

MORPHOLOGICAL CHARACTERIZATION OF SPONGE GOURD (*Luffa aegyptiaca* Mill.) GENOTYPES FROM THE EASTERN MEDITERRANEAN REGION OF TURKEY

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Having wide range of genetic resources, Hatay is the largest sponge gourd producer of province of Turkey. This study was conducted to determine the status and morphological diversity of the livestock breeding with a field survey in the districts of Hatay Province. As a result of the survey, 34 genotypes were collected that thought to be morphologically different. When the distributions of genotypes were examined, the genotypes were selected from Arsuz (5 genotypes), Defne (7 genotypes), Samandağ (1 genotypes), Antakya (5 genotypes), Dört Yol (6 genotypes), Yayladağı (4 genotypes), Altınözü (4 genotypes), Payas (1 genotypes) and Erzin (1 genotypes). Two genotypes ('31 AN 03' and '31 AL 04') from which the seeds did not germinate were extracted from the morphological characterization studies. Thirty-two genotypes selected from Hatay with 3 genotypes obtained from Adana, South Korea, and China in total of 35 genotypes were compared in terms of 49 different morphological characteristics. Variations between the genotypes were not identified for the observations made on these 49 features regarding cotyledon color, stem shape, tendrils, leaf margin, growth habit, sex type and peduncle separation from fruit. As a result of analysis of basic components and cluster analysis based on morphological characterization features, genotypes were included in six different groups. However, the effect of the districts on which genotypes were collected on this grouping could not be determined.

Keywords Cucurbits, Genetic diversity, Morphologic characterization, Sponge gourd

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INTRODUCTION

The *Cucurbitaceae* family, which includes the *Luffa* sub-family, consists of approximately 130 genera and 800 species, according to the last taxonomic classification (JEFFREY, 1990). *Cucurbitaceae*, which are used for different purposes especially in the human diet, is a very important family that includes both old and new world species (BISOGNIN, 2002). The most important cultivated *Cucurbitaceae* species are *Cucurbita*, *Cucumis*, *Citrullus*, *Lagenaria*, *Luffa*, and *Sechium* of the *Cucurbitaceae* subfamily (WHITAKER and DAVIS, 1962).

In addition to high commercial value and production volume species such as watermelon, melon, cucumber, and squash, many species within the *Cucurbitaceae* family are used as vegetables in local cuisine such as bottle gourd (*Lagenaria*), sponge gourd (*Luffa*), ash gourd (*Benincasa hispida*), chayote (*Sechium edule*), fluted gourd (*Telfairia occidentalis*), kiwano (*Cucumis metuliferus*), white melon (*Cucumeropsis mannii*), and bitter melon (*Momordica charantia*). Fruits of the *Cucurbitaceae* family can be consumed unripe (cucumber) and ripe (melon). Also, fruits can be cooked and consumed in the form of pickles, canned food, and jam. In addition to fruits, seeds (*Telfairia*), flowers (zucchini) and roots (*Sechium*) can be used in the human diet.

Especially with the determination that some species have a higher resistance to soil-borne diseases and pests, grafting applications have gained great importance in *Cucurbitaceae* cultivation. Some species can be used as a rootstock in melon and cucumber cultivation due to their different characteristics. The compatibility of the species to be used as rootstock with the graft and rooting characteristics are important. For this purpose, *Cucurbita*, *Lagenaria*, *Luffa* and *Benincasa* species are used (YETİŞİR and SARI, 2004).

Sponge gourd is an annual, monoic, yellow-flowered and self-clinging species. In Asia, varieties suitable for consumption have been developed especially as vegetables especially in China and India. Within this diversity, the size and thickness of the fruit vary greatly. The length of unripe fruit varies between 33 and 84 cm (12 days after flowering), while the length of ripe fruit varies between 39 and 102 cm (60 days after flowering), depending on the variety (ZHANG *et al.*, 2007).

Anatolia is an important gene center located at the intersection of the Mediterranean and the Near East gene centers and has a very important role in the emergence of grains and horticultural plants (VAVILOV, 1926). Among the many plant species found in the natural flora, superior ones are selected, cultured, or protected. However, there are still untouched natural areas with many extincting or endangered fruit and vegetable species. In these valuable genetic resources of Anatolia, sponge gourd is one of these species rapidly extincting because of the reasons such as monoculture and consumption of the wild genotypes.

Hatay Province is the largest producer of sponge gourd in Turkey, known as having a wide range of genetic resources of sponge gourd from ancient times. However, these genetic sources have been lost in recent decades. In addition to being a valuable rootstock for *Cucurbitaceae*, its use as a natural sponge for humans and its consumption in a small amount as a vegetable, it is very important to investigate and identify the genotypes of the sponge gourd which are among the important genetic resources in Turkey. Accordingly, studies have been carried out to investigate and characterize the genetic resources of different sponge gourd species in different regions of the world. PANDEY *et al.* (2001) in Nepal, and QUAMRUZZAMAN *et al.*

(2011) and RABBANI (2012) in Bangladesh, PHAN *et al.* (2015) and NGUYEN (2016) in Vietnam, and BLIND (2016) in Brazil collected genotypes of different sponge gourd species and characterized their morphological characteristics. There are no studies found in the literature related to the examined sponge gourd in Turkey. However, the diversity in this region, which is located at the intersection area of many trade routes, especially the Silk Road, is so precious that it cannot be abandoned to extinction.

This study aimed to determine the genetic diversity of the sponge gourd genotypes found in Hatay Province of Turkey and to collect this valuable species and to characterize the morphology of the genotypes.

MATERIALS AND METHODS

In this study, the genotypes of sponge gourd were investigated in Altınözü, Antakya, Arsuz, Belen, Defne, Dörtiyol, Erzin, Hassa, Iskenderun, Kirikhan, Kumlu, Payas, Reyhanli, Samandag and Yayladağı districts of Hatay Province of Turkey. As a result of the collection trips, a total of 34 sponge gourd genotypes which were thought to be morphologically different from each other were collected. The codes of the collected sponge gourd genotypes, the names of the districts and neighborhoods they were collected are given in Table 1, and the distribution of districts and neighborhoods where the genotypes were collected are given in Figure 1.

Table 1. Codes and collected areas of sponge gourd genotypes

| No | Code | Neighborhood | District | No | Code | Neighborhood | District |
|----|----------|---------------|----------|----|----------|-------------------------|-----------|
| 1 | 31 AR 01 | Merkez | Arsuz | 20 | 31 DÖ 02 | Merkez | Dörtiyol |
| 2 | 31 AR 02 | Gülcihan | Arsuz | 21 | 31 DÖ 03 | Altınçağ | Dörtiyol |
| 3 | 31 AR 03 | Gülcihan | Arsuz | 22 | 31 DÖ 04 | Şenmahmut-Kuzuculu | Dörtiyol |
| 4 | 31 AR 04 | Avcılar | Arsuz | 23 | 31 DÖ 05 | Şenmahmut-Kuzuculu | Dörtiyol |
| 5 | 31 AR 05 | Karahüseyinli | Arsuz | 24 | 31 DÖ 06 | Merkez | Dörtiyol |
| 6 | 31 DE 01 | Sinanlı | Defne | 25 | 31 YA 01 | Yukarı Okçular | Yayladağı |
| 7 | 31 DE 02 | Sinanlı | Defne | 26 | 31 YA 02 | Yukarı Okçular | Yayladağı |
| 8 | 31 DE 03 | Aknehir | Defne | 27 | 31 YA 03 | Dutlubahçe | Yayladağı |
| 9 | 31 DE 04 | Büyükçat | Defne | 28 | 31 YA 04 | Çamaltı | Yayladağı |
| 10 | 31 DE 05 | Büyükçat | Defne | 29 | 31 AL 01 | Sofular | Altınözü |
| 11 | 31 DE 06 | Sinanlı | Defne | 30 | 31 AL 02 | Alakent | Altınözü |
| 12 | 31 DE 07 | Dursunlu | Defne | 31 | 31 AL 03 | Tokaçlı | Altınözü |
| 13 | 31 SA 01 | Hıdırbey | Samandağ | 32 | 31 AL 04 | Merkez | Altınözü |
| 14 | 31 AN 01 | Karaali | Antakya | 33 | 31 PA 01 | İstiklal Mah. | Payas |
| 15 | 31 AN 02 | Karaali | Antakya | 34 | 31 ER 01 | Bahçelievler Mah. | Erzin |
| 16 | 31 AN 03 | Karaali | Antakya | 35 | 01 AD 01 | - | Adana |
| 17 | 31 AN 04 | Serinyol | Antakya | 36 | Korea | <i>Luffa aegyptiaca</i> | |
| 18 | 31 AN 05 | Akasya | Antakya | 37 | China | <i>Luffa acutangula</i> | |
| 19 | 31 DÖ 01 | Merkez | Dörtiyol | | | | |

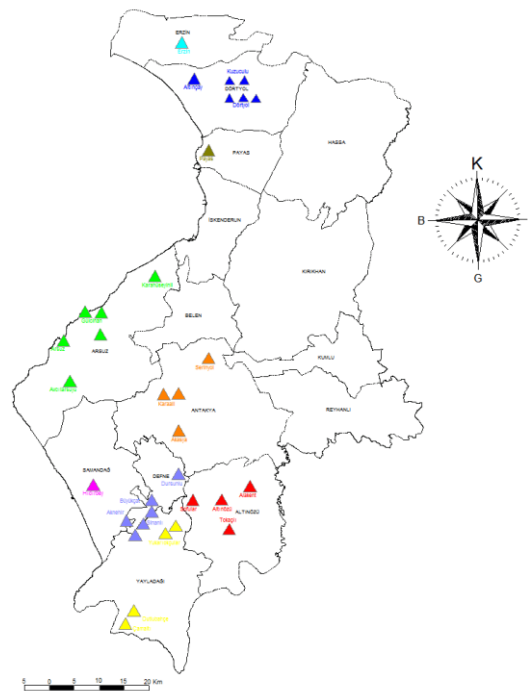


Figure 1. Distribution of neighborhoods and districts of Hatay Province that sponge gourd genotypes were collected

The seeds of the genotypes collected for morphological characterization were planted in peat-filled viols on March 28, 2017. Two genotypes ('31 AN 03' and '31 AL 04') were excluded from the study because of the poor germination. Field studies were carried out with a total of 35 genotypes including 32 genotypes collected from Hatay, 1 genotype obtained from Adana, 1 cultivar from South Korea and 1 cultivar from China (*Luffa acutangula*).

