

# Morpho-Genetic Characterization of Fig (*Ficus carica* Var. *Rupestris* (Hausskn.) Browicz) Genotypes Aiming to Be Used As Rootstock

Ercan YILDIZ

Erciyes Üniversitesi: Erciyes Üniversitesi

Erdal Ağlar

Van Yuzuncu Yıl University: Van Yuzuncu Yıl Üniversitesi

Ahmet SÜMBÜL

Sivas Cumhuriyet Üniversitesi

mehmet yaman (✉ [mhmt.-07@hotmail.com](mailto:mhmt.-07@hotmail.com))

Erciyes Üniversitesi <https://orcid.org/0000-0002-2899-2238>

Oğuzhan ÇALIŞKAN

Hatay MKÜ: Hatay Mustafa Kemal Üniversitesi

Georghe Christian POPESCU

Universitatea din Pitesti

Monica POPESCU

Universitatea din Pitesti

Metin GÖNÜLTAŞ

Erciyes Üniversitesi: Erciyes Üniversitesi

---

## Research Article

**Keywords:** *Ficus carica* var. *Rupestris*, genetic resource, dwarf rootstock, morphological characteristic, molecular markers

**Posted Date:** June 15th, 2023

**DOI:** <https://doi.org/10.21203/rs.3.rs-3051615/v1>

**License:** © ⓘ This work is licensed under a Creative Commons Attribution 4.0 International License.

[Read Full License](#)

---

**Version of Record:** A version of this preprint was published at Genetic Resources and Crop Evolution on July 4th, 2023. See the published version at <https://doi.org/10.1007/s10722-023-01654-0>.

# Abstract

Türkiye, which has very rich gene resources, is the homeland of figs as well as many plant species. The common fig species found in the natural population of our country is *Ficus carica* var. *caprificus* (male figs), *Ficus carica* var. *domestica* (female figs; edible figs) and *Ficus carica* var. *rupestris*. In the study, morphological and molecular characterization of a total of 42 genotypes, including genotypes obtained by selection breeding method from the *Ficus carica* var. *rupestris* (Hauskn.) Browicz population, which is naturally spread in a limited area in Tunceli province, was performed. In this study, the qualitative and quantitative characteristics of 23 fig genotypes were evaluated. It was determined that tree growth habit, lateral shoot formation, apical dominance and leaf length characteristics had the highest effect on phenotypic descriptions in fig genotypes. The genetic relationship between the genotypes was demonstrated with 12 SRAP primer combinations and 9 ISSR primers. As a result of the study, it was determined that the genetic similarity values ranged between 0.52 and 0.94. According to the weight grading test results, the genotypes had scores between 290 and 910. In terms of these selection criteria, the genotype FCR-19 received the highest score with 910, while this genotype received 865 points with FCR-6, FCR-7, FCR-14, FCR-15, FCR-20, FCR-24, FCR-27, FCR-31 and FCR-42 genotypes followed. At the end of the study, very detailed results on the genetic variation in the fig population in the region were obtained by morphological features and molecular methods. The 7 genotypes selected were propagated to determine their potential for dwarf rootstocks. The results of the present study may provide significant leads for further studies on this subject. Dwarf rootstocks for grafting fig is an essential tool for modern fruit growing.

## INTRODUCTION

Fig, which is in the Morecea family and cultivated in the temperate climate of the Mediterranean basin, can be also grown in tropical and subtropical climate regions (Aksoy et al., 2007). Fig can be produced in a few countries due to its climatic and ecological demands, and its export is carried out by these countries (Ministry of Customs and Trade, 2018). Türkiye is one of these rare countries, and it ranks first among the world countries in the production of both dried and table figs. Although it changes depended on years, according to FAO data, the world fig production was approximately 1.3 million tons in 2020. Approximately 25% of the production is carried out by Türkiye. Especially dried figs are among the important agricultural products in the export of dried fruit of Türkiye. Fig is an important product for Türkiye in terms of providing income and employment as well as providing foreign exchange input. Another importance of fig is that it is rich in nutritional value and its contribution to human health (Ministry of Agriculture and Forestry, 2018). The common fig species found in the natural population of Türkiye is *Ficus carica* var. *caprificus* (male figs), *Ficus carica* var. *domestica* (female figs; edible figs) and *Ficus carica* var. *rupestris*. Ozbek (1978) reported that Anatolia has very rich fig forms, and these species are grouped into four subspecies, and they are *F. carica* var. *rupestris* (Hauskn), *F. carica* var. *kurdica* (Kotschy), *F. carica* var. *riparium* (Hauskn) and *F. carica* var. *Johannis* (Boiss). Tunceli province, which constitutes the study area, offers a great biodiversity due to its geographical properties, climatic

differences and very rich water resources, and draws attention with the presence of *Ficus* subspecies and botanical varieties. ,

As in many fruit species, the using of the possible dwarf rootstocks in figs ensures easier and more economical making of cultural practises such as harvesting and struggling with diseases and pests easier by reducing tree growth. Moreover, it increases the yield obtained from the unit area by allowing more planting per unit area, (Atkinson and Else, 2001). When the natural spread and growth characteristics of *Ficus carica* var. *rupestris* (Hausskn.) Browicz fig species are considered, it is thought that this species will make an important contribution to the development of traditional fig cultivation, especially as dwarf rootstock.

Molecular markers have been widely used in recent years for the accurate selection of breeding material and for the determination of genetic diversity. However, molecular markers play an important role in identifying genetic resources and the protecting of the breeder rights. RFLP (Khadari et al., 2005), RAPD (Salhi-Hannachi et al., 2006; Dalkilic et al., 2011), ISSR (Khadari et al., 2004), AFLP (Cabrita et al.) ., 2001; Baraket et al., 2009), SRAP (Ikten et al., 2010) and SSR (Ikegami et al., 2009; Aradhya et al., 2010; Caliskan et al., 2012; Essid et al., 2015; Caliskan et al., 2018) marker systems were used to reveal genetic diversity in *F. carica* var. *domestica* (female figs) and *F. carica* var. *caprificus* (male figs) species. There is no molecular study relative to *Ficus carica* var. *rupestris* (Hausskn.) Browicz. However, it has been reported that this species is included in the studies that carried out to determine the diversity in the natural flora of Türkiye by plant botanists. As a matter of fact, botanists reported that there are plants of this species in Baskil (Kursat et al., 2005) and Maden (Cakiloglu and Civelek, 2011) of Elazığ, in Berit Mountain (Yildiz, 2001) and Şekeroba (Ilcim et al., 2008) of Kahramanmaraş, in Tavşantepe (Yildiz et al., 2004) of Malatya, in Öğütçü and Uyuzpınar (Akan et al., 2005) of Şanlıurfa. This study was carried out to characterize morphologically and molecularly of 42 genotypes obtained by selection breeding method from the naturally spread *Ficus carica* var. *rupestris* (Hausskn.) Browicz population in a limited area in Tunceli province.

