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RESEARCH PAPER

Breeding improvement of fennel genotypes of different origins (*Foeniculum vulgare* L.) using morphological and yield parameters

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Abstract

G. Yaldiz, and M. Camlica. 2022. Breeding improvement of fennel genotypes of different origins (*Foeniculum vulgare* L.) using morphological and yield parameters. Int. J. Agric. Nat. Resour. 97-111. Fennel (*Foeniculum vulgare* L.) is a reputed spice plant and is used as an industrial medicinal plant due to its pharmaceutical and food applications, exhibiting a wide array of genetic variations depending on morphological and yield properties. Along with the current study, thirty-two different fennel genotypes and five local genotypes from Turkey were used to determine the morphological and yield properties in 2017 and 2018. A wide range of variation in plant height (39.22-129.60 cm), 1000 fruit yield (1.92-7.70 g), and fruit yield (0.12-8.68 g) was observed. As deduced from previous reports and from the current findings of the study, those relevant parameters could be considered for breeding purposes. To visualize or clarify the findings, a dendrogram was constructed to reveal the genetic variability regarding the morphological and yield properties of fennel genotypes. The dendrogram revealed that genotypes of different origins occurred in different groups, but local genotypes collected from Turkey occurred in the same group and subgroup. Additionally, correlation analysis was carried out to reveal the relationships between the relevant agronomic parameters. Of those correlation coefficients, a high correlation coefficient was noted between the number of fruits and fruit yield (r=0.849). Overall, the findings of the study revealed notable genetic variation related to fruit yield and other relevant agronomic traits for fennel genotypes, suggesting that this remarkable variation might be used for selecting superior genotypes in breeding programs. Of the genotypes analyzed, Ames30289 was the best genotype due to the highest fruit yield according to two successive years. Consequently, the findings can be considered useful information for fennel breeders, researchers and farmers in Turkey or other countries.

Keywords: Augmented design, dendrogram analysis, fennel, genetic diversity.

Introduction

Fennel (*Foeniculum vulgare* L.), which belongs to the Umbelliferae family, exhibits a high variation within each population because of cross-pollinating crops and has long been cultivated and introduced into many regions (Rather et al., 2012; Rahimmalek et al., 2014). Fennel is commonly used in folk medicine due to its balsamic, cardiotonic, digestive, galactagogue and tonic properties, including essential oil, phenolic glycosides, flavonoids, triterpenes and saponins (Saleha, 2011; Saravanaperumal & Terza, 2012). Specifically, its essential oil and mature fruit are

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of great interest for pharmaceutical products, cosmetics and food products as flavorings. Another important factor is to consider fennel as a functional food in everyday life (Faudale et al., 2008; Ghasemzadeh et al., 2012). Fennel should be produced in the desired amounts and quality using sustainable production and making use of the market potential because of its particular economic importance. Recently, fennel has become a point of attraction for many international seed companies that have improved their research breeding programs.

The conservation of genetic variability for the future and the efficient utilization of available genotypes are important for efficient germplasm management and long-term breeding programs. Such information would be important for indicating the effect of geographic origin on agro-morphological traits for fennel fruit cultivars. Therefore, genetic variation is key to the ability of genotypes and species to persist over an evolutionary period through changing environments (Nass & Paterniani, 2000). It is thought to be a powerful cue for breeding habitat selection because it integrates the effects of all environmental factors on breeding success (Danchin et al., 2001). Therefore, studying the phenotypic variations of fruit is helpful for understanding the effects of environmental and genetic factors on species and how well plants adapt to environmental changes in distributed areas through long-term selection and evolution. In addition, it was reported that in general, phenotypic variance was higher than genotypic coefficient variance, indicating the role of environmental factors on character expression (Meena et al., 2019).

Since fennel is an open cross-pollinated crop, it has a wide genetic variability and offers a wide genetic background for breeders. Furthermore, it has been reported that there are considerable variabilities in the morphological traits within and among geographical provenances under the influence of eco-environmental stress, and the morphological traits of the fruit may vary greatly among individuals, even within the same geographical provenance (Yaldiz & Camlica 2019; Yaldiz & Camlica, 2021a). Therefore, the standard identifier list was used in the Guide for Conducting the Differences, Uniformity and Stability Tests by the International Union for the Protection of New Varieties of Plants (UPOV) to identify the varieties correctly (UPOV, 2000). The UPOV system of plant variety protection based on individual test guidelines represents an agreed-upon and harmonized approach for the examination of new cultivars of a species of interest. This study can shed new light on the ecophysiological effects of environmental factors in the two years under research, such as the temperature, rainfall and humidity, to improve the performance of different fennel genotypes.

There have been many studies on the secondary metabolites and yield values in fennel, but there is limited information available on the morphological and yield properties together with the UPOV criteria of different origins and local fennel genotypes. With the current study, we aimed to i) determine the morphological and yield values in fennel genotypes of different origins in two successive years; ii) evaluate the genetic diversity based on the morphological and yield properties and UPOV criteria and find diversity patterns of fennel genotypes; iii) reveal the relationship between examined properties in fennel genotypes; and iv) identify the genetically important overseas genotype for desired morpho-chemotypes for future breeding practices.

Materials and Methods

Plant material and experimental design

Seeds of fennel genotypes were obtained from the United States Department of Agriculture (USDA), and local genotypes were collected from farmers in Turkey (Table 1 and Figure 1).

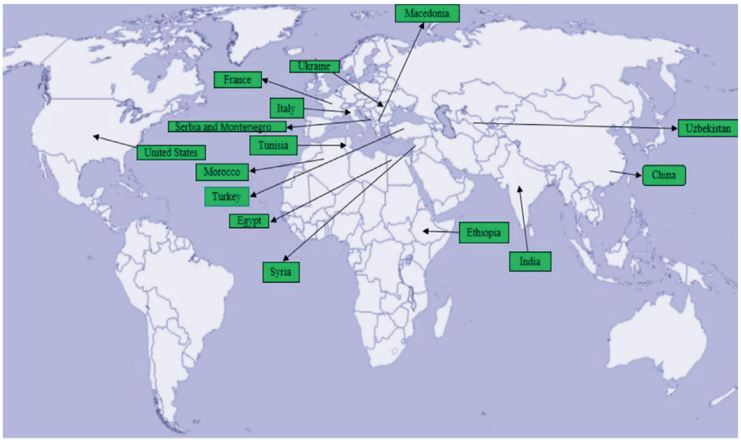

Figure 1. Origin map of fennel genotypes.

Table 1. Accession number and origin of fennel genotypes.

