

Folia Hort. 33(1) (2021): 49-78

DOI: 10.2478/fhort-2021-0005

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RESEARCH ARTICLE

http://www.foliahort.ogr.ur.krakow.pl

## Genetic characterisation and population structure analysis of Anatolian figs (*Ficus carica* L.) by SSR markers

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## ABSTRACT

The common fig (*Ficus carica* L.) is a tree species and is one of the oldest fruit trees cultivated in Turkey. The Western Anatolian region of Turkey produces nearly a quarter of the total dried fig production of the world. This region also harbours a rich fig germplasm. However, so far this germplasm has remained largely uncharacterised. In this study, using 14 simple sequence repeat (SSR) primer pairs, we analysed a total of 310 fig accessions from six different regions of Anatolia. In structure analyses, Western Anatolian accessions formed a group, which was correlated with their geographical distribution. In addition, 7 identical, 36 synonymous, and 22 homonymous fig accessions were identified. In multilocus lineages (MLLs) analysis a total of 54 accessions were matched to different accessions as clone assignment. The results will facilitate future germplasm management and breeding efforts in this economically important tree species by identifying genetic diversity, genetic relations and characterising the structure of studied populations and accessions.

Keywords: Anatolia germplasm, Ficus carica L., genetic structure analysis, microsatellite

## **INTRODUCTION**

The common fig (*Ficus carica* L.; 2n = 2x = 26) is one of the earliest cultivated tree species from Moraceae, a family which is constituted by approximately 40 genera and over 1,400 species (Boudchicha et al., 2018). The fig was originated from a region in western Asia, between the Caspian Sea and Northeast Turkey, and has

been spread through the Mediterranean basin (Stover et al., 2007; Caliskan et al., 2012; Gündeşli, 2020). Fig trees can be found throughout Turkey in the internal valleys of Central and Southeast Anatolia as well as in regions near the Black Sea, Marmara, the Aegean and the Mediterranean coast. The world fresh fig production

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in 2017 was more than 1 million tons and Turkey, with around 305,450 tons of annual fig production, was the top fig-producing country in the world. Turkey was followed by Algeria and Egypt with 131,798 tons and 167,622 tons of annual fig production, respectively (FAO, 2017). The fig tree has not been the subject of intensive breeding efforts. Therefore, in case of precise identification and classification, existed rich genetic diversity within the fig populations could be exploited (Perez-Jiménez et al., 2012).

Morphological characters and chemical properties are considered to be an option for the selection and classification of fruits' germplasm (Polat et al., 2015; Gündeşli et al., 2020; Kafkas et al., 2020). The advent of DNA-based genetic characterisation methods of fruits germplasm, especially the simple sequence repeat (SSR) or microsatellite markers, have circumvented some of the limitations associated with the use of morphological traits and chemical properties in germplasm characterisation (Giraldo et al., 2004; Zavodna et al.; 2005, Bandelj et al., 2007; Chatti et al., 2010; Wang et al., 2011; Ikhsan et al., 2016; Güney et al., 2018; Güney et al., 2019; Yılmaz et al., 2020). SSRs have several advantages over morphological markers due to their co-dominant inheritance and transferability, hyper-variability and the ease of assessment (Xu et al., 2013; Zaloglu et al., 2015).

Indeed, SSRs were successfully used for genetic characterisation of figs procured from various regions of the world (Giraldo et al., 2008; Boudchicha et al., 2018; Saddoud et al., 2008; Do Val et al., 2013; Abou-Ellail et al., 2014; Ferrara et al., 2016; Costa et al., 2017). However, only a few studies using molecular markers were conducted previously on a limited number of Anatolian fig accessions. Akbulut et al. (2009) analysed 14 wild figs from the Coruh valley located near the

Black Sea coast of Turkey by RAPD markers. Similarly, Ikten et al. (2009) analysed the population structure of some female Anatolian fig accessions by DNA markers. The genetic diversity of fig accessions from the Hatay province of Turkey was evaluated through the SSR analysis by Caliskan et al. (2012). Further, Belttar et al. (2017) estimated genetic relationships among 86 fig accessions collected from Algeria and Turkey using 16 SSR primers.

In the current study, a total of 310 Anatolian fig accessions that included both male and female figs were analysed using 14 SSR markers. Possible associations between these fig accessions were examined using different structure analysis methods and a comprehensive SSR database was developed by identifying clones, synonymous (genetically similar accessions known by different names) and homonymous (genetically different accessions known by the same name) fig accessions.