## MATERIALS AND METHODS

### Material

The study was carried out in Tunceli province, which is located in a high region surrounded by the extensions of the Eastern Taurus Mountains within the Euphrates basin in 2021 and 2022 years (Fig. 1). In Tunceli, the mountains turn into high plateaus by being deeply carved by surface waters and streams while the valleys are very narrow and steep. A very important bio-diversity has emerged in the province depending on the physical geography characteristics, climate differences and very rich water resources. There is a rich vegetation consisting of elm, maple, alder, ash, plane tree, vine, birch, walnut, wild hazelnut, poplar, willow and bush species in the Munzur Valley. The lower flora is rich in terms of oaks that are groves. In the flora of Munzur Valley National Park, which is very rich in vegetation, 1518 various plants are registered, 43 of which are endemic to the Munzur Mountains and 227 to Turkey (Anonymous, 2022).

As the plant material in the study, the genotypes of *Ficus carica* var. *rupestris* (Hauskn.) Browicz species, which grows naturally in the province, were used. It has been observed that there is a population that will represent morphological variation in 5 different areas where fig genotypes are intense. Within the scope of the project, 42 genotypes were selected as the basic material depending on the population density by scanning. 12 genotypes from Tunceli Central district, 5 genotypes each from Hozat and Mazgirt districts, and 10 genotypes each from Ovacık and Pülümür districts were evaluated. Tunceli province was chosen because it is the natural spread area of the aforementioned species and there was no study on fig there.

## Method

### Morphological characteristics

Analyzes of morphological descriptions of rootstock candidate genotypes determined depending on population density were evaluated with some modifications according to the “Fig Descriptor” developed by CIHEAM and IPGRI (Anonymous, 2003). The measurements made on the shoots (shoot length, shoot thickness and the leaf number of shoot) were carried out on 10 pieces annual shoots during the fruit ripening period. The shoot thickness was determined with a digital caliper in the middle of the annual shoot, and for the internode length, the class intervals were taken as reference the descriptor prepared by UPOV for apple rootstocks. 30 leaves located between the 3rd and 5th nodes of the shoot were harvested during the fruit ripening period, and leaf area readings were made with the aid of the electronic LI-3100 Area Meter (LI-COR-Biosciences). Measurements and subjective observations of fruit characteristics were made on 20 fruits harvested from different sides of the tree during the intensive fruit ripening period (August- September). Since the genotypes have very small fruits compared to the cultivated figs, the fruit size has been modified.

### Molecular characteristics

SRAP and ISSR techniques were used for the molecular characterization of 42 rootstock candidate genotypes. DNA extraction was performed by modifying the CTAB method of Doyle and Doyle (1990). In the PCR studies, SRAP primers, which were successfully applied by İkten et al. (2010) in fig, were used. The DNAs obtained were mixed and tested with 208 SRAP primer combinations (Me1-13; Em1-16). In PCR studies, 9 ISSR primers, which were used by Ikegami et al. (2009), were used. PCR products obtained from PCR studies performed in SRAP and ISRR techniques were loaded on a 2.0% agarose gel and run under 115 V electric current for 3.5 hours. After electrophoresis, the gels were taken to the gel imaging unit (Kodak Gel Logic 200, Eastman Kodak Company, USA) connected to the computer and the gel images were recorded on the computer under UV.

### The evaluation of the results

Principal Component Analysis (ANOVA) of all morphological data obtained in the study was carried out with the PRINCOMP process in the SAS package program and the morphological similarities of the genotypes were evaluated by cluster analysis PROC CLUSTER (with AVERAGE) command by using the PCA data. Correlation analysis was performed to determine feature (eigen) relationships. Subjective data

among the morphological data were converted into numerical information specified in the “Fig Descriptor” and used in principal component analysis. In the study, 100 bp DNA marker was used to evaluate the bands after electrophoresis for each primer. In the presence of bands; 1, in the absence of bands; 0 (zero), and in the absence of amplification; the bands seen on the gel were evaluated by giving the number 9, and these data were analyzed in the computer package program NTSYS (Numerical Taxonomy Multivariate Analysis System, NTSYS-pc version 2.1, Exeter Software, Setauket, N.Y., USA; Rohlf, 1988) in order to reveal the genetic relationships of individuals. Similarity index was calculated according to the Dice (1945) method. The obtained matrix was used for cluster analysis and a dendrogram was drawn with the UPGMA (Unweighted Pair Group Method using Arithmetic Average) method.

## RESULTS AND DISCUSSION

### Morphological characteristics

In the study, the wild fig (*Ficus carica var. rupestris* (Hausskn.) Browicz) genotypes were evaluated in terms of 23 different morphological characteristics, and the results of the distribution of genotypes in terms of the characteristics were presented in Fig. It is given in 2. In terms of tree shape, 40% (17 units) of genotypes showed creeping growth, 38% vertical (16 units) growth while 9 genotypes had splay and drooping growth characteristics. When the distribution of tree growth vigor among the genotypes was examined, it was determined that 50% (21 units) of them were medium, 38% (16 units) were weak, and 12% (5 units) were vigorous. In terms of apical bud dominance, 55% of the genotypes were absent class and 45% were in the present class. It was determined that 23 of the genotypes (55%) had lateral shoot formation and 19 (45%) did not have lateral shoot formation. It was determined that in the genotypes included in the study, the apical bud color was green in 48% (20 units), light green in 33% (14 units), and pinkish-brown (7 units) and brown (1 unit) in the remaining genotypes. It was determined that 55% (23 units) of the genotypes were in the middle class of the shoot length, 8 genotypes were weak and vigorous, and 3 genotypes were very vigorous in terms of this characteristics. When the distribution of shoot thickness of the genotypes was examined, only 1 genotype was found in the thick group while 52% (22 units) of the genotypes were medium and 45% (19) were thin. It was determined that in terms of internode length, 57% (24 units) of genotypes were short, 43% (18 units) were medium, and in terms of shoot color, 55% (23 units) of genotypes were gray, 45% (19 units) were green. 76% (32 units) of 42 genotypes had a high tendency to form bottom shoots, 7 genotypes showed medium and 3 genotypes showed low bottom shoot-forming characteristics. 74% (31 pieces) of the genotypes were in the middle class in terms of the number of leaves in the shoot, 8 genotypes were found to be more, 2 genotypes too many, and 1 genotype less in terms of this characteristic.