The seedlings were planted in three-real-leaf periods (on May 01, 2017) with seven rows with 1.9-meter-inter-row density and 5 genotypes in each row. Following the sowing procedure, fertilization (N:P:K 10:20:12 kg/da) and other maintenance procedures were performed properly, and no negative effects were observed during the experiment.

Phenological observations, plant, and pomological descriptions of 35 genotypes were analyzed according to the 'Sponge Gourd Descriptor' developed by NARC, LIBIRD, and IPGRI (JOSHI *et al.*, 2004). Other than the size and color of cotyledons, observations about plant characteristics were made in the same period in all genotypes after the 20-leaf period of the genotypes. Also, pomological analyses were carried out on 5 fruits, each randomly selected in the ripe and unripe periods. Observations, measurements, and analyses of plant characteristics of sponge gourd genotypes were carried out and the results that were evaluated based on a scale are given in Table 2.

Table 2. The list of characteristics evaluated according to the scales

| Characteristics | Evaluation Scale |
|---|--|
| <i>Plant growth characteristics</i> | |
| Cotyledon size | 1= small, 2= medium, 3= large, 4= very large |
| Cotyledon color | 1= light green, 2= intermediate, 3= dark green |
| Stem shape | 1= rounded, 2=intermediate, 3= angular |
| Tendrils | 1= present, 2= absent |
| Leaf shape (Figure 2) | 1= ovate, 2= orbicular, 3= reniform |
| Leaf size | 1= small, 2= intermediate, 3= large, 4= very large |
| Leaf margin | 1= smooth, 2= dented |
| Leaf lobes | 1= absent, 2= shallow, 3= intermediate, 4= deep |
| Leaf pubescence | 1= absent, 2= low, 3= intermediate, 4= high |
| Growth habit | 1= bushy, 2= intermediate, 3= prostrate |
| Stem pubescence | 1= absent, 2= thin, 3= dense, 4= very dense |
| <i>Flower, fruit and seed characteristics</i> | |
| Flower color | 1= white, 2= light yellow, 3= yellow, 4= orange, 5= other |
| Sex type | 1= androecious, 2= monoecious, 3= andromonoecious, 4= gynomonoecious, 5= gynoecious, 6= hermaphroditic |
| Male female flower ratio | 1= high, 2= medium, 3= low |
| Peduncle shape | 1= round, 2= smoothly angled, 3= sharply angled |
| Peduncle separation from fruit | 1= easy, 2= intermediate, 3= difficult |
| Fruit shape (Figure 2b) | 1= oblong blocky, 2= elongate slim, 3= elongate blocky, 4= elliptical, 5= elongate tapered, 6= pyriform, 7= elongate elliptical |
| Blossom end fruit shape (Figure 2c) | 1= depressed, 2= flattened, 3= rounded, 4= pointed |
| Stem-end fruit shape (Figure 2d) | 1= depressed, 2= flattened, 3= rounded, 4= pointed |
| Fruit ribs | 1= absent, 2= superficial, 3= intermediate, 4= deep |
| Unripe fruit color | 1= light green, 2= green, 3= dark green, 4= white mottled, 5= blackish, 6= others |
| Fruit skin texture | 1= smooth, 2= grainy, 3= finely wrinkled, 4= shallowly wavy, 5= nettled, 6= with warts, 7= scabrous |
| Flesh color | 1= white, 2= cream, 3= yellow |
| Flesh taste | 1= no taste, 2= sweet, 3= intermediate, 4= bitter |
| Unripe flesh texture | 1= smooth, 2= grainy, 3= spongy, 4= gelatinous, 5= fibrous |
| Unripe skin hardness | 1= soft, 2= intermediate, 3= hard |
| Fruit size variability | 1= low, 2= medium, 3= high |
| Sponge quality | 1= soft, 2= intermediate, 3= hard |
| Seed color | 1= black, 2= gray, 3= brown, 4= white |
| Seed surface | 1= smooth, 2= wrinkled, 3= slightly pitted, 4= scaly, 5= creased |

Other than the ones given in the table, internode length (cm), tendril length (cm), stem thickness (mm), the number of lateral shoots, petiole length (cm) values were measured. In addition, fruit peduncle length (cm), unripe fruit length (cm), unripe fruit diameter (cm), ripe fruit length (cm), ripe fruit diameter (cm), TSS (%), number of fruits (pcs), unripe fruit weight

(g), ripe fruit weight (g), sponge weight (g), number of seeds (pcs / fruit), 100-seed weight (g), seed length (mm), and seed width (mm) values were measured. Morphological characterization studies were performed on 9 plants of each genotype.

In order to provide an example in measurements and observations, internode length (cm) was determined between the 10th and 15th nodes in all genotypes. Observation and measurements of leaf shape, leaf size, leaf margin, leaf lobes, leaf pubescence and petiole length (cm) were determined in all genotypes with leaves between 6 and 10 leaves. Trunk thickness (mm) was measured between the 10th-15th internodes using a digital caliper. The weight values were determined using a digital scale, while measurements related to width and length were determined with a caliper and a ruler. Unripe fruit properties were determined on fresh fruits which can be used as vegetables. The hardness values were determined using a penetrometer and total soluble solids (TSS) were determined by a digital hand refractometer. The number of fruits in the plant was determined during the 25-node plant period.

The firmness values measured by a penetrometer were characterized as soft, intermediate, and hard in the descriptor, and those less than 1.54 kg / N were soft, those between 1.54 and 2.54 were intermediate and those higher than 2.54 were hard. Fruit flesh taste and sponge hardness were evaluated by five trained professionals. Flesh taste was evaluated by carrying out a taste sensory analysis. Sponge hardness was determined subjectively by squeezing five sponges and evaluating the feeling it left in the palm. Fruit properties were characterized on 5 fruits from each genotype.

The data obtained from the characterization studies were subjected to statistical analyses by using the SAS package software program. The Principal Component Analysis (PCA) was applied to the data sets and PC axes of the genotypes were obtained to highlight the characteristics representing the genotypes and to group the populations according to their characteristics. The PC axes and their variance and cumulative variance ratios, and the factor coefficients indicating the weight values of the main components for each characteristic were determined. Then dendrograms of the genotypes showing similarities and the differences between each other were created.

RESULTS

The results of the plant growth characteristics of the collected sponge gourd (*Luffa aegyptiaca* Mill.) genotypes are given in Table 3, and the leaf and stem characteristics in Table 4. The changes in flower characteristics are presented in Table 5, and the fruit characteristics in Table 5 and Table 6. The seed characterization results are shown in Table 8.

In terms of cotyledon size, 9 of the genotypes were large, 21 were medium, and 4 were small and 1 was very large (China). In terms of cotyledon color, all but the Chinese genotype was determined as 'dark green', while the Chinese genotype was determined as 'light green'. The internode lengths varied between 9.02 cm ('31 AR 04') and 17.47 cm ('31 DÖ 04'). The shape of the stem was determined as 'angular' in all genotypes. Tendril status was found to be 'present' in all the genotypes. Tendril lengths ranged between 17.80 cm ('31 AR 04') and 36.83 cm ('31 DÖ 01'). In terms of leaf shape, 4 genotypes were 'oval', 11 genotypes were 'round' and 20 genotypes were 'reniform' (Figure 2). In terms of leaf size, 14 of the genotypes were 'large', 14 were 'medium', 5 were 'small' and 2 were 'very large'. In terms of growth habit, all the

genotypes were identified as 'prostrate'. The number of lateral shoots varied from 4 to 20 (Table 3).

