Evaluation of Genetic Diversity Among Superior Cucumbers (*Cucumis sativus*) via Morphological and Pomological Characteristics in Warm Greenhouse Conditions

Karim Arab Salmani[1], Yousef Hakimi[2]*

1 Greenhouse Research Department, Agricultural and Natural Resources Research and Education Center of Tehran Province (AREEO), Tehran, Iran

2 Seed Breeding Department, Agricultural and Natural Resources Research and Education Center of Tehran Province (AREEO), Tehran, Iran

ARTICLE INFO

ABSTRACT

Genetic variability in a crop population is essential for successful plant breeding. Fifteen cucumber genotypes (*Cucumis sativus* L.) were evaluated in the greenhouse under warm conditions to estimate the magnitude of their genetic variability, trait heritability, morphological features, and pomological characteristics. The genotypes appeared in five categories based on their performance and determination of the most reliable discriminative features that accounted for more significant variability. Cluster Analysis and Principal Component Analysis (PCA) assisted in the classification. The measured characteristics were cucurbit chlorotic yellows virus, fungal severities of infestation, off-type plant, stem, internode, leaf, petiole, fruit and fruit trail length, leaf width, male flower percentage, fruit color and groove, fruit diameter, fruit fresh weight, fruit dry matter and ash percentage, fruit pH, EC and TSS, fruit yield, and total fruit count. The IR4 and IR5 genotypes showed the highest fruit yield (460.85 and 425.86 kg/plot) and number (108.72 and 84.22 fruit/plant). IR11 had the highest value of fruit length (16.60 cm). High broad-sense heritability was associated with all the traits except for cucurbit chlorotic yellows virus and fungal severities of infestation, fruit pH, and total fruit yield. Cluster analysis and its comparison of means showed that IR4 and IR5 from the fifth cluster expressed the best agronomic traits and yield potentials in warm conditions (40 °C/32 °C day/night). Hence, selection for any characteristic would favor genotypes in these clusters. The PCA involved fruit dry matter and TSS as the most discriminating trait that accounted for more significant cucumber variability, which can become crucial information in cucumber improvement programs.

Introduction

The family Cucurbitaceae consists of 98 genera and about 950-980 species of food and ornamental plants that are annual or perennial herbs native to temperate and tropical areas (Chomicki et al., 2020). The genus *Cucumis* includes almost 66 species, among which *Cucumis sativus* (2n=24) is one of the most valuable species from the southern Himalayan foothills region of Asia (Weng, 2021). Domesticated from the wild, the Indian *C. sativus* var. 'Hardwickii' has small bitter-tasting or sour fruits that are ellipsoid or subglobose and 5-8 cm long (Qi et al., 2013). Cucumber is an annual, monoecious stem with trailing stems up to 10 m long. The root system is extensive and largely superficial. Leaves are alternate and simple. The petiole measures 5-20 cm long. Male flowers occur in three to seven-flowered fascicles,

*Corresponding author's email: yousef.hakimi1@ut.ac.ir

with pedicel lengths of 0.5-2 cm. There are three stamens. Female flowers are solitary, with a short, thick pedicel up to 0.5 cm long. The ovary rests on the interior. Fruits are globose to cylindrical, berry-shaped, and over 30 cm long. The seedlings show epigeal germination (Nicodemo et al., 2012).

Because of its low calories and high soluble dietary fiber, cucumber is an ideal source for hydration and obesity management (Sharma et al., 2020). Cucumber fruits contain 96.4% moisture, 2.8% carbohydrates, 0.4% protein, 0.3% minerals, and 0.1% fat. Also, its seeds have high amounts of protein, fat, and minerals (Abiodun and Adeleke, 2010). Fruits have carminative and antacid confidants and help remove constipation and aid digestion (Dhiman et al., 2012; Saboo et al., 2013). Mature cucumber can relieve celiac disease and strengthen the skin. Furthermore, unripe cucumber assists in treating dysentery. Seed juice is also helpful for expelling parasitic worms (Uthpala et al., 2020).

Cucumber is among the most cultivated and consumed vegetable crops worldwide (Zargar Shooshtari et al., 2020). In 2020, cucumber was grown on approximately 2,260,000 hectares of land, with a total production of 91.2 million tons, which shows an increase of 2.95 and 9.74%, respectively, compared to 2016.

China, Iran, Russia, Turkey, and the United States top the list of cucumber producers. China was the largest producer, accounting for 79.81% of world production and 56.61% of the global cucumber-cultivated area. Also, Iran is one of the largest cucumber producers, accounting for 1.32% of world production and 1.79% of the cucumber-cultivated area (FAO, 2020).

Extensive research on selecting high-quality cucumber genotypes from seed masses with well-known cucumber cultivars appeared effective in selecting and evaluating genotypes. A study on 21 cucumber genotypes showed that cucumber lengths measured from 5.50 to 20.95 cm with an average of 12.19 cm. Cucumber width was between 3.00 and 8.30 cm, averaging 5.97 cm. Their heritability was 84.36 and 93.23%, respectively (Shet et al., 2018). In another research on the genetic evaluation of 38 cucumber genotypes, the fruit length ranged from 6.57 to 35.71 cm with a mean of 20.73 cm; the fruit width was between 2.25 and 10.71 cm with a mean of 6.44 cm. The fruit's fresh weight was between 65.85 and 540 gr, averaging 278.32 grams. Their coefficient of variation (CV) was 7.71, 9.50, and 17.78%, respectively (Veena et al., 2012). Pal et al. (2017) indicated that the fruit length ranged from 8.83 to 20.82 cm with a mean of 15.83 cm, the fruit diameter was between 2.89

and 5.56 cm with a mean of 4.53 cm, the fruit fresh weight was between 75.25 and 310.42 grams, averaging 206.40 gr and the fruit TSS were between 3.80 and 5.38% with a mean of 4.31%. Research on the evaluation of 30 cucumber genotypes indicated that the incidence severity of powdery mildew ranged from 8.50 to 29.40%, averaging 19.62%. The incidence severity of anthracnose was between 7.70 to 26.20%, averaging 15.20%. The fruit fresh weight was between 95.00 to 430.00 gr, averaging 249.63 gr, and the fruit TSS was between 2.03 and 4.07%, averaging 2.75% (Kumar et al., 2013).

This study evaluated and determined morphological, phenological, and pomological characteristics. We selected the best cucumber genotypes and recorded their measurable characteristics in warm greenhouse conditions.

Material and Methods
Experimental design
This study was carried out in the research greenhouse of the Agricultural Research Center, Tehran Province (Varamin), with a latitude of 35 degrees, a longitude of 51 degrees, and an altitude of about 1300 meters above sea level. The research was arranged based on a completely randomized design with three replications. Eleven superior cucumber genotypes from selected populations and four control cultivars were arranged in three replicates. They were examined in terms of quantitative and qualitative traits. Each replication consisted of 70 plants. The genotypes were coded. Morphological and pomological studies were conducted for each genotype based on Table 1.

Plant materials and growth condition
The seeds of the cucumber genotypes were disinfected using sodium hypochlorite and washed twice with distilled water (Hakimi et al., 2021). The seeds were sown in plots of 15×1.2 m in two rows and irrigated using a drip irrigation system in a greenhouse in spring and summer. Seedlings were grown under average temperature (28 °C/22 °C day/night) and relative humidity of ~60% for 45 days. The temperature was gradually increased by 2 °C each day to avoid any osmotic shock to seedlings up to 40 °C/32 °C day/night by using temperature controller thermostats. This temperature was maintained for 60 days.

Measurement of morphological and pomological characteristics
To measure plant dimensions such as stem length, internode length, leaf length and width, petiole

length, fruit length, and fruit tail length, a tape measure and ruler were used. A scale was used for measuring fruit fresh weight, dry matter percentage, ash percentage, and product yield. To

measure the pH, EC, and TSS, a pH meter, EC meter, and refractometer were used, respectively.

Table 1. Characteristics evaluated in the experiment related to cucumber genotypes.

Character	Abbreviation	Unit	Measurement method
Cucurbit Chlorotic Yellows Virus	CCYV	%	(sensitive plant/total plant)×100
fungal severity	FS	%	(sensitive plant/total plant)×100
Off-type plant	OP	%	(off-type plant/total plant)×100
Stem length	VL	m	Tape measure
Internode length	IL	cm	Ruler
Leaf length	LL	cm	Ruler
Leaf width	LW	cm	Ruler
Petiole length	PL	cm	Ruler
Male flower percentage	MFP	%	(male flower/total flower)×100
Fruit color	FC	Code	1=very light green, 2=light green 3=normal green, 4=dark green
Fruit groove	FG	Code	1=without groove, 2=normal groove 3=deep groove
Fruit length	FL	cm	Ruler
Fruit diameter	FD	mm	Caliper
Fruit trail length	FTL	cm	Ruler
Fruit fresh weight	FFW	gr	Scale
Fruit dry matter	FDM	%	(sample dry weight/sample weight)×100
Fruit ash	FA	%	(sample ash weight/sample dry weight)×100
Fruit pH	pH	0-14	pH meter
Fruit EC	EC	$\mu S\ m^{-1}$	EC meter
Fruit TSS	TSS	°Brix	Refractometer
Fruit yield per plot	FYP	kg	Scale
Fruit number per plant	FN	N	Counting

Plant materials and growth condition

The seeds of the cucumber genotypes were disinfected using sodium hypochlorite and washed twice with distilled water (Hakimi et al., 2021). The seeds were sown in plots of 15×1.2 m in two rows and irrigated using a drip irrigation system in a greenhouse in spring and summer. Seedlings were grown under average temperature (28 °C/22 °C day/night) and relative humidity of ~60% for 45 days. The temperature was gradually increased by 2 °C each day to avoid any osmotic shock to seedlings up to 40 °C/32 °C day/night by using temperature controller thermostats. This temperature was maintained

for 60 days.

Measurement of morphological and pomological characteristics

To measure plant dimensions such as stem length, internode length, leaf length and width, petiole length, fruit length, and fruit tail length, a tape measure and ruler were used. A scale was used for measuring fruit fresh weight, dry matter percentage, ash percentage, and product yield. To measure the pH, EC, and TSS, a pH meter, EC meter, and refractometer were used, respectively.

Measurement of the severity of fungal disease

Anthracnose and powdery mildew were considered fungal disease agents and were diagnosed based on objective observations based on the characteristics developed on the leaves. Anthracnose symptoms include small brown spots and marks on the foliage, which rapidly grow in size and make a yellow edge, with pink mold developing on the stems and stalks (Ma et al., 2018). Powdery mildew on cucumber leaves appeared as patches of white fungal growth on the leaves and stems, eventually affecting the entire foliage (Ma et al., 2018).

Phenotypic, genotypic variances, and heritability

Genotypic variance (Al-Jibouri et al., 1958), phenotypic variance (Al-Jibouri et al., 1958), and broad sense heritability (Lush, 1949) were computed as per standard formulas.