According to the distribution of the leaf shapes of the genotypes, it has been determined that 60% (25 units) of them were group H, 26% (11 units) were group G, 10% (4 units) were group C and 4% (2 units) were group A. In terms of the number of leaf lobes, 60% (25 units) of the genotypes were absent, 26% (11 units) were in the 3 lobes, 14% (6 units) were in the 5 lobes class. When the leaf length and width of the

genotypes were examined collectively, it has been determined that the genotypes were mostly in the middle class in terms of these characteristics 1 genotype had very large leaf length and 3 genotypes had very large leaf width. In terms of leaf area, 48% (20 units) of the genotypes were determined as small, 40% (17 units) as medium, 10% (4 units) large and 4% (1 unit) as very large. Considering the leaf hispidity in genotypes, it was determined that 29 (69%) of them were dense, 7 (17%) hairless, 5 (12%) sparse and 1 (4%) medium. In terms of leaf veining, 81% (34 units) of genotypes were very explicit, 19% (8 units) were explicit, and in terms of petiole length, 76% (32 units) of genotypes were short, 45% (10 units) was determined to be medium. In terms of leaf serrulation, all genotypes showed completely serrated characteristics. In terms of fruit size, 79% (33 units) of genotypes were determined as small and 21% (9 units) as medium. It was recorded that according to the distribution of the fruit shapes of the genotypes, 79% (33 units) of them were group C, 12% (5 units) were group E, 5% (2 units) were group A and 5% (2 units) were F group. It was determined that 48% (20 units) of the genotypes were low yielding, 29% (12 units) medium yielding and 24% (10 units) fruitfull. Considering the distribution of genotypes in terms of gender status, it was determined that 74% (31 units) of them were female and 26% (11 units) were male.

## **Principal Component Analysis**

PCA is performed to identify the models of the variation between genotypes and to differentiate variables in the data set (Iezzoni and Pritts, 1991). PCA analysis of table figs (Caliskan and Polat, 2008; Saddoud et al., 2008; Giraldo et al., 2010; Podgornik et al., 2010; Hssaini et al., 2020; Dogan et al., 2021) and wild figs (Khadivi-Khub et al. Anjam, 2014) is widely used to determine phenotypic diversity. The aim of this analysis is to classify the examined genotypes and to determine the effect levels of the examination criteria. The eigenvalues (eigen), percentages of variation and load coefficients of the first five components were calculated by using PCA analysis based on the correlation matrix for the criteria examined. In principal component analysis, the components with eigen greater than 1.00 were preserved to maintain the reliability of the final output. It was determined that the first five basic components constituted 20.87%, 13.21%, 10.66%, 9.58% and 7.11% of the variations, respectively, and the cumulative rate of the variation corresponded to 61.43% of the total variance (Table 1).

Table 1  
The variation values in principal components (PCs) in fig genotypes

| Characteristics             | PCA1        | PCA2         | PCA3         | PCA4         | PCA5         |       |
|-----------------------------|-------------|--------------|--------------|--------------|--------------|-------|
| Tree growth habit           | -0.09       | <b>-0.34</b> | -0.12        | 0,13         | -0,18        |       |
| Tree vigour                 | 0.08        | <b>0.33</b>  | <b>0.33</b>  | -0,25        | 0,18         |       |
| Apical dominancy            | 0.12        | <b>-0.36</b> | <b>0.31</b>  | 0,25         | 0,06         |       |
| Lateral shoot formation     | -0.12       | <b>0.36</b>  | <b>-0.31</b> | -0,25        | -0,06        |       |
| Terminal bud colour         | -0.03       | -0.01        | <b>0.31</b>  | -0,15        | 0,20         |       |
| Shoot length                | <b>0.32</b> | 0.09         | -0.03        | 0,17         | 0,22         |       |
| Shoot width                 | 0.22        | 0.13         | 0.05         | 0,14         | <b>-0,31</b> |       |
| Shoot internode length      | 0.14        | -0.03        | 0.05         | 0,09         | <b>0,45</b>  |       |
| Shoot colour                | -0.26       | 0.16         | -0.02        | -0,21        | 0,05         |       |
| Tendency to form suckers    | 0.08        | -0.29        | -0.06        | -0,04        | -0,05        |       |
| Number of leaves per shoot  | 0.26        | 0.14         | 0.15         | <b>0,33</b>  | 0,12         |       |
| Leaf shape                  | -0.18       | 0.11         | <b>0.38</b>  | 0,13         | <b>-0,41</b> |       |
| Number of lobes             | 0.20        | -0.16        | <b>-0.33</b> | -0,13        | <b>0,39</b>  |       |
| Leaf length                 | <b>0.30</b> | 0.27         | -0.16        | 0,05         | -0,10        |       |
| Leaf width                  | <b>0.35</b> | 0.01         | -0.16        | -0,01        | -0,12        |       |
| Leaf area                   | <b>0.33</b> | 0.15         | -0.09        | 0,02         | <b>-0,31</b> |       |
| Density of spicules on leaf | 0.23        | -0.07        | 0.05         | <b>-0,36</b> | -0,14        |       |
| Leaf venation               | -0.07       | 0.05         | <b>-0.37</b> | 0,08         | -0,05        |       |
| Petiole length              | <b>0.31</b> | 0.02         | 0.03         | 0,09         | -0,12        |       |
| Fruitlet size               | -0.21       | 0.12         | -0.14        | <b>0,46</b>  | 0,15         |       |
| Fruit shape                 | -0.16       | 0.23         | -0.05        | <b>0,38</b>  | 0,01         |       |
| Fruit yield                 | 0.01        | <b>0.38</b>  | 0.18         | 0,04         | 0,18         |       |
| Gender                      | 0.14        | -0.07        | 0.24         | -0,16        | -0,01        |       |
| Eigen value                 | 4.80        | 3.04         |              | 2.45         | 2.20         | 1.64  |
| Variattion (%)              | 20.87       | 13.21        |              | 10.66        | 9.58         | 7.11  |
| Total variattion (%)        | 20.87       | 34.08        |              | 44.74        | 54.31        | 61.43 |

It showed that the variance inferred by the five principal components (PC) decreased between PC1 and PC2, but the variance reduction slowed down from PC2. PC1 explained 20.87% of the total variance and occurred positive correlations represented by leaf width (0.35), leaf area (0.33), shoot length (0.32), petiole length (0.31) and leaf length (0.30). PC2 explained 13.21% of the total variance. The positive correlations were formed by productivity (0.38), lateral shoot formation (0.36) and tree growth vigor (0.33), but the negative correlations were formed by apical bud dominance (-0.36) and tree shape (-0.34). It explained 10.66% of the total variability in PC3. The observed positive correlations; leaf shape (0.38), tree growth vigor (0.33), apical bud dominance (0.31) and apical bud color (0.31) values were determined. The observed negative correlations; leaf veining status (-0.37), leaf lobe number (-0.33) and lateral shoot formation (-0.31) values were determined (Fig. 3).

## Molecular characterization

A total of 42 wild fig genotypes obtained from natural flora were used. Pre-screening was performed with SRAP primer combinations and ISSR primers by mixing the DNA samples obtained from these materials. As a result of these tests, PCR and electrophoresis were performed with 12 SRAP combinations (Table 2) and 9 ISSR primers (Table 3), in which the highest and scoreable number of polymorphic bands were obtained, and the bands were evaluated after gel imaging. A total of 93 bands were obtained from 12 SRAP primer combinations yielding PCR products, and 84.7% of them were polymorphic. On average, 7.8 bands were obtained per SRAP primers, and the number of polymorphic bands was calculated as 6.6 per primer. When the primers were compared in terms of the total number of bands, the highest number of bands was obtained from the Me6-Em13 primer combination with 13 bands, followed by Me8-Em4 with 12 bands and Me10-Em10 and Me5-Em3 primer combinations with 11 bands each. When the primers were examined in terms of polymorphism ratio, this ratio was 100.0% in the 4 primer combinations while the lowest ratio was 50.0% obtained from the Me7-Em5 primer combination.

