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Research Article

Morphological Characterization and Selection in Some Summer Squash (*Cucurbita pepo* L.) Genotypes

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Abstract: This study was carried out to determine stage progression and specific plant and fruit characteristics in purposefully created summer squash genotypes. In this study, which was carried out in 2019, 59 squash genotypes were assessed with 24 morphological measurements and observations involving plant and fruit characteristics, and one-generation advancement was achieved. Cluster and PCA were implemented to determine the relationship between genotypes determined at the end of single plant selection. A dendrogram was constructed to assess the morphological similarities between the genotypes. In this respect, four main groups and 12 subgroups were determined in the cluster analysis performed among squash genotypes based on 24 morphological variables, while the 10 PC axis explained 94.3% of the total variation in the PCA. When the variance values of the principal component axis were examined, it was seen that the first principal component axis explained 28.8% of the total variation, the second principal component axis explained 26% of the variation, and the third principal component axis explained 11.2% of the total variation. Principal component analyses revealed that (i) 66% of the qualitative (neck in unripe fruit, curving of the neck in unripe fruit, mottling in unripe fruit, and type of mottling in unripe fruit) variation was explained by the first three components. At the end of the study, the phenotypic diversity that exists in this core collection provides valuable information to improve agronomic traits in the summer squash breeding program.

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1. Introduction

Cucurbita pepo L., which belongs to the *Cucurbitaceae* family, is an important species with a high economic value. The total global production of summer squash is 27 962 481 tons (FAO,2022). In Türkiye, 609 622 tons of summer squash are produced, according to 2021 data (TÜİK, 2022). Summer squash can be grown throughout the world and in our country with no problems due to the suitability of ecological conditions, its economic value, and its place in the diet. Summer squash is widely grown for different purposes almost in all regions of Türkiye, especially in the coastal areas of the Mediterranean and Aegean regions (Vural et al., 2000). However, productivity and quality in squash farming require good cultivation techniques as well as a high genetic performance. For this purpose, high productivity and quality are crucial in commercial varieties, in addition to resistance to various diseases and pests. Today, hybrid varieties are used almost exclusively in commercially cultivated summer squash in Türkiye (Kesici et al., 2004; Nacar et al., 2011).

F1 hybrid variety breeding is one of today's most commonly practiced breeding methods. The first step of hybrid squash breeding is obtaining well-defined inbred lines and identifying their characteristics. Accordingly, the formation of a seed collection rich in genetic variation at the beginning of breeding, the knowledge of morphological variations within the gene pool, and the distribution of this variation provide significant opportunities to the breeder. Numerous researchers in our country and around the world performed various characterizations on *Cucurbitaceae* family and *C. pepo* species according to the fruit and plant characteristics, and the existing morphological variations were identified in detail (Paris, 2001; Sarı et al., 2008; Méndez-López et al., 2010; Seymen, 2010; Nacar et al., 2011; Nacar, 2014; Türkmen et al., 2016; Aslan et al., 2019; Çetin et al., 2019; Seymen, 2020; Kayak and Türkmen, 2021; Kumar et al., 2022).

Multivariate analysis techniques are used to evaluate the data obtained from qualified gene pools established in breeding programs. Morphological characteristics must be evaluated from multiple aspects to detect variability observed in specific characteristics (Tan, 2005; Alkan, 2011). The data obtained at the end of the characterization studies are used in cluster analysis and principal component analysis, which easily shows similarities and groupings of genotypes (Karaağaç and Balkaya, 2010; Karaağaç, 2013). This study aimed to identify the morphological characteristics of the genetic sources of squash according to the criteria of the UPOV (TG/119/3). Convention, determine the current variation level within the population and explain in detail from which characteristics the factors creating the variation emerge. Another aim was to create a good gene pool by including the selected genotypes in the prospective breeding studies.