No	Accession	Origin country	No	Accession number	Origin country
1	Ames 23130	Italy	20	PI 273660	Ethiopia, Harer
2	Ames 27588	Italy	21	PI 288283	India, Uttar Pradesh
3	Ames 30289	Tunisia, Sfax	22	PI 288285	India, Rajasthan
4	Ames 30290	Tunisia, Sfax	23	PI 288477	India
5	Ames 30693	United States, Oregon	24	PI 358460	Macedonia
6	Ames 7551	United States, Illinois	25	PI 414189	Egypt, Cairo
7	Bucak	Turkey/Burdur	26	PI 414190	United States, Maryland
8	Denizli	Turkey/Denizli	27	PI 414191	United States, Maryland
9	Erzurum	Turkey/Erzurum	28	PI 414192	United States
10	Eskişehir	Turkey/Eskişehir	29	PI 601795	United States, California
11	Nazilli	Turkey/Aydın	30	PI 649460	Italy, Lotium
12	NSL 6409	United States, California	31	PI 649463	China, Shanxi
13	PI 172898	Turkey, Mardin	32	PI 649464	China, Guangxi
14	PI 174212	Turkey, Ş. Urfa	33	PI 649465	Uzbekistan
15	PI 174213	Turkey, Ş. Urfa	34	PI 649466	France, Loire-Atlantique
16	PI 194892	Ethiopia	35	PI 649469	Syria
17	Ames20029	Ukraine	36	PI 649470	China, Yunnan
18	PI 251085	F. Serbia and Montenegro	37	PI 649471	Morocco
19	PI 273659	Ethiopia			

An augmented trial design was established in the experimental area of Bolu Abant İzzet Baysal University (40.7325° N, 31.6082° E, 752 m) in 2017 and 2018. Thirty-two USDA genotypes and 5 local genotypes were used as materials. These seeds were sown on 17 April 2017 in four blocks with sixteen entries, and the block size was measured as 7.2 m×5.0 m with a spacing of 45 cm in 2017. In 2018, genotypes were sown on 14 April 2018 with 4 blocks with thirteen entries in each block and a plot size of 5.85 m×5.0 m, with a spacing of 45 cm.

As experimental factors, 60 kg ha^{-1} diammonium phosphate (DAP) as the base fertilizer and 4 kg ha^{-1} ammonium nitrate (AN) as the top fertilizer were applied in both experimental years.

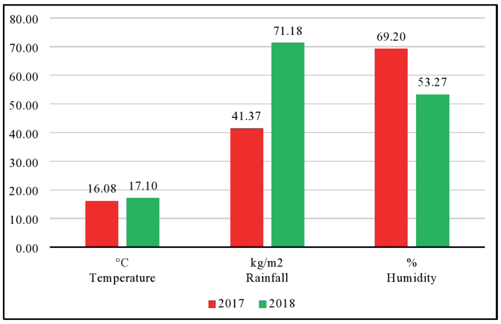

Figure 2. Climatic data for the two vegetation periods.

The experimental years had similar temperatures of 16.08 °C and 17.10 °C in 2017 and 2018, respectively (Figure 2). The precipitation in 2018 (71.18 kg m^{-2}) was greater than that in 2017 (41.37 kg m^{-2}). The relative humidity values of the experimental years were 69.20% in 2017 and 53.27% in 2018.

Experimental soils had a clay-loam texture, 4.70% organic matter, 2.8% lime, 10.3 ppm phosphorus, 235 ppm potassium and a pH value of 7.80 (Table 2). Climatic conditions such as rainfall and humidity were found to be different, but the temperature was noted to be similar in the two vegetation periods.

All required agronomic applications were applied for successful crop raising during the growing season. Morphological research was carried out in 2017 and 2018. Each genotype was represented by ten plants, and a total of 370 plants were analyzed for morphological traits in both experimental years. Twenty-seven traits were scored according to the UPOV Guidelines for the Conduct of Tests for Distinctness, Uniformity and Stability, in which the qualitative traits were expressed in discontinuous states, whereas the expression of each quantitative trait was divided into a number of discrete states for the purpose of description. Fennel genotypes did not contain other criteria outside of the 15 UPOV criteria (Table 3). All states were necessary to describe the full range of the traits, and every form of expression could be described by a single state. Thus, all the recorded data were qualitative in nature.

Statistical analysis

Variance analysis was conducted for individual years as per an augmented design by using the JMP-13 statistical program. The mean values of the examined properties were calculated separately in each year for fennel genotypes and were statistically analyzed vis-a-vis the controls using the least significant differences test to determine promising genotypes ($p<0.01$). The statistical analysis included the mean, coefficient of variation (CV) and the Least Significant Difference (LSD) values in 2017 and 2018. Constellation plot analysis was performed depending on the morphological, yield and UPOV criteria among the fennel genotypes using Ward's method and the squared Euclidian distance of the mean of the experimental years. Correlation analysis was conducted to determine the relationships among the morphological and yield properties by using the means of the 2017 and 2018 experimental years.

Results

Variation in the morphological and yield parameters of fennel genotypes

The variation among the pooled means of the accessions (37 genotypes) was highly significant ($p < 0.01$) for the examined traits (Tables 4 and 5). The fennel genotypes exhibited significant

Table 2. Properties of experimental area soil.

Soil texture	pH	Organic matter	Salt content	Lime content	Phosphorus ratio	Potassium ratio
		%			ppm	
clay-loam	7.80	4.70%	0.008	2.8	10.3	235

Table 3. Description of UPOV criteria in fennel genotypes.

No	Character	State	Note	No	Character	State	Note
1	Only varieties without grumolo: Young plant: length of cotyledons (LC)	Short	3	8	Leaf: length (LL)	Short	3
		Medium	5			Medium	5
		Long	7			Long	7
2	Only varieties without grumolo: Young plant: length of petiole of first leaf (LPPFL)	Short	3	9	Leaf: curvature of tip (LCT)	Absent	1
		Medium	5			Weakly expressed	2
		Long	7			Strongly expressed	3
3	Only varieties with grumolo: Plant: height at harvest maturity (PHHM)	Short	3	10	Main umbel: diameter (UD)	Small	3
		Medium	5			Medium	5
		Long	7			Large	7
4	Foliage: attitude (FA)	Erect	1	11	Time of appearance of main umbel (TAMU)	Early	3
		Semi-erect	3			Medium	5
		Horizontal	5			Late	7
5	Foliage: density (FD)	Sparse	3	12	Time of beginning of flowering (TBF)	Early	3
		Medium	5			Medium	5
		Dense	7			Late	7
6	Foliage: intensity of green color (IGC)	Very light	1	13	Fruit: thousand fruit weight (TFW)	Low	3
		Light	3			Medium	5
		Medium	5			High	7
		Dark	7	14	Time of beginning of harvest time (TBH)	Early	3
		Very dark	9			Medium	5
7	Main stem: height at flowering (HF)	Short	3			Late	7
		Medium	5	15	Grumolo formation (GF)	Absent	1
		Long	7			Present	9

differences in terms of the examined properties in different years: the 50% seedling emergence day was between 9.80 and 20.60 days (average 16.63 days) in 2017 and between 13.00 and 24.00 days (average 17.49 days) in 2018 (Table 4). The earliest 50% seedling emergence was observed in the PI649469 and PI172898 genotypes in two successive years. The latest 50% of seedling emergence days were for Ames30693 and PI649471 in 2017 and 2018, respectively.