Table 2  
*Total and polymorphic band numbers and polymorphism rates obtained as a result of using SRAP primer combinations in fig genotypes*

| Number | Primers   | Base lenght | Total Bant<br>Number | Polymorphic Bant<br>Number | Polymorphism<br>rate (%) |
|--------|-----------|-------------|----------------------|----------------------------|--------------------------|
| 1      | Me3-Em7   | 300–1000    | 5                    | 4                          | 80.0                     |
| 2      | Me13-Em16 | 150–900     | 8                    | 6                          | 75.0                     |
| 3      | Me8-Em8   | 250–850     | 9                    | 9                          | 100.0                    |
| 4      | Me7-Em9   | 190–570     | 5                    | 5                          | 100.0                    |
| 5      | Me11-Em12 | 300–400     | 2                    | 2                          | 100.0                    |
| 6      | Me10-Em10 | 200–1200    | 11                   | 9                          | 81.8                     |
| 7      | Me7-Em5   | 150–250     | 2                    | 1                          | 50.0                     |
| 8      | Me5-Em3   | 230–1100    | 11                   | 10                         | 90.9                     |
| 9      | Me6-Em13  | 150–1300    | 13                   | 11                         | 84.6                     |
| 10     | Me2-Em2   | 180–950     | 8                    | 7                          | 87.5                     |
| 11     | Me6-Em4   | 220–1050    | 7                    | 7                          | 100.0                    |
| 12     | Me8-Em4   | 180–1100    | 12                   | 8                          | 66.7                     |
| Total  |           | -           | 93                   | 79                         | -                        |
| Mean   |           | -           | 7.8                  | 6.6                        | 84.7                     |

70.5% of the 62 bands obtained from the 9 ISSR primers used in the study were polymorphic. Average 6.9 bands were obtained per ISSR primer, and the number of polymorphic bands was calculated as 4.9 per primer. When the primers were compared, the highest number of bands was obtained from the primers (GA)8YG (11 bands) and (AG)7YC (10 bands). When the primers were examined in terms of polymorphism rate, the polymorphism rate ranged between 20.0% and 100.0%, and the lowest rate was obtained from the (TCC)5RY primer.

Table 3  
*Total and polymorphic band numbers and polymorphism rates obtained by using ISSR primers in fig genotypes*

| Number | Primers                | Base lenght | Total Bant<br>Number | Polymorphic Bant<br>Number | Polymorphism<br>rate (%) |
|--------|------------------------|-------------|----------------------|----------------------------|--------------------------|
| 1      | (AG) <sub>8</sub> T    | 320–750     | 7                    | 4                          | 57.1                     |
| 2      | BDB(CA) <sub>7</sub> C | 250–950     | 6                    | 5                          | 83.3                     |
| 3      | DBDA(CA) <sub>7</sub>  | 350–1000    | 9                    | 6                          | 66.7                     |
| 4      | (AG) <sub>7</sub> YC   | 150–1100    | 10                   | 5                          | 50.0                     |
| 5      | (AGC) <sub>6</sub> G   | 200–900     | 7                    | 7                          | 100.0                    |
| 6      | (CA) <sub>8</sub> R    | 350–470     | 3                    | 2                          | 66.7                     |
| 7      | (CAC) <sub>3</sub> GC  | 250–600     | 4                    | 4                          | 100.0                    |
| 8      | (TCC) <sub>5</sub> RY  | 200–800     | 5                    | 1                          | 20.0                     |
| 9      | (GA) <sub>8</sub> YG   | 180–1200    | 11                   | 10                         | 90.9                     |
| Total  |                        | -           | 62                   | 44                         | -                        |
| Mean   |                        | -           | 6.9                  | 4.9                        | 70.5                     |

When the studies were examined, it is seen that the morphological characteristics were mainly used in plant species and variety identification. Until today, the genotypes have been defined by considering morphological parameters in studies on figs in Türkiye. However, it is among the common opinions of different researchers that these characteristics in plants are sensitive to environmental conditions. On the other hand, these criteria used are limited in number and do not allow to distinguish groups with different phenotypic characteristics (Khadari et al., 2003; Baraket et al., 2009). To solve these problems, the development of the molecular markers with full polymorphism continues today. For this purpose, DNA-based methods are used to identify polymorphism within and between species. Techniques such as RAPD, ISSR, SSR, and AFLP in fig species have been successfully used to identify the difference between genotypes (Khadari et al., 2003; Saddoud et al., 2005; Baraket et al., 2009).

Two main groups were formed in the pedigree obtained as a result of SRAP and ISSR analyzes on fig genotypes (Fig. 4). There were 3 genotypes (FCR-1, FCR-2 and FCR-28) in the first main group, the second main group was divided into two subgroups as II-A and II-B. There were 2 genotypes (FCR-19 and FCR-23) in group II-A, group II-B was divided into 2 subgroups. In the II-B-I group, only the FCR-29 genotype was formed, and in the II-B-II group, two more subgroups were formed, one with 11 genotypes and the other with 25 genotypes. Khadari et al. (2003) found an average of four alleles, between 2 and 6 at each locus,

in their study with six SSRs in 30 fig genotypes. They found that there were differences in the number of alleles detected from the same primers in the fig genotypes in two different research areas. Khadari et al. (2004) reported that they obtained 38 alleles from six SSR loci in their research on 75 fig genotypes. Researchers reported that the number of alleles at each locus ranged from 3 to 14, with an average of 6.3. Giraldo et al. (2005) examined 15 fig cultivars with 26 polymorphic SSR primers and reported that they detected between 2 and 8 alleles, with an average of three alleles and a total of 79 alleles. Bandelj et al. (2007) used 15 SSR primers in their study to identify some fig cultivars and genotypes. They detected four alleles from primer FCUP027-4, eight alleles from primer FCUP038-6, four alleles from primer FCUP066-7 and five alleles from primer FCUP068-1 in 22 fig genotypes. They reported that allele size, allele number, and expected and observed heterozygosity values of all primers used in the study varied between cultivars and genotypes. Ikegami et al. (2009) used 13 ISSR, 19 SSR and 13 RAPD marker combinations in their study with 19 fig genotypes selected from Europe and Asia. A total of 71 bands were obtained in ISSR primers, the rate of polymorphism ranged from 0% ((AGC)<sub>6</sub> primer) to 100% ((CA)<sub>8</sub>A and (CT)<sub>8</sub>G primers). On average, 5.5 bands were obtained per ISSR primer, and the number of polymorphic bands was determined as 3.5 per primer. It was emphasized that di-nucleotide repeats (ie, (AG)<sub>8</sub>T, (GA)<sub>8</sub>T and (CT)<sub>8</sub>T) are more informative than tri-nucleotide repeats. Caliskan et al. (2018) detected a total of 124 alleles at 15 loci in male fig genotypes. In the study, the total number of alleles in the loci varied between 3–14, but average number of alleles was determined as 8.3. The highest number of alleles was determined at the FCUP0038 and FCUP008 loci (14 alleles), and the lowest number of alleles was determined at the LMFC18 and LMFC23 loci (3 alleles).