2. Material and Methods

The study was carried out in the R&D greenhouse of Beta Tohumculuk company. The plant material consisted of 59 summer squash genotypes selected from the previous year's breeding studies and left for open pollination. During the choosing, the genetic expansion (homogeneous/heterogeneity) within the gene collection was taken into consideration. For the trial, two to three seeds per seedbed were planted directly in the soil on 25 October 2019 with a row spacing and intra-row spacing of 90 × 60 cm in a way that five squash seedlings would be obtained from each squash genotype. When seedlings with two or three actual leaves emerged for genotypes in which seed emergence occurred, the number of plants in each seedbed was reduced to one. Irrigation and fertilization were performed with drip irrigation. Fertilization containing magnesium sulphate, MAP (mono ammonium phosphate), humic acid, and microelements were applied until the fruit formation period. A potassium-based fertilization program was applied to ensure nitrogen-phosphorus-potassium balance after the fruit was formed and towards fruit ripening. The designated morphological parameters were evaluated in each plant with seed emergence, and self-pollination was performed to obtain an advanced stage of breeding in the existing genotypes for the selection breeding of squash (Upov, Document No: TG/119/3). Measurements and observations were performed in squash genotypes. The measurements and observations involve growth habit, branching, the degree of branching, the attitude of petioles (excluding lower external leaves), green color on the stem, tendrils on the stem, incisions on leaf blade, the green color of the upper surface of leaf blade, leaf blade marbling, leaf blade surface area, petiole length, petiole thickness, the shape of the cross-section of petioles, and prickliness of petioles. The observations regarding fruits are related to the neck in unripe fruit, curving of the neck in unripe fruit, the number of major colors in unripe fruit, major colors in unripe fruit, the intensity of major colors in unripe fruit, glossiness in unripe fruit, mottling in unripe fruit, the type of mottling in unripe fruit, the general shape of the fruit, and major color in fully-developed fruit (UPOV, 2006).

In recent years, it has been possible to determine the level of variation existing in populations through taxonomic classification methods called multivariate analyses (Karaağaç, 2006; Balkaya et al., 2010; Karaağaç and Balkaya, 2010; Kobal Bekar et al., 2019). The study used Minitab (16.00) statistical software for cluster and principal component analysis (PCA), which shows the similarities and differences between squash genotypes (MINITAB, 2016).

3. Results and Discussion

Table 1 shows the plant observations investigated in the study, and Table 2 presents fruit observations. All the plants in the study were observed to be semi-creeping regarding growth habit and showed branching. Their degree of branching was identified as weak in 38 genotypes, medium in 14 genotypes, and strong in seven genotypes. In terms of tendril development on the stem, 39 genotypes had no tendrils or underdeveloped tendrils, whereas 20 genotypes had well-developed tendrils. The stem color was light and dark green in only two plants, while 27 genotypes had only green, and 30 plants had only dark green color.

According to the observations about leaves, the attitude of petioles was identified as erect in three genotypes, semi-erect in 35 genotypes, and prostrate in 21 genotypes. The petiole length was identified as short in 10 genotypes, long in 19 genotypes, and medium in 30 genotypes. The petiole thickness was detected as thin in 24 genotypes, thick in four genotypes, and medium in 31 genotypes. Regarding prickliness in petioles, 16 genotypes showed a medium level, while there were a few prickles in 43 genotypes. The shape of the cross-section of petioles was identified as circular in all the genotypes. According to the observations of leaf blades, marbling in leaf blades was observed in none of the genotypes. Incisions on leaf blade were found in 30 genotypes to be minimum/very slight, 23 genotypes as slight, and six genotypes as medium. The surface areas of leaf blades were identified as small (three genotypes), medium (17 genotypes), large (26 genotypes), and very large (13 genotypes). Finally, the green color of the upper surface of the leaf blade was identified as light in only five genotypes, whereas 33 genotypes had medium, and 21 genotypes had dark green color.