Genetic variance
$$(V_g) = \frac{MSV - V_E}{r}$$

V_g=Genotypic variance, MSV=Mean square for varieties, V_E=Error mean square and r=Number of replications

Phenotypic variance $(V_P) = V_g + V_E$

V_P=Phenotypic variance, V_g=Genotypic variance and V_E=Error variance

Heritability
$$(h^2) = \frac{V_g}{VP} \times 100$$

h^2=Heritability (broad sense), V_g= Genotypic variance and V_P=Phenotypic variance

Statistical analysis

The SPSS software version 26 (SPSS, Chicago, USA) operated in the analysis of variance (ANOVA), Duncan's multiple range test, mean comparison test (DMRT), characteristic correlation (Pearson's method), cluster analysis (Ward method), and principal component analysis. Data were recorded and graphs were designed using Microsoft Excel. Data are mean values ± SD of three replications.

Results

The analysis of variance showed that the studied genotypes had significant differences among all traits due to the diversity in the measured characteristics. Therefore, it was possible to select the genotypes for different trait values. With a high coefficient of variation, some had a more comprehensive range of character variation and quantities and provided a broader range of choices for selection (Mousavi et al., 2015).

Cucurbit Chlorotic Yellows Virus severity

The CV observed in the CCYV severity trait among genotypes was 34.47%, and the range of CCYV severity in the studied genotypes was from 15.96 to 54.47%, with a mean of 30.31%. The most resistant genotype to CCYV was the 'Nagene' genotype control, with a mean of 15.96%. The genotype IR2 was the most sensitive, respectively 38.51, 29.14, 30.85, and 24.56% higher than 'Nagene,' 'Veolla,' 'Datis,' and 'Ballistic' cultivars. The heritability of this trait among genotypes was 69% (Fig. 1A). A significant negative correlation occurred between the CCYV with the FG (r=-0.377), FL (r=-0.364), FDM (r=-0.363), FA (r=-0.369), and TSS (r=-0.364) and vice versa. Also, a significant positive correlation was observed between the CCYV with the FS (r=0.834) and OP (r=0.640) and vice versa (Table 2).
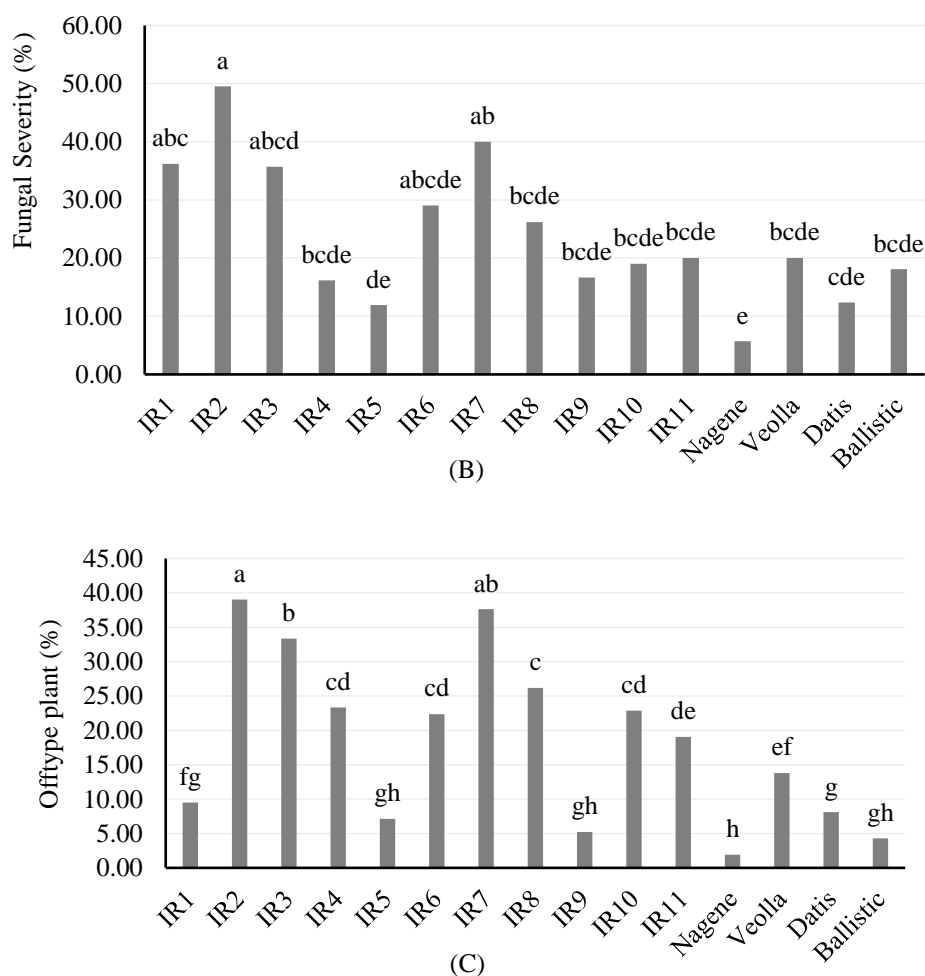

(A)
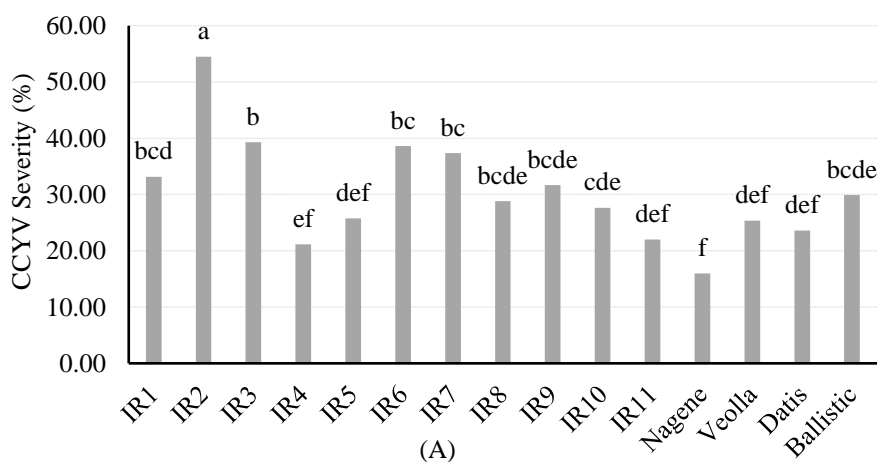
Fig. 1. Mean comparison of (A) CCYV severity, (B) fungal severity, (C) off-type plants among superior cucumber genotypes. According to Duncan's multiple range test (DMRT), means with the same letter do not have a significant difference (p<0.05).

Fungal severity

Mean fungal severity varied from 5.72 to 49.52%, with a total mean of 23.78%. Also, the CV of this trait was 65.41%. The most resistant genotype to fungal severity also belongs to the 'Nagene' cultivar, which is respectively 14.28, 17.90, and 24.19% less than 'Veolla,' 'Datis,' and 'Ballistic' cultivars. The genotype IR2 was the most sensitive, with fungal infestation severities that were 43.8, 29.52, 37.14, and 31.42% higher than those of 'Nagene,' 'Veolla,' 'Datis,' and 'Ballistic' cultivars, respectively. The heritability of this trait among genotypes was 38.94% (Fig. 1B). There was a significant positive correlation between mean FS with OP (r=0.688) and vice versa. Also, a significant negative correlation occurred between the FS and the FG (r=-0.328), FL (r=-0.295), FDM (r=-0.303), FA (r=-0.306), TSS (r=-0.304) and FYP (r=-0.313) and vice versa (Table 2).

Off-type plant

Based on the results of the present study, 20% of the genotypes were off-types in the range of 30-45%, 33.33% of the genotypes were off-types in 15-30%, and 46.67% of the genotypes were off-types in 0-15% regarding off-type severity. Also, the mean value of off-type severity in plants among all genotypes was 18.25%, and the CV observed in the off-type plant trait among genotypes was 67.42%. The heritability of this trait among genotypes was 93.37% (Fig. 1C). A significant negative correlation was observed between the OP with the VL (r=-0.415), PL (r=-0.383), FC (r=-0.456), FG (r=-0.506), FL (r=-0.474), FFW (r=-0.486), FDM (r=-0.435), FA (r=-0.441), and TSS (r=-0.432) and vice versa. Also, a significant positive correlation was observed between the OP and the MFP (r=0.309) and vice versa (Table 2).

Arab Salmani and Hakimi

Int. J. Hort. Sci. Technol. 2024 11 (2): 229-248

Table 2. Simple correlation coefficients of some quantitative and qualitative traits measured in cucumber genotypes.

	CCYV	FS	OP	VL	IL	LL	LW	PL	MFP	FC	FG
CCYV	1										
FS	0.834**	1									
OP	0.640**	0.688**	1								
VL	-0.155	-0.206	-0.415**	1							
IL	-0.036	-0.018	-0.138	-0.446**	1						
LL	0.92	-0.001	-0.263	-0.159	0.340*	1					
LW	0.207	0.116	-0.183	-0.152	0.252	0.895**	1				
PL	-0.104	-0.141	-0.383**	-0.319*	0.644**	0.705**	0.594**	1			
MFP	0.089	0.199	0.309*	-0.224	-0.231	-0.260	-0.204	-0.318*	1		
FC	0.084	-0.129	-0.456**	0.254	0.365*	0.362*	0.318*	0.344*	-0.453**	1	
FG	-0.377*	-0.328*	-0.506**	0.55	0.034	0.175	0.162	0.464**	-0.317*	0.037	1
FL	-0.364*	-0.295*	-0.474**	0.381**	-0.231	0.154	0.079	0.211	0.171	0.128	0.560**
FD	0.124	-0.092	-0.185	-0.300*	0.346*	0.357*	0.322*	0.353*	-0.246	0.511**	-0.179
FTL	-0.123	-0.138	-0.143	-0.209	0.117	-0.031	-0.156	0.224	-0.260	0.047	0.072
FFW	-0.118	-0.244	-0.486**	-0.222	0.191	0.583**	0.513**	0.658**	-0.151	0.393**	0.364*
FDM	-0.363*	-0.303*	-0.435**	-0.149	0.472**	0.723**	0.564**	0.771**	-0.232	0.282	0.296*
FA	-0.369*	-0.306*	-0.441**	-0.152	0.473**	-0.725**	0.566**	0.768**	-0.236	0.285	0.301*
pH	-0.155	-0.122	-0.195	-0.002	-0.114	0.402**	0.502**	0.297*	-0.309*	0.014	0.573**
EC	0.092	-0.001	-0.263	-0.159	0.340*	0.887**	0.895**	0.705**	-0.260	0.362*	0.175
TSS	-0.364*	-0.304*	-0.432**	-0.151	0.469**	0.716**	0.558**	0.764**	-0.223	0.281	0.300*
FYP	-0.211	-0.313*	-0.074	0.299*	-0.271	-0.149	-0.081	-0.168	-0.046	-0.190	0.228
FN	-0.097	-0.088	0.181	0.362*	-0.316*	-0.365*	-0.277	-0.455**	0.008	-0.313*	-0.023

*, **: Significant difference at the 5% and 1% of probability levels, respectively.

Continued Table 2. Simple correlation coefficients of some quantitative and qualitative traits measured in cucumber genotypes.