#### **MATERIALS AND METHODS**

#### Plant material

We used 310 fig accessions which were collected from different eco-geographical sites (Figure 1) in Anatolia and deposited at the National Fig Germplasm Repository, Fig Research Institute, Erbeyli-Aydın, Turkey. The names, accession numbers, locations and the gender of the figs studied here are presented in Supplementary Table 1.

#### DNA isolations

DNA was extracted from leaf tissue as described by Lefort et al. (1998) and its concentration was estimated spectrophotometrically as described in detail by Akçay et al. (2014) and Burak et al. (2014).



**Figure 1.** Eco-geographical sites of Anatolian fig accessions used in this study. The number of fig accessions collected from each different eco-geographical province is given in brackets.

Locus no	Locus name	N	Не	Но	PI
L1	MFC1	6	0.592	0.845	0.362
L2	MFC2	9	0.706	0.680	0.198
L3	MFC3	8	0.554	0.409	0.373
L4	MFC8	6	0.339	0.319	0.505
L5	FCUP008-2	11	0.763	0.761	0.161
L6	FCUP027-4	9	0.778	0.732	0.135
L7	FCUP038-6	15	0.805	0.696	0.093
L8	FCUP066-7	8	0.701	0.754	0.240
L9	FCUP068-1	11	0.726	0.748	0.189
L10	FCUP070-2	11	0.831	0.764	0.094
L11	LMFC23	2	0.413	0.383	0.600
L12	LMFC25	5	0.521	0.532	0.424
L13	LMFC30	9	0.833	0.819	0.093
L14	FM4-70	6	0.736	0.658	0.212
	Mean	7.75	0.652	0.685	_

**Table 1.** Genetic parameters of Anatolian fig accessions

 examined in this study.

Allele numbers (*N*), expected heterozygosity (*He*), observed heterozygosity (*Ho*) and probability of identity (*PI*) values for the SSR loci are shown.

#### SSR analysis

Fourteen SSR markers, namely MFC1, MFC2, MFC3, MFC8 (Khadari et al., 2001), LMFC23, LMFC25, LMFC30 (Giraldo et al., 2005), FCUP068-1, FCUP038-6, FCUP008-2, FCUP070-2, FCUP027-4, FCUP066-7 (Bandelj et al., 2007) and FM4-70 (Zavodna et al., 2005) were used in this study (Supplementary Table 2). PCR amplifications were performed as previously described by Akçay et al. (2014). Briefly, 15-200 ng DNA, 0.5 mM dNTP, 5 pmol of labelled forward and reverse primers, 0.5 unit DNA polymerase (Promega) (containing 1.5 mM MgCl<sub>2</sub>) and 1 µl 10X buffer were used and a total of 10 µl of PCR reaction mixture was prepared. PCR program: 1 cycle (94°C for 3 min), 35 cycles (94°C for 1 min, 53–58°C depending on the primers for 1 min, 72°C for 2 min), followed by 72°C for 10 min and 4°C forever (Supplementary Table 2). The amplification control of PCR products was checked by 2% agarose gel electrophoresis.

Capillary electrophoresis conditions were previously described by Akçay et al. (2014) and Burak et al. (2014) in detail. A Beckman CEQ fragment analysis software was used to determine the allele size of each SSR locus. The analyses were repeated at least twice to ensure that the results are reproducible. In each run, 'Sarılop' and 'Kadota' cultivars were included as controls.

For each locus, the number of alleles (n), allele frequency, expected (He) and observed heterozygosity (Ho) and the probability of identity (PI) values were calculated as previously described (Akçay et al., 2014; Burak et al., 2014). The software IDENTITY was used to detect identical accessions; the proportion of shared alleles was calculated using Microsat (version 1.5) (Minch et al., 1995) and a dendrogram was constructed with the unweighted pair-group method with arithmetic

Excluding the Beyaz Bukele accession which showed tri allelic cases for SSR loci, the Arlequin software (Excoffier et al., 2005) was used to estimate the population genetic parameters of 309 diploid fig accessions. A neighbour-joining tree constructed from Nei's genetic distances was used (1972). Genetix 4 (Belkhir et al., 1996–1998) was used to perform factorial correspondence analysis (FCA) and gene flow estimates. We used the BAPS (Bayesian Analysis of Population Structure) software (version 6.0) (http://www.helsinki. fi/bsg/soft-ware/BAPS) (Corander et al., 2008) to analyse individual elements of data from each province to distinguish population structures. The STRUCTURE software (Pritchard et al., 2000) was employed to analyse population structures of fig accessions. In these analyses, the same computing parameters were used with the exception of measuring the K level for K:1-8 for unknown reconstructed panmictic populations (RPPs) with 25 replications as reported by Pereira-Lorenzo et al. (2018). Structure Harvester (Earl and von Holdt, 2012) was also used for the estimation of the best K value supported by the data (Evanno et al., 2005). We used Bayesian model-based clustering methods to identify RPPs. The number of accessions strongly assigned to each RPPs was determined based on the qI (probability of membership) probabilities greater than 80%.