According to the observations about the neck in unripe fruit, six genotypes did not have a neck in the fruit, while the neck existed in 53 genotypes. Curving was detected in the neck in 17 genotypes, but 42 did not have to curve. The number of major colors in unripe fruit was identified as one in all the genotypes, and the major color in unripe fruit was identified as yellow in only one genotype and green in the rest. When the intensity of major colors and the glossiness in unripe fruit were investigated, the color intensity was identified as light in 43 genotypes, medium in 10 genotypes, and dark in six genotypes. On the other hand, the glossiness was slight in 46 genotypes and medium in 13 genotypes. Significant differences were found in the study in terms of the general shape of the fruit, mottling, and major color in fully-developed fruit. When the parameters of the general shape of the fruit were studied, 10 genotypes were ovate, seven genotypes were cylindrical, one genotype was pyriform, and 41 genotypes were elliptic. As for mottling in fruit, mottling was not detected in the fruit of 50 genotypes, whereas mottling existed in nine genotypes. Among these nine fruits, the type of mottling was diffused in five genotypes and diffused in linear bands in four genotypes. Finally, when the major color in the fully-grown fruit was investigated, eight genotypes were identified as cream, one genotype as orange, 10 as green, and 40 as yellow. According to the study results, all the parameters except growth habit, branching, the shape of the cross-section in the petiole, marbling in the leaf blade, and the number of major colors in unripe fruit were effective in determining the level of variation. In this study, which aimed to create a good gene pool by including the selected genotypes in the prospective breeding studies, it is expected that the mean of the population will increase with respect to specific characteristics when selection is implemented in a population. The targeted outcomes were mostly achieved in the characteristics investigated with regard to the wide variation we obtained through selection, which significantly supports the literature (Özbakır et al., 2011; Nacar, 2014; Çetin et al., 2019; Kayak and Türkmen, 2021).

