowering, eventually decreasing productivity (Rebecca, 2021).

In developing improved cucumber cultivars, utilizing new germplasm was more suitable for planting in open fields in the Republic, with good fruit quality, resistance to powdery and downy mildew diseases, more maternal flowers, high-yielding cultivars, and the strategy of F₁ hybrids is a practical way to find a solution to all these relevant constraints (Yunusov, 2019). Downy mildew is one of the most harmful diseases in cucumbers in Kazakhstan. High variability of the fungus to the emergence of new aggressive pathotypes and, consequently, loss of resistance by some crop cultivars causes the ever-growing destructiveness of *P. cubensis* (Amirkhanova and Rsaliyev, 2017). Cucumber planting transpires worldwide, making it a highly influential cucurbitaceous crop (Miller *et al.*, 1970; Borasulov, 2021).

Knowledge of the genetic manifestation of quantitative traits is crucial for breeders creating new cultivars and hybrids (Bandyopadhyay, 2011). Depending on the nature of the function of genes controlling the manifestation of the traits, determining the selection method for these traits is also necessary for cultivating new cultivars. The success of selection primarily depends upon the assortment of source material and its in-depth study based on various related aspects. Determining the combining ability is one of the main methods for identifying and selecting promising genotypes. Selection of heterocyst hybrids is essential in choosing through

combining ability in terms of economically valuable traits, including early maturity, fruit weight, and final productivity (Liu *et al.*, 2021).

Combining ability of the genotypes is a genetically determined parameter, which depends upon the complex systems of interaction of hereditary factors. Proof has long existed that cultivars with high combining ability provide higher-yielding hybrids than cultivars with low combining ability. Given that carrying out cultivar selection is mainly for high combining ability, the elucidation of the genetic basis of these parameters, and further advancement in its evaluation, become one of the most significant tasks of breeding (Yong, 2015). The analysis of combining ability effects for harvest showed reliable differences in general combining ability (GCA) effects of the parental genotypes and specific combining ability (SCA) effects in particular hybrids. One of the critical steps in the analysis was to compare the varied values of the genotypes, and the GCA of the genotypes is comparable to the SCA of the hybrids by quantifying their effects (Griffing, 1956). Significant GCA and SCA variances resulting in all the traits implied that both the additive and non-additive gene effects operated in the genetic expression of the attributes (Madhu, 2010; Bunphan *et al.*, 2015).

Positive heterosis for juice-dissolved solids was not evident; however, five hybrids had negative mid-parent heterosis for this trait. Positive heterosis for biomass yield, theoretical juice yield, and grain yield emerged in some hybrids. Better Parent Heterosis (BPH), genetic variances, gene effects, and heritability of the traits underwent estimation for hybrids. A high level of epistasis controlled some of the quantitative characteristics and hybridization evidenced by the result effectively developed new tomato cultivars with positive heterotic effects on fruit yield (Acquaah, 2007).

In addition to comparing the variance due to SCA of different hybrids, equating the relative variances due to GCA and SCA of the same genotype is interesting. A genotype with high GCA variance means that the said genotype is much better than other compared lines (Alsharar *et al.*, 2023). Based on the GCA

variance, assessing the importance of the genes can depend on their additive type of action. The hybrids' SCA variance indicates that those cross combinations involving a given accession are relatively better or worse than expected based on the average values of the accession. Genotypes with low SCA variance can also receive an assessment through their genotypes' GCA variances. Specific combining ability depends upon the genes with dominant and epistatic effects (Chaudhary, 1987; Chikezie *et al.*, 2001; Mule and Khandelwal, 2011). Combining ability studies have continued for primary and economically valuable cucumber traits (Lopez and Staub, 2002; Golabadi *et al.*, 2015). The latest research sought to study the GCA and SCA in the diallel crosses for economically important cucumber traits.

MATERIALS AND METHODS

The research proceeded from 2020 to –2023 at the Samarkand State University of Veterinary Medicine, Animal Husbandry, and Biotechnology, Tashkent branch, Uzbekistan. The soil's characteristic was typically sulfurous. The research experiment commenced in field conditions according to the recommendations and guidelines for cucumbers' selection and seed production (Kononkova and Pivovarov, 1999). The experiment comprised four replicates of diallel-crossed hybrids with an area of 4.2 m². The total number of cucumber plants in each plot is 16, following the planting scheme below.

$$\text{Sowing scheme } \frac{(140 + 70)}{2} \times 30 \text{ cm}$$

The pH of the nutrient solution requires maintaining 5.5–6.5. Electrical conductivity (EC) should not be a method of determining precise fertility of the nutrient solution because EC can vary with water quality and source of fertilizer. However, EC can serve as a quick check on the total soluble salts in the nutrient solution. Maintaining EC should be between 1.5–2.5 deciSiemens/meter (1

deciSiemen/meter = 1 millimhos/centimeter = 640 parts per million). An emitter placed in a plastic jug collected a sample to test the EC and pH of the solution (Lamb *et al.*, 2001).