For clone differentiation, the GenAlEx v6.5 program (Peakall and Smouse, 2012) was used to identify multilocus genotypes (MLGs) in populations. Using the same program, number of different alleles (*Na*), effective alleles (*Ne*), observed heterozygosity (*Ho*), Nei's (1978) unbiased expected heterozygosity (*uHe*) and private alleles summary (*PAS*) values for each population were determined.

In addition, a histogram of pairwise distances generated using the software GenoType v1.2 (Meirmans and van Tienderen, 2004) was used to determine whether somatic mutations are present. A possible number of clones (representing clone number) and Simpson's diversity based on multilocus lineages (MLLs) calculations was conducted using the GenoDive v1.1 program (Meirmans and van Tienderen, 2004). In addition, an effective number of genotypes (accessions) (eff), genotypic diversity (div), eveness (eve) and Shannon-Wiener (shw) diversity index values were calculated using the GenoDive v1.1 program. In the analysis of MLGs, different mutational threshold or T values (T shows the maximum distance allowed to identify a clone between two individuals with the same 'MLG (accession)' value) were tested (e.g. from threshold = 0 to threshold = 10) to minimise potential scoring errors and mutational problems. The groupings of MLGs within MLLs were considered, and the accessions with similar mutational threshold values were considered to represent the clones.

#### RESULTS

#### SSR analysis

In this study, a total of 310 fig accessions were analysed for 14 SSR loci and a total of 124 alleles were identified. The lowest number of alleles (2) was observed for the LMFC23 and the highest number of alleles (15) was found for the FCUP038-6 locus. The average allele number per locus was 7.75 and the mean *He* and *Ho* values were 0.652 and 0.685, respectively. The highest *Ho* values of 0.845 and 0.819 were observed for MFC1 and LMFC30, and the lowest values of 0.319 and 0.383 for MFC8 and LMFC23, respectively. FCUP038-6 with 15 alleles (*PI*: 0.093), FCUP070-2 with 11 alleles (*PI*: 0.094) and LMFC30 with 9 alleles (*PI*: 0.600) with two alleles was the least informative locus (Table 1).

#### Genetic relationships of fig accession groups

Various genetic parameters, such as *Ho* and *He*, polymorphic loci and the mean number of alleles per locus, estimated for six fig accession groups, are summarised in Table 2.

The highest gene flow (Nm) (31.23) was found between Central Anatolia and Marmara accession groups and the lowest gene flow (2.94) was found between Aegean and Black Sea accession groups (Table 3). Genetic similarity between the accessions was estimated using the coefficient for Nei's standard genetic distance (1972) (Supplementary Table 3), which showed relatively high genetic similarities. The tree constructed using neighbour-joining analysis was consistent with the findings from genetic distance analyses (Supplementary Figure 1).

Marmara accessions showed relatively high similarity to the geographically close Aegean and Central Anatolian accessions with high gene flow rates (10.16 and 31.23, respectively) between these accession groups (Supplementary Figure 1, Table 3 and Supplementary Table 3). Southeast Anatolian accessions showed relatively low similarity to the accessions from other regions, especially to Aegean and Central Anatolia groups, as evidenced by high genetic distance and low gene flow values. Overall, genetic distance and adjacent joining analyses revealed that genetic similarities between the groups were high.

The FCA (Figure 2) showed partial sub-structuring of fig accession groups. Mediterranean and Black Sea accessions were grouped separately and showed relatively little overlap with other accession groups. Southeast Anatolian accessions were similar to Mediterranean and Black Sea accessions and showed a partial overlap with these two groups (Figure 2). In contrast, Aegean and Marmara accessions showed a strong overlap with accessions from Central Anatolia, most likely due to potential gene flows occurring between these populations (Table 3).

**Table 2.** Expected and observed heterozygosities, polymorphic locus at both 95% and 99% probability levels and the mean number of alleles per locus in six Anatolian fig populations (sample size of each population).