Table 1. Observations about the plant investigated in the study

Observations	G.H	G.B	D.B	T.S	G.C.S	A.P	P.L	P.T	P.P	S.C.S.P	L.B.M	I.L.B	L.B.S.A	G.C.U.L.B
1	2	9	3	1	1	5	5	5	3	1	1	3	5	7
2	2	9	3	1	3	7	5	3	3	1	1	3	3	7
3	2	9	3	1	2	7	5	5	3	1	1	1	7	5
4	2	9	3	1	2	5	5	5	3	1	1	3	5	5
5	2	9	3	1	2	7	5	3	3	1	1	1	5	3
6	2	9	3	1	1	5	3	3	5	1	1	1	7	7
7	2	9	3	1	1	5	5	5	3	1	1	1	7	7
8	2	9	3	1	2	7	5	5	3	1	1	3	7	7
9	2	9	5	2	2	5	5	5	3	1	1	3	5	7
10	2	9	3	1	1	5	3	3	3	1	1	3	7	5
11	2	9	3	1	1	5	3	5	3	1	1	3	7	7
12	2	9	3	1	1	5	7	5	5	1	1	1	7	5
13	2	9	5	2	2	5	5	7	3	1	1	1	9	5
14	2	9	3	1	1	7	5	3	3	1	1	1	5	5
15	2	9	5	2	1	5	5	5	3	1	1	1	7	7
16	2	9	3	1	2	3	5	5	3	1	1	5	7	5
17	2	9	5	2	1	5	7	5	3	1	1	3	7	5
18	2	9	3	1	2	5	5	3	3	1	1	1	7	7
19	2	9	5	2	2	5	3	5	3	1	1	1	5	5
20	2	9	3	1	1	5	5	3	5	1	1	3	5	5
21	2	9	3	1	2	7	5	5	3	1	1	3	7	5
22	2	9	5	2	1	7	7	3	3	1	1	3	5	7
23	2	9	3	1	2	5	7	5	3	1	1	5	7	5
24	2	9	3	1	1	5	7	3	3	1	1	1	5	5
25	2	9	3	1	2	5	5	3	5	1	1	5	7	5
26	2	9	5	2	1	7	5	5	3	1	1	3	5	5
27	2	9	5	2	2	5	5	5	5	1	1	1	7	5
28	2	9	3	1	2	5	7	3	3	1	1	7	7	7
29	2	9	3	1	2	3	5	3	3	1	1	1	7	5
30	2	9	7	2	1	5	7	5	5	1	1	5	9	7
31	2	9	3	1	2	5	3	3	5	1	1	1	3	3
32	2	9	3	1	2	5	7	5	3	1	1	1	7	5
33	2	9	3	1	1	7	7	3	5	1	1	1	5	5
34	2	9	7	2	2	5	7	5	5	1	1	3	7	7
35	2	9	1	1	2	5	3	3	3	1	1	5	5	3
36	2	9	3	1	1	7	5	5	3	1	1	1	7	7
37	2	9	3	1	2	7	7	3	5	1	1	3	5	5
38	2	9	1	1	2	3	3	5	3	1	1	1	5	5
39	2	9	3	1	1	7	5	3	3	1	1	3	5	5
40	2	9	3	1	1	5	5	3	5	1	1	3	7	5
41	2	9	3	1	3	7	7	7	3	1	1	5	9	5
42	2	9	5	2	1	5	7	5	3	1	1	1	9	3
43	2	9	5	2	2	7	7	7	5	1	1	3	9	5
44	2	9	3	1	2	7	7	3	3	1	1	1	5	5
45	2	9	3	1	2	5	5	3	3	1	1	1	9	5
46	2	9	7	2	1	5	5	5	3	1	1	3	9	5
47	2	9	3	1	1	7	5	7	3	1	1	3	9	5
48	2	9	7	2	1	5	7	5	5	1	1	1	9	7
49	2	9	5	2	1	7	5	5	5	1	1	3	9	5
50	2	9	7	2	2	5	3	5	3	1	1	1	7	7
51	2	9	3	1	2	5	3	5	3	1	1	1	7	5
52	2	9	5	2	1	7	7	3	3	1	1	3	7	7
53	2	9	3	1	1	7	3	3	3	1	1	1	3	7
54	2	9	3	1	1	5	7	3	5	1	1	3	9	5
55	2	9	7	2	2	5	5	5	3	1	1	1	9	7
56	2	9	7	2	1	7	5	5	3	1	1	3	9	7
57	2	9	3	1	2	5	5	5	3	1	1	1	7	5
58	2	9	5	2	2	7	5	5	3	1	1	1	7	7
59	2	9	5	2	3	5	7	3	5	1	1	1	5	3