In studying cucumbers' six accessions and their 30 F₁ hybrids, the recommended agricultural technology was generally operational for the conditions of Uzbekistan (Kulakova, 1977). The 30 F₁ hybrids resulted from diallel crosses in six accessions of cucumber. The research sought to evaluate the combining ability of cucumber parental genotypes and their F₁ hybrids based on economically valuable traits and their subsequent use in breeding programs to develop high-yielding and high-quality cultivars and hybrids.

In 2020-2023, 19 cucumber (*Cucumis sativus* L.) accessions received from the World Vegetable Center, Taiwan, underwent scrutiny at the experimental base of the Samarkand State University of Veterinary Medicine, Animal Husbandry and Biotechnology, Tashkent branch, Uzbekistan. The soil was typically chernozem. Climatic conditions during the experimental period were close to average based on the long-term data. The studies progressed according to the recommendations and methodological guidelines for cucumber breeding and seed production (Country Commercial Guide, Uzbekistan, 2023).

Six cucumber accessions' identification was on the complex of economically valuable traits, i.e., C-25/1, C-25/2, C-26, C-29, A-6, and A-9, which consisted of the hybridization program for complete diallel crosses. The diallel crosses resulted in 36 hybrid combinations, and the hybridization analysis occurred according to the first method of Griffing (1956), where direct and reciprocal crosses were samples along with parental genotypes for further comparative study. Standard, generally accepted methods help determine the general and specific combining ability of the parental genotypes and their diallel hybrids (Paulo and Adriano, 2023).

Data recorded

Data recording ensued on the following quantitative traits included the number of days

from mass sprouting to the opening of female flowers, the number of days from mass sprouting to physiological ripening of fruits, the number of fruits per plant, the average fruit weight, and fruit productivity per plant.

Statistical analysis

Data based on the cucumber parental genotypes and their F₁ hybrids having significant differences in the means obtained through analysis of variance (ANOVA) further underwent the combining ability analysis according to Method I based on Eisenhart's Model-II (Singh and Chaudhary, 1979). Generally accepted methods were also operational to determine the GCA and SCA effects (Gomez and Gomez, 1984). The computer application MS-Excel ran all the statistical and genetic analyses.

RESULTS AND DISCUSSION

The results enunciated that cucumber traits, i.e., the number of days from seed germination to the female flowering and the number of days until physiological maturity of fruits in the studied cucumber parental genotypes and their F₁ hybrids, the ratio of GCA and SCA variances ($\sigma^2_{gi} < \sigma^2_{si}$) was evident, along with the dominant role of the genes with their epistatic effects. The trait number of fruits per plant received control from dominant and epistatic gene effects ($\sigma^2_{gi} < \sigma^2_{si}$) in almost all the cucumber accessions, while additive gene effects ($\sigma^2_{gi} > \sigma^2_{si}$) were in the accession A-6. It can be due to the small chromosome size and interference of secondary metabolites, with relatively low genetic diversity and heterozygosity attained. Self-compatibility, using a few plants to obtain fruits, and backyard cultivations could explain the relatively low diversity (Dane, 1991).

The phenomenon ($\sigma^2_{gi} < \sigma^2_{si}$) was noticeable for average fruit weight, where the dominant genes with their epistatic effects controlled the trait expression in three cucumber accessions (C-25/1, A-6, and A-9), while additive gene effects ($\sigma^2_{gi} > \sigma^2_{si}$) were more significant in the inheritance of the said

trait in three other accessions. The fruit productivity per plant's management was by the dominant genes with their epistatic effects ($\sigma^2_{gi} < \sigma^2_{si}$) in the three cucumber accessions, while in the three other accessions (C-25/1, A-6, and A-9), the additive gene effects play a unique role for the expression of the said trait. The promising cucumber hybrid combinations with the best productivity and quality were better choices to use as a base material for further growth and future breeding programs. The combining ability analysis of the cucumber parental accessions and their F₁ diallel hybrids also showed differences in the onset of phenomenological phases of development and productivity.

Studies on correlation and path coefficient analysis carried out in eight genotypes of cucumber showed that yield per plant had a strong positive association with the main vine length, number of secondary branches, leaf area, fruiting percentage, the number of fruits per plant, fruit weight, and fruit length both at genotypic and phenotypic levels. Path coefficient analysis revealed that the number of fruits per plant had the maximum direct genotypic effect on yield, followed by fruit weight. These traits were valuable parameters in any selection program for cucumber yield improvement (Dhiman and Prakash, 2005).