The results of the analysis of variance for flowering days showed a wide range of variation, and there were significant differences among all evaluated fennel genotypes (Tables 4 and 5). This characteristic changed from 56.10 to 115.10 days in 2017 and from 62 to 105 days in 2018. The earliest value was obtained from the PI288283 genotype in both years, and the latest genotypes were PI414192 and PI273659 in 2017 and 2018, respectively.

Significant differences were found among the fennel genotypes in the values of fruit setting days ($p<0.01$). The fruit setting days ranged from 102.55 to 140.35 days in 2017 and from 95 to 151 days in 2018. The earliest fruit setting was found in the Ames30290 and Ames30693 genotypes at 102.55 and 95 days, respectively; the latest fruit setting was found in the PI649465 and PI273659 genotypes at 140.35 and 151.00 days in 2017 and 2018, respectively. The Ames30290 genotype was the earliest genotype in both years (Table 4).

The mean plant height ranged from 39.22 to 104.64 cm in 2017 and from 42.33 to 129.60 cm in 2018. The tallest plant height was for the PI649471 (104.64 cm) and Ames23130 (129.60 cm) genotypes in the two successive years. The PI414192 and PI649460 genotypes had the smallest plant height in both years of evaluation.

Table 5 shows that the fennel genotypes had a significant effect on the number of branches produced. The PI251085 genotype exhibited the highest average number of branches (8.50), followed by the Ames23130 and PI649465 genotypes

Table 4. Morphological properties of fennel genotypes.

No	Genotypes	2017	2018	2017	2018	2017	2018
		SD (day)		DFT (day)		FSD (day)	
1	Ames20029	18.60a-d	17d-h	67.90h-k	65ıj	105.55lmn	112gh
2	Ames23130	17.80a-e	21a-d	59.10ıjk	101a	111.95fgh	141bc
3	Ames27588	17.40a-g	18c-g	101.90abc	97ab	121.15cd	122e
4	Ames30289	17.60a-f	14gh	86.90def	80cde	117.55de	113fg
5	Ames30290	16.60a-g	14gh	74.90fgh	73d-j	102.55n	95n
6	Ames30693	20.60a	14g-h	75.90fgh	70d-j	102.55n	110ghı
7	Ames7551	15.20c-ı	22abc	91.10cde	89bc	122.35cd	125e
8	NSL6409	17.40a-g	16e-h	93.90bcd	89bc	118.15de	116f
9	PI172898	13.80e-j	13h	59.10ıjk	66hıj	107.95h-m	109hıj
10	PI174212	18.80a-d	16e-h	69.10h-k	65ıj	109.95h-k	108ıjk
11	PI174213	16.60a-g	17d-h	73.90fgh	66hıj	105.55lmn	103lm
12	PI194892	16.40a-g	14g-h	102.90abc	68f-j	121.15cd	111ghı
13	PI251085	20.60a	17d-h	73.90fgh	73d-j	106.55k-n	109hıj
14	PI273659	19.40abc	16e-h	81.90d-h	105a	115.15ef	151a
15	PI273660	19.40abc	23ab	81.90d-h	102a	114.15efg	138c
16	PI288283	10.80ıj	18c-g	56.10k	62j	104.95mn	106jkl
17	PI288285	15.80b-h	16e-h	57.10jk	80cde	106.95j-m	103lm
18	PI288477	18.60a-d	16e-h	69.90g-k	67g-j	107.55ı-m	103lm
19	PI358460	19.40abc	15fgh	77.90e-h	79c-f	108.15h-m	105kl
20	PI414189	18.20a-e	14g-h	73.10f-ı	65ıj	110.35g-k	111ghı
21	PI414190	18.20a-e	19b-f	68.10h-k	74d-ı	105.35lmn	109hıj
22	PI414191	20.20ab	14g-h	74.10fgh	70d-j	138.35a	110ghı
23	PI414192	17.80a-e	18c-g	115.10a	67g-j	139.95a	106jkl
24	PI601795	13.20f-j	18c-g	102.10abc	96ab	132.35b	131d
25	PI649460	20.20ab	19b-f	72.10ghı	78c-g	111.35f-ı	111ghı
26	PI649463	15.40c-h	14gh	81.90d-h	81cd	114.15efg	113fg
27	PI649464	17.80a-e	19b-f	72.10ghı	67g-j	111.95fgh	111ghı
28	PI649465	18.20a-e	20a-e	107.10abc	81cd	140.35a	116f
29	PI649466	18.20a-e	16e-h	71.10g-j	65ıj	114.35efg	105kl
30	PI649469	9.80j	17d-h	71.10g-j	67g-j	110.95ghı	100m
31	PI649470	10.80ıj	21a-d	72.10ghı	81cd	111.95fgh	113fg
32	PI649471	15.40c-h	24a	83.90d-g	98ab	114.15efg	142b
33	Bucak	13.00g-j	19a-f	74.50fgh	74d-ı	110.00h-k	109hıj
34	Denizli	14.50d-ı	21a-d	70.00g-k	74d-ı	107.50ı-m	110g-j
35	Erzurum	13.75e-j	18c-h	74.75fgh	69e-j	108.50h-m	109hıj
36	Eskişehir	11.75hıj	18c-h	74.50fgh	77d-h	109.00h-l	111ghı
37	Nazilli	18.00a-e	21a-e	79.75d-h	67hıj	110.75g-j	108h-k
	Check mean	14.20	19.40	74.70	72.20	109.15	109.40
	Genotype mean	17.01	17.19	78.73	77.72	114.54	114.31
	General mean	16.63	17.49	78.18	76.97	113.81	113.65
	Genotype×year	**	**	**	**	**	**
	LSD (1%)	4.57	4.97	14.66	11.39	4.03	3.73
	CV (%)	14.73	12.3	8.99	7.57	1.69	1.8

SD: Seedling day, DFT: 50% days to flowering time, FSD: fruit setting day, LSD: least significant difference, CV: coefficient of variation.

Values followed by the same letters are not significantly different at P<0.01 according to the LSD test.

(7.60) in 2017. Overall, the PI251085 and PI649460 genotypes were superior genotypes in the two successive years on average.