	FL	FD	FTL	FFW	FDM	FA	pH	EC	TSS	FYP	FN
FL	1										
FD	-0.331*	1									
FTL	-0.116	0.561**	1								
FFW	0.265	0.718**	0.527**	1							
FDM	0.360*	0.288	0.208	0.587**	1						
FA	0.363*	0.291	0.211	0.592**	0.931**	1					
pH	0.374*	-0.067	-0.103	0.284	0.363*	0.364*	1				
EC	0.154	0.357*	-0.031	0.583**	0.716*	0.718*	0.402*	1			
TSS	0.359*	0.291	0.209	0.592**	0.942**	0.937**	0.362*	0.716**	1		
FYP	0.064	-0.471**	-0.441**	-0.383**	-0.247	-0.251	0.135	-0.149	-0.248	1	
FN	-0.091	-0.673**	-0.602**	-0.750**	-0.440*	-0.437*	0.011	-0.365*	-0.441**	0.882**	1

*, **: Significant difference at the 5% and 1% of probability levels, respectively.

Stem length

The CV of the stem length among genotypes was 12.62%, and the values of stem length in the studied genotypes ranged from 5.62 to 8.66 m, averaging 7.01 m. The highest stem length belonged to the IR9 genotype, with a mean value of 8.66 cm. The second highest stem length (8.13 cm) was observed in IR4. The genotype IR8 had the lowest stem length, which was 15.99, 13.80, 24.46, and 13.27% lower than that of 'Nagene,' 'Veolla,' 'Datis,' and 'Ballistic' cultivars, respectively. The heritability of this trait among

Arab Salmani and Hakimi

Int. J. Hort. Sci. Technol. 2024 11 (2): 229-248

genotypes was 96.83% (Table 3). There was a significant positive correlation between mean VL and FL (r=0.381), FYP (r=0.299), and FN (r=0.362) and vice versa. Also, a significant negative correlation was observed between the VL and the IL (r=-0.446), PL (r=-0.319), and FD (r=-0.300), and vice versa (Table 2).

Table 3. Comparison of the mean morphological characteristics in the studied genotypes of cucumber.

Genotypes	Stem length (m)	Internode length (cm)	Leaf length (cm)	Leaf width (cm)	Petiole length (cm)
IR1	8.06±0.16[bc]	8.58±0.35[d]	27.63±0.71[c]	26.65±0.55[bc]	20.74±0.33[c]
IR2	7.27±0.13[f]	7.63±0.24[ef]	28.20±1.25[bc]	28.70±0.62[b]	20.67±1.68[c]
IR3	6.16±0.12[i]	7.59±0.20[ef]	23.57±1.50[ef]	23.50±1.50[ef]	18.20±1.11[ef]
IR4	8.13±0.20[b]	6.81±0.32[g]	24.50±0.64[ef]	24.07±0.55[ef]	18.63±1.15[f]
IR5	7.81±0.15[cd]	6.51±0.27[g]	20.20±1.06[h]	22.13±0.45[ef]	17.70±0.66[ef]
IR6	6.31±0.14[hi]	8.26±0.13[d]	25.50±0.50[d]	26.10±0.66[cd]	18.87±1.00[cdef]
IR7	6.11±0.25[i]	7.28±0.28[f]	21.30±1.04[gh]	21.53±0.50[f]	19.47±0.60[cde]
IR8	5.62±0.18[j]	11.21±0.27[a]	28.30±0.89[bc]	27.27±1.12[bc]	22.97±0.95[b]
IR9	8.66±0.08[a]	7.55±0.28[ef]	25.37±1.39[d]	24.45±2.50[de]	20.33±0.68[cd]
IR10	6.40±0.11[ghi]	6.81±0.11[g]	24.50±0.96[de]	24.07±1.89[de]	18.63±1.48[def]
IR11	7.55±0.22[de]	5.27±0.34[h]	23.50±0.50[ef]	23.27±0.80[ef]	17.20±0.82[f]
Nagene	6.69±0.13[g]	9.19±0.25[c]	29.83±1.04[b]	27.50±1.08[bc]	25.63±1.55[a]
Veolla	6.52±0.12[gh]	10.02±0.15[b]	22.57±0.72[fg]	22.73±1.00[ef]	23.37±0.75[b]
Datis	7.44±0.17[ef]	9.01±0.22[c]	24.33±0.78[de]	23.53±1.27[ef]	20.47±0.93[cd]
ballistic	6.48±0.18[gh]	7.79±0.20[e]	33.57±0.57[a]	32.87±1.99[a]	25.43±1.10[a]
Mean	7.01	7.94	25.44	25.20	20.45
CV (%)	12.62	18.77	13.85	12.32	13.92
Heritability (%)	96.83	97.33	92.98	84.35	86.86

*Means with at least one common letter are not significantly different in each column, according to Duncan's test at the 5% probability level.

Internode length

Average internode lengths varied from 5.27 to 11.21 cm, with a total mean value of 7.94 cm. Also, the CV of this trait was 18.77%. The highest internode length also belonged to the IR8 cultivar, respectively 21.98, 11.88, 24.42, and 43.90% more than 'Nagene,' 'Veolla,' 'Datis,' and 'Ballistic' cultivars, respectively. Genotype IR11 had the lowest internode length. The heritability of this trait among genotypes was 97.33% (Table 3). A significant negative correlation was observed between the IL and FN (r=-0.316) and vice versa. Also, a significant positive correlation was observed with the LL (r=0.340), PL (r=0.644), FC (r=0.365), FD (r=0.346), FDM (r=0.472), FA (r=0.473), EC (r=0.340) and TSS (r=0.469) and vice versa (Table 2).

Leaf length

Leaf length averaged 25.44 cm, and the CV was 13.85%. The results showed a low difference between genotypes in this trait. The highest leaf lengths (33.57 and 29.83 cm) belonged to the 'Ballistic' and 'Nagene' genotypes, respectively. The lowest leaf length (20.20 cm) appeared in genotype IR5 and happened to be 32.28, 10.50, 16.97, and 39.83% lower than those of 'Nagene,' 'Veolla,' 'Datis,' and Ballistic cultivars, respectively. The heritability of this trait among genotypes was 92.98% (Table 3). There was a significant positive correlation between the mean LL and LW (r=0.895), PL (r=0.705), FC (r=0.362), FD (r=0.357), FFW (r=0.583), FDM (r=0.723), pH (r=0.402), EC (r=0.887), TSS (r=0.716), and vice versa. Also, a significant negative correlation was observed with the FA (r=-0.725) and FN (r=-0.365) and vice versa (Table 2).

Leaf width

The CV observed in the leaf width among genotypes was 12.32%, and the leaf width in the studied genotypes ranged from 21.53 to 32.87 cm, averaging 25.20 cm. The highest leaf width occurred in 'Ballistic,' with a mean of 32.87 cm. The second highest leaf width (27.50cm) was in 'Nagene.' Genotype IR7 had the lowest value of leaf width and was 21.71, 5.28, 8.50, and 34.50% lower than those of 'Nagene,' 'Veolla,' 'Datis,' and 'Ballistic' cultivars, respectively. The heritability of this trait among genotypes was 84.35% (Table 3). No significant negative correlation was observed between the LW and other characteristics. However, a significant positive correlation was observed among PL (r=0.594), FC (r=0.318), FD (r=0.322), FFW (r=0.513), FDM (r=0.564), FA (r=0.566), pH (r=0.502), EC (r=0.895), TSS (r=0.558), and vice versa (Table 2).

Petiole length

Average petiole lengths varied from 17.20 to 25.63 cm, with a total mean of 20.45 cm. Also, the CV of this trait was 13.92%. The highest petiole length belonged to 'Nagene' and was 9.67, 25.21,

and 0.79% more than those of 'Veolla,' 'Datis,' and 'Ballistic' cultivars, respectively. Genotype IR11 had the lowest internode length and was 32.89, 26.40, 15.97, and 32.36% lower than those of 'Nagene,' 'Veolla,' 'Datis,' and Ballistic cultivars, respectively. The heritability of this trait among genotypes was 86.86% (Table 3). There was a significant positive correlation between mean PL and FC (r=0.344), FG (r=0.464), FD (r=0.353), FFW (r=0.658), FDM (r=0.771), FA (r=0.768). pH (r=0.297), EC (r=0.705), TSS (r=0.764), and vice versa. A significantly negative correlation was observed between the MFP (r=-0.318) and FN (r=-0.455) and vice versa (Table 2).

Male flower percentage

Male flower percentages averaged 33.52%, and the CV was 66.10%. The highest male flower percentages (73.00 and 68.25%) belonged to the IR11 and IR7 genotypes, respectively. The lowest male flower percentage (4.66%) occurred in the IR10 genotype. The heritability of this trait among genotypes was 96.35% (Fig. 2A). A significantly negative correlation was observed among MFP, FC (r=-0.453), FG (r=-0.317), pH (r=-0.309), and vice versa (Table 2).
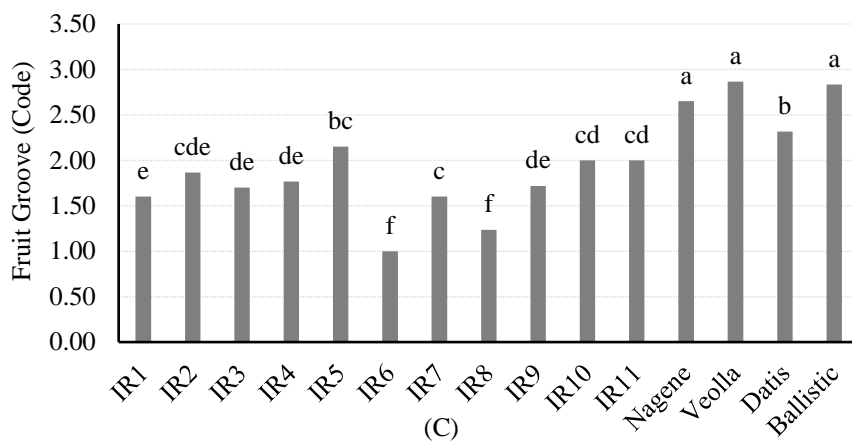

(A)

(B)
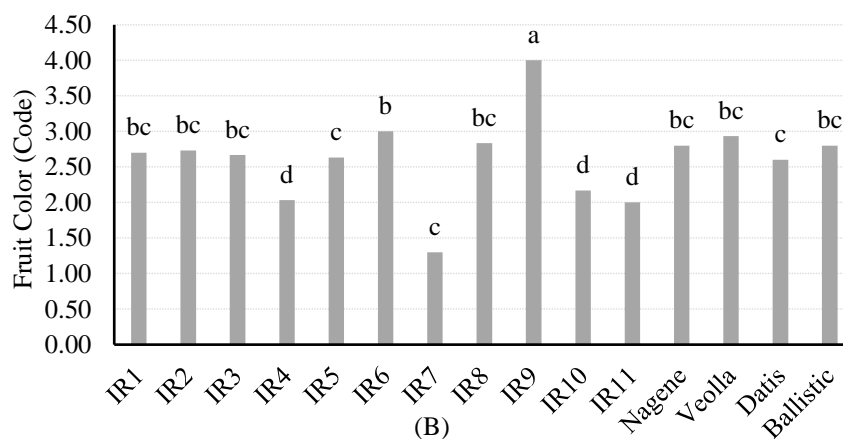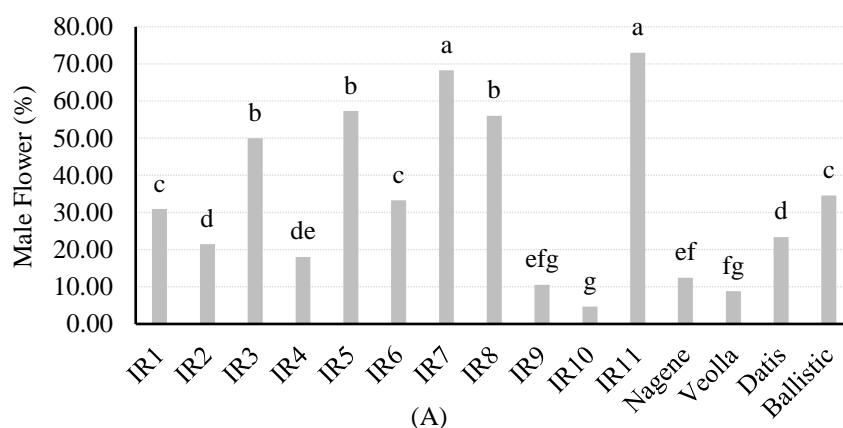
Fig. 2. Mean comparison of (A) male flower percentage, (B) fruit color, and (C) fruit groove among superior cucumber genotypes. According to Duncan's multiple range test (DMRT), means with the same letter do not have a significant difference (p<0.05).