According to the dendrogram created in the study, the similarity values varied between 0.52 and 0.94. The most genetically distant genotypes were FCR-2 with FCR-39 with 52% similarity, FCR-1 with FCR-8 with 53% similarity, FCR-1 with FCR-9 with 54% similarity, FCR-2 with FCR-7 and FCR-35 was also stated to be between FCR-1 and FCR-19, FCR-33 and FCR-39 genotypes with a similarity rate of 55%. The genetically closest genotypes were FCR-3 and FCR-6 with 94% similarity rate, these genotypes are seen to be ranked with FCR-3 and FCR-42 and FCR-4 and FCR-6 genotypes with 93% similarity rate. Genotypes with 90% or more similarity were genetically like each other. These were FCR-6 with FCR-42 (0.92), FCR-3 with FCR-4 (0.91), FCR-3 with FCR-15 and FCR-20, FCR-4 with FCR-20 and FCR-42 (0.90) genotypes. In the pedigree obtained because of the analysis of molecular data, 2 main groups were indicated. There are 3 genotypes (FCR-1, FCR-2 and FCR-28) in the first main group, the second main group was divided into two subgroups, one of them had 2 genotypes (FCR-19 and FCR-23), and the other (II-B group). ) consisted of 2 subgroups. It is stated that in the II-B-I group there were only FCR-29 genotypes, and in the II-B-I group there were two more subgroups, one with 11 genotypes and the other with 25 genotypes.

## CONCLUSION

In the study, morphological and molecular characterization of a total of 42 genotypes, including genotypes obtained by selection breeding method from the *Ficus carica* var *rupestris* (Hausskn.) Browicz population, which is naturally spread in a limited area in Tunceli province, was performed. When the graph drawn according to the position levels of the criteria examined in terms of morphological

characteristics is examined, the tree shape, lateral shoot formation, apical bud dominance and leaf length characteristics of the genotypes were in a different region compared to other characteristics. On the other hand, the apical bud color and leaf veining had the lowest effect on the differentiation of genotypes. The genetic relationship between the genotypes was demonstrated with 12 SRAP primer combinations and 9 ISSR primers. As a result of the study, it was determined that the genetic similarity values ranged between 0.52 and 0.94. In the pedigree obtained because of the analysis of molecular data, 2 main groups were formed. There were 3 genotypes (FCR-1, FCR-2 and FCR-28) in the first main group, the second main group was divided into two subgroups. There were 2 genotypes (FCR-19 and FCR-23) in one of them, 2 subgroups were formed in the other (group II-B). At the end of the study, very detailed data on the genetic variation in the wild fig population in the region were obtained by morphological features and molecular methods. According to the weighted rating (data do not show) of the fig genotypes, the genotypes had scores between 290 and 910. In this context, 7 genotypes were reproduced to be used in the determination of the dwarfing rootstock potential. We believe that comprehensive studies with these genotypes will contribute to the development of modern fig cultivation techniques in our country.

## Declarations

### Competing Interests

The authors have no relevant financial or non-financial interests to disclose.

### Acknowledgment

This study was supported by Scientific Research Projects Department of Erciyes University (Project no: FBA-2021-11015).

## References

1. Aksoy, U., Zafer, H.C., Meyvacı, B., Şen, F. (2007). Kuru İncir: Türk Sultanları Çekirdeksiz Kuru Üzüm, Kuru İncir ve Kuru Kayısı. Ege Kuru Meyve ve Mamulleri İhracatçıları Birliği, 139 s.
2. Anonim, (2022). <http://www.tunceli.gov.tr/doga-ve-cografya>
3. Anonymous, (2003). Descriptors for Figs. International Plant Genetic Resources Institute, Rome, Italy, and International Centre for Advanced Mediterranean Agronomic Studies, Paris, France.
4. Aradhya, M.K., Stover, E.D., Velasco, D., Koehmstedt, A. (2010). Genetic Structure and Differentiation in Cultivated Fig (*Ficus carica* L.). *Genetica*, 138: 681–694.
5. Atkinson, C., Else, M. (2001). Understanding How Rootstocks Dwarf Fruit Trees. Presented at the 44th Ann. IDFTA Con., February 17-21, Grand Rapids, Michigan.
6. Bandelj, D., Javornik, B., Jakse, J. (2007). Development of microsatellite markers in the common fig, *Ficus carica* L. *Molecular Ecology Notes*, 7, 1311-1314.

7. Baraket, G., Chatti, K., Saddoud, O., Mars, M., Marrakchi, M., Trifi, M., Hannachi, A.S. (2009). Genetic Analysis of Tunisian Fig (*Ficus carica* L.) Cultivars using Amplified Fragment Length Polymorphism (AFLP) Markers. *Sci. Hort.*, 120: 487-492.
8. Cabrita, L.F., Aksoy, U., Hepaksoy, S., Leitao, J.M. (2001). Suitability of Isozyme, RAPD and AFLP Markers to Assess Genetic Differences and Relatedness among Fig (*Ficus carica* L.) Clones. *Sci. Hort.*, 87: 261-273.
9. Çakıloğlu, U., Civelek, Ş. (2011). Flora of the Region between Copper Mine and Tekevler Village (Maden-Elâziğ/Turkey). *Biological Diversity and Conservation*, 4(1): 54-66.
10. Çalışkan, O., Polat, A.A. (2008). Fruit Characteristics of Fig Cultivars and Genotypes Grown in Turkey. *Science Horticulture*, 115(4): 360-367.
11. Çalışkan, O., Bayazit, S., Ilgın, M., Karataş, N., Ergül, A. (2018). Genetic Diversity and Population Structure in Caprifigs (*Ficus carica* var. *caprificus*) using SSR Markers. *Spanish Journal of Agricultural Research*, 16(3): 1-12.
12. Çalışkan, O., Polat, A.A., Çelikkol, P., Bakır, M. (2012). **Molecular Characterization of Autochthonous Turkish Fig Accessions**. *Spanish Journal of Agricultural Research*, 10: 130-140.
13. Dice, L.R. (1945). Measures of the Amount of Ecologic Association between Species, *Ecology*, 26, 297-302.
14. Doğan, A., Kurt, H., Özrenk, K. (2021). İncir (*Ficus carica* L.) Genotipleri Arasındaki Fenotipik Varyasyonun Kümeleme ve Temel Bileşen Analizi Metodu ile Belirlenmesi. *Turk. J. Agric. Res.*, 8(3): 282-294.
15. Doyle, J., Doyle, J.L. (1990). Isolation of Plant DNA from Fresh Tissue, *Focus*, 12: 13-15.
16. Essid, A., Aljane, F., Ferchichi, A., Hormaza, J.I. (2015). Analysis of Genetic Diversity of Tunisian capri Fig (*Ficus carica* L.) Accessions using Simple Sequence Repeat (SSR) Markers. *Hereditas*, 152(1): 1-7.
17. Flaishman, M.A., Rover, V., Stover, E. (2008). The Fig: Botany, Horticulture and Breeding. *Hort. Rev.*, 34: 113-197.
18. Giraldo, E., López-Corrales, M., Hormaza, J.I. (2010). Selection of the Most Discriminating Morphological Qualitative Variables for Characterization of Fig Germplasm. *Journal of the American Society for Horticultural Science*, 135(3): 240-249.
19. Giraldo, E., Viruel, M. A., López-Corrales, M., Hormaza, J.I. (2005). Characterization and Cross-Species Transferability of Microsatellites in the Common Fig (*Ficus carica* L.). *J. Hortic. Sci. Biotechnol.*, 80: 217-224.
20. Hssaini, L., Hanine, H., Razouk, R., Ennahli, S., Mekaoui, A., Ejilani, A., Charafi, J. (2020). Assessment of Genetic Diversity in Moroccan fig (*Ficus carica* L.) Collection by Combining Morphological and Physicochemical Descriptors. *Genetic Resources and Crop Evolution*, 67(2): 457- 474
21. Iezzoni, A.F., Pritts, M.P. (1991). Applications of Principal Component Analysis to horticultural research. *HortScience*, 26(4): 334-338.