Populations (sample size	Heteroz	zygosity	Polymorphic locus		Mean of alleles/loci
of each population)	Hexp	Hobs	P(0.95)	P(0.99)	
Aegean (157)	$0.624\pm0.146$	$0.625\pm0.160$	1.000	1.000	6.86
Central Anatolia (11)	$0.625\pm0.154$	$0.623\pm0.214$	1.000	1.000	4.79
Mediterranean (42)	$0.658 \pm 0.176$	$0.668\pm0.192$	1.000	1.000	6.36
Marmara (53)	$0.655\pm0.193$	$0.685\pm0.219$	1.000	1.000	6.36
Black Sea (34)	$0.641 \pm 0.169$	$0.687\pm0.209$	1.000	1.000	5.50
Southeast Anatolia (13)	$0.638\pm0.185$	$0.687\pm0.221$	1.000	1.000	5.50

Genetic differentiation (*Fst*) values are shown in Table 3. Based on the *Fst* values, some accession groups were significantly different from others (Table 3).

**Table 3.** Pairwise population differentiation (*Fst*) and gene flow (*Nm*) between Anatolian fig populations.

Populations (Fst/Nm)	Aegean	Central Anatolia	Mediterranean	Marmara	Black Sea
Aegean	-				
Central Anatolia	0.035***/6.92	_			
Mediterranean	0.067***/3.50	0.067***/3.47	_		
Marmara	0.024***/10.16	0.007ns/31.23	0.048***/4.92	-	
Black Sea	0.078***/2.94	0.043***/5.40	0.068***/3.41	0.037***/6.40	_
Southeast Anatolia	0.71***/3.26	0.069***/3.39	0.028**/8.70	0.048***/4.90	0.054***/4.28

Ns, not significant.

\*\**p* < 0.01.

\*\*\*p < 0.001.



**Figure 2.** FCA of six fig populations. Different colours indicate different geographical regions where different fig accessions are originated from. The first axis of the FCA accounts for 38.76% of the variation within the data whereas the second axis accounts for an additional 28.63%. Both axes together account for 67.39% of the variability in the dataset. FCA, factorial correspondence analysis.

Southeast Anatolian accessions, which showed relatively high genetic distance from the accessions of other regions, displayed a homogenous (monocoloured) BAPS structure (Supplementary Table 3 and Supplementary Figure 2). Central Anatolia, which showed overlap with other regions in the FCA, formed a homogenous structure according to the BAPS analysis. Marmara accessions, which showed the low genetic distance to other populations with a significant overlap in the FCA, displayed an admixture BAPS structure (Figure 2; Supplementary Figure 2).

#### Genetic relationships of Anatolian fig accessions

In this study, we identified 22 homonymous (genetically different accessions known by the same name), 36 synonymous (genetically same accessions known by the different name) and 7 identical accession groups (Supplementary Tables 4–6).

A maximum K value at K = 2 corresponding to the two main RPPs (Figure 3; Supplementary Figure 3; Supplementary Tables 1 and 2) (RPP1 and RPP2) was identified using STRUCTURE analyses of diploid fig populations. Furthermore, RPP analyses showed that 87% (271) of accessions could be assigned to individual RPPs with at least 80% probability whereas 13% of accessions either could not be assigned or could be assigned only with a low probability value to a representative RPP (Figure 3).

RPP1 contained 81% of the Aegean population, followed by Central Anatolia (55%) and Marmara (51%) populations. In RPP1, 127 out of 165 accessions (77%) were observed with a probability of membership ratio qI (>80%), whereas a total of 38 accessions (23%) of different populations were identified as <80%. In RPP1, the highest number of accessions (126) was found in the Aegean population whereas the lowest number of accessions (4) was found in the Mediterranean population (Figure 3, Supplementary Table 1).

In RPP2, the populations with the highest numbers of accessions were Southeast Anatolia (100%), Mediterranean (93%) and Black Sea (79%). In RPP2, the qI (>80%) value of 72% was similar to that of RPP1. In RPP2 populations, the highest number of entries was found in the Mediterranean (39 accessions) and the lowest number of accessions (5 accessions) was found in Central Anatolia. In addition, the qI value was <80% for 40 accessions (28%), which included 4 accessions from the Black Sea, 3 accessions from Southeast Anatolia, 10 accessions from Marmara, 4 accessions from the Mediterranean, 2 accessions from Central Anatolia and 17 accessions from Aegean populations.

In both RPPs, RPP1 and RPP2, a total of 70 accessions were identified as admixed accessions (qI < 80%). The populations with the highest number of admixed accessions for both groups were Aegean (35 accessions) and Marmara (22 genotypes) (Figure 3; Supplementary Table 1).

When male–female distribution was examined in RPP analyses, female figs were distributed in two RPPs, whereas 40 out of 45 male (caprifig) figs originating from Aegean-Aydın and Aegean-İzmir, respectively, were found in RPP1, and the remaining 5 in RPP2.