Fruit color

The CV observed for fruit color among genotypes was 23%, and genotype fruit color ranged from 1.3 (very light green) to 4.00 (dark green) with a mean of 2.61 (common green). Based on the results, 6.67, 20, 66.67, and 6.66% of the genotypes had very light green, light green, common green, and dark green fruits, respectively. The highest fruit color belonged to IR9, with a mean of 4. The second-highest fruit color (3) was observed in IR6. The heritability of this trait among genotypes was 90.96% (Fig. 2B). There was a significant positive correlation among mean FC and FD (r=0.511), FFW (r=0.393), and EC (r=0.362) and vice versa. A significantly negative correlation was observed with the FN (r=-0.313) and vice versa (Table 2).

Fruit groove position

The mean fruit groove varied from 1 (without groove) to 2.87 (deep groove) and had a total mean of 1.95 (normal groove). Also, the CV of this trait was 28.05%. Based on the results, 13.33, 66.67, and 20.00% of genotypes had no groove, normal groove, and deep groove fruits, respectively. The highest fruit groove also belonged to 'Veolla,' 'Nagene,' and 'Ballistic.' The genotypes IR6 and IR8 had the lowest groove value. The heritability of this trait among genotypes was 90.72% (Fig. 2C). A significant positive correlation was observed among the FG and FL (r=0.560), FFW (r=0.364), FDM (r=0.296), FA (r=0.301), pH (r=0.573), TSS (r=0.300), and vice versa (Table 2).

Fruit length

Fruit length averaged 13.86 cm, and the CV was 9.00%. The highest fruit length of 16.60 and 15.00

cm belonged to IR11 and Ballistic genotypes, respectively. The lowest fruit length (11.12 cm) occurred in IR6, which was respectively 25.57, 20.80, 21.63, and 25.87% lower than the value observed in 'Nagene,' 'Veolla,' 'Datis,' and 'Ballistic' cultivars. The heritability of this trait among genotypes was 98.47% (Table 4). There was a significant positive correlation between mean FL and FDM (r=0.360), FA (r=0.363), pH (r=0.374), TSS (r=0.359), and vice versa. A significantly negative correlation occurred with the FD (r=-0.331) and vice versa (Table 2).

Fruit diameter

The CV for fruit diameter among genotypes was 8.89%, and the fruit diameter ranged from 26.11 to 35.35 mm with a mean of 29.41 mm. The highest fruit diameter belonged to IR6. The second-highest fruit diameter (33.28 mm) occurred in IR9. The genotype IR4 had the lowest fruit diameter. The heritability of this trait among genotypes was 99.23% (Table 4). A significant negative correlation was observed between the FD with the FYP (r=-0.471) and FN (r=-0.673) and vice versa, and also a significant positive correlation was observed between the FD and FTL (r=0.561), FFW (r=0.718), EC (r=0.357), and vice versa (Table 2).

Fruit trail length

Mean fruit trail length varied from 4.41 to 7.02 cm, with a total mean of 5.60 cm. Also, the CV of this trait was 15.04%. The highest fruit trail length belonged to 'Nagene,' which was 17.59, 17.79, and 41.25% more than the values in 'Veolla,' 'Datis,' and 'Ballistic' cultivars, respectively. The genotype IR4 had the lowest fruit trail length, which was respectively 37.18,

26.13, 26.01, and 11.27% less than 'Nagene,' 'Veolla,' 'Datis,' and 'Ballistic' cultivars. The heritability of this trait among genotypes was 97.98% (Table 4). There was a significant positive correlation between mean FTL with FFW (r=0.527) and vice versa. Also, a significant negative correlation was observed with the FYP (r=-0.441) and FN (r=-0.602) and vice versa (Table 2).

Table 4. Comparison of mean pomological traits in the studied cucumber genotypes.

Genotypes	Fruit length (cm)	Fruit diameter (mm)	Fruit trail length (cm)	Fruit fresh weight (gr)	Fruit dry matter (%)	Fruit ash (%)
IR1	13.68±0.12[e]	26.54±0.23[k]	4.96±0.09[f]	68.87±0.70[i]	4.12±0.01[ef]	11.86±0.03[ef]
IR2	13.57±0.06[ef]	27.85±0.10[i]	4.95±0.07[f]	70.67±1.40[hi]	4.06±0.03[f]	11.70±0.09[f]
IR3	13.56±0.10[ef]	27.97±0.16[i]	4.77±0.12[fg]	69.27±1.11[i]	3.77±0.08[j]	10.85±0.23[j]
IR4	13.06±0.16[g]	26.11±0.09[l]	4.41±0.10[h]	60.47±1.30[j]	4.08±0.02[ef]	11.74±0.07[ef]
IR5	14.47±0.08[c]	27.14±0.26[j]	4.72±0.16[g]	72.20±1.11[g]	3.86±0.04[i]	11.11±0.13[i]
IR6	11.12±0.14[i]	35.35±0.26[a]	6.64±0.18[b]	86.17±1.56[d]	3.92±0.03[h]	11.28±0.10[h]
IR7	12.87±0.12[gh]	29.35±0.23[g]	6.68±0.09[b]	79.57±1.76[e]	3.97±0.04[g]	11.44±0.12[g]
IR8	13.33±0.13[f]	30.76±0.23[d]	4.83±0.13[fg]	76.30±1.45[f]	4.67±0.02[b]	13.46±0.07[b]
IR9	14.85±0.09[b]	33.28±0.28[b]	6.27±0.10[c]	90.63±1.36[c]	4.31±0.02[d]	12.42±0.06[d]
IR10	12.66±0.23[h]	29.88±0.33[f]	6.34±0.12[c]	76.47±1.32[f]	4.09±0.01[ef]	11.78±0.03[ef]
IR11	16.60±0.14[a]	26.15±0.25[l]	5.52±0.19[e]	76.30±1.67[f]	4.13±0.03[e]	11.89±0.10[e]
Nagene	14.94±0.22[b]	30.33±0.35[e]	7.02±0.11[a]	94.37±1.78[b]	4.90±0.02[a]	14.10±0.07[a]
Veolla	14.04±0.23[d]	28.56±0.24[h]	5.97±0.15[d]	78.87±2.20[ef]	4.10±0.02[ef]	11.81±0.07[ef]
Datis	14.19±0.20[d]	30.01±0.19[ef]	5.96±0.18[d]	76.70±2.45[f]	4.09±0.01[ef]	11.77±0.04[ef]
ballistic	15.00±0.22[b]	31.87±0.18[c]	4.97±0.16[f]	104.17±2.06[a]	4.54±0.03[c]	13.07±0.09[c]
Mean	13.86	29.41	5.60	78.73	4.17	12.02
CV (%)	9.00	8.89	15.04	13.93	7.28	7.21
Heritability (%)	98.47	99.23	97.98	97.94	98.96	97.56

*Mean values with at least one common letter using Duncan's test (p≤0.05) are not significantly different in each column.

Fruit fresh weight

Fruit fresh weight averaged 78.73 g, and the CV was 13.93%. The highest fruit fresh weight (104.17 and 94.37 g) belonged to the 'Ballistic' and 'Nagene' genotypes, respectively. The lowest fruit fresh weight (60.47 g) occurred in IR4, which was 35.92, 23.33, 21.16, and 41.95% lower than the values observed in 'Nagene,' 'Veolla,' 'Datis,' and Ballistic cultivars, respectively. The heritability of this trait among genotypes was 97.94% (Table 4). A significant negative correlation was observed between the FFW with the FYP (r=-0.383) and FN (r=-0.750) and vice versa, and also a significant positive correlation was observed with the FDM (r=0.587), FA (r=0.592), EC (r=0.583), TSS (r=0.592), and vice versa (Table 2).

Fruit dry matter

The CV for fruit dry matter among genotypes was 7.28%, and the fruit dry matter ranged from 3.77 to 4.90%, with a mean of 4.17%. The highest fruit dry matter belonged to 'Nagene.' The second-highest fruit dry matter (4.67%) occurred in IR8. The genotype IR3 had the lowest fruit dry matter, which was respectively 1.13, 0.37, 0.36, and 0.77% lower than the values observed in 'Nagene,' 'Veolla,' 'Datis,' and 'Ballistic' cultivars. The heritability of this trait among genotypes was 98.96% (Table 4). There was a significant positive correlation occurred between mean FDM with FA (r=0.931), pH (r=0.363), EC (r=0.716), and TSS (r=0.942) and vice versa, and also a significant negative correlation was observed with the FN (r=-0.440) and vice versa (Table 2).

Fruit ash

Mean fruit ash percentage varied from 10.85 to 14.10%, with a total mean of 12.02%. Also, the CV of this trait was 7.21%. The highest fruit ash percentage belonged to 'Nagene,' which was 2.29, 2.33, and 1.03% more than the values in 'Veolla,' 'Datis,' and 'Ballistic' cultivars, respectively. Genotype IR3 had the lowest fruit ash percentage, which was 3.25, 0.96, 0.92, and 2.22% lower than the values in 'Nagene,' 'Veolla,' 'Datis,' and 'Ballistic' cultivars, respectively. The heritability of this trait among genotypes was 97.56% (Table 4). A significant negative correlation was observed between the FA and FN (r=-0.437) and vice versa. Also, a significant positive correlation was observed between the FA with the pH (r=0.364), EC (r=0.718), and TSS (r=0.937) and vice versa (Table 2).