22. Ikegami, H., Nogata, H., Hirashima, K., Awamura, M., Nakahara, T. (2009). Analysis of Genetic Diversity among European and Asian Fig Varieties (*Ficus carica* L.) using ISSR, RAPD and SSR Markers. Genet. Resour. Crop Ev., 56: 201-209.
23. Khadari, B., Grout, C., Santoni, S., Kjellberg, F. (2005). Contrasted Genetic Diversity and Differentiation among Mediterranean Populations of *Ficus carica* L.: A Study using mtDNA RFLP. Gen. Res. Crop Ev., 52: 97-109.
24. Khadari, B., Hochu, I., Santoni, S., Oukabli, A., Ater, M., Roger, J.P., Kjellberg, F. (2003). Which molecular markers are best suited to identify fig cultivars: a comparison of RAPD, ISSR and microsatellite markers. Acta Horticulturae, 605, 69-75.
25. Khadari, B., Oukabli, A., Ater, M., Mamouni, A., Roger, J.P., Kjellber, F. (2004). Molecular Characterization of Moroccan Fig Germplasm using Intersimple Sequence Repeat and Simple Sequence Repeat Markers to Establish a Reference Collection. Hort. Sci., 40(1): 29-32.
26. Khadivi, A., Anjam, R., Anjam, K. (2018). Morphological and Pomological Characterization of Edible Fig (*Ficus carica* L.) to Select the Superior Trees. Scientia Horticulturae, 238: 66-74.
27. Khadivi-Khub, A., Anjam, K. (2014). Characterization and Evaluation of Male Fig (*caprifig*) Accessions in Iran. Plan Systematics and Evolution, 300(10): 2177- 2189.
28. Kürşat, M., Civelek, Ş., Türkoğlu, İ. (2005). Elâziğ, Baskil Merkez İlçe-Altınkürek Köyü (Keban) Arasındaki Yüksek Sahanın Florası. Fırat Üniversitesi Fen ve Müh. Bil. Der., 17(3): 541-557.
29. Norman, P.E., Tongoona, P., Shanahan, P.E. (2011). Determination of Interrelationships among agr-Morphological Traits of Yams (*Discorea* spp.) using Correlation and Factor Analyses. Journal of Applied Biosciences, 45: 3059-3070.
30. Özbek, S. (1978). Özel Meyvecilik (Kışın Yaprığını Döken Meyve Türleri). Çukurova Üniv. Ziraat Fakültesi Yayınları: 128, Ders Kitabı: 11, Adana.
31. Podgornik, M., Vuk, I., Vrhovnik, I., Mavsar, D.B. (2010). A Survey and Morphological Evaluation of Fig (*Ficus carica* L.) Genetic Resources from Slovenia. Scientia Horticulturae, 125(3): 380-389.
32. Rohlf, F.J. (1988). NTSYS-pc Numerical Taxonomy and Multivariate Analysis System, Version 2.11V. Exeter software, Setauket, New York.
33. Saddoud, O., Baraket, G., Chatti, K., Trifi, M., Marrakchi, M., Salhi-Hannachi, A., Mars, M. (2008). Morphological Variability of Fig (*Ficus carica* L.) Cultivars. International Journal of Fruit Science, 8(1-2): 35-51.
34. Saddoud, O., Salhi-Hannachi, A., Chatti, K., Mars, M., Rhouma, A., Marrakchi, M., Trifi, M. (2005). Tunisian fig (*Ficus carica* L.) genetic diversity and cultivar characterization using microsatellite markers. Fruits, 60, 143-153.
35. Salhi-Hannachi, A., Chatti, K., Saddoud, O., Mars, M., Rhouma, A., Marrakchi, M., Trifi, M. (2006). Genetic Diversity of Different Tunisian Fig (*Ficus carica* L.) Collections Revealed by RAPD Fingerprints. Hereditas, 143: 15-22.
36. T.C. Ekonomi Bakanlığı (2017), Kuru İncir Sektör Raporları, İhracat Genel Müdürlüğü Tarım Ürünleri Daire Başkanlığı.

37. T.C. Gümrük ve Ticaret Bakanlığı Kooperatifçilik Genel Müdürlüğü 2017 Yılı Kuru İncir Raporu Nisan, (2018)
38. TC. Tarım ve Orman Bakanlığı, (2018). <https://www.tarim.orman.gov.tr/Konular/Tarimsal-Destekler>
39. Yıldız, B. (2001). **Floristical Characteristics of Berit Dağı (Kahramanmaraş)**, Turkish Journal of Botany, 25: 63-102.
40. Yıldız, B., Bahçecioğlu, Z., Arabacı, T. (2004). Floristic Characteristics of Beydağı (Malatya), Turk. J. Bot., 28(4): 391-419.