#### **Clonal analysis**

In MLG analyses, a total of 96 different MLGs (accessions) and 213 unique accessions were identified. In line with the number of populations, the highest number of MLGs was 38 and these were found in the Aegean population; on the other hand, the lowest number of MLGs was 3 and these were found in the Central Anatolia population. The mean number of



**Figure 3.** A: Illustration of two RPPs (RPP1 and RPP2) (K = 2, ql = 100-0%) B: Distribution of fig accessions by RPPs; accession no (population no: (1): Aegean, (2): Central Anatolia, (3): Mediterranean, (4): Marmara, (5): Black Sea, (6): Southeast Anatolia). See Supplementary Table 1 for corresponding accession numbers. RPPs, reconstructed panmictic populations.

different alleles (*Na*) and effective alleles (*Ne*), which were 5.87 and 3.35, respectively, were similar in all 6 populations. Observed heterozygosity (*Ho*) values were 0.68 in Marmara, Black Sea and Southeast Anatolia populations. These *Ho* values were higher than the *uHe* values of the same populations. However, in the Aegean population, *Ho* and *uHe* values were identical. The lowest *PAS* value with 4 alleles at 2 different loci was found in the Black Sea and Southeast Anatolia populations, whereas the highest *PAS* value with 12 alleles at 5 different loci was found in Aegean and Mediterranean populations (Table 4).

In MLLs analyses performed using different threshold values, some minor differences were observed in the number of different MLLs. There was no difference in the number of MLLs between threshold = 2 and threshold = 3 values. Therefore, threshold = 2 is considered as the threshold value.

Based on clonal diversity values, all populations except Central Anatolia and one accession of Southeast

Population	MLG	Na	Ne	Но	uНe	PAS (Locus no: alleles (bp))
Aegean	38	6.85	3.07	0.62	0.62	L3:137, L6:246, L8:142, L10:155–159–179, L11:176
Central Anatolia	3	4.78	3.03	0.62	0.65	L4:156, L12:124
Mediterranean	19	6.35	3.60	0.66	0.66	L3:141, L6:160, L7:190, L9:153, L15:196
Marmara	15	6.35	3.67	0.68	0.66	L6:148-168, L7:158, L8:186, L14:249
Black Sea	15	5.42	3.35	0.68	0.64	L2:160, L8:144
Southeast Anatolia	6	5.50	3.40	0.68	0.66	L2:186, L11:152
Total	96	35.25	20.12	3.94	3.89	_

**Table 4.** Multilocus genotypes (MLG), number of different alleles (*Na*), effective alleles (*Ne*), observed heterozygosity (Ho), unbiased expected heterozygosity (uHe) and PAS values found in different fig populations studied.

PAS, private alleles summary.

Table 5. Number of genotypes (accessions) (gen)/clonality, effective number of genotypes (accessions) (eff), genotypic diversity (*div*), eveness (*eve*) and Shannon-Wiener (*shw*) values (for threshold = 2) determined in MLLs analysis.

Population	Number of genotypes	Effective number of	Genotypic	Eveness	Shannon-
	(accessions) (gen)/Clonality	genotypes (accessions) (eff)	diversity (div)	(eve)	wiener (shw)
Aegean	124/33	87	0.994	0.702	2.035
Central Anatolia	11/0	11	1.000	1.000	1.041
Mediterranean	33/9	26	0.986	0.809	1.479
Marmara	46/7	41	0.994	0.911	1.644
Black Sea	29/4	26	0.992	0.915	1.445
Southeast Anatolia	12/1	11	0.987	0.938	1.067

MLLs, multilocus lineages.

Anatolia were found to contain unique accessions (Table 5).

The genotypic diversity (div) value, also known as expected heterozygosity, was similarly found to be high in all populations (mean 0.991). The lowest eveness (eve) value, which shows distribution status of accessions within a population, was 0.702 in the Aegean population, whereas the highest eveness value, which was the same as the number of effective number of genotypes (accessions) (eff), was 1.000 in the Central Anatolia population. This indicates that all accessions of the Central Anatolia population have the same frequency. The higher Shannon-Wiener (shw) value (2.035) which was observed in the Aegean population as compared with other populations, was consistent with the high-diversity features of this population (Table 5).

Among accessions, 54 clones/multilocus accessions were found for threshold = 2. Especially in Aegean (33 clones) and Mediterranean (9 clones) populations, accession-clone matches were found to occur mostly within the same population. Detailed information (accession name, accession no, geographical region and province) on clones determined based on threshold = 2value is given in Supplementary Table 7.