The mean values of the number of branches in the first year were higher than those in the second year, which was related to their height and habitat, and in all experimental years, the highest branch numbers were obtained in the first experimental year. This result can be explained by the weather conditions in 2018 because the temperature was higher in the vegetative growth period and the rainfall was much lower than that in the 2017 experimental year (BMGD, 2019).

There was a significant difference among the fennel genotypes in both evaluation years regarding their number of umbels. The number of umbels ranged from 1.18 to 14.43 in 2017 and from 4.40 to 20.00 in 2018. The highest values were obtained from the PI414191 and PI174212 genotypes, and the lowest values were observed from the PI414192 and PI273660 genotypes in 2017 and 2018, respectively.

According to our experimental results, the increasing temperature and rainfall values in the second year positively affected the number of umbels. Furthermore, the number of umbels increased or decreased according to the genotypes' flowering days. There was a negative relationship between the number of umbels and flowering days.

There was also a significant difference among genotypes in terms of the number of umbellates per umbel (Table 5). The number ranged from 6.80 to 22.43 in 2017 and from 10.20 to 25.60 in 2018. The highest values were obtained in PI172898 in 2017 and in PI649460 in 2018. The lowest values were noted for the PI194892 (6.80) and PI273659 (7.47) genotypes in 2017 and for the PI649471 (10.00) genotype in 2018.

During the first agronomic year, the fruit number per plant varied from 7.38 to 1214.78, with an average of 519.10 (Table 4). The highest fruit number was observed in the PI649464 and PI649463 genotypes, and the lowest fruit number was recorded in the PI288283 genotype. In the second agronomic year, the fruit number per plant varied between 322.20 and 1,306.00 (Table 5). The highest fruit number was found in the Ames20029 genotype, followed by that in the Ames23130 and NSL6409 genotypes. The lowest seed number was observed in the Eskişehir local genotype.

The one thousand fruit weight of fennel genotypes showed statistically significant differences among the fennel genotypes, ranging from 1.92-8.14 g and 2.26-7.70 g in both agronomic years. The PI649470 and PI194892 genotypes had maximum values in 2017 and 2018. The PI414192 genotype from the United States and the PI174213 genotype from Turkey had the lowest 1000 fruit weight in both years (Table 5).

Fruit yield was significantly different among the fennel genotypes in different years, ranging between 0.15 and 8.14 g in 2017 and between 0.12 and 8.68 g in 2018 (Figure 3). The highest seed yields (8.85 g and 8.68 g) were obtained from the Ames30289 and Ames20029 genotypes, and the lowest seed yields (0.15 g and 0.12 g) were obtained from the PI28883 and PI273659 genotypes in 2017 and 2018, respectively (Table 5). The Ames20029 genotype also had the highest fruit number and fruit yield. The mean fruit yield per plant of local genotypes was found to be higher than that for genotypes from different origins and the general mean of fennel genotypes in the two vegetation years. Additionally, differences between the lowest fruit yield and the highest fruit yield per plant were found to be more than 50-fold in both years.

UPOV criteria of fennel genotypes

The UPOV criteria (15 properties) were noted to find genetic differences in genotypes of different origins. Breeders still use a wide range of their phenotypic performance to select desired

Table 5. Yield properties of fennel genotypes.