Table 3. Results of assessed plant growth characteristics

| Genotype | CS | CC | IL | SS | Tendrils | TL | GH | NLS |
|----------|----|----|-------|----|----------|-------|----|-----|
| 31 AR 01 | 2 | 3 | 16.76 | 3 | 1 | 26.27 | 3 | 8 |
| 31 AR 02 | 3 | 3 | 14.19 | 3 | 1 | 24.25 | 3 | 9 |
| 31 AR 03 | 3 | 3 | 15.39 | 3 | 1 | 22.77 | 3 | 10 |
| 31 AR 04 | 1 | 3 | 9.02 | 3 | 1 | 17.80 | 3 | 12 |
| 31 AR 05 | 2 | 3 | 14.94 | 3 | 1 | 21.80 | 3 | 11 |
| 31 DE 01 | 3 | 3 | 14.77 | 3 | 1 | 28.33 | 3 | 5 |
| 31 DE 02 | 2 | 3 | 15.40 | 3 | 1 | 31.58 | 3 | 12 |
| 31 DE 03 | 3 | 3 | 13.40 | 3 | 1 | 33.83 | 3 | 10 |
| 31 DE 04 | 2 | 3 | 15.13 | 3 | 1 | 28.05 | 3 | 12 |
| 31 DE 05 | 3 | 3 | 13.47 | 3 | 1 | 25.50 | 3 | 8 |
| 31 DE 06 | 2 | 3 | 14.97 | 3 | 1 | 25.50 | 3 | 8 |
| 31 DE 07 | 2 | 3 | 12.51 | 3 | 1 | 30.12 | 3 | 16 |
| 31 SA 01 | 3 | 3 | 16.82 | 3 | 1 | 27.00 | 3 | 11 |
| 31 AN 01 | 2 | 3 | 12.42 | 3 | 1 | 29.05 | 3 | 12 |
| 31 AN 02 | 3 | 3 | 14.27 | 3 | 1 | 24.95 | 3 | 8 |
| 31 AN 04 | 2 | 3 | 16.86 | 3 | 1 | 35.60 | 3 | 16 |
| 31 AN 05 | 2 | 3 | 14.28 | 3 | 1 | 27.85 | 3 | 18 |
| 31 DÖ 01 | 2 | 3 | 13.45 | 3 | 1 | 36.83 | 3 | 20 |
| 31 DÖ 02 | 2 | 3 | 11.89 | 3 | 1 | 29.88 | 3 | 15 |
| 31 DÖ 03 | 2 | 3 | 12.00 | 3 | 1 | 19.45 | 3 | 10 |
| 31 DÖ 04 | 2 | 3 | 17.47 | 3 | 1 | 28.97 | 3 | 11 |
| 31 DÖ 05 | 1 | 3 | 14.66 | 3 | 1 | 25.35 | 3 | 7 |
| 31 DÖ 06 | 2 | 3 | 10.04 | 3 | 1 | 34.28 | 3 | 20 |
| 31 YA 01 | 2 | 3 | 13.00 | 3 | 1 | 30.70 | 3 | 12 |
| 31 YA 02 | 2 | 3 | 16.94 | 3 | 1 | 27.78 | 3 | 8 |
| 31 YA 03 | 2 | 3 | 15.80 | 3 | 1 | 24.03 | 3 | 11 |
| 31 YA 04 | 2 | 3 | 12.73 | 3 | 1 | 24.02 | 3 | 4 |
| 31 AL 01 | 1 | 3 | 10.53 | 3 | 1 | 20.97 | 3 | 8 |
| 31 AL 02 | 3 | 3 | 13.31 | 3 | 1 | 23.80 | 3 | 8 |
| 31 AL 03 | 2 | 3 | 14.35 | 3 | 1 | 29.10 | 3 | 13 |
| 31 PA 01 | 1 | 3 | 9.96 | 3 | 1 | 24.73 | 3 | 13 |
| 31 ER 01 | 3 | 3 | 12.64 | 3 | 1 | 28.68 | 3 | 11 |
| 01 AD 01 | 2 | 3 | 16.88 | 3 | 1 | 24.27 | 3 | 12 |
| S. Korea | 2 | 3 | 12.74 | 3 | 1 | 18.80 | 3 | 7 |
| China | 4 | 1 | 12.60 | 3 | 1 | 23.00 | 3 | 10 |

CS: Cotyledon Size, CC: Cotyledon Color, IL: Internode Length, SS: Stem Shape, TL: Tendril Length, GH: Growth Habit, NLS: Number of Lateral Shoots

Table 4. Results of assessed leaf and stem characteristics

| Genotype | LSH | LSI | LM | LL | LP | ST | SP | PL |
|----------|-----|-----|----|----|----|------|----|-------|
| 31 AR 01 | 2 | 2 | 2 | 3 | 2 | 5.98 | 2 | 13.57 |
| 31 AR 02 | 1 | 2 | 2 | 3 | 2 | 5.67 | 2 | 11.85 |
| 31 AR 03 | 1 | 3 | 2 | 3 | 2 | 6.14 | 2 | 12.35 |
| 31 AR 04 | 3 | 2 | 2 | 3 | 2 | 5.87 | 2 | 11.45 |
| 31 AR 05 | 3 | 1 | 2 | 3 | 2 | 6.04 | 2 | 12.42 |
| 31 DE 01 | 3 | 3 | 2 | 3 | 3 | 6.59 | 2 | 11.98 |
| 31 DE 02 | 3 | 4 | 2 | 3 | 1 | 7.31 | 2 | 11.92 |
| 31 DE 03 | 3 | 3 | 2 | 3 | 1 | 6.35 | 2 | 13.94 |
| 31 DE 04 | 3 | 2 | 2 | 2 | 2 | 5.35 | 2 | 15.12 |
| 31 DE 05 | 3 | 3 | 2 | 3 | 1 | 5.64 | 1 | 11.86 |
| 31 DE 06 | 2 | 3 | 2 | 2 | 1 | 7.07 | 1 | 11.49 |
| 31 DE 07 | 2 | 3 | 2 | 4 | 2 | 6.44 | 2 | 12.70 |
| 31 SA 01 | 3 | 3 | 2 | 3 | 2 | 6.96 | 2 | 13.45 |
| 31 AN 01 | 3 | 3 | 2 | 3 | 2 | 6.23 | 2 | 13.15 |
| 31 AN 02 | 3 | 2 | 2 | 3 | 2 | 5.92 | 2 | 12.52 |
| 31 AN 04 | 2 | 3 | 2 | 2 | 2 | 7.16 | 2 | 13.40 |
| 31 AN 05 | 3 | 2 | 2 | 3 | 2 | 5.82 | 2 | 12.48 |
| 31 DÖ 01 | 3 | 3 | 2 | 3 | 2 | 7.55 | 2 | 13.21 |
| 31 DÖ 02 | 2 | 2 | 2 | 2 | 2 | 6.09 | 2 | 13.49 |
| 31 DÖ 03 | 2 | 1 | 2 | 2 | 2 | 5.37 | 2 | 13.59 |
| 31 DÖ 04 | 1 | 3 | 2 | 4 | 2 | 6.97 | 2 | 13.22 |
| 31 DÖ 05 | 1 | 3 | 2 | 4 | 2 | 6.37 | 2 | 12.94 |
| 31 DÖ 06 | 3 | 2 | 2 | 2 | 2 | 6.74 | 2 | 8.97 |
| 31 YA 01 | 3 | 1 | 2 | 3 | 2 | 5.32 | 2 | 12.02 |
| 31 YA 02 | 3 | 2 | 2 | 3 | 2 | 6.05 | 2 | 12.06 |
| 31 YA 03 | 3 | 2 | 2 | 3 | 2 | 6.56 | 2 | 11.72 |
| 31 YA 04 | 3 | 1 | 2 | 3 | 1 | 5.28 | 2 | 11.78 |
| 31 AL 01 | 2 | 2 | 2 | 2 | 1 | 4.94 | 2 | 12.87 |
| 31 AL 02 | 2 | 3 | 2 | 3 | 1 | 6.18 | 2 | 14.32 |
| 31 AL 03 | 3 | 3 | 2 | 2 | 2 | 7.01 | 2 | 12.90 |
| 31 PA 01 | 3 | 1 | 2 | 3 | 2 | 5.85 | 2 | 11.98 |
| 31 ER 01 | 3 | 2 | 2 | 2 | 2 | 5.44 | 2 | 12.26 |
| 01 AD 01 | 2 | 2 | 2 | 2 | 2 | 5.74 | 2 | 13.05 |
| S. Korea | 2 | 2 | 2 | 2 | 1 | 5.16 | 2 | 11.67 |
| China | 2 | 4 | 2 | 1 | 1 | 5.60 | 1 | 12.63 |

LSH: Leaf Shape, LSI: Leaf Size, LM: Leaf Margin, LL: Leaf Lobes, LP: Leaf Pubescence, ST: Stem Thickness, SP: Stem Pubescence, PL: Petiole Length

In terms of leaf margin, all the genotypes were found to be ‘dented’. In terms of leaf lobe, 3 genotypes were identified as ‘deep’, 20 genotypes as ‘intermediate’, 11 genotypes as ‘shallow’ and 1 genotype as ‘absent’. In terms of leaf pubescence, 1 genotype was ‘intermediate’, 25

genotypes were 'low' and 9 genotypes were 'absent'. Stem thicknesses ranged from 4.99 mm ('31 AL 01') to 7.55 mm ('31 DÖ 01'). In terms of stem pubescence, most of the genotypes were identified as 'thin'. Petiole length ranged from 8.97 to 13.94 cm (Table 4).