Fruit pH

Fruit acidity averaged 5.62 on the pH scale, and the CV was 5.04%. The highest fruit acidity (6.11 and 5.92) belonged to the 'Ballistic' and 'Nagene' genotypes, respectively. The lowest fruit acidity (5.22) occurred in IR6. The heritability of this trait among genotypes was 57.66% (Fig. 3A). A significant positive correlation was observed among the fruit pH, the EC (r=0.402), TSS (r=0.362), and vice versa (Table 2).
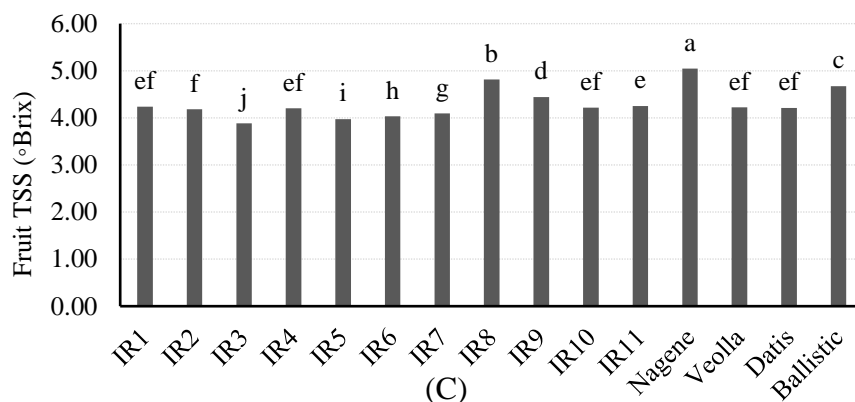

(A)

(B)

239
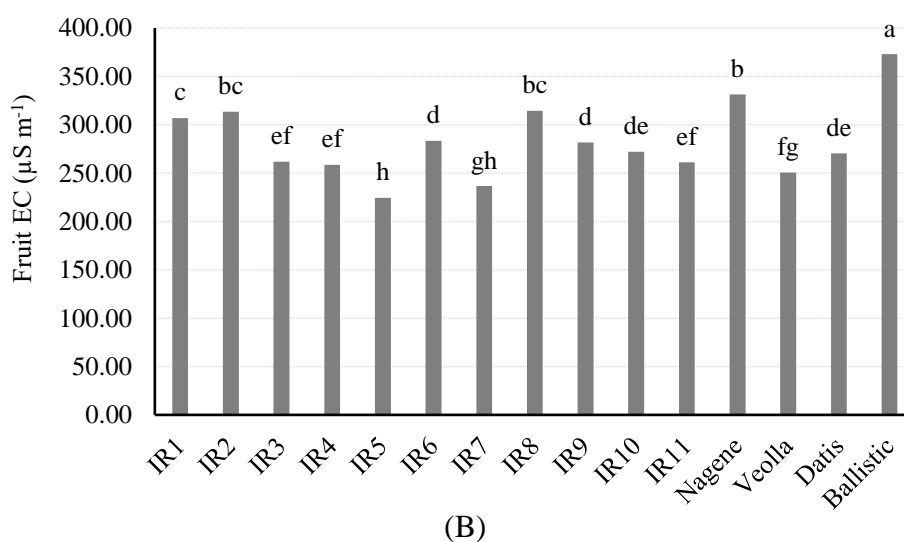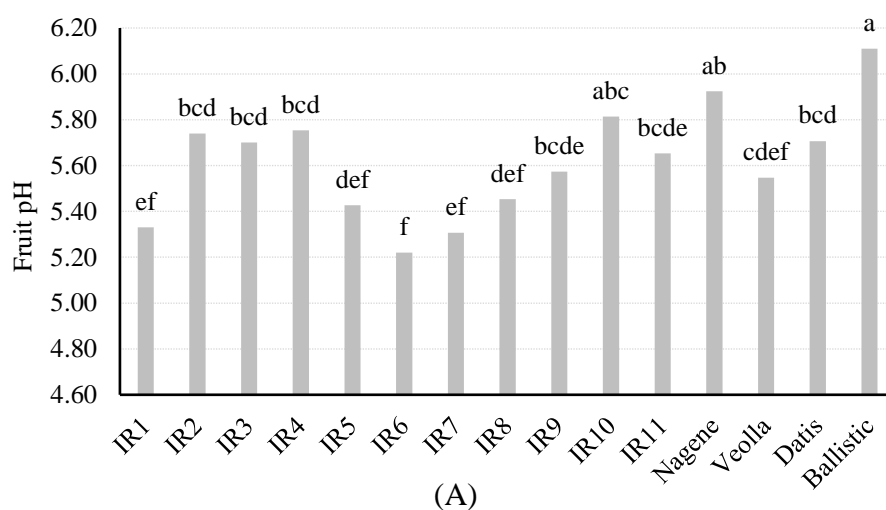
Fig. 3. Mean comparison of (A) fruit pH, (B) fruit EC, (C) fruit TSS among superior cucumber genotypes. According to Duncan's multiple range test (DMRT). Means with the same letter do not have a significant difference (p<0.05).

Fruit EC

The CV observed in the fruit EC among genotypes was 13.87%, and the range of fruit EC in the studied genotypes was from 224.42 to 372.92 μS m-1 with a mean of 288.66 μS m^{-1}. The highest fruit EC belonged to the Ballistic cultivar. The second highest fruit EC (331.45 μS m^{-1}) occurred in 'Nagene.' Genotype IR5 had the lowest fruit EC. The heritability of this trait among genotypes was 92.98% (Fig. 3B). There was a significant positive correlation between mean fruit EC and TSS (r=0.716) and vice versa. Also, a significant negative correlation was observed with the FN (r=-0.365) and vice versa (Table 2).

Fruit TSS

The mean fruit TSS varied from 3.88 to 5.04 °Brix and had a total mean of 4.30 °Brix. Also, the CV of this trait was 7.33%. The highest fruit TSS belonged to 'Nagene,' which was 19.43, 19.71, and 7.92% more than 'Veolla,' 'Datis,' and Ballistic cultivars, respectively. Genotype IR3 had the

lowest fruit TSS, which was 23.02, 8.06, 7.84, and 16.92% lower in value than 'Nagene,' 'Veolla,' 'Datis,' and 'Ballistic' cultivars, respectively. The heritability of this trait among genotypes was 99.02% (Fig. 3C). A significant negative correlation was observed between the fruit TSS and the FN (r=-0.441) and vice versa (Table 2).

Total yield

Total yield averaged 347.14 kg/plot, and the obtained CV was 17.49%. The highest total yield (460.85 and 425.86 kg/plot) belonged to IR4 and IR5 genotypes, respectively. The lowest total (263.53) occurred in the IR9 genotype, which was 24.26, 26.46, 29.98, and 24.33% lower than the values in 'Nagene,' 'Veolla,' 'Datis,' and 'Ballistic' cultivars, respectively. The heritability of this trait among genotypes was 55.55% (Fig. 4A). A significant positive correlation was observed between the FYP and the FN (r=0.882) and vice versa (Table 2).
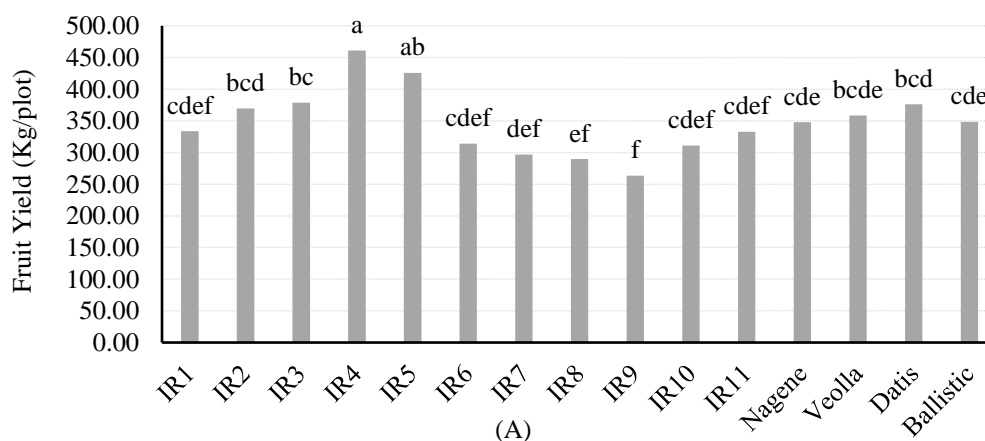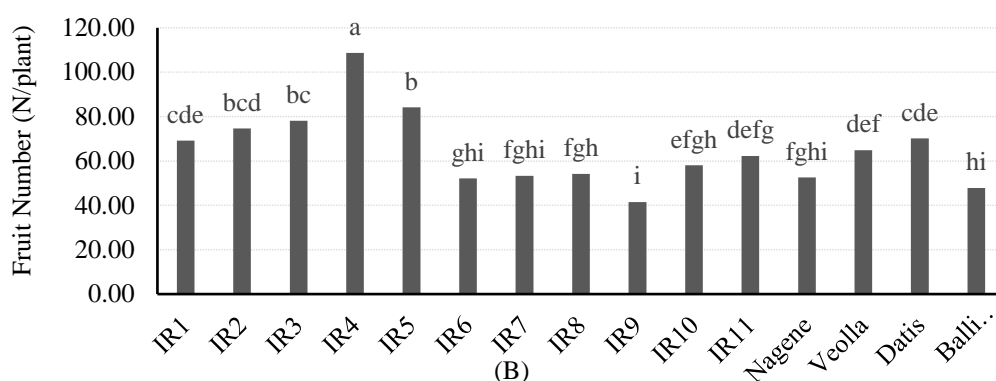
Fig. 4. Mean comparisons of (A) fruit yield and (B) fruit count among superior cucumber genotypes. According to Duncan's multiple range test (DMRT), means with the same letter do not have a significant difference (p<0.05).

Fruit count

The CV for the fruit count among genotypes was 27.10%, and the fruit count in the studied genotypes ranged from 41.44 to 108.72 plant^{-1} with a mean value of 64.78 plant^{-1}. The highest fruit number belonged to IR4. The second-highest fruit count (84.22) occurred in IR5. The genotype IR9 had the lowest fruit count, which was 21.20, 36.12, 40.99, and 13.43% lower than those in 'Nagene,' 'Veolla,' 'Datis,' and 'Ballistic' cultivars, respectively. The heritability of this trait among genotypes was 85.89% (Fig. 4B).

Yield component

The highest yield was observed in genotype IR4 with a value of 113.57 kg/plot in the 2nd harvest, which was 25.19, 28.94, 38.42, and 31.40% higher than those in the 1st, 3rd, 4th, and 5th harvests, respectively. The highest mean yield (91.50 kg/plot) occurred in the 2nd harvest, which was 20.38, 19.83, 36.30, and 33.86 kg/plot more than the 1st, 3rd, 4th, and 5th harvests, respectively (Table 5).

Table 5. Comparison of mean yield components (kg/plot) in the cucumber genotypes.