No	Genotypes	2017	2018	2017	2018	2017	2018	2017	2018	2017	2018	2017	2018	2017	2018
		PH (cm)		NB (number plant^{-1})		NU (number plant^{-1})		NUT (number NU^{-1})		NF (number plant^{-1})		1000 FW (g)		FY (g plant^{-1})	
1	Ames20029	60.36h-n	104.60bc	6.40a-ı	6.60abc	7.47h-k	16.00bc	11.64j-p	21.80ab	374.44d-g	1306.00a	4.29ghı	5.41a-e	1.70ef	8.68a
2	Ames23130	55.18ı-n	129.60a	4.24ıjk	7.60a	12.58a-d	4.60q	15.53e-k	14.00c-g	760.78bcd	1236.80ab	4.39e-ı	2.34fg	3.16c-f	2.66def
3	Ames27588	54.64j-o	103.80bc	8.26ab	5.40b-d	5.12j-m	4.60q	16.97c-f	17.80bcd	420.68c-f	1073.00a-d	4.28ghı	2.98d-g	1.85e-f	2.30efg
4	Ames30289	91.36ab	97.40c-d	7.10a-f	4.80cd	7.27h-k	13.80de	21.24a-b	16.20b-e	1248.44a	1191.40abc	6.99abc	3.19d-g	8.85a	3.49cd
5	Ames30290	84.06bcd	75.20g-m	7.90a-d	5.00bcd	9.07b-j	13.60def	16.74c-g	17.60bcd	1131.19ab	1115.60a-d	5.79b-h	3.68c-g	6.69ab	3.00cde
6	Ames30693	76.81b-g	93.80cde	6.80a-g	5.80a-d	5.07j-m	13.20d-g	12.43h-n	14.80c-g	202.04fg	943.80c-f	2.99ıj	2.75efg	0.71f	1.77f-k
7	Ames7551	73.54c-h	88.20d-g	6.80a-g	5.00bcd	7.23h-k	8.60mno	20.33a-d	13.20c-g	492.30c-f	910.00d-h	4.83d-ı	3.64c-g	2.45def	2.22e-h
8	NSL6409	68.10e-j	91.20c-f	6.67a-h	5.40bcd	7.92e-k	14.20cd	18.13b-e	18.80bc	1030.48ab	1245.80ab	5.00c-ı	3.43c-g	5.25bcd	6.61b
9	PI172898	70.27d-ı	71.80h-n	5.74d-k	4.40d-d	10.78a-h	9.60lmn	22.43a	13.20c-g	816.38bc	644.40h-m	5.14b-h	4.23b-g	4.07b-e	1.46g-n
10	PI174212	52.17k-o	72.80g-n	4.44h-k	6.00a-d	11.18a-h	20.00a	15.70e-j	13.60c-g	323.38efg	406.20mn	6.69a-d	7.61a	2.07def	0.81k-p
11	PI174213	64.76f-ı	56.00o-q	6.50a-ı	5.00bcd	12.07a-f	12.20e-ı	15.29e-l	13.40c-g	459.69c-f	549.20j-n	6.34a-g	2.26g	2.98c-f	0.56m-p
12	PI194892	62.44g-m	76.20f-m	4.26ıjk	6.00a-d	7.52h-k	19.00a	6.80q	11.20efg	289.68efg	545.20j-n	4.00hıj	7.70a	1.20ef	1.89f-ı
13	PI251085	61.96g-m	78.20f-l	8.50a	5.60a-d	3.74klm	10.60ı-l	11.94ı-o	15.00c-g	333.24efg	502.60j-n	5.81b-h	3.53c-g	2.00def	0.72l-p
14	PI273659	70.54d-ı	91.00c-f	3.76k	4.80cd	5.12j-m	5.80pq	7.47pq	18.60bc	445.68c-f	389.00mn	4.40e-ı	2.39fg	2.02def	0.12p
15	PI273660	86.84bc	100.00cd	6.66a-h	4.20d	9.72b-ı	4.40q	10.30mq	10.20g	331.28efg	402.00mn	5.13b-h	5.41a-e	1.75ef	1.16ı-o
16	PI288283	70.47d-ı	68.60k-p	3.94jk	5.40bbd	0.78m	12.60d-h	11.68j-p	14.00c-g	7.38g	595.00ı-m	6.99abc	6.23abc	0.15f	1.84f-j
17	PI288285	69.07d-j	66.20k-p	5.74d-k	5.20bcd	10.73a-h	7.60op	16.20d-h	10.20g	496.38c-f	526.00j-n	5.01c-ı	3.71c-g	2.31def	0.84k-p
18	PI288477	73.56c-h	72.80g-n	8.10abc	5.80a-d	5.07j-m	12.00e-j	11.19l-p	10.40fg	468.24c-f	648.00g-m	4.42e-ı	4.14b-g	2.17def	1.44g-n
19	PI358460	65.74e-k	70.20j-o	7.26a-f	5.40bcd	13.10ab	11.80f-k	12.47h-n	13.20c-g	390.28d-g	553.20j-n	6.67a-d	5.02a-g	2.67c-f	1.27h-o
20	PI414189	45.57no	67.20k-p	6.33a-ı	6.00a-d	5.18j-m	13.60def	10.00m-q	16.20b-e	240.44efg	914.60d-g	4.59d-ı	4.77b-g	1.27ef	3.88c
21	PI414190	86.84bc	58.00nop	6.60a-h	5.00bcd	10.73a-h	10.20j-m	10.93m-q	13.60c-g	353.90efg	440.00lmn	4.82d-ı	2.51fg	1.82ef	0.35op
22	PI414191	56.49ı-n	71.60h-n	6.50a-ı	5.40bcd	14.43a	13.80de	13.17f-m	14.40c-g	467.10c-f	1106.00a-d	4.88c-ı	4.91a-g	2.35def	3.96c
23	PI414192	39.22o	79.60e-k	7.04a-f	6.60abc	1.18m	11.80f-k	7.91opq	15.20c-g	379.78d-g	596.00ı-m	1.92j	4.74b-g	0.34f	1.40g-n
24	PI601795	48.14mno	115.60ab	6.90a-g	4.60cd	4.93j-m	8.20no	12.53h-n	16.20b-e	468.63c-f	601.40ı-m	4.97c-ı	2.48fg	2.40def	0.75l-p
25	PI649460	69.46d-j	42.33q	7.44a-f	6.60abc	12.72abc	16.40b	12.33h-n	25.60a	272.10efg	546.40j-n	5.31b-h	5.64a-d	1.56ef	1.39g-n
26	PI649463	81.24b-e	85.20d-j	6.16b-j	4.20d	2.32lm	7.40op	20.93abc	11.80efg	1135.48ab	530.00j-n	5.89b-h	3.83c-g	6.81ab	0.88j-p
27	PI649464	92.37ab	63.60l-p	5.54e-k	5.60a-d	11.98a-g	11.40g-l	16.42d-h	13.20c-g	1214.78a	678.60f-l	4.82d-ı	3.95c-g	5.77abc	1.50g-n
28	PI649465	49.99l-o	95.20cd	5.90c-k	7.60a	6.10n-q	11.20h-l	8.88n-q	13.40c-g	567.23c-f	859.80d-ı	5.17b-h	2.73efg	2.96c-f	1.53g-m
29	PI649466	55.24ı-n	86.80d-h	4.67g-k	5.80a-d	7.08h-k	11.6g-k	15.37e-l	16.00c-f	629.41cde	1003.00b-e	5.35b-h	3.65c-g	3.36c-f	2.57def
30	PI649469	69.17d-j	53.60pq	5.34f-k	4.60cd	7.68f-k	11.80f-k	11.33k-p	12.4d-g	310.38efg	582.00j-n	5.42b-h	5.50a-e	1.50ef	1.55g-l
31	PI649470	103.07a	73.80g-m	7.74a-e	5.00bcd	7.38h-k	5.20q	16.28d-h	25.20a	357.58efg	414.80lmn	8.14a	4.72b-g	2.93c-f	0.54nop
32	PI649471	104.64a	86.00d-ı	5.36f-k	5.50bc d	7.07h-k	8.50mno	18.21a-e	10.00g	502.68c-f	723.40f-k	4.37e-ı	2.22g	2.26def	0.94ı-p
33	Bucak	68.20e-j	65.73k-p	6.45a-ı	5.73a-d	7.62g-k	12.13e-ı	10.97m-q	16.67b-e	296.85efg	399.07mn	6.43a-f	5.09a-f	1.94ef	1.88f-ı
34	Denizli	78.33b-f	66.07k-p	7.73a-e	6.07a-d	14.33a	11.73f-k	16.06e-ı	14.87c-g	622.05cde	742.13e-j	6.50a-e	6.94ab	4.06b-e	3.88c
35	Erzurum	80.03b-f	70.80ı-o	6.23a-j	5.53bcd	8.15d-k	12.20e-ı	12.97f-n	16.80b-e	427.55c-f	459.40k-n	6.08a-h	5.34a-e	2.63c-f	2.70def
36	Eskişehir	72.18c-h	62.40m-p	6.33a-ı	5.93a-d	8.28c-j	11.27h-l	11.50j-p	11.80efg	353.83efg	322.20n	5.95b-h	5.09a-f	2.17def	2.15e-h
37	Nazilli	59.56h-n	57.30n-q	6.88a-g	6.90ab	12.27a-e	10.07k-n	16.10d-ı	17.80bd	584.90c-f	600.50ı-m	7.17ab	4.89a-g	4.36b-e	3.48cd
	Check mean	71.66	64.46	6.72	6.03	10.13	11.48	13.52	15.59	457.04	504.66	6.43	5.47	3.03	2.82
	Genotype mean	69.17	80.82	6.27	5.50	7.82	11.10	14.02	15.01	528.80	743.10	5.15	4.10	2.79	2.00
	General mean	69.50	78.61	6.33	5.57	8.13	11.15	13.96	15.09	519.10	710.88	5.32	4.29	2.83	2.11
	Genotype×year	**	**	**	**	**	**	**	**	**	**	**	**	**	**
	LSD (1%)	15.61	15.54	2.29	2.04	4.45	1.87	4.26	5.62	397.26	269.92	2.11	2.81	2.33	0.99
	CV (%)	9.98	11.5	15.62	16.14	20.11	8.63	14.43	17.2	39.82	46.82	15.03	27.11	49.70	18.52

PH: Plant height, NB: Number of branches; NU: Number of umbels, NUT: Number of umbellates, NF: Number of fruits, 1000FW: 1000 fruit weight, FY: Fruit yield, LSD: Least significant difference, CV: Coefficient of variation. Values followed by the same letters are not significantly different at P < 0.01 according to the LSD test.