Table 5. Results of assessed flower characteristics

| Genotype | FC | ST | MFFR | PS | PL | PSF | BFS | SFS |
|----------|----|----|------|----|------|-----|-----|-----|
| 31 AR 01 | 3 | 2 | 2 | 1 | 9.0 | 3 | 3 | 3 |
| 31 AR 02 | 3 | 2 | 2 | 1 | 17.2 | 3 | 3 | 3 |
| 31 AR 03 | 3 | 2 | 3 | 1 | 16.7 | 3 | 3 | 3 |
| 31 AR 04 | 2 | 2 | 1 | 1 | 6.1 | 3 | 4 | 3 |
| 31 AR 05 | 3 | 2 | 2 | 1 | 6.4 | 3 | 2 | 2 |
| 31 DE 01 | 3 | 2 | 3 | 1 | 17.4 | 3 | 2 | 3 |
| 31 DE 02 | 3 | 2 | 2 | 2 | 15.4 | 3 | 3 | 3 |
| 31 DE 03 | 3 | 2 | 1 | 1 | 19.3 | 3 | 3 | 3 |
| 31 DE 04 | 3 | 2 | 1 | 3 | 17.0 | 3 | 3 | 3 |
| 31 DE 05 | 3 | 2 | 2 | 1 | 9.7 | 3 | 3 | 3 |
| 31 DE 06 | 3 | 2 | 2 | 2 | 14.6 | 3 | 3 | 3 |
| 31 DE 07 | 3 | 2 | 1 | 2 | 8.8 | 3 | 4 | 3 |
| 31 SA 01 | 3 | 2 | 3 | 3 | 8.9 | 3 | 2 | 3 |
| 31 AN 01 | 3 | 2 | 3 | 1 | 11.8 | 3 | 3 | 3 |
| 31 AN 02 | 3 | 2 | 2 | 1 | 12.8 | 3 | 3 | 3 |
| 31 AN 04 | 3 | 2 | 1 | 1 | 20.3 | 3 | 3 | 3 |
| 31 AN 05 | 3 | 2 | 1 | 1 | 11.7 | 3 | 4 | 4 |
| 31 DÖ 01 | 3 | 2 | 3 | 1 | 20.6 | 3 | 3 | 3 |
| 31 DÖ 02 | 3 | 2 | 3 | 1 | 12.0 | 3 | 3 | 3 |
| 31 DÖ 03 | 2 | 2 | 1 | 3 | 6.6 | 3 | 3 | 3 |
| 31 DÖ 04 | 3 | 2 | 1 | 1 | 10.0 | 3 | 3 | 3 |
| 31 DÖ 05 | 3 | 2 | 2 | 1 | 15.6 | 3 | 3 | 3 |
| 31 DÖ 06 | 3 | 2 | 1 | 1 | 11.2 | 3 | 4 | 3 |
| 31 YA 01 | 3 | 2 | 2 | 2 | 11.7 | 3 | 4 | 3 |
| 31 YA 02 | 2 | 2 | 2 | 3 | 13.7 | 3 | 3 | 3 |
| 31 YA 03 | 3 | 2 | 2 | 1 | 16.4 | 3 | 3 | 3 |
| 31 YA 04 | 3 | 2 | 1 | 1 | 10.4 | 3 | 3 | 3 |
| 31 AL 01 | 2 | 2 | 3 | 1 | 9.8 | 3 | 2 | 2 |
| 31 AL 02 | 3 | 2 | 2 | 1 | 17.1 | 3 | 3 | 3 |
| 31 AL 03 | 2 | 2 | 3 | 2 | 17.0 | 3 | 2 | 4 |
| 31 PA 01 | 3 | 2 | 3 | 1 | 16.9 | 3 | 3 | 3 |
| 31 ER 01 | 3 | 2 | 2 | 2 | 10.1 | 3 | 2 | 2 |
| 01 AD 01 | 2 | 2 | 1 | 3 | 16.9 | 3 | 3 | 3 |
| S. Korea | 3 | 2 | 3 | 1 | 10.5 | 3 | 3 | 3 |
| China | 2 | 2 | 2 | 2 | 9.3 | 3 | 3 | 3 |

FC: Flower Color, ST: Sex Type, MFFR: Male Female Flower Ratio, PS: Peduncle Shape, PL: Peduncle Length, PSF: Peduncle Separation from Fruit, BFS: Blossom-end Fruit Shape, SFS: Stem-end Fruit Shape

Table 6. Results of assessed fruit characteristics

| Genotype | FS | FR | FT | FC | UFL | FL | UFD | FD | FST | FFC | UFT |
|----------|----|----|----|----|-------|-------|------|-------|-----|-----|-----|
| 31 AR 01 | 3 | 3 | 4 | 3 | 15.67 | 34.47 | 2.90 | 8.87 | 2 | 2 | 2 |
| 31 AR 02 | 7 | 3 | 3 | 3 | 15.99 | 28.17 | 3.46 | 8.81 | 2 | 3 | 2 |
| 31 AR 03 | 3 | 4 | 2 | 3 | 16.67 | 28.60 | 4.12 | 8.03 | 4 | 2 | 2 |
| 31 AR 04 | 2 | 3 | 3 | 3 | 15.73 | 33.83 | 2.44 | 6.50 | 6 | 1 | 2 |
| 31 AR 05 | 1 | 3 | 2 | 3 | 17.33 | 40.40 | 4.26 | 6.27 | 3 | 2 | 2 |
| 31 DE 01 | 7 | 3 | 2 | 2 | 14.73 | 51.10 | 2.87 | 11.33 | 2 | 2 | 2 |
| 31 DE 02 | 7 | 2 | 4 | 5 | 15.70 | 47.23 | 2.83 | 11.00 | 7 | 2 | 3 |
| 31 DE 03 | 7 | 3 | 1 | 2 | 16.50 | 46.93 | 2.53 | 11.17 | 7 | 3 | 3 |
| 31 DE 04 | 5 | 3 | 4 | 3 | 16.87 | 48.00 | 2.52 | 10.70 | 7 | 3 | 2 |
| 31 DE 05 | 2 | 3 | 1 | 2 | 23.50 | 52.67 | 3.34 | 9.73 | 7 | 2 | 1 |
| 31 DE 06 | 7 | 3 | 2 | 3 | 14.87 | 50.83 | 2.28 | 11.00 | 7 | 2 | 2 |
| 31 DE 07 | 2 | 3 | 2 | 3 | 20.87 | 29.33 | 3.51 | 8.64 | 7 | 2 | 2 |
| 31 SA 01 | 7 | 3 | 3 | 2 | 15.47 | 48.80 | 2.91 | 9.20 | 7 | 3 | 2 |
| 31 AN 01 | 2 | 3 | 1 | 5 | 13.67 | 42.37 | 2.82 | 10.23 | 7 | 2 | 2 |
| 31 AN 02 | 7 | 3 | 2 | 2 | 22.77 | 47.47 | 3.86 | 9.27 | 3 | 2 | 2 |
| 31 AN 04 | 7 | 3 | 1 | 2 | 16.27 | 49.40 | 3.04 | 11.80 | 7 | 2 | 2 |
| 31 AN 05 | 3 | 1 | 2 | 3 | 16.80 | 30.77 | 3.57 | 8.47 | 7 | 3 | 2 |
| 31 DÖ 01 | 7 | 3 | 3 | 2 | 16.67 | 52.77 | 3.18 | 9.80 | 7 | 2 | 2 |
| 31 DÖ 02 | 7 | 2 | 3 | 2 | 17.77 | 39.87 | 3.27 | 9.07 | 7 | 1 | 3 |
| 31 DÖ 03 | 7 | 3 | 2 | 5 | 13.63 | 33.80 | 3.31 | 8.57 | 2 | 1 | 2 |
| 31 DÖ 04 | 7 | 3 | 2 | 5 | 18.40 | 30.77 | 2.91 | 8.03 | 6 | 2 | 3 |
| 31 DÖ 05 | 7 | 3 | 3 | 3 | 17.50 | 56.33 | 2.77 | 13.47 | 4 | 2 | 2 |
| 31 DÖ 06 | 5 | 3 | 4 | 2 | 16.70 | 32.10 | 2.66 | 6.87 | 2 | 1 | 2 |
| 31 YA 01 | 2 | 3 | 2 | 2 | 22.77 | 74.00 | 3.16 | 11.37 | 2 | 2 | 2 |
| 31 YA 02 | 7 | 3 | 3 | 5 | 14.13 | 49.53 | 2.43 | 11.63 | 7 | 2 | 2 |
| 31 YA 03 | 5 | 3 | 1 | 3 | 25.33 | 72.07 | 3.24 | 10.83 | 7 | 1 | 2 |
| 31 YA 04 | 7 | 3 | 1 | 3 | 14.70 | 39.63 | 3.26 | 9.63 | 2 | 2 | 1 |
| 31 AL 01 | 2 | 3 | 3 | 3 | 11.57 | 33.43 | 3.70 | 10.83 | 1 | 2 | 2 |
| 31 AL 02 | 3 | 3 | 3 | 3 | 14.30 | 55.10 | 3.16 | 11.83 | 2 | 1 | 2 |
| 31 AL 03 | 3 | 4 | 1 | 1 | 20.17 | 39.37 | 4.46 | 10.30 | 2 | 2 | 2 |
| 31 PA 01 | 5 | 3 | 1 | 2 | 12.33 | 36.53 | 2.63 | 8.53 | 7 | 2 | 2 |
| 31 ER 01 | 3 | 3 | 1 | 3 | 13.10 | 27.90 | 3.47 | 8.57 | 2 | 2 | 2 |
| 01 AD 01 | 5 | 2 | 4 | 3 | 21.23 | 40.57 | 2.59 | 10.67 | 2 | 2 | 2 |
| S. Korea | 6 | 2 | 3 | 2 | 13.92 | 37.67 | 3.26 | 7.90 | 1 | 2 | 2 |
| China | 5 | 5 | 2 | 3 | 23.93 | 43.53 | 2.88 | 6.43 | 3 | 2 | 2 |

FS: Fruit Shape, FR: Fruit Ribs, FT: Flesh Taste, FC: Fruit Color, UFL: Unripe Fruit Length, FL: Fruit Length, UFD: Unripe Fruit Diameter, FD: Fruit Diameter, FST: Fruit Skin Texture, FFC: Fruit Flesh Color, UFT: Unripe Flesh Texture

Flower characteristics of the genotypes are given in Table 4. In terms of flower color, 28 of the genotypes were 'yellow' and 7 of them were 'light yellow'. The sex in the flower was found to be 'monoic' in all the genotypes. In terms of male female flower ratios, 11 genotypes

were determined to have 'high' and 10 genotypes had 'low' ratios and the other genotypes were scored as 'moderate'.