It has been observed that the clone matching groups determined in the MLL analysis are partially similar to the groups determined in the RPP analysis.

#### DISCUSSION

To date, Anatolian figs have been identified mostly based on their morphological features and current accessions have been often named by individual collectors/curators of such germplasms. Therefore, it is suspected that due to the lack of a reliable genetic characterisation system, a number of homonymous and synonymous fig accessions from Anatolia have remained uncharacterised. In this study, we used SSR markers, which have been used extensively for genetic diversity, linkage mapping and population genetic studies (Verma et al., 2013), for the characterisation of Anatolian figs. The database constructed for Anatolian figs in this study will be a useful national and international reference for future studies.

#### SSR analysis

Based on the PI values, the most informative locus was FCUP038-6 (PI: 0.093; 15 alleles), and the least informative locus was LMFC23 (PI: 0.600; 2 alleles). The FCUP038-6 locus has also been identified as the locus which demonstrates the highest number of alleles in previous investigations (Bandelj et al., 2007; Caliskan et al., 2012; Ferrara et al., 2016; Caliskan et al., 2018). The number of alleles per locus ranged from 2 for LMFC23 to 15 for FCUP038-6 and the allele sizes ranged from 121bp for MFC3 to 261bp for LMFC30. Similarly, the LMFC23 locus displayed low polymorphism in other studies (Giraldo et al. 2005; Giraldo et al., 2008; Ferrara et al., 2016). The MFC and LMF group loci (Khadari et al., 2003; Saddoud et al., 2008; Achtak et al., 2009; Aradhya et al., 2010; Do Val et al., 2013; Caliskan et al., 2018; Ganopoulos et al., 2015; Teoman et al., 2017) and the FM4-70 locus (Zavodna et al., 2005; Caliskan et al., 2012; Ikten et al., 2018) have also been used by other

workers for genetic identification of figs and, overall, our results are in accordance with these previous studies. In a study by Teoman et al. (2017), 24 LMF loci were studied on 45 caprifigs (*F. carica* var. *caprificus*) and 2 female figs from the Marmara and Aegean regions of Turkey, and the LMF-30 locus was found to have the highest number of alleles per locus (9 alleles). Similar results were also obtained by Achtak et al. (2009) and Aradhya et al. (2010).

#### Genetic relationships of fig accession groups

Estimates of genetic similarity were obtained from SSR markers data. The genetic distance matrix varied between 0.055 and 0.232 suggesting that fig accessions analysed had relatively high genetic diversity. The lowest similarity value was found between the accessions from Southeast and Central Anatolia whereas the maximum similarity was found between Marmara and Aegean accessions. Additionally, high similarities between accessions from Marmara and other regions were found (Supplementary Table 3). The Marmara region is known for having the highest rate of human commute due to its historical past (the former capital of Turkey throughout history), and this genetic similarity of Marmara accessions and other regions can be due to the comparatively high level of genetic material exchange with these regions throughout history.

Based on SSR analyses, 310 accessions were classified into six accession groups (dendrogram not shown). Similarly, Caliskan et al. (2018) divided 90 caprifig accessions from the Eastern Mediterranean into five groups. In our study, reference accessions from geographically distant Aegean region clustered separately from eastern accessions. The most significant genetic differentiation value (0.078) was found between Aegean and Black Sea fig accession groups whereas the lowest  $F_{ST}$  value (0.007) was identified between Marmara and Central Anatolian fig populations. Similarly, significant genetic differentiation values were found within Anatolian fig populations, with the highest and lowest  $F_{st}$  values being 0.182 and 0.007, respectively (Caliskan et al., 2018). The results of gene flow analyses revealed that the accessions from geographically distant regions had lower levels of gene flow, whereas the accessions originated from closer geographical locations had higher levels of gene flow.

The observed heterozygosity values, which were higher than expected heterozygosity for all groups except for those from Central Anatolia, indicated a high level of cross-pollination in different *F. carica* populations. This finding agrees with that of Aradhya et al. (2010), who studied fig samples from Europe, Asia and North America. According to the BAPS structure analysis, fig accessions from Southeast Anatolia displayed a homogeneous structure which is consistent with the FCA analysis. In addition, Southeast Anatolian accessions showed the highest genetic distance among the remaining regions studied (Supplementary Table 3). Central Anatolian accessions showed a homogeneous structure. Based on genetic distance and the rate of gene flow analyses, genetic similarity between accessions from this region and those of Marmara indicated gene flow from Central Anatolia to the Marmara region. Marmara and Aegean accessions with an admixture (heterogeneous) structure had some overlap with other accessions (Figure 2; Supplementary Figure 2), suggesting that gene flows to these regions from other regions had been also occurred.