## Figures

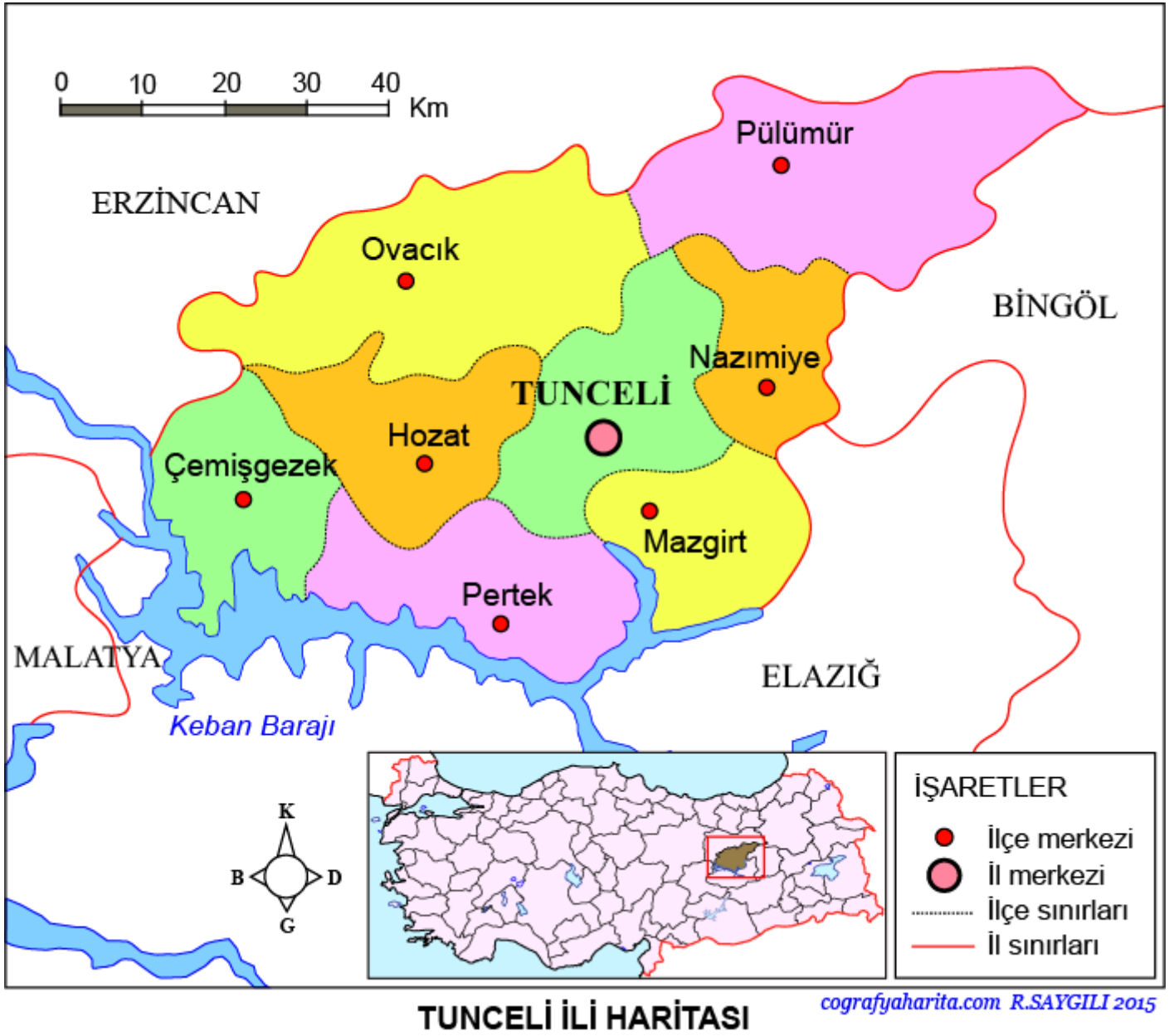


Figure 1

Tunceli province map

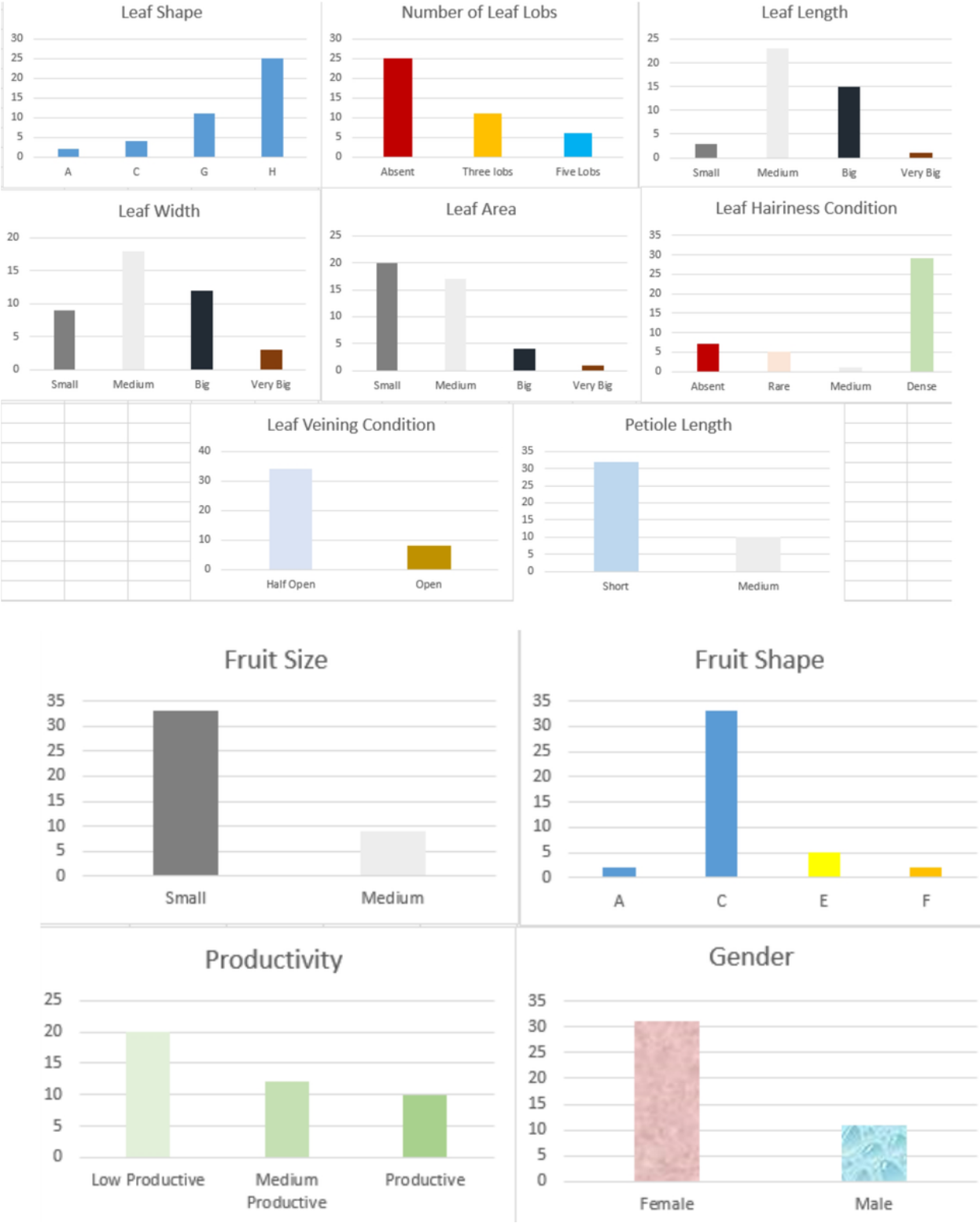
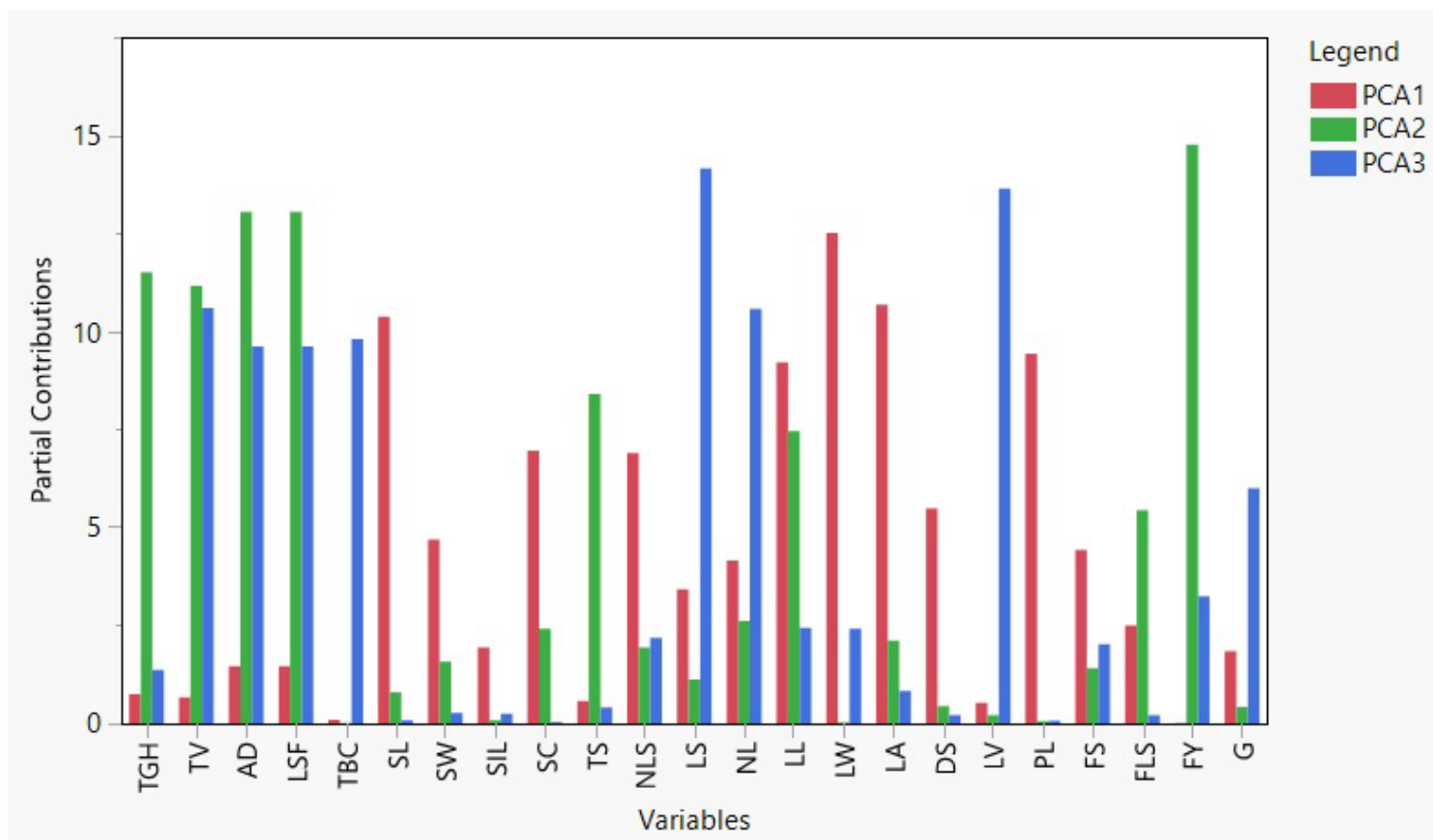


Figure 2

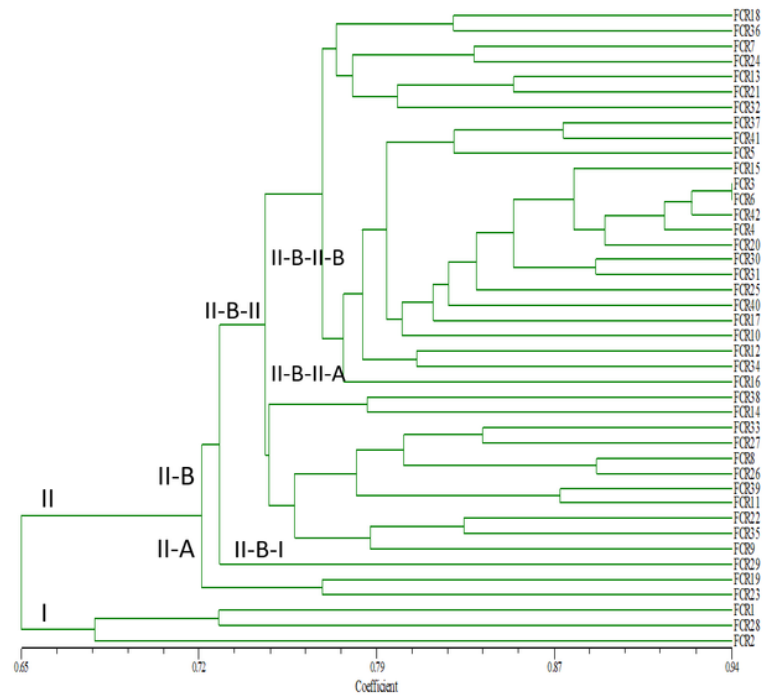
The distribution of some morphological characteristics of fig plants.



**Figure 3**

The range of the variation in morphological characters according to the first 3 basic components

TGH: Tree growth habit, TV: Tree vigour, AD: Apical dominance, LSF: Lateral shoot formation, TBC: Terminal bud colour, SL: Shoot length, SW: Shoot width, SIL: Shoot internode length, SC: Shoot colour, TS: Tendency to form suckers, NLS: Number of leaves per shoot, LS: Leaf shape, NL: Number of lobes, LL: Leaf length, LW: Leaf width, LA: Leaf area, DS: Density of hairs/spicules on leaf upper surface, LV: Leaf venation, PL: Petiole length, FS: Fruit shape, FLS: Fruitlet size, FY: Fruit yield, G: Gender



**Figure 4**

*Dendrogram obtained by using SRAP and ISSR data on fig genotypes.*