Genotypes	1st 10harvests (kg/plot)	2nd 10harvests (kg/plot)	3rd 10harvests (kg/plot)	4th 10harvests (kg/plot)	5th 10harvests (kg/plot)
IR1	64.73±13.69[ab]	81.94±16.49[bc]	69.33±12.73[c]	59.00±5.77[bcd]	58.68±14.13[bcd]
IR2	73.07±14.82[ab]	89.67±11.18[abc]	76.32±11.37[abc]	62.97±2.32[bc]	67.66±9.96[abc]
IR3	70.01±7.76[ab]	88.13±9.46[bc]	77.91±11.17[abc]	67.84±10.63[ab]	74.72±9.18[ab]
IR4	90.72±17.08[a]	113.57±11.17[a]	88.08±8.22[ab]	82.05±9.41[a]	86.43±4.42[a]
IR5	72.00±9.62[ab]	97.62±14.51[ab]	90.79±6.82[a]	78.57±10.78[a]	86.89±12.47[a]
IR6	65.82±13.43[ab]	89.31±10.55[abc]	64.05±3.38[cd]	49.09±8.84[cdef]	45.69±23.15[cd]
IR7	64.15±5.49[ab]	86.10±12.66[bc]	66.58±4.92[c]	42.98±1.42[def]	37.02±7.89[d]
IR8	52.49±14.03[b]	80.90±9.15[bc]	63.05±6.43[cd]	42.48±0.56[ef]	50.71±7.21[bcd]
IR9	68.26±27.76[ab]	72.15±16.88[c]	51.28±11.77[d]	35.86±12.80[f]	35.97±24.91[d]
IR10	75.97±16.77[ab]	92.22±15.21[abc]	63.72±7.25[cd]	44.92±4.33[def]	34.12±4.68[d]
IR11	69.77±9.95[ab]	93.02±11.78[abc]	69.24±3.19[c]	49.91±5.38[cdef]	50.65±7.82[bcd]
Nagene	78.19±20.88[ab]	89.19±17.28[abc]	67.07±9.25[c]	54.48±3.83[bcde]	59.00±10.91[bcd]
Veolla	71.97±15.23[ab]	99.34±13.75[ab]	77.60±3.90[abc]	55.31±9.26[bcde]	54.11±11.18[bcd]
Datis	82.13±9.85[a]	100.04±7.07[ab]	76.02±0.81[abc]	51.26±6.24[cdef]	66.91±9.20[abc]
ballistic	67.45±2.02[b]	99.33±10.73[ab]	74.05±9.56[bc]	51.34±16.23[cdef]	56.08±21.80[bcd]
Mean	71.12	91.50	71.67	55.20	57.64
CV (%)	20.75	15.66	16.66	26.29	34.13

*Means with at least one common letter using Duncan's test (p≤0.05) are not significantly different in each column.

Cluster analysis

At a distance of 5 out of 25, the genotypes were divided into five main groups, and each group was divided into smaller clusters with more common characteristics (Fig. 5). Genotype cluster mean values are shown in Table 6. Comparing cluster means with the studied traits revealed considerable variation among different groups. The first group included two subgroups, with characteristics such as high CCYV (35.68%), FS (29.40%), IL (8.56 cm), and FC (2.73 normal green) and consisted of 'Veolla,' 'Datis,' 'IR2,' and 'IR3.' The second group consisted of 'Nagene' and 'ballistic' and included traits such as high IL (8.49 cm), LL (31.70 cm), LW (30.19 cm), PL (25.53

mm), FC (2.80 normal green), FG (2.74 deep groove), FL (14.97 cm), FD (31.10 mm), FFW (99.28 gr), FDM (4.72 %), FA (13.59 %), and TSS (4.86 °Brix). The third group consisted of one subgroup that included traits such as high FS (30.00%), OP (28.34%), MFP (70.63%), FL (14.74 cm), and FTL (6.10 cm), which consisted of IR7 and IR11. The fourth group consisted of two subgroups with IR9, IR10, IR1, IR6, and IR8 genotypes, involving traits such as high FS (25.43%), IL (8.48 cm), FC (2.94 normal green), and FD (31.16 mm). The fifth group had traits such as VL (7.97 m), FYP (443.36 kg/plot), and FN (96.47 fruits/plant) and consisted of IR4 and IR5 genotypes.
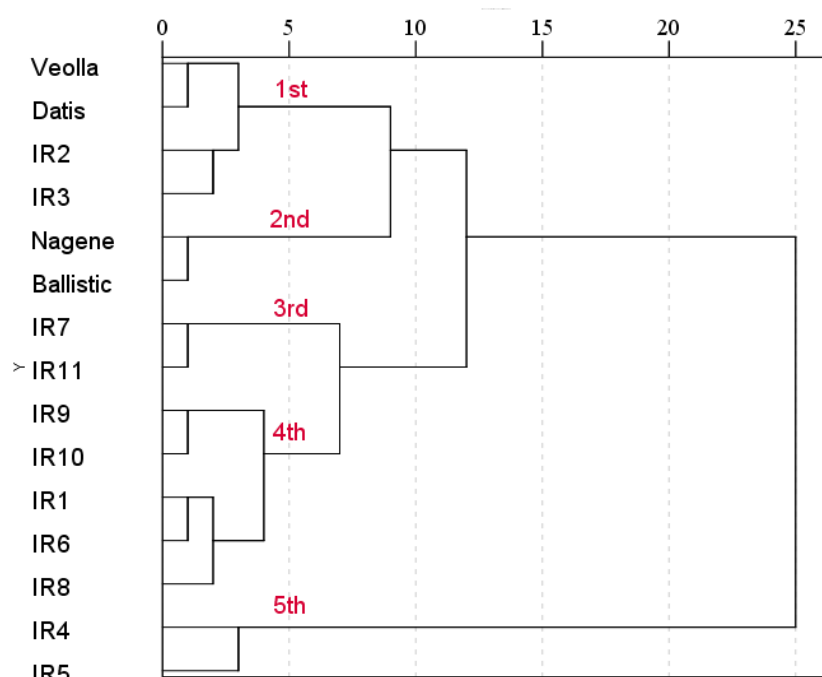

Fig. 5. Cluster analysis of 15 cucumber genotypes based on traits with high heritability via Ward's method.

Table 6. Mean comparison of cucumber traits among cluster group.

Group	CCYV (%)	FS (%)	OP (%)	VL (m)	IL (cm)	LL (cm)	LW (cm)	PL (cm)	MFP (%)	FC (code)
1st	35.68[a]	29.40[a]	23.57[b]	6.85[b]	8.56[a]	24.67[c]	24.62[b]	20.68[b]	25.92[cd]	2.73[a]
2nd	22.94[c]	11.91[b]	3.10[d]	6.59[c]	8.49[a]	31.70[a]	30.19[a]	25.53[a]	23.55[d]	2.80[a]
3rd	29.67[b]	30.00[a]	28.34[a]	6.83[b]	6.28[b]	22.40[d]	22.40[c]	18.34[c]	70.63[a]	1.65[c]
4th	31.97[ab]	25.43[a]	17.24[c]	7.01[b]	8.48[a]	26.26[b]	25.71[b]	20.31[b]	27.09[c]	2.94[a]
5th	23.45[c]	14.05[b]	15.24[c]	7.97[a]	6.45[b]	21.74[d]	22.95[c]	17.40[d]	37.68[b]	2.33[b]

*Means with at least one common letter using Duncan's test (p≤0.05) are not significantly different in each column.

Continued Table 6. Mean comparison of cucumber traits among cluster group.

Group	FG (code)	FL (cm)	FD (mm)	FTL (cm)	FFW (gr)	FDM (%)	FA (%)	TSS (°Brix)	FYP (kg)	FN (number)
1st	2.19[b]	13.84[b]	28.60[b]	5.41[c]	73.88[c]	4.01[cd]	11.53[cd]	4.12[cd]	370.74[b]	71.96[b]
2nd	2.74[a]	14.97[a]	31.10[a]	6.00[ab]	99.27[a]	4.72[a]	13.59[a]	4.86[a]	348.09[bc]	50.23[c]
3rd	1.80[c]	14.74[a]	27.75[c]	6.10[a]	77.94[b]	4.05[c]	11.67[c]	4.17[c]	314.72[c]	57.77[c]
4th	1.51[d]	13.13[c]	31.16[a]	5.81[b]	79.69[b]	4.22[b]	12.16[b]	4.35[b]	302.35[c]	54.99[c]
5th	1.96[c]	13.77[b]	26.63[d]	4.57[d]	66.34[d]	3.97[d]	11.43[d]	4.09[d]	443.36[a]	96.47[a]

*Means with at least one common letter using Duncan's test (p≤0.05) are not significantly different in each column.

Principal component analysis (PCA)

PCA is a powerful multivariate statistical method that can put the number of evaluated attributes into influential groups. Using PCA, various traits can be placed in the factors or components, each containing several characteristics. This analysis can clarify the main differences between genotypes and reduce data load. The relative variance per component indicated the importance of each in the variance of the studied traits, expressed as percentages. In this study, PCA revealed 22 evaluated traits as six main components, among which the first, second, and third components had the largest share in justifying variance. Six main and independent components had more than one variance and explained 85.14% of the total variance. The first component (PC1) correlated with nine traits, including leaf length and width, petiole length, fruit fresh weight, fruit dry weight, fruit ash, fruit EC, fruit TSS and fruit number, which explained 36.46% of the variance. In PC2, the traits included CCYV, fungal severity, off-type plant, stem length, fruit groove, fruit length, fruit diameter, and fruit yield, which accounted for 16.91% of the variance. Fruit trail length was observed in PC3, making 11.39% of the variance. The PC4 had the MFP and fruit color, which explained 7.87% of the variance. In PC5, internode length explained 6.84% of the variance. PC6 explained 5.67% of the variance and correlated with fruit pH (Table 7).

Discussion

Around the world, germplasm collections receive protection from governments, universities, botanical gardens, private investors, individuals, and industries. By maintaining diverse perennial plants in one location through multiple years, germplasm collections offer an essential opportunity to describe phenotypic and interannual variation in large numbers of accessions under typical conditions (Migicovsky et al., 2019). Evaluation of the genetic diversity of cucumber germplasm to select new genotypes with desirable traits is one of the advantages of germplasm preservation (Hakimi et al., 2022).

The lowest CCYV among genotypes, except for 'Nagene,' was observed in the IR4 genotype with 21.14%, which was 4.19, 2.48 and 8.77% less than 'Veolla,' 'Datis,' and 'Ballistic' cultivars, respectively (Fig. 1A). Cucurbit chlorotic yellows virus (CCYV) belongs to the genus *Crinivirus* and is part of a complex of whitefly-transmitted viruses that cause yellowing disease in cucurbits (Kavalappara et al., 2022). This virus has been widely reported in most countries, resulting in lower yields and poorer quality fruit, but one of the best ways to deal with it is to identify genotypes resistant to this disease (Sun et al., 2017). According to the results, as the amount of groove, length, dry matter, ash percentage, and TSS of fruits increases, the amount of CCYV decreases and vice versa. Selecting genotypes with these traits can lead to CCYV control (Table 2). The lowest fungal severity (11.90%) among genotypes, except for 'Nagene,' was observed in the IR5 genotype, which was 8.10, 0.48, and 6.2% less than 'Veolla,' 'Datis,' and 'Ballistic' cultivars, respectively (Fig. 1B). The most important fungal diseases in cucumber production are downy mildew, powdery mildew, anthracnose, Cercospora leaf spot, and Alternaria leaf blight, which are the precursors of rotting in roots and aerial parts, thus decreasing yield (Meena et al., 2019). Identifying genotypes resistant to fungal diseases and management methods can help better control these pathogens. Based on the results, as the amount of groove, length, dry matter, ash percentage, TSS, and yield of fruits increases, the fungal severity decreases (Table 2).

Table 7. Eigenvectors and total percentage variation for the PCA of the cucumber genotypes.