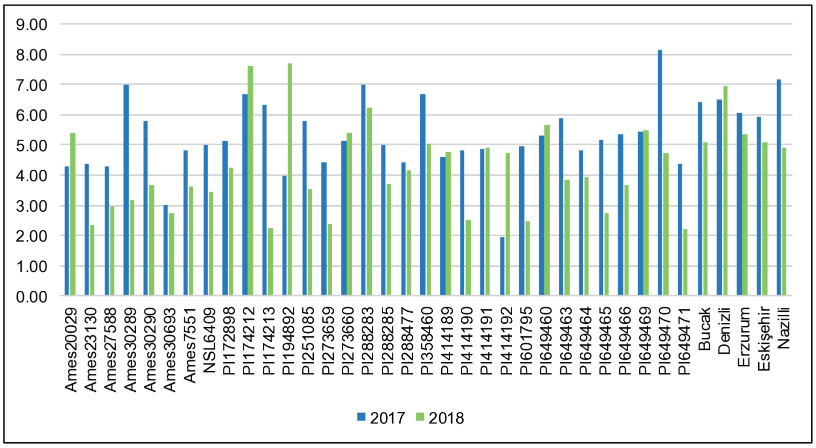

Figure 3. FY and 1000 FW values of fennel genotypes.

characteristics, such as agronomic and quality properties and pest and disease resistance.

The Ames30289, NSL6409 and Ames20029 genotypes, which were found to have the highest mean fruit yields, had similar plant height at harvest maturity, foliage attitude, green color intensity of foliage, main stem height at flowering time, thousand fruit weight and time of beginning harvest time in the UPOV criteria (Table 6). The PI273660, PI288477 and PI649470 genotypes showed differences from other genotypes as being sparse (3) in terms of foliage density. The intensity of green color in the foliage was found to be similar in the US origin genotypes (Ames7551 and PI414190) as light (3), and the very light (1) property for the intensity of green color was not found in any of the genotypes. The Ames20029 (for appearance time of the main umbel) and PI273660 (for thousand fruit weight) genotypes differed from the other genotypes.

Grumolo formation of fennel genotypes was found to be absent (1), and the other 11 properties associated with this property were not recorded. Additionally, male sterility of fennel genotypes was not noted.

Genetic diversity of fennel genotypes

Plant variation is an important issue concerning the conservation of genetic diversity. This genetic diversity in a plant population might be associated with the origin of the species, the breeding method and the variation in plants (Zanella et al., 2011). In this study, high genetic diversity was found among the different origins and local fennel genotypes by using the UPOV criteria (Figure 4).

Genetic diversity was determined among the 37 fennel genotypes in 2018 by using dendrogram analysis. Genetic differences were divided into two main groups (Groups A and B). The first group (Group A) included seven genotypes, and they were separated into two subgroups. The A1 subgroup included only one genotype originating from Ethiopia, Harer (PI273660), and subgroup A2 included six genotypes. Most of the genotypes were grouped into Group B. The second group (Group B) had 30 fennel genotypes, and this group was divided into two subgroups (B1 and B2). Subgroup B1 had 8 genotypes, and the genotypes originated from six different countries. The most crowded group was determined in subgroup B2, with 22 genotypes, and

Table 6. UPOV criteria of fennel genotypes.

Genotypes	LC	LPPFL	PHHM	FA	FD	IGC	HF	LL	LCT	UD	TAMU	TBF	TFW	TBH	GF
Ames20029	3	3	7	1	5	5	5	5	2	3	7	7	3	7	1
Ames23130	5	5	7	5	5	9	7	7	1	5	5	7	3	7	1
Ames27588	3	3	7	1	7	5	3	7	1	3	5	5	3	7	1
Ames30289	3	5	7	1	7	5	5	5	2	3	3	5	3	7	1
Ames30290	7	5	5	3	5	5	3	5	2	5	3	3	3	3	1
Ames30693	7	7	7	1	5	7	3	7	2	5	3	3	3	5	1
Ames7551	5	3	5	3	7	3	3	5	2	3	5	7	3	7	1
NSL6409	7	5	7	1	7	5	5	3	1	7	5	7	3	7	1
PI172898	7	7	5	3	5	7	3	7	2	5	3	3	3	3	1
PI174212	7	7	5	1	7	9	3	7	3	5	3	3	5	3	1
PI174213	3	5	3	3	5	9	3	7	2	5	3	3	3	3	1
PI194892	3	5	5	3	5	5	3	7	2	7	3	3	5	3	1
PI251085	3	5	5	1	7	9	3	7	3	5	3	3	3	3	1
PI273659	5	5	7	3	5	7	3	7	2	7	3	3	5	3	1
PI273660	3	3	7	1	3	7	5	3	3	3	5	5	7	7	1
PI288283	7	7	3	3	5	9	3	5	3	7	3	3	5	3	1
PI288285	3	5	3	1	5	5	3	5	2	3	3	3	3	3	1
PI288477	3	3	5	3	3	9	3	5	3	5	3	3	3	3	1
PI358460	3	3	3	1	5	7	3	5	1	5	3	3	5	3	1
PI414189	7	7	3	1	7	5	3	7	3	7	3	3	5	3	1
PI414190	3	5	3	3	5	3	3	3	2	3	3	5	3	5	1
PI414191	7	5	5	1	7	7	3	7	2	5	3	3	5	3	1
PI414192	3	3	5	1	5	7	3	7	3	7	3	3	5	3	1
PI601795	3	3	7	3	7	5	5	7	1	3	5	5	3	7	1
PI649460	3	3	3	1	7	9	3	7	2	5	3	3	5	3	1
PI649463	3	5	5	3	5	5	3	5	3	3	3	5	3	7	1
PI649464	7	5	3	3	7	7	3	7	2	7	3	3	3	3	1
PI649465	5	5	5	1	5	7	5	5	2	3	3	5	3	7	1
PI649466	7	7	5	3	5	9	3	7	2	7	3	3	3	5	1
PI649469	3	5	3	3	5	9	3	5	3	3	3	3	5	3	1
PI649470	7	7	5	1	3	5	3	7	3	3	3	5	5	5	1
PI649471	7	5	5	3	5	7	3	3	3	3	5	7	3	7	1
Bucak	3	5	3	5	7	7	3	7	2	5	3	3	3	3	1
Denizli	5	5	3	5	7	7	3	7	3	5	3	3	5	3	1
Erzurum	7	5	3	5	7	7	3	7	2	5	3	3	3	3	1
Eskişehir	7	5	3	5	5	7	3	7	2	5	3	3	3	3	1
Nazilli	3	5	3	5	7	7	3	7	2	5	3	3	3	3	1

*The abbreviations are explained in Table 3.

this subgroup included local fennel genotypes (Bucak, Nazilli, Denizli, Eskişehir and Erzurum) and with Turkish-originated fennel genotypes obtained from the USDA (PI172898, PI174212 and PI174213). A strong relationship was observed between Group A and Group B (Figure 4). This relationship can be explained by the fruit yield properties, and the features of these genotypes had similarly high or low values.