Days from sprouting to female flowering

The combining ability analysis revealed that the lowest values of GCA determining the

relative early maturity were prominent in cucumber two accessions C-25/2 ($\hat{g}_i = -1.81$) and C-26 ($\hat{g}_i = -0.65$). However, their SCA variants differed. For example, accession C-25/2 has the highest variant SCA ($\sigma^2_{si} = 1.30$), while accession C-26 ($\sigma^2_{si} = -1.57$) has a relatively low SCA variant. The cucumber accessions C-25/1 and A-9 have the lowest GCA variants ($\sigma^2_{gi} = -1.99$ and $\sigma^2_{gi} = -1.93$, respectively). The accession C-29 also differed from other cucumber accessions due to maximum GCA effects ($\hat{g}_i = 1.48$), and GCA ($\sigma^2_{gi} = 0.20$) and SCA ($\sigma^2_{si} = 0.20$) variants have moderate significance. Cucumber fruit development follows a canonical sigmoidal growth pattern. Unlike many fruits, however, they are typically immature when harvested toward the end of the exponential growth stage, at approximately 10 to 12 days post-pollination (DPP) (Mansfeld and Grumet, 2016).

The results indicated that the longer duration of the interphase period from mass sprouts to the opening of female flowers in hybrid combinations with the abovementioned accessions is relative to the average values. For the said trait, the SCA variances were higher in accessions A-9 ($\sigma^2_{si} = 3.85$) and C-26 ($\sigma^2_{si} = 3.75$), although their effect indices and GCA variances were relatively low ($\hat{g}_i = 0.25$, $\sigma^2_{gi} = -1.93$ and $\hat{g}_i = -0.65$, $\sigma^2_{gi} = -1.57$, respectively) (Table 1). The variability of agrotechnical and phenological dates in the region varied from 3.0% to 5.4%. The smallest time variability pointed to the date of sowing

Table 1. Assessment of GCA effects and variances due to GCA and SCA in diallel crosses and their parental genotypes for number of days from sprouting to female flowering in cucumber.

Female forms	Male form						<i>gi</i>	<i>Ggi</i> ²	<i>Gsi</i>
	C-25/1	C-25/2	C-26	C-29	A-6	A-9			
C-25/1	55.00	46.00	51.75	55.75	55.50	59.00	0.02	-1.99	6.44
C-25/2	53.75	53.75	50.50	53.75	54.00	51.25	-1.81	1.30	1.81
C-26	48.50	47.75	54.50	54.00	59.75	55.50	-0.65	-1.57	3.75
C-29	56.50	50.75	58.00	55.00	56.25	53.25	1.48	0.20	0.94
A-6	49.50	52.25	51.25	55.00	55.75	52.50	0.71	0.90	1.83
A-9	56.75	53.50	49.00	57.25	53.75	52.00	0.25	-1.93	3.85
Standard error	Restrictions						HCP ₀₅	HCP ₀₁	
							2.08	2.75	
<i>gi - gj</i>	0.60	<i>i = j</i>					1.20	1.59	
<i>sij - sik</i>	1.35	<i>i = j, k; j = k</i>					2.69	3.55	
<i>sij - skl</i>	1.21	<i>i = j, k; l; j = k, k = l</i>					2.40	3.18	

and the largest to the date of harvesting. However, the mean forecast error determined for the dates of the beginning of flowering and harvesting of cucumber did not exceed 2% (Kalbarczyk, 2006).

In almost all studied cucumber accessions, the SCA variances for the number of days from mass sprouting to female flowering prevail over the values of GCA variances ($\sigma_{\hat{g}_i}^2 < \sigma_{s_i}^2$). This phenomenon indicates the predominant role of the dominant genes and their epistatic effects in the inheritance of the said trait. The promising hybrid combinations with a shorter period of interphase from mass sprouting to the opening of female flowers were the selections of C-25/1 x C-25/2, C-26 x C-25/2, C-26 x C25/1, A-9 x C-26, and A-6 x C-25/1, wherein female flowering begins at 46 to 49 days after sprouting.