Character	Component					
	1	**2**	**3**	**4**	**5**	**6**
CCYV	-0.227	0.690	0.467	0.244	0.282	0.057
Fungal severity	-0.274	0.648	0.479	-0.035	0.262	0.033
Off-type plant	-0.535	0.576	0.380	-0.260	-0.059	0.145
Stem length	-0.191	-0.569	-0.052	0.515	0.323	-0.336
Internode length	0.504	0.308	-0.041	0.020	-0.630	-0.074
Leaf length	0.825	0.099	0.460	0.102	0.030	-0.074
Leaf width	0.702	0.120	0.580	0.150	0.108	0.020
Petiole length	0.864	0.035	0.100	-0.071	-0.189	0.125
MFP	-0.357	0.139	0.071	-0.634	0.199	-0.445
Fruit color	0.477	0.060	-0.125	0.698	0.067	-0.268
Fruit groove	0.395	-0.584	-0.008	-0.120	0.169	0.498
Fruit length	0.301	-0.622	0.004	-0.266	0.508	-0.250
Fruit diameter	0.525	0.542	-0.386	0.318	0.022	0.078
Fruit trail length	0.304	0.302	-0.697	-0.065	0.103	0.347
Fruit fresh weight	0.810	0.135	-0.269	-0.009	0.329	0.139
Fruit dry matter	0.902	-0.119	0.040	-0.225	-0.146	-0.170
Fruit ash	0.901	-0.118	0.039	-0.224	-0.145	-0.169
Fruit pH	0.419	-0.381	0.380	-0.071	0.272	0.481
Fruit EC	0.825	0.099	0.460	0.102	0.030	-0.074
Fruit TSS	0.902	-0.118	0.039	-0.226	-0.147	-0.170
Fruit yield	-0.324	-0.644	0.332	0.171	-0.303	0.171
Fruit number	-0.609	-0.533	0.395	0.154	-0.352	0.046
% of variance	36.46	16.91	11.39	7.87	6.84	5.67
Cumulative %	36.46	53.37	64.76	72.63	79.47	85.14

IR4 and IR5 genotypes were deemed promising cucumber genotypes for breeding programs to produce resistant cucumber varieties due to their relative resistance to viral and fungal diseases. Among the studied genotypes, except for the control cultivars, IR5 and IR9 showed the lowest off-type plants (Fig. 1C). To produce hybrid cultivars with a high degree of purity, it is necessary to remove off-type plants from inbred lines (Brandes et al., 2009). According to the results, an increase in the stem length, petiole length, color, groove length, fresh weight, dry matter, ash percentage, and TSS of fruits caused a decrease in off-type plants (Table 2). The comparison of the cluster groups also showed that except for the second cluster, including the control cultivars, these three traits in the fifth cluster showed the least amount compared to the others (Table 6). Also, these three traits belong to the second main component, which expresses a state of resistance to diseases and physiological disorders (Table 7).

The stem length of IR9 and IR4 genotypes was 16.40 and 9.27% higher than those of the 'Datis' (Table 3). Based on the results, with an increase in fruit length, fruit yield, and fruit number, there was an inrease in stem length (Table 2). The heritability for this trait was above 95%. Based on the correlation results, selecting genotypes with higher stem lengths can be crucial in producing cultivars with higher yield and fruit length. These results are consistent with the results of Kumari (2017). The internode length of the IR11 genotype was 42.66, 47.41, 41.51 and 32.35% less than the 'Nagene,' 'Veolla,' 'Datis,' and 'Ballistic' cultivars, respectively (Table 3). The

Arab Salmani and Hakimi

Int. J. Hort. Sci. Technol. 2024 11 (2): 229-248

selection of genotypes with long stem lengths, short internode, and a high number of fruits per node is vital for breeding and production programs (Pushpalatha et al., 2016). The heritability for this trait was above 95%, and according to the results, the decrease in leaf length, petiole length, color, dry matter, ash content, EC, and TSS of fruits was parallel with lower internode length (Table 2), similar to a previous finding (Sharma et al., 2018). Also, the internode length was attributed to the fifth main component, expressing its highest variance (Table 7). It seems that among the leaf-related indices, control genotypes have superiority over others. 'Ballistic' had 31.96 and 30.44% more leaf length and width than the mean index. Also, 'Nagene' had 25.33% more petiole than the mean index (Table 3). A higher leaf area index and a larger canopy reportedly increased temperatures among plants. Warm conditions can lead to the closing of the leaf stomata and an increase in evaporation and transpiration, thereby decreasing plant growth and yield (Jeon et al., 2022). For this reason, in high-temperature greenhouses, as in this study, choosing genotypes with medium leaf dimensions is the best option to deal with this issue because it improves the airflow among the plants and reduces evaporation and transpiration. Based on this, IR4 and IR6 genotypes seem the best option. Also, the correlation results showed that the number of fruits decreases with the increase in the dimensions of the leaves (Table 2). Also, these three traits belong to the first main component, which expresses a state of vegetation and stem yield components (Table 7).

MFP of IR10 was 7.82, 4.16, 18.76, and 29.95% lower than the values in 'Nagene,' 'Veolla,' 'Datis,' and 'Ballistic' cultivars, respectively. Male flowers reportedly increased with the increase in temperature (Miao et al., 2011). It seems that under warm greenhouse conditions, genotypes IR11, IR7, IR5, IR8, and IR3 showed more sensitivity to high temperatures and produced more male flowers (Fig. 2A). It seems that except for IR9 (dark green), IR10 (light green), IR11 (light green), and IR7 (very light green) genotypes, other genotypes showed normal green fruit color, which is the most desirable color in greenhouse cucumber production (Fig. 2B). According to the results, the control cultivars showed the deepest fruit groove (Fig. 2C). Also, the correlation results showed that the fruit groove increased with the increase in the fruit length, fresh weight, dry matter, and ash (Table 2). In other words, genotypes with deeper grooves had better-quality fruits.

The fruit length of the IR11 genotype was 11.11,

18.23, 16.98, and 10.67% more than the values in 'Nagene,' 'Veolla,' 'Datis,' and 'Ballistic' cultivars, respectively (Table 4). According to the results, as the fruit length increased, the fruit dry matter, fruit ash percentage, acidity, and TSS increased likewise. Thus, fruit length is directly related to quality traits, and genotypes with longer fruit length and deep grooves had longer post-harvest and shelf life (Table 2). These results are consistent with the results of Kumari (2017). The maximum fruit length in a previous study (Kumar et al. 2013) was 22.76 cm in the LC-25 genotype, which was 37.11% more than the value in the IR11 genotype in this study. According to the results, the heritability of this trait was above 95% and belonged to the second main component (Table 7). Fruits with a smaller diameter are more desirable among people, so choosing genotypes with a smaller width is more appropriate. IR4 had the smallest fruit diameter, which was 13.91, 8.58, 13.00, and 18.07 less than the value in 'Nagene,' 'Veolla,' 'Datis,' and 'Ballistic' cultivars, respectively (Table 4). According to the correlations, the smaller the fruit diameter, the higher the fruit yield and fruit count (Table 2). This correlation likewise and reportedly occurred in a previous study (Bozorgzad and Golabadi, 2019).

Among the cluster group, the fifth cluster's fruit diameter was 6.89, 14.37, 4.04, and 14.54% less than the 1st, 2nd, 3rd, and 4th clusters (Table 6). The smallest fruit diameter occurred in a study by Sadiq et al. (2019), with a value of 2.5 cm in the 'Liza' variety, which was 6.12% less than the value observed in IR4 in this study.

Based on the results, 33.33, 46.67, and 20% of the genotypes had fruit fresh weights ranging between 60-75, 75-90, and 90-105 gr, respectively (Table 4). The highest fruit fresh weight (99.27 gr) belonged to the 2nd cluster, which was 34.37, 27.37, 24.57, and 49.64% more than the 1st, 3rd, 4th, and 5th clusters, respectively (Table 6). Ullah et al. (2012) showed that fruit fresh weight ranged between 82.33-303.30 gr by evaluating 12 cucumber genotypes. Based on the correlation results, an increase in fruit fresh weight was parallel with a decrease in fruit yield and count (Table 2). For this reason, selecting genotypes with medium fruit weight and higher quality can lead to higher yield than genotypes with higher fruit weight. However, these results do not agree with previous results by Kumar et al. (2022). The dry matter percentage of 'Nagene' was 0.80, 0.81, and 0.36% higher than 'Veolla,' 'Datis,' and 'Ballistic,' respectively. Also, 26.67% of the genotypes were above the average fruit dry matter, and the rest were below the average (Table 4). Beilari et al.

(2022) evaluated nine cucumber genotypes, showing that fruit dry matter percentages ranged between 1.269 and 6.599%. The highest fruit dry matter percentages (4.72%) belonged to the 2nd cluster, 0.71, 0.67, 0.50, and 0.75% more than the 1st, 3rd, 4th, and 5th clusters, respectively (Table 6). Based on the correlation results, an increase in fruit dry matter percentage was parallel with an increase in fruit pH, EC, and TSS (Table 2). Valverde-Miranda et al. (2021) showed a positive correlation between dry matter and TSS of fruits with shelf-life. As a result, selecting genotypes with a higher percentage of dry matter led to a longer shelf life in post-harvest conditions. The heritability of fresh weight, dry matter percentage, and ash content of the fruits were above 95%. These traits belonged to the first main component, describing vegetative yield and stem yield components (Table 7).

Fruit acidity in genotypes ranged between 5.22 and 6.11. Fruit acidity in IR6 was 11.82, 5.95, 8.58, and 14.57% lower than the values observed in 'Nagene,' 'Veolla,' 'Datis,' and 'Ballistic' cultivars, respectively (Fig. 3A). Based on the correlation results, greater leaf and fruit dimensions were parallel with higher fruit acidity (Table 2). Fruit acidity was related to the fifth principal component and constituted the largest share of the variance in this factor (Table 7). Fruit EC of IR5 was 32.29, 10.49, 16.99, and 39.82% lower than the values observed in 'Nagenea,' 'Veolla,' 'Datis,' and 'Ballistic' cultivars, respectively (Fig. 3B). Similar to fruit acidity, greater leaf and fruit dimensions were parallel with an increase in EC in the fruits (Table 2). However, this trait belonged to the first principal component (Table 7). TSS is one of the most essential marketability traits among horticultural products, including cucumber. TSS depends on carbohydrates, organic acids, proteins, fats, and minerals (Valverde-Miranda et al., 2021). Except for the 'Nagene,' the highest amount of fruit TSS was observed in IR8, which was 13.98, 14.25, and 3.00% higher than the values observed in 'Veolla,' 'Datis,' and 'Ballistic' cultivars, respectively (Fig. 3C).