Explanation: G.H: Growth habit (bush(1), semi-trailing(2), trailing(3)), G.B: Growth branching (absent(1), present(9)), D.B: Degree of branching (very weak (1), medium(5), strong(7)), T.S: Tendrils on the stem (absent to rudimentary(1), well developed(2)), G.C.S: Green color on the stem (light(1), dark(2), light and dark(3)), A.P: Attitude of petioles (erect(3), semi erect(5), horizontal(7)), P.L: Petiole length (short(3), medium(5), long(7)), P.T: Petiole thickness (thin(3), medium(5), thick(7)), P.P: Prickliness of petioles (very few(3), medium(5), many(7)), S.C.S.P: Shape of the cross-section of petioles (circular(1), triangular(2)), L.B.M: Leaf blade marbling (absent(1), present(9)), I.L.B: Incisions on leaf blade (wery weak(1), weak(3), medium(5), strong(7), very strong(9)), L.B.S.A: Leaf blade surface area (very small(1), small(3), medium(5), large(7), very large(9)) and G.C.U.L.B: Green color of the upper surface of leaf blade (light(3), medium(5), dark(7)).

Table 2. Characteristics of the fruit investigated in the study

Observations	N.U.F	C.N.U.F	N.M.C.U.F	M.C.U.F	I.M.C.U.F	G.U.F	G.S.F	M.U.F	T.M.U.F	M.C.D.F
1	1	1	1	4	3	5	5	1	0	3
2	1	1	1	4	5	3	5	9	5	5
3	9	9	1	4	3	3	7	1	0	3
4	9	1	1	4	5	3	5	9	7	5
5	9	1	1	4	5	3	5	9	7	5
6	9	9	1	2	3	3	5	1	0	3
7	9	9	1	4	3	3	5	1	0	3
8	9	9	1	4	3	3	7	1	0	3
9	9	1	1	4	5	5	5	1	0	3
10	9	1	1	4	3	3	5	1	0	3
11	9	1	1	4	5	3	7	1	0	2
12	9	1	1	4	3	3	5	1	0	3
13	9	1	1	4	7	5	5	9	5	5
14	9	1	1	4	3	3	5	1	0	3
15	9	1	1	4	3	3	2	1	0	2
16	9	9	1	4	7	5	5	1	0	5
17	9	1	1	4	3	3	2	1	0	3
18	9	9	1	4	5	5	5	9	5	3
19	9	1	1	4	3	3	5	1	0	3
20	9	1	1	4	3	3	5	1	0	3
21	9	9	1	4	7	5	7	1	0	5
22	9	1	1	4	3	3	5	1	0	3
23	9	1	1	4	7	3	5	9	5	5
24	9	1	1	4	3	3	9	1	0	3
25	9	1	1	4	3	3	2	1	0	3
26	9	1	1	4	3	3	5	1	0	3
27	9	9	1	4	3	3	5	1	0	3
28	9	1	1	4	3	5	5	1	0	2
29	1	1	1	4	3	3	2	1	0	3
30	9	1	1	4	3	3	2	1	0	3
31	9	1	1	4	3	3	5	1	0	2
32	9	1	1	4	3	5	2	1	0	3
33	1	1	1	4	3	3	5	1	0	2
34	9	1	1	4	3	3	2	1	0	3
35	9	1	1	4	3	3	5	1	0	2
36	9	1	1	4	5	3	5	1	0	3
37	9	1	1	4	3	5	5	1	0	4
38	9	9	1	4	3	3	5	1	0	2
39	9	1	1	4	3	3	5	1	0	3
40	9	1	1	4	3	3	5	1	0	3
41	9	1	1	4	7	5	5	1	0	5
42	9	1	1	4	3	3	2	1	0	3
43	9	1	1	4	3	3	5	1	0	3
44	9	1	1	4	3	3	5	1	0	3
45	9	9	1	4	3	3	5	1	0	3
46	9	9	1	4	3	3	7	1	0	3
47	9	9	1	4	3	3	5	1	0	3
48	9	9	1	4	3	3	7	1	0	3
49	1	1	1	4	3	3	5	1	0	3
50	9	1	1	4	3	3	5	1	0	3
51	9	9	1	4	7	5	2	9	5	5
52	1	1	1	4	3	3	5	1	0	3
53	9	9	1	4	3	3	5	1	0	2
54	9	1	1	4	3	3	7	1	0	3
55	9	1	1	4	5	5	5	1	0	3
56	9	1	1	4	3	5	2	1	0	3
57	9	1	1	4	5	3	5	9	7	3
58	9	9	1	4	5	3	5	9	7	5
59	9	9	1	4	3	3	5	1	0	3

Explanation: N.U.F: Neck in unripe fruit(absent(1), present(9)), C.N.U.F: Curving of the neck in unripe fruit (absent(1), present(9)), N.M.C.U.F: Number of major colors in unripe fruit (one(1), two(2), three(3)), M.C.U.F: Major colors in unripe fruit (whitish(1), yellow(2), orange(3), green(4), partly white and partly yellow(5), partly green and partly yellow(6)), I.M.C.U.F: Intensity of major colors in unripe fruit (light(3), medium(5), dark(7)), G.U.F: Glossiness in unripe fruit (light(3), medium(5), strong(7)), G.S.F: General shape of the fruit (scallop-shaped(1), ovate(2), globular(3), elliptical(5), cylindrical(7), club shaped(8), pear shaped(9)), M.U.F: Mottling in unripe fruit (absent(1), present(9)), T.M.U.F: Type of mottling in unripe fruit (sparse(3), sparse pieced(5), sparse bands(7), sparse pieced and bands(9)), and M.C.D.F: Major color in fully-developed fruit (whitish(1), cream(2), yellow(3), orange(4), green(5)).

Cluster and principal component analyses (PCA) were conducted to determine the relationships between the populations and obtain information about the usefulness of the relevant plant and fruit characteristics in identifying the groups. According to the cluster analysis, the genotypes were grouped under four main groups and 12 subgroups. There were five genotypes in Group 1, seven genotypes in Group 2, six genotypes in Group 3, five genotypes in Group 4, five genotypes in Group 5, nine genotypes in Group 6, six genotypes in Group 7, three genotypes in Group 8, six genotypes in Group 9, 10 genotypes in Group 10, two genotypes in Group 11, and two genotypes in Group 12 (Figure 1).