Days from mass sprouting to fruits technical ripeness

Based on the combining ability analysis, the lowest values of GCA effects were evident in accessions C-26 ($\hat{g}_i = -1.78$) and C-25/2 ($\hat{g}_i = -1.40$), in which the GCA variances ($\sigma_{\hat{g}_i}^2 = 1.34$, $\sigma_{s_i}^2 = 0.15$) and SCA ($\sigma_{\hat{g}_i}^2 = 3.14$, $\sigma_{s_i}^2 = 1.23$) had average values, respectively. High GCA effects were visible in the cucumber accessions C-25/1 ($\hat{g}_i = 0.99$) and A-6 ($\hat{g}_i = 0.91$), and the GCA and SCA variances differed. In the accession C-25/1, the GCA variant had a relatively low value ($\sigma_{\hat{g}_i}^2 = -0.83$), however, the SCA variant had the highest significance ($\sigma_{s_i}^2 = 4.48$). A similar pattern emerged for the accession A-9. The cucumber accession C-26 had high and medium values of the OKC variances ($\sigma_{\hat{g}_i}^2 = 1.34$) and SCA ($\sigma_{s_i}^2 = 3.14$), although, it had the lowest GCA effect ($\hat{g}_i = -1.78$) (Table 2).

The genetic arsenal was characteristic of various vegetative and commercial traits: (i) days to 50% curd initiation: DCI; (ii) days to 50% curd maturity: DCM; (iii) plant height: PH (cm); (iv) gross plant weight: GPW (kg); (v) marketable curd weight: MCW (kg); (vi) net curd weight: NCW (kg); (vii) leaf length: LL (cm); (viii) leaf width: LW (cm); (ix) number of leaves: NoL; (x) curd length: CL (cm); (xi)

curd diameter: CD (cm); (xii) core length: CoL (cm); (xiii) harvest index: HI (%); and (xiv) Total marketable yield: TMY (t/ha) (Dey *et al.*, 2017; Bazargaliyeva *et al.*, 2023; Fathurrahman, 2023).

The ratio of $\sigma_{\hat{g}_i}^2 < \sigma_{s_i}^2$ was notable in all studied cucumber accessions for the trait days from mass sprouting to physiological ripeness of fruits, for which the predominant role of the dominant genes with epistatic effects was evident in the inheritance of the said trait. Hybrid combinations C-26 x C-26, C-25/1 x C-25/2, A-9 x C-26, A-6 x A-9, and C-26 x C-25/1 appeared as the promising ones for the number of days from mass sprouting to the technical ripening of the fruits. In these cucumber accessions, fruits reached physiological ripeness in 57 to 60 days from the mass sprouting (Table 2).

Fruits per plant

Analysis of the combining ability of the studied cucumber accessions exhibited that the number of fruits per plant showed the highest significance of the GCA effects ($\hat{g}_i = 0.53$) in the accession A-6, which also revealed the highest and average values of GCA variants ($\sigma_{\hat{g}_i}^2 = 0.33$) and SCA ($\sigma_{s_i}^2 = 0.09$). The higher values of SCA variances were apparent in accessions C-25/1 ($\sigma_{s_i}^2 = 0.18$), C-26 ($\sigma_{s_i}^2 = 0.15$), and A-9 ($\sigma_{s_i}^2 = 0.14$); however, the GCA variances had relatively higher negative values ($\sigma_{\hat{g}_i}^2 = -0.14$, $\sigma_{\hat{g}_i}^2 = -0.18$ and $\sigma_{\hat{g}_i}^2 = -0.18$, respectively). Meanwhile, the accessions C-26 ($\hat{g}_i = 0.18$) and A-9 ($\hat{g}_i = 0.17$) owned the medium positive GCA effects, and the accession C-25/1 showed a significant negative index ($\hat{g}_i = -0.26$) (Table 3).

The GCA mean square appeared considerably larger than the SCA for IL, NFP, and LW, indicating that additive genetic effects were crucial in governing these traits. A close agreement also occurred between the yield per fruit and the yield per plant, as affected by GCA (Cramer and Wehner, 2000). In all studied cucumber accessions, except for accession A-6, the SCA variance was superior to GCA variance ($\sigma_{\hat{g}_i}^2 < \sigma_{s_i}^2$), and the dominant genes with epistatic effects were more pronounced than the additive effects in the

inheritance of the number of fruits per plant. However, the opposite phenomenon emerged in accession A-6, where the additive gene effects have more influence on the manifestation of this trait. Hybrid combinations C-25/1 x C-26, A-6 x C-26, C-26 x C-29, and A-6 x A-6 were the best for the number of fruits per plant, which on average, formed 7.0 to 7.7 fruits per plant during the whole vegetation period (Table 3).