The RPP analyses confirmed the results of structuring by other population analyses (FCA, BAPS structure, gene flow, etc.). RPP1 included 81% of the Aegean population, half of the Marmara population and 50% of the Central Anatolia population. As a result, these three populations overlapped in FCA, showing high gene flow and low genetic distance to one another.

RPP2 was the most diverse RPP and consisted of accessions from all populations. In particular, the Mediterranean and Southeast Anatolia, which showed high similarity to each other, were included in this group (Figure 3; Supplementary Tables 1 and 2).

In MLG analysis carried out in our research, 96 MLGs that showed correspondence to 31% of the total population were distinguished. In similar MLG analyses performed on different plants, this rate was 78% in Halophila ovalis population (Xu et al., 2019), 48% in olive population (Barazani et al., 2014) and 14% in wild population of Ziziphus celata (Rhamnaceae) (Gitzendanner et al., 2012). The rate of MLGs in a population may vary significantly depending on the total population number, the number of SSR markers used and discrimination power (Hamadeh et al., 2018). Accordingly, about 56% of 96 MLGs determined in MLG analysis were distinguished as clone in MLL analysis (threshold = 2) (Table 5) and proved that the discrimination power of SSR markers used in the clonal analysis is sufficient.

As it is known, heterozygosity values (unbiased heterozygosity (*uHe*) expected and observed heterozygosity) determined in MLG analysis provide information about genetic diversity and kinship relations between MLGs (Harris and DeGiorgio, 2017). In MLG analysis performed on 1,747 Pueraria montana (Lour.) Merr. var. lobata (also known as kudzu) plants belonging to 87 different locations in the United States, the average number of samples for 87 locations was 20, and based on the unbiased expected heterozygosity (*uHe*) value (0.398) and observed heterozygosity value (Ho) (0.444), it was clear that kudzu plant had high genetic diversity and it was explained that this situation was caused by high clonal reproduction (Bentley and Mauricio, 2016). In addition, in MLG analysis based on SSR markers in 429 genotypes belonging to 22 different populations of the perennial tree Platanus orientalis living in the Mediterranean region, unbiased expected heterozygosity (uHe) was found between 0.267 and 0.607, and observed heterozygosity (Ho) was found

between 0.207 and 0.564, and despite the high number of analysed population, low heterozygosity values observed at the clonal level were attributed to geographic isolation and low gene flow (Rinaldi et al., 2019).

In MLG analysis of our study, it was interestingly revealed that expected heterozygosity (uHe) and observed heterozygosity (Ho) values were quite close to each other in all six populations, and values of both heterozygosities were observed to be 0.620 and higher. This situation reveals the possible genetic variation among MLGs in each population (Harris and DeGiorgio, 2017).

#### Genetic relationships of fig accessions

As explained in detail later, in this study, 36 synonymous, 22 homonymous and 7 identical fig accessions were identified (Supplementary Tables 4–6).

#### Homonymous groups

The accessions named 'Siyah' (e.g. accessions 105, 106, 214, 215, 251 and 252) and 'Siyah İncir' (e.g. accessions 216, 241 and 295) are most likely homonymous. A similar situation can also be seen in the case of 'Beyaz' (203) and 'Beyaz incir' accessions. It should be noted that the words/adjectives used in accession names such as 'Siyah' (meaning 'black' in Turkish), 'Beyaz' (meaning 'white' in Turkish) and 'Mor' (meaning 'purple' in Turkish) all refer to the colour of the fruit. The accessions called 'Datça 1' (145), 'Datça 2' (146), 'Datça 3' (147), 'Datça 4' (148) and 'Datça 5' (157) formed a homonymous group with <70% genetic similarity. Despite having the same name, the homonymous group accessions Halebi (298) and Halebi (299) showed only 56.7% similarity to each other whereas Halebi (298) and Halebi (299) showed 86.7% similarity to 'Armut sapı' (178) and 66.7% similarity to 'Mor özer' (297) accessions, respectively (Supplementary Table 4).

#### Synonymous groups

The two 'Kadota' accessions (134 and 168) originated from Italia and a Turkish accession called 'Lop Yemiş' (132) formed a synonymous group. 'Lop Yemiş' was not similar to other similarly called accessions (i.e. 'Lop Figs') and, therefore, it is likely that 'Lop Yemiş' (132) is a 'Kadota' accession. Of the fig accessions from the Aydın province, three accessions, namely 'Bağcılar' (41), an 'unnamed' accession (45) and 'Sarılop' (46), were found to be synonymous (Supplementary Table 5). It is likely that 'Bağcılar' (41) and the 'unnamed' accession (46) may, in fact, be 'Sarılop' (46), which is a widely grown fig accession in the Aegean region.