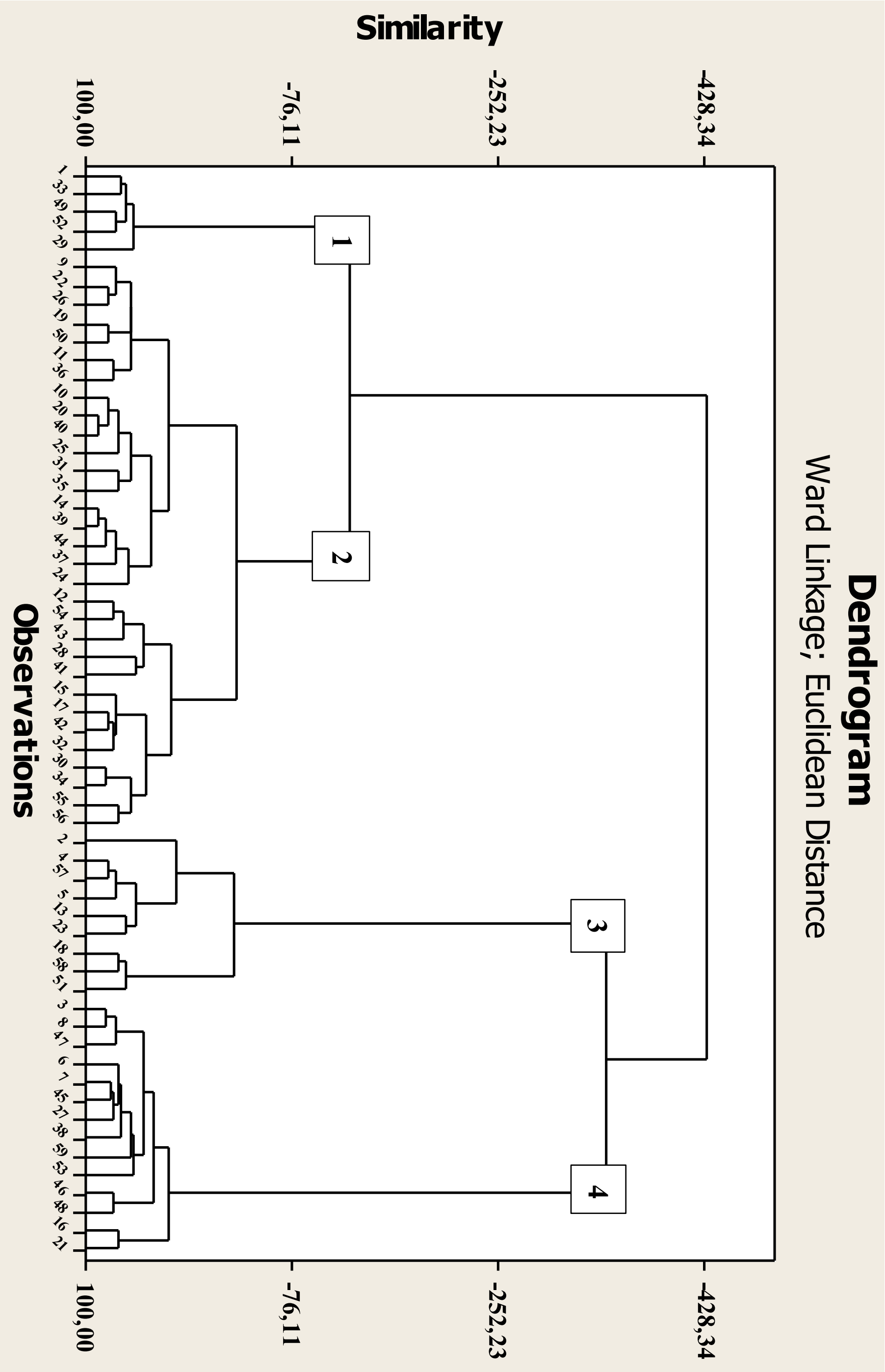

Figure 1: Dendrogram obtained at the end of the cluster analysis performed with morphological data.