Correlation analysis

Correlation analysis was carried out using the means of the examined properties of 2017 and 2018 among the fennel genotypes (Table 7). Generally, 17 correlations were found between the morphological and yield properties of fennel genotypes, and there were both positive and negative correlations. Six highly significant and

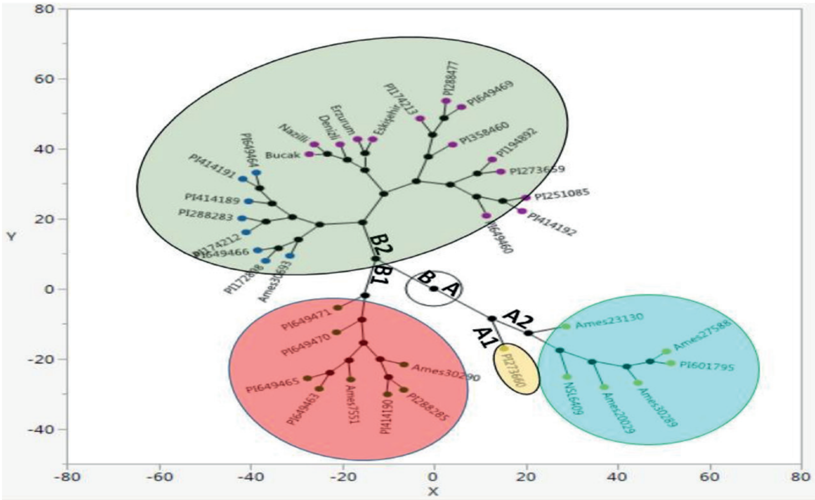

Figure 4. Dendrogram analysis of fennel genotypes with different origins.

significant positive correlations were found. Four highly significant negative correlations and one negative correlation were found. The highest correlation was observed between the NF and FY properties, with r=0.849, followed by the DFT and FLD properties, with r=0.814. The fruit yield per plant in fennel genotypes had a positive correlation with the number of umbels per plant and the fruit number per plant as yield components (Table 7).

Discussion

The prediction of plant genetic diversity has been a focus of plant breeding. This is the initial step for crop development in changing global scenarios of diminishing food security, malnutrition, global warming and climate change (Ali Shah et al., 2018). Variations for can be used for the further improvement of different yield and yield values of fennel. In addition, to improve seed yield in fennel, more emphasis should be given to plant height (cm) and the number of primary branches (Yogi et al., 2013).

Specific and genetically stable external reproductive characteristics that have a similar pattern of variability across morphological traits among genotypes result from interactions between genetic variation and environmental factors (Napoli et al., 2010; Saleha, 2011; Saravanaperumal & Terza,

Table 7. Correlation analysis results among the examined properties for two-year means.

Properties	PH	NB	NU	NUT	DFT	FSD	NF	1000FW	FY
SD	0.19	0.388*	0.021	-0.061	0.338*	0.406*	0.002	-0.275	-0.099
PH		-0.155	-0.436**	0.229	0.428**	0.411*	0.417*	-0.327*	0.271
NB			0.125	0.201	0.082	-0.144	0.12	-0.033	0.181
NU				0.061	-0.449**	-0.401*	0.089	0.44**	0.272
NUT					-0.041	-0.108	0.492**	0.116	0.555**
DFT						0.814**	0.134	-0.446**	-0.041
FSD							0.091	-0.441**	-0.121
NF								-0.31	0.849**
1000FW									0.093

Significant at *5%, **1%; SD: Seedling day, PH: Plant height, NB: Number of branches; NU: Number of umbels, NUT: Number of umbellates, DFT: Days to flowering time, FSD: Fruit setting day, NF: Number of fruits, 1000FW: 1000 fruit weight, FY: Fruit yield

2012). In addition, it has been reported that under the influence of eco-environmental stress, there are considerable variations in the morphological traits within and among geographical provenances, and fruit morphological traits can vary greatly between individuals, even within the same geographical provenance (Yaldiz & Camlica 2019; Yaldiz & Camlica 2021b).

In this study, fennel genotypes of different origins were studied for their variations in morphology, yield values and UPOV criteria diversity. We observed important genetic diversity for all obtained data. The results of the study showed important differences among the fennel genotypes between the two years of evaluation. Our results agree with some researchers who reported that fennel genotypes had a high variation in economic traits among different genotypes and years of cultivation (Lal, 2008).

The examined properties were remarkably influenced by the environmental conditions during the two years of evaluation. In particular, the first year was performed for the adaptation and obtained high fruit yields from the genotypes, and the second year was performed for the more uniform data of the examined properties. For this reason, the genotype × year interaction was revealed to select and suggest the best fennel genotype for all properties, mainly seed yield, by the mean of data in the vegetation years.

The results of the study showed similar findings among the fennel genotypes for the examined properties. There were statistically significant differences among the different genotypes with respect to the examined properties in the two experimental years. The presence of a difference between the highest and lowest values indicated that the genotypes included in the present study were quite diverse. These increases or decreases in properties could be due to adaptation, different genotypic characteristics, temperature and relative humidity and seemed to be reflected in the morphology and consequent yield (Tables 1, 2 and 3). The Ames30289, NSL6409 and Ames20029 genotypes were found to have the highest average fruit yield in both years, and they had similar plant heights at harvest maturity, foliage attitudes, green color intensity of foliage, main stem height in flowering time, thousand fruit weight and time of beginning harvest time in UPOV criteria (Table 2).

In a previous study, Abou El-Nasr et al. (2013) determined the phenotypic and molecular variability of 45 fennel varieties in Egypt. Plant height, number of branches, and fruit yield per plant were reported to be 52.33-132.00 cm, 6.00-14.33 and 42.33-205.00 g, respectively.