Average fruit weight

The combining ability analysis revealed that the highest positive values for GCA effects ($\hat{g}_i = 10.44$) and GCA ($\sigma^2_{\hat{g}_i} = 98.20$) and SCA ($\sigma^2_{si} = 70.67$) variances manifested in the cucumber accession A-9. A similar phenomenon was also prominent in accession A-6; however, the GCA effects and GCA and SCA variances were slightly lower than in accession A-9. Higher values of the SCA variances showed in accessions C-26 ($\sigma^2_{si} = 132.08$) and C-29 ($\sigma^2_{si} = 111.77$), although, the GCA variance values were different. The accession C-26 ($\sigma^2_{\hat{g}_i} = 14.65$) had a positive value and the accession C-29 ($\sigma^2_{\hat{g}_i} = -10.59$) had a negative one. The accessions C-25/2 ($\sigma^2_{\hat{g}_i} = 10.16$, $\sigma^2_{si} = 66.68$) and C-25/1 ($\sigma^2_{\hat{g}_i} = 29.11$, $\sigma^2_{si} = 27.57$) gave positive values of GCA and SCA variances, although the GCA effects had a significant negative value ($\hat{g}_i = -4.58$ and $\hat{g}_i = -6.32$, respectively) (Table 4).

The greater part of the diversity resulted in fruit diameter, weight, length and width, fruit cavity length and diameter, seed length, and color. The flesh area of the fruit, flesh thickness, leaf size, seed weight, and seed index did not account for variation in the first six principal components of the melon collection. The scatter diagram segregated the acidulus and momordica into separate clusters (Kirkbride, 1993).

Three cucumber accessions C-25/1, A-6, and A-9 showed differences in the ratio $\sigma^2_{\hat{g}_i} < \sigma^2_{si}$ for average fruit weight, with dominant genes and epistatic effects controlling the inheritance of the said trait and playing a significant role. In other cucumber accessions, the additive gene effects ($\sigma^2_{\hat{g}_i} > \sigma^2_{si}$) were prominent for the said trait. The cucumber F_1 hybrids C-26 x C-29, A-9 x A-6, and A-9 x C-25/2 were distinct with

bigger fruits weighing 108.2 to 113.1 g (Table 4).

Fruit productivity per plant

A significant wide variability occurred in the GCA and SCA variances for the fruit productivity per plant. It was also noteworthy that accessions A-6 and A-9 showed highest indices for GCA effects ($\hat{g}_i = 82.1$ and $\hat{g}_i = 78.6$) and GCA ($\sigma^2_{\hat{g}_i} = 7176.9$ and $\sigma^2_{\hat{g}_i} = 3989.1$) and SCA ($\sigma^2_{si} = 1074.4$ and $\sigma^2_{si} = 3579.5$) variances. Average positive variances of GCA and SCA resulted in cucumber accessions C-25/2 ($\sigma^2_{\hat{g}_i} = 2072.6$ and $\sigma^2_{si} = 2702.2$) and C-25/1 ($\sigma^2_{\hat{g}_i} = 1447.2$ and $\sigma^2_{si} = 1443.6$); however, the GCA effects had relatively negative significance ($\hat{g}_i = -60.2$ and $\hat{g}_i = -60.3$, respectively). The highest values of SCA variances came from the accessions S-29 ($\sigma^2_{si} = 4887.9$) and S-26 ($\sigma^2_{si} = 4863.2$), although the GCA variances ($\sigma^2_{\hat{g}_i} = -1906.3$ and $\sigma^2_{\hat{g}_i} = -1841.2$) and effects ($\hat{g}_i = -16.7$ and $\hat{g}_i = -18.5$) had negative values. The maximum values of SCA variances surfaced in the accessions C-29 ($\sigma^2_{si} = 4887.9$) and C-26 ($\sigma^2_{si} = 4863.2$), and the GCA variances ($\sigma^2_{\hat{g}_i} = -1906.3$ and $\sigma^2_{\hat{g}_i} = -1841.2$) and effects ($\hat{g}_i = -16.7$ and $\hat{g}_i = -18.5$) were negative (Table 5).

The relative importance of GCA vs. SCA for fruit number was relevant after the first harvest, with values higher than 0.75. The GCA estimates for this trait vary in magnitude and direction depending on the harvest. Estimates of GCA for fruit number were most variable in Harvest 1 but were relatively consistent in Harvest 3 and three cumulative harvests (Lopez and Staub, 2002). By comparing the GCA and SCA variances of the studied cucumber accessions C-25/2, C-26, and C-29, the SCA variance for the fruit productivity per plant prevails over higher values of SCA variance ($\sigma^2_{\hat{g}_i} < \sigma^2_{si}$), indicating the predominant role of dominant genes and epistatic effects in the inheritance of the said trait. In accessions C-25/1, A-6, and A-9, the manifestation of the studied trait had the additive gene effects ($\sigma^2_{\hat{g}_i} > \sigma^2_{si}$) controlling them. The most productive hybrid combinations were C-26 x C-29, A-9 x A-6, and A-6 x A-9, with total fruit productivity of 691 to 769 g per plant

Table 2. Assessment of GCA effects and variances due to GCA and SCA in diallel crosses and their parental genotypes for days from mass sprouting to technical ripeness of fruits in cucumber.