At the end of the principal component analysis, 10 independent principal component axes were obtained between the plants (Table 3). According to the principal component analysis results, these 10 principal component axes represent 94.3% of the total variation in the squash population (Table 3). The literature has reported that principal component axes with eigenvalues greater than 1 in PCA are highly reliable (Özdamar, 2004; Balkaya et al., 2010; Kanal and Balkaya, 2021). The study revealed that the coefficients of the eigenvalues of the first 10 principal components varied between 15.15 and 1.023 (Table 3). When the variance values of the principal component axis were examined, it was seen that the first principal component axis explained 28.8% of the total variation, the second principal component axis explained 26% of the variation, and the third principal component axis explained 11.2% of the total variation. Principal component analyses revealed that (i) 66% of the qualitative (neck in unripe fruit, curving of the neck in unripe fruit, mottling in unripe fruit, and type of mottling in unripe fruit) variation was explained by the first three components. Moreover, the genotypes were grouped under four groups in the principal component analysis (Figure 2). Numerous studies in the literature have been carried out to determine the existing variation levels of populations of *C. Pepo* L.. In their study carried out with 46 C. pepo genotypes selected from 5000 genotypes, Méndez-López et al. (2010) reported that three groups were identified with respect to morphological characteristics. The study by Nacar et al. (2011) on *Cucurbita pepo* L. squash lines established that 14 cluster groups were formed. In our study, 12 different cluster groups were identified. In the cluster analysis performed based on 21 morphological variables in squash, Balkaya et al. (2010) found that 10 different groups were created, and the first five principal component axes explained 65.0% of the total variation between the populations. Mladenoviç et al. (2014), who aimed to determine the morphological characterization in 20 squash genotypes, reported at the end of the PCA that these genotypes were divided into five groups on the PCA axis. Martins et al. (2015) identified 54 *C. pepo* genotypes, 32 *C. maxima* genotypes, and 21 *C. moschata* genotypes collected from the central and northern parts of Portugal based on 20 morphological characteristics. According to their study, three species clearly diverged from each other in the PCA, and the total variation was 52.5%. When the data of the present study and the data from the literature are taken into consideration, it can be understood that the existence of variation was sufficient.

Table 3: Factor groups based on the principal component analysis of the characteristics examined in the study and the corresponding principal component axes

	Principal Component Axes									
Eigenvalue	15.146	13.662	5.859	4.38	2.681	2.088	1.866	1.591	1.23	1.023
Variance value	0.288	0.26	0.112	0.083	0.051	0.04	0.036	0.03	0.023	0.019
Cumulative value	0.288	0.549	0.66	0.744	0.795	0.835	0.87	0.9	0.924	0.943
	Factor Coefficients									
Features	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**	**PC7**	**PC8**	**PC9**	**PC10**
G.H	0	0	0	0	0	0	0	0	0	0
G.B	0	0	0	0	0	0	0	0	0	0
D.B	-0.059	0.043	0.171	-0.394	-0.366	-0.241	-0.205	-0.255	-0.087	-0.574
T.S	-0.02	0.008	0.047	-0.125	-0.125	-0.087	-0.049	-0.067	0.014	-0.214
G.C.S	0.054	-0.034	0.008	0.011	0.057	0.084	0.047	0.004	0.114	-0.21
A.P	-0.014	-0.029	-0.062	0	0.153	-0.419	-0.064	-0.193	0.485	0.134
P.L	-0.099	-0.045	0.071	-0.242	0.204	-0.369	0.597	-0.226	0.263	0.081
P.T	0.056	0.012	0.2	-0.325	0.047	-0.003	-0.232	0.307	0.251	-0.154
P.P	-0.058	0.04	-0.009	-0.022	-0.055	-0.084	0.308	-0.055	-0.207	-0.162
S.CS.P	0	0	0	0	0	0	0	0	0	0
L.B.M	0	0	0	0	0	0	0	0	0	0
I.L.B	-0.101	-0.046	0.114	-0.12	0.612	0.328	0.031	-0.471	-0.335	-0.197
L.B.S.S	0.018	0.086	0.273	-0.606	0.062	-0.042	0.134	0.363	-0.325	0.397
G.C.U.L.B	0.003	0.03	-0.049	-0.213	-0.026	-0.096	-0.523	-0.487	-0.039	0.471
N.U.F	0.155	0.173	0.872	0.392	-0.045	-0.067	0.002	-0.123	0.027	0.086
C.N.U.F	0.678	0.663	-0.215	-0.094	0.019	0.069	0.121	-0.13	0.037	-0.047
N.M.C.U.F	0	0	0	0	0	0	0	0	0	0
M.C.U.F	-0.007	-0.014	0.008	-0.008	0.015	-0.013	0.008	0.008	0.035	-0.049
I.M.C.U.F	0.186	-0.146	0.104	-0.104	0.338	0.183	-0.21	0.208	0.264	-0.139
G.U.F	0.026	-0.02	0.054	-0.101	0.169	0.191	-0.12	0	0.272	0.022
G.S.F	0.075	0.092	-0.092	0.211	0.451	-0.631	-0.265	0.255	-0.356	-0.152
M.U.F	0.526	-0.549	-0.003	-0.031	-0.084	-0.049	0.053	-0.089	-0.131	0.041
T.M.U.F	0.387	-0.411	0.013	0.007	-0.092	-0.096	0.058	-0.062	-0.123	0.022
M.C.D.F	0.122	-0.105	0.038	-0.09	0.186	0.018	0.047	0.041	0.209	-0.176