Ozyılmaz (2015) reported that the morphological and yield properties of fennel genotypes showed large variations in the Tokat-Kazova conditions from 2012-2014. Morphological and yield properties such as time to 50% seedling (10-32 days), time to 50% flowering (58-71 days), time to 50% fruit setting days (54-102 days), plant height (54.6-105 cm), number of branches (3.40-8.40), number of umbels (15.4-31.5 per plant), number of umbellates (55.2-501.2 per plant), fruit number (364.0-1666 per plant), 1000 fruit yield (3.20-5.53 g) and fruit yield (4.04-22.70 g/per plant) were determined for 33 local fennel genotypes.

Likewise, Kumar et al. (2017) reported that morphological and yield parameters varied in fennel germplasm. Plant height changed by 160-201.80 cm, branch number ranged from 6-9.4, the number of umbellates changed from 28.2 to 58.4 and fruit yield changed by 22.5-35.6 g.

In contrast, Poudineh et al. (2018) conducted a study to determine the genetic and morphological diversity of fennel by using ISSR markers and biplot analysis of ten different genotypes collected from different areas in Iran. They were found to be within the ranges of 40.56-55.80 cm for plant height, 10.93-17.80 for fruit in umbels, 8.83-15.33 for number of umbels, and 46.63-88.45 g for economic yield.

Similarly, genetic variability studies in 60 fennel genotypes according to an augmented block design were carried out in India by Seet et al. (2020). It was reported that the days to 50% flowering, plant height (cm), number of branches per plant, number of umbels per plant, number of umbellets per umbel, number of fruit per umbellets, days to maturity, 1000 fruit weight (g) and fruit yield per plant (g) changed by 92.03-111.03 days, 126.79-182.65 cm, 5.35-11.28 in number, 41.78-112.90 in number, 19.69-36.80 in number, 219.94-233.79 days, 4.65-7.74 g, and 29.53-58.80 g, respectively.

Regarding the various research results, there were some differences between the values of each study. The variability in the number of umbellates in umbels between these findings and previous studies can be explained by the fact that plant density and sparse sowings affect the umbellate number of fennel (Ozkan & Gurbuz, 2000). Furthermore, Lefort et al. (2021) reported that the flowering stage is critical for producing fennel fruits and that they vary depending on climatic factors.

Fruit yield was affected by the number of fruits and umbellates; increasing the number of fruits and umbellates positively affected the fruit yield among the fennel genotypes. In addition, our findings were consistent with those of Heywood (2002), who reported that different genotypes exhibited genetic variation that may influence phenotypic traits and, consequently, fruit yield. The fruit yield of fennel genotypes in this study was generally within the usual range reported in a previous study (Abou-El-Nasr et al., 2013); however, Seet et al. (2020) and Kumar et al. (2017) reported higher results than our findings. Differences in the fennel fruit yield between this study and others could be attributed to genotypic differences, growing conditions or environmental factors.

Correlation analysis was performed by Ozyılmaz (2015) among the fennel genotypes in Turkey. It was reported that the number of fruits was correlated with fruit yield. In our study, it was noted that fruit yield was also correlated with the number of umbellates in umbels.

The results of dendrogram analysis showed that there was no integration consistency between the geographical similarity and UPOV criteria of fennel genotypes. It was reported that the genetic diversity was not necessarily interrelated with the geographical variations (Meena et al., 2010; Yaldiz et al., 2018; Camlica & Yaldiz, 2019).

Conclusions

In this study, different fennel genotypes were evaluated to explain their use in plant breeding programs for further crop improvement. In the first year, 43 fennel genotypes were sown, and 32 genotypes were adapted among these genotypes. Selected genotypes were sown again depending on their adaptation and yield criteria in the second year. These fennel genotypes had a high polymorphism depending on morphology, yield and UPOV criteria. The Ames30289 genotype originating from Tunisia was found to be a superior genotype, with a high seed yield based on two successive years. Dendrogram analysis showed a wide variation depending on 15 UPOV criteria and divided the two main groups. Local genotypes were found in the same main group (Group B) and same subgroup (Group B2). Correlation analysis revealed that the greatest correlation was noted between the plant height and the number of branches per plant, time to 50% of flowering, days to fruit setting, fruit number, and weight of 1000 fruits, either positively or negatively. As a result of these studies, the best genotypes, Ames30289, NSL6409 and Ames20029, will be selected as parental candidates for a fennel breeding program.

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Resumen

G. Yaldiz, y M. Camlica. 2022. Mejora genética de genotipos de hinojo de diferentes orígenes (*Foeniculum vulgare* L.) utilizando parámetros morfológicos y de rendimiento. Int. J. Agric. Nat. Resour. 97-111. El hinojo (*Foeniculum vulgare* L.) es una planta especia de renombre y se utiliza como planta medicinal industrial debido a sus aplicaciones farmacéuticas y alimentarias, exhibiendo una amplia gama de variaciones genéticas dependiendo de las propiedades morfológicas y de rendimiento. Junto con el estudio actual, se utilizaron treinta y dos genotipos de hinojo diferentes y cinco genotipos locales de Turquía para determinar las propiedades morfológicas y de rendimiento en 2017 y 2018. Se observó un amplio rango de variación en la altura de la planta (39,22-129,60 cm), de 1000 frutos (1,92-7,70 g) y rendimiento de frutos (0,12-8,68 g). Como se deduce de informes anteriores y de los hallazgos actuales del estudio, esos parámetros relevantes podrían considerarse con fines de mejoramiento. Para visualizar o aclarar los hallazgos, se construyó un dendrograma para revelar la variabilidad genética con respecto a las propiedades morfológicas y de rendimiento de los genotipos de hinojo. El dendrograma reveló que los genotipos de diferentes orígenes ocurrieron en diferentes grupos, pero los genotipos locales recolectados de Turquía ocurrieron en el mismo grupo y subgrupo. Además, se llevó a cabo un análisis de correlación para revelar las relaciones entre los parámetros agronómicos relevantes. De esos coeficientes de correlación, se observó un alto coeficiente de correlación entre el número de frutos y el rendimiento de frutos (r =0.849). En general, los hallazgos del estudio revelaron una notable variación genética relacionada con el rendimiento de la fruta y otras características agronómicas relevantes para los genotipos de hinojo, lo que sugiere que esta notable variación podría usarse para seleccionar genotipos superiores en los programas de mejoramiento. De los genotipos analizados, Ames30289 fue el mejor genotipo debido al mayor rendimiento de frutos según dos años sucesivos. En consecuencia, los hallazgos pueden considerarse información útil para los criadores, investigadores y agricultores de hinojo en Turquía u otros países.

Palabras clave: Análisis de dendogramas, diseño aumentado, diversidad genética, hinojo.

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