Female form	Male form						<i>gi</i>	<i>Ggi</i> ²	<i>Gsi</i>
	C-25/1	C-25/2	C-26	C-29	A-6	A-9			
C-25/1	65.25	57.75	62.25	65.75	65.50	69.00	0.99	-0.83	4.48
C-25/2	64.50	63.75	61.50	64.00	64.00	62.25	-1.40	0.15	1.23
C-26	59.75	60.00	57.00	64.25	69.75	65.50	-1.78	1.34	3.14
C-29	65.75	61.50	67.00	64.75	65.75	63.50	1.26	-0.22	1.62
A-6	69.75	62.00	61.00	64.75	65.25	59.50	0.91	1.19	3.98
A-9	66.75	63.50	59.00	68.75	63.75	62.00	0.01	-1.82	4.09
Standard error	Restrictions						HCP ₀₅	HCP ₀₁	
<i>gi - gj</i>	0.56	<i>i = j</i>					1.94	2.56	
<i>sij - sik</i>	1.26	<i>i = j, k; j = k</i>					1.12	1.48	
<i>sij - skl</i>	1.12	<i>i = j, k; l; j = k, k = l</i>					2.50	3.30	
							2.24	2.96	

Table-3. Assessment of GCA effects and variances due to GCA and SCA in diallel crosses and their parental genotypes for fruits on per plant in cucumber.

Female form	Male form						<i>gi</i>	<i>Ggi</i> ²	<i>Gsi</i>
	C-25/1	C-25/2	C-26	C-29	A-6	A-9			
C-25/1	5.45	5.45	7.68	4.73	4.80	5.23	-0.21	-0.21	0.30
C-25/2	4.93	4.43	5.13	4.60	4.93	5.23	-0.42	-0.08	0.06
C-26	4.78	5.68	4.43	7.03	5.70	4.80	0.07	-0.25	0.17
C-29	5.20	5.80	4.35	4.70	5.90	6.60	-0.23	-0.20	0.05
A-6	6.93	5.63	7.58	6.48	6.23	6.78	0.48	0.28	0.10
A-9	4.40	6.25	6.83	4.68	6.10	7.25	0.32	-0.15	0.19
Standard error	Restrictions						HCP ₀₅	HCP ₀₁	
<i>gi - gj</i>	0.23	<i>i = j</i>					0.79	1.04	
<i>sij - sik</i>	0.51	<i>i = j, k; j = k</i>					0.46	0.60	
<i>sij - skl</i>	0.46	<i>i = j, k; l; j = k, k = l</i>					1.02	1.35	
							0.91	1.21	

Table 4. Assessment of GCA effects and variances due to GCA and SCA in diallel crosses and their parental genotypes for average fruit weight in cucumber.

Female form	Male form						<i>gi</i>	<i>Ggi</i> ²	<i>Gsi</i>
	C-25/1	C-25/2	C-26	C-29	A-6	A-9			
C-25/1	78.35	66.25	69.23	75.95	86.70	79.53	-5.78	19.01	33.09
C-25/2	66.83	77.18	67.00	76.78	73.33	91.58	-4.18	3.14	37.67
C-26	51.63	65.58	69.90	108.13	75.95	78.95	-5.59	16.86	83.13
C-29	88.00	88.18	80.85	71.93	92.08	80.40	1.85	-10.93	79.94
A-6	83.55	81.25	81.23	85.70	93.73	90.83	4.78	25.68	10.24
A-9	88.30	100.68	96.60	84.28	101.23	98.33	8.92	65.20	40.98
Standard error	Restrictions						HCP ₀₅	HCP ₀₁	
<i>gi - gj</i>	1.91	<i>i = j</i>					6.58	8.70	
<i>sij - sik</i>	4.27	<i>i = j, k; j = k</i>					3.80	5.02	
<i>sij - skl</i>	3.82	<i>i = j, k; l; j = k, k = l</i>					8.50	11.23	
							7.60	10.05	

Table 5. Assessment of GCA effects and variances due to GCA and SCA in diallel crosses and their parental genotypes for fruit productivity per plant.