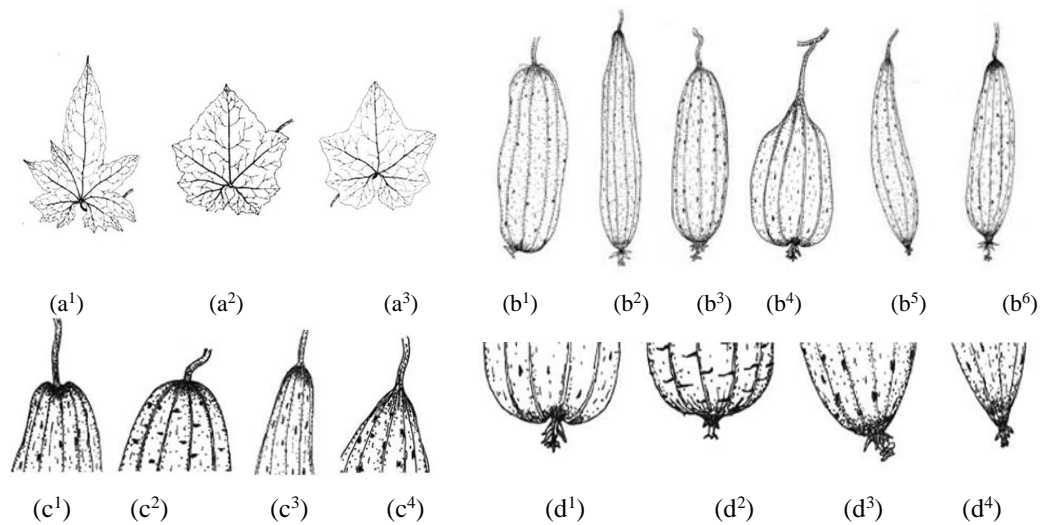


Figure 2. Shape illustrations leaf (a), fruit (b), stem-end fruit (c), and blossom-end fruit (d) samples

a¹- ovate, a²- orbicular, a³- reniform

b¹- oblong blocky, b²- elongate slim, b³- elliptical, b⁴- pyriform, b⁵- elongate tapered, b⁶- elongate elliptic

c¹- depressed, c²- flattened, c³- rounded, c⁴- pointed

d¹- depressed, d²- flattened, d³- rounded, d⁴- pointed

Examining the fruit characteristics of sponge gourd genotypes, the shape of the fruit stem was determined as 'rounded' in 23 genotypes, 'slightly angular' in 6 genotypes and 'angular' in 5 genotypes. Fruit peduncle length ranged from 6.1 cm to 20.3 cm while peduncle separation from fruit was determined to be 'difficult'. There were variations among genotypes in terms of fruit shape, while in most genotypes the shape of the fruit was 'elongate elliptical' and the fruit rib was determined to be 'intermediate' (Figure 3a). Ripe fruit lengths ranged between 27.90 cm ('31 ER 01') and 74 cm ('31 YA 01'). There were also variations in ripe fruit diameters and the highest fruit diameter was obtained in '31 DÖ 05' with 13.47 cm (Figure 3b). The smallest fruit diameter was obtained in '31 AR 05' with 6.27 cm. There was also a difference in terms of fruit skin texture; 1 genotype was 'smooth', 10 genotypes were 'grainy', 3 genotypes were 'finley wrinkled', 2 genotypes were 'shallowly wavy', 2 genotypes were 'with warts' and 15 genotypes were 'scabrous'. In terms of flesh taste, genotypes were distributed to all 'insipid', 'intermediate', 'bitter', and 'favorable' classifications. Including the genotype obtained from China, the flesh taste of 11 genotypes was found to be 'favorable' (Table 6).

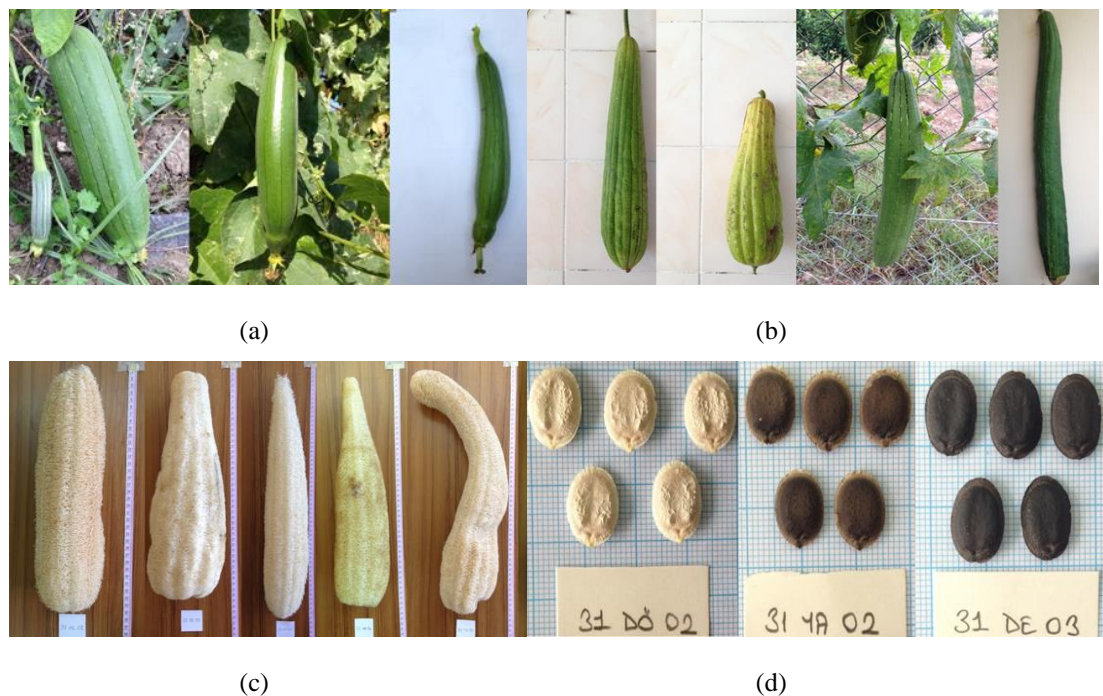


Figure 3. Unripe sponge gourd that can be consumed as a vegetable (a) sponge gourd samples suitable for sponge production (b) differences in sponge sizes of some genotypes (c) examples of color differences in seeds (d)

As shown in Table 7, Fruit size was found to be 'intermediate' in 4 genotypes while it was determined to be 'low' in other genotypes. The TSS content of the genotypes varied between 3.10 % and 5.93 %, while the number of fruits per plant varied between 6.0 and 19.33. The ripe fruit weights of the genotypes varied between 29.09 g ('31 DÖ 06') and 222.38 g ('31 DÖ 05'). In terms of sponge quality, it was determined that they were generally of 'medium' quality. In terms of sponge weight, the highest value was obtained in '31 YA 02' with 47.98 g whereas the lowest value was in '31 DÖ 06' with 5.84 g (Figure 3c).

Seed characteristics of sponge gourd genotypes are given in Table 8. The seed colors were generally determined as 'black' while '31 DÖ 02' genotype was identified as 'white' (Figure 3d). The number of seeds varied depending on the genotypes and the highest number of seeds was seen in '31 DE 07' with 461 seeds. The lowest number of seeds was determined to be 36 in '31 DÖ 06'. The highest value in terms of 100-seed weight was obtained from '31 DÖ 04' genotype with 15.72 g, whereas the lowest value was determined in '31 DÖ 06' genotype with 7.41 g.

Making a general evaluation, the mean values of the characters examined were subjected to the principal components analysis (PCA) of the multiple variable analyses. As a result of the analysis, the first three components explained 16.4%, 9.1%, 9.0% of the variance, respectively.