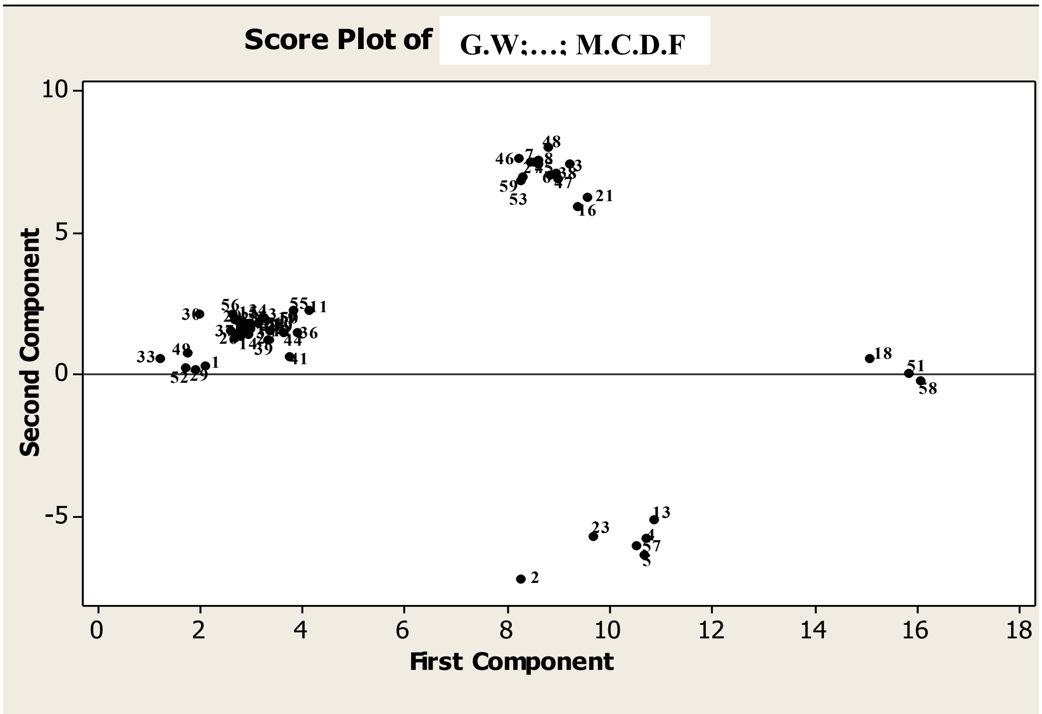

Figure 2: Two-dimensional graphic obtained through the principal component analysis performed with morphological data.

4. Conclusion

The production and consumption of summer squash have gradually increased in recent years. In this study, we identified the accession of Summer squash exhibited the variation in qualitative and quantitative characteristics to develop an F1 hybrid variety of squash, which is also a suitable alternative crop for greenhouse cultivation. Cluster and principal component analyses (PCA) were conducted to determine the relationships between the populations and obtain information about the usefulness of the relevant plant and fruit characteristics in identifying the groups. According to the cluster analysis, the genotypes were grouped under four main groups and 12 subgroups.PCA identified neck in unripe fruit, curving of the neck in unripe fruit, mottling in unripe fruit, and type of mottling in unripe fruit as important traits for variation. Based on agro-morphological traits and cluster analysis, accessions were categorized into four groups. This phenotypic variation observed for agro-morphological traits revealed that agronomic traits can be improved by a selection program. In addition, an assessment of phenotypic variability among the accessions would be useful for germplasm management.

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