Female form	Male form						<i>gi</i>	<i>Ggi</i> ²	<i>Gsi</i>
	C-25/1	C-25/2	C-26	C-29	A-6	A-9			
C-25/1	510.75	378.23	534.13	340.13	417.38	474.50	-62.60	-0.21	1417.19
C-25/2	381.43	353.58	346.63	388.15	430.68	569.63	-67.58	-0.08	2760.20
C-26	263.35	421.38	409.10	853.25	516.38	428.35	-13.83	-0.25	7018.56
C-29	507.60	507.10	461.50	350.60	553.50	530.58	-11.98	-0.20	6926.88
A-6	587.15	488.40	618.78	577.03	721.83	691.30	79.76	0.28	1045.23
A-9	414.48	641.30	643.08	507.20	703.90	690.73	76.23	-0.15	3772.51
Standard error	Restrictions						HCP ₀₅	HCP ₀₁	
							68.21	90.15	
<i>gi - gj</i>	19.79	<i>i = j</i>					39.38	52.05	
<i>sij - sik</i>	44.25	<i>i = j, k; j = k</i>					88.06	116.38	
<i>sij - skl</i>	39.58	<i>i = j, k; l; j = k, k = l</i>					78.76	104.09	

CONCLUSIONS

The results revealed that for average fruit weight, the phenomenon ($\sigma^2_{\hat{g}i} < \sigma^2_{si}$) was valid, and the manifestation of the said trait had dominant genes with epistatic effects ($\sigma^2_{\hat{g}i} < \sigma^2_{si}$) controlling these three cucumber accessions (C-25/1, A-6, and A-9), while in three other accessions, the additive gene effects ($\sigma^2_{\hat{g}i} > \sigma^2_{si}$) were more significant in inheritance. The dominant genes and epistatic effects ($\sigma^2_{\hat{g}i} < \sigma^2_{si}$) in three cucumber accessions controlled fruit productivity per plant. However, in three other accessions (C-25/1, A-6, and A-9) the additive gene effects were more prominent and vital in expressing the said trait. Promising hybrid combinations with the best performance were options for their use as source material for further selection.

REFERENCES

Acquaah G (2007). Principles of Plant Genetics and Breeding. Blackwell Publishing, Oxford. pp. 127-128.

Alsharar SF, Ibrahim AA, Okasha SA (2023). Combining ability for yield, oil content, and physio-biochemical characters of canola (*Brassica napus* L.) under salt stress conditions. *SABRAO J. Breed. Genet.* 55(4): 1003-1024.

Amirkhanova NT, Rsaliyev AS (2017). Screening of cucumber varieties and hybrids for selection of downy mildew resistance sources.

Vavilovskii Zhurnal Genetiki i Seleksii - Vavilov J. Genet. Breed. 21(6): 677-685.

Bandyopadhyay T (2011). Molecular marker technology in genetic improvement of tea. *Int. J. Plant Breed. Genet.* 5: 23-33.

Bazargaliyeva A, Utarbayeva N, Nussupova A, Admanova G, Yechshanova G, Kuanbay Z, Sarzhigitova A, Baubekova A (2023). Ecological varietal evaluation of cucumber (*Cucumis sativus* L.) under field conditions. *SABRAO J. Breed. Genet.* 55(1): 90-96. <http://doi.org/10.54910/sabrao2023.55.1.8>.

Borasulov A (2021). Use of new germplasm in the breeding of varieties and F1 hybrids with complex economic characteristics of cucumber. Dissertation. pp. 87.

Bunphan D, Prasit J, Jirawat S, Joseph EK, Anderson FW (2015). Heterosis and combining ability of F1 hybrid sweet sorghum in Thailand. *Crop Sci.* 55: 178-187.

Cavagnaro PF, Senalik DA, Yang L, Simon PW, Harkins TT, Kodira CD, Huang S, Weng Y (2010). Genome-wide characterization of simple sequence repeats in cucumber (*Cucumis sativus* L.). *BMC Genomics* 11: 569.

Chaudhary S (1987). Studies heterosis, combining ability, and correlation in bitter melon (*Momordica charantia* L.). Ph.D. Thesis. Mahatma Phule, University, Rahuri, Maharashtra. pp. 211.

Chikezie O, Ejimofor PO, Christian UA (2001). Heterosis and combining ability in cucumber (*Cucumis sativus* L.) Department of Crop Science, University of Nigeria.

Country Commercial Guide, Uzbekistan (2023). International Trade Administration, Uzbekistan.

Cramer CS, Wehner TC (2000). Fruit yield and yield component correlations of four pickling