Table 7. Results of assessed fruit (continued) characteristics

| Genotype | USH | FSV | TSS | NF | UFW | FW | SQ | SW |
|----------|-----|-----|------|--------|--------|--------|----|-------|
| 31 AR 01 | 2 | 1 | 5.53 | 7.00 | 101.71 | 89.12 | 2 | 16.99 |
| 31 AR 02 | 1 | 1 | 5.93 | 11.00 | 71.18 | 88.63 | 2 | 19.57 |
| 31 AR 03 | 1 | 1 | 4.10 | 9.33 | 104.90 | 65.77 | 2 | 15.26 |
| 31 AR 04 | 2 | 1 | 3.60 | 9.33 | 57.43 | 54.27 | 2 | 7.56 |
| 31 AR 05 | 1 | 2 | 4.60 | 7.33 | 140.77 | 89.39 | 2 | 22.74 |
| 31 DE 01 | 1 | 1 | 5.10 | 8.33 | 79.66 | 192.32 | 3 | 44.61 |
| 31 DE 02 | 1 | 1 | 4.67 | 9.00 | 126.49 | 168.22 | 2 | 36.50 |
| 31 DE 03 | 1 | 1 | 4.97 | 8.67 | 125.34 | 217.00 | 3 | 46.74 |
| 31 DE 04 | 3 | 1 | 4.37 | 7.33 | 114.51 | 151.23 | 3 | 41.89 |
| 31 DE 05 | 2 | 1 | 5.23 | 7.00 | 135.30 | 180.97 | 2 | 36.15 |
| 31 DE 06 | 3 | 2 | 5.83 | 7.67 | 77.18 | 120.71 | 3 | 39.23 |
| 31 DE 07 | 1 | 1 | 4.47 | 0.00** | 136.38 | 55.90 | 2 | 27.87 |
| 31 SA 01 | 2 | 1 | 5.07 | 6.67 | 97.53 | 126.34 | 2 | 20.30 |
| 31 AN 01 | 1 | 1 | 3.40 | 6.67 | 73.06 | 137.92 | 2 | 29.46 |
| 31 AN 02 | 1 | 1 | 4.30 | 7.00 | 269.89 | 130.05 | 2 | 30.52 |
| 31 AN 04 | 1 | 1 | 5.33 | 8.33 | 98.94 | 113.30 | 2 | 24.94 |
| 31 AN 05 | 3 | 1 | 3.50 | 19.33 | 74.52 | 79.78 | 2 | 7.73 |
| 31 DÖ 01 | 1 | 1 | 4.80 | 6.00 | 105.96 | 144.26 | 3 | 47.95 |
| 31 DÖ 02 | 1 | 1 | 4.57 | 8.00 | 98.27 | 59.13 | 2 | 11.72 |
| 31 DÖ 03 | 3 | 2 | 3.07 | 9.00 | 125.16 | 64.80 | 2 | 14.90 |
| 31 DÖ 04 | 1 | 1 | 5.67 | 10.67 | 78.56 | 29.73 | 2 | 11.73 |
| 31 DÖ 05 | 2 | 1 | 5.63 | 8.33 | 92.62 | 222.38 | 3 | 57.85 |
| 31 DÖ 06 | 3 | 1 | 4.27 | 10.67 | 56.81 | 29.09 | 1 | 5.84 |
| 31 YA 01 | 1 | 1 | 4.27 | 7.00 | 137.23 | 137.46 | 1 | 45.07 |
| 31 YA 02 | 1 | 1 | 5.10 | 6.33 | 54.57 | 199.08 | 3 | 47.98 |
| 31 YA 03 | 2 | 1 | 4.10 | 7.33 | 165.78 | 98.28 | 2 | 36.87 |
| 31 YA 04 | 1 | 1 | 5.03 | 8.33 | 89.03 | 95.59 | 3 | 31.42 |
| 31 AL 01 | 1 | 1 | 5.10 | 9.67 | 80.74 | 125.68 | 2 | 17.25 |
| 31 AL 02 | 2 | 1 | 5.10 | 7.67 | 73.25 | 145.99 | 3 | 40.53 |
| 31 AL 03 | 1 | 1 | 3.57 | 10.00 | 117.86 | 80.70 | 1 | 13.74 |
| 31 PA 01 | 1 | 1 | 3.47 | 7.33 | 53.71 | 104.12 | 2 | 12.17 |
| 31 ER 01 | 1 | 2 | 5.33 | 11.33 | 113.92 | 44.11 | 1 | 9.43 |
| 01 AD 01 | 1 | 1 | 4.07 | 7.00 | 87.13 | 184.69 | 3 | 44.74 |
| S. Korea | 1 | 1 | 4.60 | 15.00 | 61.13 | 74.52 | 2 | 19.07 |
| China | 1 | 1 | 3.10 | 10.33 | 71.29 | 63.03 | * | * |

USH: Unripe Skin Hardness, FSV: Fruit Size Variability, TSS: Total Soluble Solids, NF: Number of Fruits, UFW: Unripe Fruit Weight, FW: Fruit Weight, SQ: Sponge Quality, SW: Sponge Weight

Table 8. Results of assessed seed characteristics

| Genotype | SC | SS | NS | 100SW | SD | SL |
|----------|----|----|-----|-------|------|-------|
| 31 AR 01 | 1 | 1 | 215 | 14.99 | 8.40 | 13.57 |
| 31 AR 02 | 1 | 1 | 334 | 12.70 | 8.36 | 11.85 |
| 31 AR 03 | 1 | 1 | 158 | 13.36 | 8.93 | 12.35 |
| 31 AR 04 | 1 | 1 | 85 | 9.43 | 7.75 | 11.45 |
| 31 AR 05 | 1 | 1 | 230 | 13.16 | 7.75 | 12.42 |
| 31 DE 01 | 1 | 1 | 302 | 11.62 | 7.85 | 11.98 |
| 31 DE 02 | 1 | 1 | 222 | 10.69 | 8.39 | 11.92 |
| 31 DE 03 | 1 | 2 | 329 | 15.09 | 9.71 | 13.94 |
| 31 DE 04 | 3 | 2 | 398 | 14.46 | 9.47 | 15.12 |
| 31 DE 05 | 1 | 1 | 231 | 10.48 | 7.74 | 11.86 |
| 31 DE 06 | 1 | 1 | 323 | 10.16 | 7.93 | 11.49 |
| 31 DE 07 | 1 | 1 | 461 | 11.83 | 8.81 | 12.70 |
| 31 SA 01 | 1 | 1 | 213 | 14.71 | 8.55 | 13.45 |
| 31 AN 01 | 1 | 2 | 153 | 13.87 | 8.65 | 13.15 |
| 31 AN 02 | 1 | 1 | 289 | 11.57 | 8.53 | 12.52 |
| 31 AN 04 | 1 | 1 | 266 | 14.20 | 8.70 | 13.40 |
| 31 AN 05 | 1 | 1 | 282 | 12.70 | 8.42 | 12.48 |
| 31 DÖ 01 | 1 | 1 | 293 | 13.89 | 7.47 | 13.21 |
| 31 DÖ 02 | 4 | 5 | 183 | 15.39 | 9.57 | 13.49 |
| 31 DÖ 03 | 1 | 1 | 218 | 12.51 | 8.78 | 13.59 |
| 31 DÖ 04 | 1 | 1 | 196 | 15.72 | 8.65 | 13.22 |
| 31 DÖ 05 | 1 | 1 | 386 | 14.74 | 8.28 | 12.94 |
| 31 DÖ 06 | 1 | 1 | 36 | 7.41 | 6.25 | 8.97 |
| 31 YA 01 | 1 | 1 | 111 | 10.58 | 7.89 | 12.02 |
| 31 YA 02 | 2 | 1 | 370 | 13.53 | 8.49 | 12.06 |
| 31 YA 03 | 1 | 1 | 62 | 11.48 | 7.83 | 11.72 |
| 31 YA 04 | 1 | 1 | 132 | 10.57 | 7.93 | 11.78 |
| 31 AL 01 | 1 | 1 | 353 | 11.78 | 8.10 | 12.87 |
| 31 AL 02 | 1 | 2 | 311 | 16.48 | 8.47 | 14.32 |
| 31 AL 03 | 1 | 1 | 116 | 12.55 | 8.20 | 12.90 |
| 31 PA 01 | 1 | 1 | 279 | 9.43 | 7.68 | 11.98 |
| 31 ER 01 | 1 | 1 | 120 | 12.96 | 8.59 | 12.26 |
| 01 AD 01 | 1 | 1 | 431 | 14.75 | 9.27 | 13.05 |
| S. Korea | 1 | 1 | 392 | 9.50 | 7.21 | 11.67 |
| China | 1 | 4 | 115 | 15.00 | 7.77 | 12.63 |

Seed Color, SS: Seed Surface, NS: Number of Seeds, 100SW: 100-Seed Weight, SD: Seed Diameter, SL: Seed Length

In other words, the total variance explained by the principal component (PC) analysis was 34.5% (Table 9).