Kumar et al. (2013) showed that TSS ranged between 2.07 and 4.07 °Brix by evaluating 30 cucumber genotypes. Based on the results, acidity, electrical conductivity, and TSS were in positive correlations, meaning that increasing each trait increased the other (Table 2). The total yield per plot of the IR4 genotype was 32.45, 28.61, 22.45, and 32.33% more than the values observed in 'Nagene,' 'Veolla,' 'Datis,' and 'Ballistic' cultivars, respectively. Also, the total yield per plot of the IR5 genotype was 22.40, 18.85, 13.16, and 22.29% more than the values in

'Nagene,' 'Veolla,' 'Datis,' and 'Ballistic' cultivars, respectively (Fig. 3A). These two genotypes showed the highest yield per plot and also belonged to the fifth cluster in the cluster grouping, with yields per plot that were 19.59, 27.37, 40.87, and 46.64% higher than 1st, 2nd, 3rd, and 4th clusters, respectively (Table 6). Furthermore, this trait belonged to the second main component (Table 7). The correlations also showed that the product yield decreased significantly, parallel to greater fruit size and weight. These results confirm previous ones by Bozorgzad and Golabadi (2019). The total fruit count per plant of the IR4 genotype was 106.73, 67.60, 54.81, and 127.12% more than the values observed in 'Nagene,' 'Veolla,' 'Datis,' and 'Ballistic' cultivars, respectively. Also, the total fruit count per plant of the IR5 genotype was 60.14, 29.83, 19.92, and 75.93% more than the values observed in 'Nagene,' 'Veolla,' 'Datis,' and 'Ballistic' cultivars, respectively (Fig. 3B). These two genotypes showed the highest total fruit number per plant and also belonged to the fifth cluster in the cluster grouping, whose total fruit count per plant was 34.06, 92.06, 66.99, and 75.43% higher than the 1st, 2nd, 3rd, and 4th clusters, respectively (Table 6). Furthermore, this trait belonged to the first main component (Table 7). Increasing the greenhouse temperature in the first days increased the mean total yield up to the 2nd harvest while keeping the temperature at 40 gradually decreased the yield. The mean yield of the 2nd harvests was 28.66, 27.67, 65.76, and 58.74% higher than the 1st, 3rd, 4th, and 5th harvests, respectively (Table 5).

Conclusions

Breeding for horticultural plants is gradually becoming more prevalent through motivations to preserve genetic diversity. While many cucumber cultivars have been registered worldwide, more breeding programs are still needed to produce better quality cucumber genotypes to solve production problems such as susceptibility to fungal and viral diseases. In conclusion, we observed a high degree of variation in morphology and phenology among superior cucumber genotypes. Evaluating biochemical characteristics via molecular markers can complete phenotypic data to study genetic variation in cucumber populations. In addition, knowledge of biochemical traits such as protein, phenolic compounds, and secondary metabolites can highly assist in introducing a superior genotype with high fruit qualities. Based on the results, the selected genotypes were superior in various aspects of phenotypic characteristics and

fruit quality. Therefore, these superior genotypes have the potential for introduction as commercial cultivars and can serve as a source of desirable genes for future cucumber breeding programs. Here, a thorough comparison with established cucumber cultivars (Nagene, Veolla, Datis, and Ballistic) showed that 'IR4' and 'IR5' are relatively superior because of their low susceptibility to fungal infestation and severity of CCYV, highest stem length, high yield, and high fruit count per plant. These genotypes can contribute to cucumber cultivation worldwide while offering a genetic resource for cucumber breeding and crossbreeding later.

Author contributions
Conceptualization: KAS, methodology: YH, software: YH, validation: KAS, formal analysis: YH, investigation: YH, resources: YH, data curation: YH, writing—original draft preparation: YH, writing—review and editing: KAS, supervision: KAS, project administration: YH. All authors have read and agreed to the published version of the manuscript.

Conflict of Interest
The authors indicate no conflict of interest for this work.

References

Abiodun OA, Adeleke RO. 2010. Comparative studies on nutritional composition of four melon seeds varieties. Pakistan Journal of Nutrition 9(9), 905-908.

Al-Jibouri H, Miller PA, Robinson HF. 1958. Genotypic and environmental variances and covariances in an upland cotton cross of interspecific origin 1. Agronomy Journal 50(10), 633-636.

Beilari A, Olfati JA, Esfahani M, Pirmoradian N. 2022. Evaluation of yield stability of a number of cucumber lines (Cucumis sativus L.) during spring and autumn cropping seasons. Journal of Crops Improvement 24(3), 961-975. https://doi.org/10.22059/jci.2022.322875.2545

Bozorgzad G, Golabadi M. 2019. Appointment of importance and portion of morphological traits on fruit yield in breeding hybrid cultivars of greenhouse cucumber. Journal of Agronomy and Plant Breeding 15(2), 1-34.

Brandes C, Joachimsthaler A, Stöger A, Ruppitsch W, Zimmermann H. 2009. Genetic characterization of the origin of offtype plants in maize inbred lines. Seed Science and Technology 37(2), 423-435. https://doi.org/10.15258/sst.2009.37.2.15

Chomicki G, Schaefer H, Renner SS. 2020. Origin and domestication of cucurbitaceae crops: insights from phylogenies, genomics and archaeology. New Phytologist 226(5), 1240-1255.

Dhiman K, Gupta A, Sharma DK, Gill NS, Goyal A. 2012. A review on the medicinally important plants of the family cucurbitaceae. Asian Journal of Clinical Nutrition 4(1), 16-26.

FAO. 2020. Food and Agriculture Organization of the United Nations-Statistic Division.

Hakimi Y, Fatahi R, Naghavi MR, Zamani Z. 2021. Seed germination indices of Papaver bracteatum populations under different temperature treatments. 1st International & 5th National Seed Science and Technology Conference of Iran.

Hakimi Y, Fatahi R, Zamani Z. 2022. Evaluation of genetic diversity among some selected walnut by using morphological and pomological characteristics. Iranian Journal of Horticultural Science 53(1), 209-224. https://doi.org/10.22059/ijhs.2021.318674.1896

Jeon Y, Cho L, Park S, Kim S, Lee C, Kim D. 2022. Canopy temperature and heat flux prediction by leaf area index of bell pepper in a greenhouse environment: experimental verification and application. Agronomy 12(8), 1807. https://doi.org/10.3390/agronomy12081807

Kavalappara SR, Riley DG, Cremonez PSG, Perier JD, Bag S. 2022. Wild radish (Raphanus raphanistrum L.) is a potential reservoir host of cucurbit chlorotic yellows virus. Viruses 14(3), 593. https://doi.org/10.3390/v14030593

Kumar R, Das Munshi A, Behera TK, Jat GS, Choudhary H, Talukdar A, Dash P, Singh D. 2022. Association mapping, trait variation, interaction and population structure analysis in cucumber (Cucumis sativus L.). Genetic Resources and Crop Evolution 69(5), 1901-1917. https://doi.org/10.1007/s10722-022-01352-3

Kumar S, Kumar D, Kumar R, Thakur KS, Dogra BS. 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.

Kumari B. 2017. Evaluation of phenotypic trait analysis of cucumber germplasm. International Journal of Engineering and Applied Sciences 4(9), 257375.

Lush JL. 1949. Heritability of quantitative characters in farm animals. Proceedings of the 8th Congress of Genetics and Hereditas 356-375.

Ma J, Du K, Zheng F, Zhang L, Gong Z, Sun Z. 2018. A recognition method for cucumber diseases using leaf symptom images based on deep convolutional neural network. Computers and Electronics in Agriculture 154, 18-24.

Meena AK, Godara SL, Meena PN, Meena AK. 2019. Foilar fungal pathogens of cucurbits. In the Vegetable Pathosystem (pp. 203-228). Apple Academic Press.

Miao M, Yang X, Han X, Wang K. 2011. Sugar signalling is involved in the sex expression response of monoecious cucumber to low temperature. Journal of Experimental Botany 62(2), 797-804. https://doi.org/10.1093/jxb/erq315

Migicovsky Z, Warschefsky E, Klein LL, Miller AJ. 2019. Using living germplasm collections to characterize, improve, and conserve woody perennials. Crop Science 59(6), 2365-2380.

Mousavi SA, Tatari M, Moradi H, Hasani D. 2015. Evaluation of genetic diversity among the superior walnut genotypes based on pomological and phenological traits in Chahar Mahal va Bakhtiari Province. Seed and Plant Improvement Journal 31(2), 365-389.

Nicodemo D, Malheiros EB, Jong DD, Couto RHN. 2012. Floral biology of greenhouse-grown of Japanese cucumber plants (*Cucumis sativus* L.). Científica (Jaboticabal) 40(1), 35-40.

Pal S, Sharma HR, Yadav NE. 2017. Evaluation of cucumber genotypes for yield and quality traits. Journal of Hill Agriculture 8(2), 144-150.

Pushpalatha N, Anjanappa M, Devappa V, Pitchaimuthu M. 2016. Genetic variability and heritability for growth and yield in cucumber (*Cucumis sativus* L.). Journal of Horticultural Sciences 11(1), 33-36.

Qi J, Liu X, Shen DI, Miao H, Xie B, Li X, Huang S. 2013. A genomic variation map provides insights into the genetic basis of cucumber domestication and diversity. Nature Genetics 45(12), 1510-1515.

Saboo SS, Thorat PK, Tapadiya GG, Khadabadi SS. 2013. Ancient and recent medicinal uses of cucurbitaceae family. International Journal of Therapeutic Applications 9, 11-19.

Sadiq GA, Omerkhil N, Zada KA, Safdary AJ. 2019. Evaluation of growth and yield performance of five cucumbers (*Cucumis sativus* L.) genotypes: case study in Kunduz province, Afghanistan. Evaluation 4(6), 22-28.

Sharma S, Kumar R, Chatterjee S, Sharma HR. 2018. Correlation and path analysis studies for yield and its attributes in cucumber (*Cucumis sativus* L.). International Journal of Chemical Studies 6(2), 2045-2048.

Sharma V, Sharma L, Sandhu KS. 2020. Cucumber (*Cucumis sativus* L.). In Antioxidants in Vegetables and Nuts-Properties and Health Benefits (pp. 333-340). Springer.

Shet RM, Shantappa T, Gurumurthy SB. 2018. Genetic variability and correlation studies for productivity traits in cucumber (*Cucumis sativus* L.). International Journal of Chemical Studies 6(5), 236-238.

Sun X, Wang Z, Gu Q, Li H, Han W, Shi Y. 2017. Transcriptome analysis of Cucumis sativus infected by cucurbit chlorotic yellows virus. Virology Journal 14(1), 18. https://doi.org/10.1186/s12985-017-0690-z

Ullah M, Hasan MJ, Chowdhury A, Saki A, Rahman A. 2012. Genetic variability and correlation in exotic cucumber (*Cucumis sativus* L.) varieties. Bangladesh Journal of Plant Breeding and Genetics 25(1), 17-23.

Uthpala TGG, Marapana RAUJ, Lakmini K, Wettimuny DC. 2020. Nutritional bioactive compounds and health benefits of fresh and processed cucumber (Cucumis sativus L.). Sumerianz Journal of Biotechnology 3(9), 75-82.

Valverde-Miranda D, Díaz-Pérez M, Gómez-Galán M, Callejón-Ferre ÁJ. 2021. Total soluble solids and dry matter of cucumber as indicators of shelf life. Post-harvest Biology and Technology 180, 111603. https://doi.org/10.1016/j.postharvbio.2021.111603

Veena R, Sidhu AS, Pitchaimuthu M, 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.

Weng Y. 2021. *Cucumis sativus* chromosome evolution, domestication, and genetic diversity: implications for cucumber breeding. Plant Breeding Reviews 44, 79-111.

Zargar Shooshtari F, Souri MK, Hasandokht MR, Kalate Jari S. 2020. Glycine mitigates fertilizer requirements of agricultural crops: case study with cucumber as a high fertilizer demanding crop. Chemical and Biological Technologies in Agriculture 7(1), 1-10.