- cucumber populations. *Cucurbit Genet. Coop. Rep.* 23: 12–15.
- Dane F (1991) Cytogenetics in genus *Cucumis*. In: Chromosome Engineering in Plants: Genetics, Breeding, and Evolution, Part B. T. Tsuchiya and P.K. Gupta (Eds.), Elsevier, Amsterdam. pp. 201–214.
- Dey SS, Bhatia R, Bhardwaj I, Mishra V, Sharma K, Parkash C (2017). Molecular-agronomic characterization and genetic study reveal the usefulness of refined Ogura cytoplasm-based CMS lines in hybrid breeding of cauliflower (*Brassica oleracea* var. botrytis L.). *Sci. Hortic.* 224: 27–36.
- Dhiman MR, Prakash C (2005). Correlation and path coefficient analysis in cucumber. *Haryana J. Hortic. Sci.* 34(1-2): 111–112.
- FAOSTAT (2020). Food and Agriculture Organization of the United Nations Statistics Division. Available online: <http://faostat.fao.org/site/567/desktopdefault.aspx>.
- FAOSTAT (2023). Food and Agriculture Organization of the United Nations Statistics Division. Available online: <https://www.fao.org/documents/card/en/c/8b1a57f5-587c-5ff6-a0da-cd5b90d8b747>.
- Fathurrahman F (2023). Growth and genetic characteristics of cucumber (*Cucumis sativus* L.) Cultivar mercy f1 hybrid and mutant populations. *SABRAO J. Breed. Genet.* 55(2): 485-494. <http://doi.org/10.54910/sabrao2023.55.2.20>.
- Golabadi M, Golkar P, Eghtedary A (2015). Combining ability analysis of fruit yield and morphological traits in greenhouse cucumber (*Cucumis sativus* L.). *Can J. Plant Sci.* 31(2): 46–58.
- Gomez K, Gomez A (1984). Statistical Procedures for Agricultural Research. The International Rice Research Institute, Los Banos, Laguna, Philippines.
- Griffing B (1956). Concept of general and specific combining ability in relation to diallel crossing systems. *Aust. J. Biol. Sci.* 9: 463–493.
- Jeffrey C (1990). Systematics of the Cucurbitaceae: An overview. In: D.M. Bates, W. Robinson, and C. Jeffrey (Eds.), *Biology and Utilization of the Cucurbitaceae*, Cornell University Press, Ithaca, NY, USA, pp. 3–9.
- Kalbarczyk R (2006). Time and spatial distribution of agrotechnical dates and phenological stages of cucumber in Western Poland. *Acta Sci. Pol., Hortorum Cultus* 5(2) 51-68. pp. 19–22.
- Kirkbride JH (1993). Biosystematic Monograph of the Genus *Cucumis* (Cucurbitaceae). Parkway Publishers, Boone. pp. 108.
- Kononkova F, Pivovarov B (1999) Recommendation and methodical instructions for selection and seed analysis in the hospital in Moscow. pp. 86.
- Kulakova MN (1977). Cucumber culture in Uzbekistan. Fan-Tashkent. pp. 18 (In Russian).
- Lamb EM, Shaw NL, Cantliffe DJ (2001). Beit Alpha Cucumber: A new Greenhouse Crop for Florida Institute of Food & Agriculture Science. pp.34.
- Liu Z, Jiang J, Ren A, Xu X, Zhang H, Zhao T, Jiang X, Sun Y, Li J, Yang H (2021). Heterosis and combining ability analysis of fruit yield, early maturity, and quality in tomato. *Agronomy* 11(4):807. <https://doi.org/10.3390/agronomy11040807>.
- Lopez S, Staub J (2002). Combining ability analysis of yield components in cucumber. *J. Am. Soc. Hortic. Sci.* 127: 931–937.
- Madhu S (2010). Gene action and heterosis studies involving gynoeious lines in cucumber (*Cucumis sativus* L.) Ph.D. Thesis. Palampur, India: Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya. pp. 150–157.
- Mamedov MI (2015). Vegetable growing in the world: Production of main vegetable crops, development trend for 1993–2013 according to FAO data. *Veg. Russia* 2015(2): 3–9.
- Mansfeld B, Grumet R (2016). Metabolomic plasticity of cucumber fruit peel - effects of developmental stage and market class. In: *Proceedings of Cucurbitaceae 2016*. Kozik (Ed.) E.U. Paris, pp. 174–179.
- Miller CH, Lower RL, Fleming HP (1970). Evaluation of pickles from cucumber plants treated with 2- chloroethylphosphonic acid. *Hort. Sci.* 5: 434–435.
- Mule PN, Khandelwal V (2011). Combining ability studies in cucumber (*Cucumis sativus* L.). *Veg. Sci.* 122–131.
- Paulo H, Adriano P (2023). Diallel analysis: Choosing parents to introduce new variability in a recurrent selection population. *Agriculture*.
- Rebecca G (2021). Genetic resources and vulnerabilities of major cucurbit crops. *Genes (Basel)*. 12(8): 1222.
- Singh RK, Chaudhary BD (1979). *Biometrical Methods in Quantitative Genetic Analysis*. Kalyani Publishers Ludhiana New Delhi. pp. 102–164.
- Yong B (2015). Understanding crop genetic diversity under modern plant breeding. *Theor. Appl. Genet.* 128(11): 2131–2142.
- Yunusov S (2019). New varieties of cucumber for the cultivation in the open area. *Asian J. Multidem. Res.* 8: 52–58.