Table 9. Eigen values, variances and correlation results of the first three principle components (PC) of assessed characteristics

| Characteristics | PC1 | PC2 | PC3 |
|--------------------------------|-------------|-------------|-------------|
| Cotyledon size | 0.09 | -0.02 | -0.13 |
| Cotyledon color | 0.00 | 0.00 | 0.00 |
| Internode length | 0.24 | -0.03 | -0.02 |
| Stem shape | 0.00 | 0.00 | 0.00 |
| Tendrils | 0.00 | 0.00 | 0.00 |
| Tendrill length | 0.16 | 0.33 | 0.02 |
| Leaf shape | -0.08 | 0.15 | -0.11 |
| Leaf size | 0.21 | 0.15 | -0.05 |
| Leaf margin | 0.00 | 0.00 | 0.00 |
| Leaf lobes | 0.10 | 0.10 | -0.12 |
| Leaf pubescence | -0.02 | 0.13 | 0.09 |
| Growth habit | 0.00 | 0.00 | 0.00 |
| Stem thickness | 0.16 | 0.30 | -0.05 |
| Number of lateral shoots | -0.07 | 0.38 | 0.19 |
| Stem pubescence | -0.03 | 0.03 | 0.21 |
| Petiole length | 0.10 | 0.11 | -0.01 |
| Flower color | 0.08 | 0.18 | -0.11 |
| Sex type | 0.00 | 0.00 | 0.00 |
| Male female flower ratio | 0.01 | -0.06 | -0.11 |
| Peduncle shape | 0.08 | -0.11 | 0.13 |
| Peduncle length | 0.24 | 0.11 | -0.05 |
| Peduncle separation from fruit | 0.00 | 0.00 | 0.00 |
| Blossom end fruit shape | -0.06 | 0.27 | 0.08 |
| Stem-end fruit shape | 0.06 | 0.27 | 0.05 |
| Fruit shape | 0.18 | 0.00 | 0.07 |
| Fruit ribs | -0.01 | -0.06 | -0.22 |
| Unripe fruit color | 0.03 | -0.13 | 0.18 |
| Unripe fruit length | 0.05 | 0.23 | -0.18 |
| Unripe fruit diameter | 0.19 | 0.09 | -0.24 |
| Fruit length | -0.14 | -0.03 | -0.11 |
| Fruit diameter | 0.29 | -0.06 | -0.11 |
| Fruit skin texture | 0.16 | 0.27 | 0.09 |
| Flesh color | 0.14 | -0.05 | -0.01 |
| Flesh taste | 0.04 | -0.07 | 0.22 |
| Unripe flesh texture | 0.11 | 0.12 | 0.29 |
| Fruit skin hardness | -0.05 | 0.03 | 0.08 |
| Fruit size variability | -0.10 | -0.19 | -0.01 |
| TSS | 0.17 | -0.15 | -0.12 |
| Number of fruits | -0.14 | -0.02 | 0.12 |
| Unripe fruit weight | 0.04 | 0.06 | -0.17 |

| | | | |
|---------------------------|------|-------|-------|
| Fruit weight | 0.26 | -0.17 | 0.02 |
| Sponge quality | 0.30 | -0.06 | -0.19 |
| Sponge weight | 0.29 | -0.11 | -0.15 |
| Seed color | 0.08 | 0.02 | 0.31 |
| Seed surface | 0.08 | 0.06 | 0.29 |
| Number of seeds | 0.19 | -0.19 | 0.07 |
| 100-seed weight | 0.24 | -0.10 | 0.21 |
| Seed length | 0.21 | -0.13 | 0.21 |
| Seed diameter | 0.21 | -0.09 | 0.27 |
| <i>Eigen values</i> | 6.9 | 3.8 | 3.8 |
| <i>Variance (%)</i> | 16.4 | 9.1 | 9.0 |
| <i>Total variance (%)</i> | 16.4 | 25.5 | 34.5 |

Of the 49 morphological characters subjected to the principal component analysis, the use of 7 (cotyledon color, stem shape, tendril, leaf margin, growth habit, flower sex and peduncle separation from fruit) was not found to be effective since there were no differences between these genotypes. PC1 was mainly composed of internode length, fruit stem length, ripe fruit weight, sponge quality, sponge weight and 10-seed weight, while tendril length, stem thickness, the number of lateral shoots, fruit shape, and fruit skin texture were effective in PC2 formation. In PC3, on the other hand, was a component in which the variables such as stem pubescence, fruit rib, the diameter of the unripe fruit, flesh taste and texture, seed color, seed skin, and seed width had higher contributions compared to other variables. It was seen that many characters contributed significantly to the formation of the first three PCs. The main components and these highly correlated characters have emerged as the characteristics that should be emphasized in future wing studies, in which morphological differences will be more clearly revealed. It was seen that those based on measurement (quantitative) were more effective in determining the morphological differences.

The same group of data was also evaluated by the cluster analysis, another multivariate analysis method that currently applied in characterization studies (KAYACETIN, 2019). The related dendrograms are given in Figure 4. As seen in the dendrograms, genotypes formed six clusters. Cluster I consist of genotype '31 AN 02'. Cluster II consists of genotype '31 DE 07'. Cluster III consisted of 15 genotypes. The genotype '31 DÖ 06' also formed a separate cluster (Cluster IV). The genotypes '31 DE 02' and '31 DE 05' formed the Cluster V. Cluster VI, the last cluster, was also consisted of 15 genotypes. Clustering analysis made by considering morphological characters enabled genotypes to be included in different groups. However, some genotypes sampled from the same districts were included in the same group. For example, the genotypes '31 DE 02' and '31 DE 05' sampled from the Defne district and the '31 DÖ 02', '31 DÖ 03' and '31 DÖ 04' genotypes sampled from the Dörtüol district were in the same groups. However, evaluating all the genotypes together, it was seen that they were not generally clustered according to districts from which they were sampled. Although the sponge gourd brought from China used as a control was different from the genotypes selected from the Hatay Province, it was not included in a different group when evaluated in terms of morphological characters.

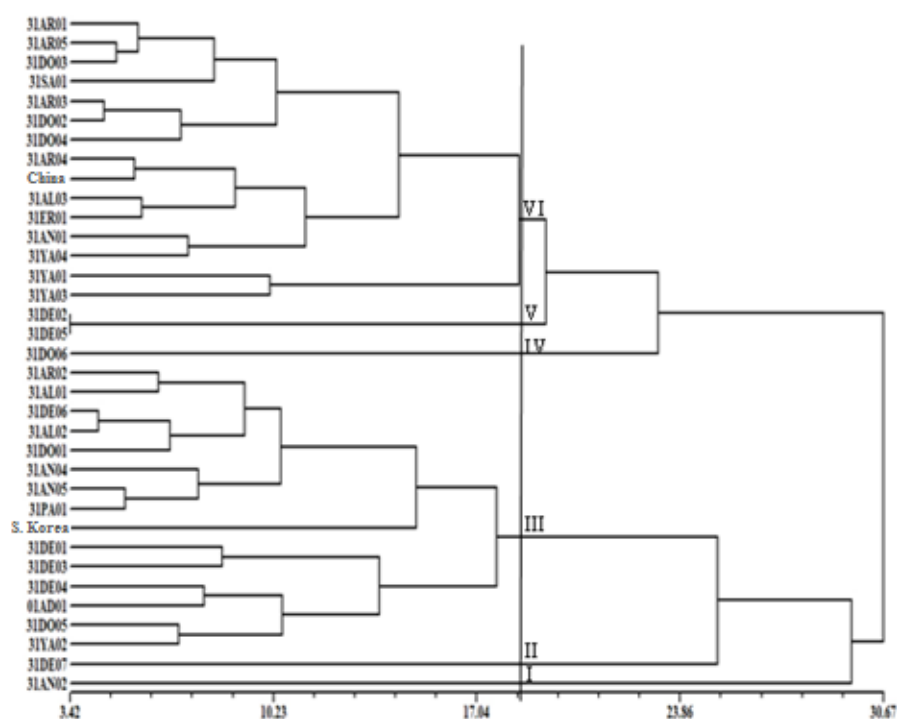


Figure 4. Groups obtained by cluster analysis of collected sponge gourd genotypes

Table 10. Mean values of the traits distinguished in principal component analysis of the groups obtained as a result of cluster analysis

| Characteristics | Means of clustering analysis groups | | | | | |
|-----------------------------------|-------------------------------------|-------|--------|-------|--------|-------|
| | I | II | III | IV | V | VI |
| Internode length (cm) | 14.27 | 12.51 | 14.14 | 10.04 | 14.44 | 13.86 |
| Tendrill length (cm) | 24.95 | 30.12 | 27.06 | 34.28 | 28.54 | 25.50 |
| Stem thickness (mm) | 5.92 | 6.44 | 6.12 | 6.74 | 6.48 | 6.02 |
| Number of lateral shoots (amount) | 8.00 | 16.00 | 10.70 | 20.00 | 9.70 | 10.80 |
| Peduncle length (cm) | 12.80 | 8.80 | 15.90 | 11.20 | 12.60 | 10.80 |
| Unripe fruit diameter (cm) | 3.86 | 3.51 | 2.93 | 2.66 | 3.09 | 3.29 |
| Fruit weight (g) | 130.10 | 55.90 | 144.20 | 29.10 | 174.60 | 79.40 |
| Sponge weight (g) | 30.50 | 27.90 | 34.10 | 5.80 | 36.30 | 20.50 |
| 100-seed weight (g) | 11.57 | 11.83 | 13.00 | 7.41 | 10.59 | 13.09 |
| Seed diameter (mm) | 8.53 | 8.81 | 8.36 | 6.25 | 7.74 | 8.35 |

Table 10 shows the evaluation of mean values of the measurable characteristics of the genotypes in clusters that were highly correlated as a result of principal components analysis. The groups were between 10.04 and 14.44 cm in terms of internode length, between 24.95 and 34.28 cm in terms of tendril length, between 5.92 and 6.74 mm in terms of stem thickness, between 8 and 20 in terms the number of lateral shoots, between 8.8 and 15.9 cm in terms of fruit stem length, between 2.66 and 3.86 cm in terms of fruit diameter, between 29.1 and 174.6 g in terms of ripe fruit weight, between 5.8 and 36.3 g in terms of sponge weight, between 7.41 and 13.09 g in terms of 100-seed weight, and between 6.25 and 8.81 mm in terms of seed width. Albeit not very wide, there were variations between the genotypes.

DISCUSSION

Within the scope of the study, sponge gourd genotypes showing different characteristics were collected from the different districts of Hatay Province. The observations and measurements were made on 49 different morphological characters in the collected genotypes and the obtained data were evaluated. Of the 49 characters, no variations between genotypes were determined for cotyledon color, stem shape, tendril, leaf margin, growth habit, flower sex and peduncle separation from fruit.

PANDEY *et al.* (2001) conducted a study to determine the diversity of Nepalese sponge gourd, and in 4 of 13 morphological characters (leaf size, tendril, seed color, and fruit stain) found no variations, while the other 9 characters were found to have variations. In the present study, no differences were found between the genotypes in terms of tendril whereas there were differences in seed color.

In studies conducted on pumpkins collected from the Black Sea Region (BALKAYA *et al.*, 2010), it has been reported that genotypes were not distributed into groups according to the geographical regions where they were collected. It has been stated that the distribution was according to fruit characteristics. Similarly, sponge gourds collected in this study were not distributed according to the districts from which they were collected.

Examining the plant growth characteristics in the genotypes (Table 3), in the seedling period, the genotypes in the present study had different cotyledon sizes. NGUYEN (2016) collected 39 sponge gourd genotypes from different regions in Vietnam. In the morphological characterization of these genotypes, it has been reported that cotyledon size, fruit weight, fruit length, and 100-seed weight values were the prominent characters. The mean internode length varied between 9.02 cm and 17.47 cm. Genotype '31 AR 04' had the shortest internode length whereas '31 DÖ 04' presented the longest internode length. YADAV *et al.* (2001) have reported that the internode length varied between 11.42 and 15.90 cm in the sponge gourd (*Luffa cylindrica* L.) genotypes selected from Nepal. Although the sponge gourd genotypes have developed strongly due to their prostrate character, a wide variation was observed between the internodes.

In terms of leaf shapes, genotypes were classified as round, reniform and oval-shaped according to the descriptor. The genotype suitable for consumption as a vegetable brought from South Korea and the *Luffa acutangula* L. genotype from China were observed to have oval leaves. Although small, intermediate, and large classification was made in the descriptor in terms of leaf size, the leaves of two genotypes were found to be much larger ('31 DE 02' and China).

The life-size values obtained in the present study were higher than those reported by YADAV *et al.* (2001). This was associated with the differences in genotypes in these studies as well as the nutritional and maintenance conditions of the plants. The differences between the leaves were not only in size large but also in leaf stem length (Table 4).

There were no differences between the genotypes in terms of flower color and flower sex (Table 5). The color of the flower was in different shades, but it was determined to be yellow, close to orange. Sponge gourd genotypes have been reported to have large yellow flowers in previous studies (HEISER and SCHILLING, 1990; ZHANG *et al.*, 2007; AKTAR, 2015). The genotypes were found to be monoic (in different parts of the plant of male and female flowers). In the studies, sponge gourd genotypes have been reported to be hermaphrodite, gnomonic and andromonoic (VARALAKSHMI and SUCHITHA, 2016). In the samples collected from the Hatay Province, genotypes of other flower types were not found. It was thought that this was due to the pollination and fertilization of monoic plants with continuous monoic plants.

Fruit shape was evaluated in three different aspects (Table 6). Examining all the fruits, no genotype was determined with an elliptical fruit. The sample genotypes for all the fruit shapes except for ellipse were included in the selected collection. PANDEY *et al.* (2001) have reported that the genotypes they collected from Nepal had genotypes with five different fruit shapes. In terms of unripe fruit color, dark green to light green colors were determined in the genotypes selected from Hatay. NGUYEN (2016) reported that the color of the unripe fruit was mostly light green. This may be due to the selection of genotypes used as vegetables.

The most important character that will facilitate the use of selected genotypes as vegetables is the unripe fruit taste. Since the cultivation in the Hatay region is for sponge production, local producers do not have any information about the unripe fruit taste. Especially in Hatay, in the Aknehir and Büyükçat neighborhoods of Defne district where sponge gourd cultivation was carried out in closed gardens, long local genotypes were developed with the selection of genotypes that yields long sponges. This caused the elimination of varieties with short fruits, sweet fruits, etc. by negative selection. One of the most important aims of the study, that was to prevent the loss of genetic diversity, has succeeded. Also, purification and quality studies should be continued to be used as an alternative vegetable in the following studies.

It was seen that the diversity of immature and mature fruit lengths was very wide. The mean length of unripe fruit ranged from 11.6 to 25.3 cm, while the mean length of ripe fruit ranged from 27.9 to 74.0 cm. In some studies, conducted in different countries, the mean length of unripe fruit has been reported as 15.1-48.6 cm (AKTAR, 2015), 34.8-36.6 cm (DAVIS, 1994), 14.8-21.8 cm (UMESH *et al.*, 2017), and 19.8-30.5 cm (ABHIJEET *et al.*, 2018) while the length of the ripe fruit varied between 29.3 and 43.7 cm (PHAN *et al.*, 2015). Since the lowest value in unripe fruit length in the present study was lower than those reported in the previous studies, it was thought that some genotypes may have been harvested in the early period since we do not fully know about their use as a vegetable.

Sponge quality and sponge weight characteristics of genotypes were also determined since it was important in the evaluation for the Hatay region and they were included in the descriptor, sponge quality was determined by the manual procedure as soft, medium and hard. A more scientific and technological determination of this property will allow the use of sponges in

different ways. The mean sponge weights of the genotypes after fruit peel separation ranged from 5.8 g to 57.9 g. In the literature, there were no studies on sponge properties (Table 7).

A wide variation was determined in the number of seeds in fruit. Examining the observations and measurements made on the seeds of the genotypes (Table 8), it was seen that the seeds had a structure called 'wings' unlike other vegetable and cucurbit seeds. While this structure was very prominent in some genotypes, it was indistinct in some genotypes. The China genotype seed had no wings. Seed colors were white, gray, brown and black. Although some studies have reported only brown and black seeds (HENEIDAK and KHALIK, 2015), the seed colors reported in the literature were consistent with the seed colors in this study (PRAKASH *et al.*, 2014). The seed weight (100 seeds) value ranged from 7.41 g to 16.48 g, and, likewise stated by PRAKASH *et al.* (2014), exhibited a significant diversity.

CONCLUSION

In the statistical cluster analysis, six different groups were determined between genotypes. It has been concluded that the descriptor used in morphological characterization was sufficient to determine the differences between the genotypes, however, due to the high similarities in some characteristics of the collected genotypes, these characters can be ignored in future studies. The descriptor used had unmeasurable criteria based only on observation. It may be useful to replace these criteria with some measurable characters to achieve clearer results.

Among the genotypes, 10 genotypes were selected which were estimated to be edible as fruit with a sweet taste. Sponge gourd, which is a fantastic vegetable in terms of its usage areas, deserves attention. Therefore, genotypes that have a favorable taste can be used in future studies to obtain pure lines and pave the way for their usability as vegetables. Thus, from this genetic source, besides its use as a vegetable, it will be determined that they can be used as a rootstock for sponge production and use as an ornamental plant and a genetic material pool will be formed for the varieties that can be developed by hybridization.

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**MORFOLOŠKA KARAKTERIZACIJA GENOTIPA SUNĐERA (*Luffa aegyptiaca* Mill.)
IZ ISTOČNOMEDITERANSKE REGIJE TURSKE**

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Izvod

Sa širokim spektrom genetskih resursa, Hatay je najveći proizvođač tikvica od sunđera u odnosu na ostale provincije Turske. Ova studija je sprovedena radi utvrđivanja statusa i morfološke raznovrsnosti stočarstva terenskim istraživanjem u okruzima provincije Hataj. Kao rezultat istraživanja prikupljena su 34 genotipa za koja se smatra da su morfološki različita. Kada su ispitane distribucije genotipova, genotipovi su odabrani između Arsuz (5 genotipova), Defne (7 genotipova), Samandağ (1 genotip), Antakya (5 genotipova), Dörtyol (6 genotipova), Yayladağı (4 genotipa), Altınözü (4 genotipa), Payas (1 genotip) i Erzin (1 genotip). Dva genotipa („31 AN 03“ i „31 AL 04“) iz kojih seme nije klijalo ekstrahovana su iz studija morfološke karakterizacije. Trideset i dva genotipa odabrana iz Hataja sa 3 genotipa dobijena iz Adane, Južne Koreje i Kine, ukupno 35 genotipova, upoređena su prema 49 različitih morfoloških karakteristika. Varijacije između genotipova nisu identifikovane za posmatranja ovih 49 karakteristika u vezi sa bojom kotiledona, oblikom stabljike, viticama, rubom lista, tipom pola i odvajanjem peteljke od ploda. Kao rezultat analize osnovnih komponenti i klaster analize na osnovu morfoloških karakteristika, genotipovi su uključeni u šest različitih grupa. Međutim, uticaj okruga u kojima su genotipovi prikupljeni na ovo grupisanje nije mogao da se utvrdi.

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