Our results also indicated the synonymous 306 (unnamed) is a 'Lop' (229) accession whereas 210 (unnamed) is a 'Siyah İncir' (149) accession. 'Bektaşi' (40) and 'Mor İncir' (107) were found to be synonymous to 'Mor Güz' (5) and 'Mor Güz' (95) and because of low similarities between 'Mor İncir' (107) and other members of the 'Mor İncir' accessions, it is likely that 'Bektaşi' (40) and 'Mor İncir' (107) were misnamed. These accessions are likely to be the same as 'Mor Güz' accessions (Supplementary Table 5).

Similarly, since 'Datça 1' (145) was found to be synonymous with 'Siyah Güz' (9), it is likely that 'Siyah Güz' (9) was misnamed. 'Yediveren' (30) formed a synonymous group with accessions 1, 28, 33, 223 and 244 but had only 36.7% similarity to another accession also, called 'Yediveren' (115), forming a homonymous group with it. This indicates that accession 30 was not 'Yediveren' but had the same genetic background with its synonymous accessions.

The synonymous accession 'unnamed' (125) seems to be a 'Izmir Bardacık' accession and 'unnamed' 141 in case 7 is a 'Mor 4' accession. Similarly, 'unnamed' (262) is an accession of 'Yediveren'. 'Unnamed' synonymous 259 and 260, showing the same similarities to all other accessions, were similar to 104 'Aydın İnciri' and may be originated from 104. Besides, because 'Mor İncir' (107) showed low similarities to other members of the 'Mor İncir' group, this accession is likely to be the same as 'Mor Güz' accessions.

#### Identical groups

In this study, seven identical groups including 'Yanako 1' (60) – 'Yanako 2' (61), 'Siyah' (215) – 'Siyah İncir' (216), 'Tarak' (183) – 'Tarak İnciri' (191), 'Morgüz' (5) – 'Morgüz' (95), 'Kırmızı İncir' (174) – 'Kırmızı İncir' (187), 'Siyah' (242) – 'Siyah İncir' (295) and 'Kadota' (134) – 'Kadota' (168) were identified (Supplementary Table 6).

#### Clonal similarity

As proposed by Ordidge et al. (2018), 16 clonal cases with 90–100% similarity required for clonality were found. Of these, nine accession groups that showed one allelic difference (or 96.9% similarity), three accession groups that showed two allelic differences (or 93.8% similarity) as well as four groups that showed three allelic differences (90.6% similarity) were identified. The number of clones determined in MLL analyzes (Supplementary Table 7) is higher than the number of clones determined by the genetic similarity index (UPGMA). However, it was determined that the accessions belonging to the clone groups in both analyses showed high similarity with each other.

Our analyses also revealed extensive clonal relationships among accession. 'Devetabani' (34) and 'Sakız' (35) were found to be 96.7% and 93.3% similar, respectively, to six synonymous accessions (1, 28, 30, 33, 223 and 244). 'Devetabani' (34) differed from these six synonymous accessions by only one allele found at the MFC4 locus and 'Sakız' (35) differed by two homozygous alleles at the LMFC25 locus.

Similarly, of the three synonymous fig accessions identified here, 'Sarılop Kim' (92) and 'Ak Sarılop' (99) from İzmir and another 'unnamed' accession (138) from Manisa showed 96.7% similarity to 'Sarılop' (46) from Aydın. In MLLs analysis, unnamed accession (138) and 'Ak Sarılop' (99) were identified as the clone of 'Bağcılar' (41) from the same population. The clonal variation shown by 'Sarılop' in the Aegean region is already known (Cabrita et al., 2001) and accordingly it is possible that accessions 41, 92, 99 and 138 are all different 'Sarılop' clones. Besides, unknown (309) accession seems to be a 'Siyah Orak' (21) clone (Supplementary Table 7).

# Unique synonymous-clonal structure and sex distribution of Anatolian figs

In general, the ecotypic variation due to somaclonal variations of fig cultivars appears to be high. Ecotypes here are defined both within and between geographical regions and provinces. Especially in Aegean, Marmara and Mediterranean ecotypes, different accessions were found homonymous (e.g. 'Datça 1' (145) – 'Datça 3' (147) – 'Datça 4' (148) – 'Datça 5' (157)), whereas similar accessions ('Bektaşi' (40) – 'Mor Güz' (95) – 'Mor İncir' (107), etc.) were found synonymous (Supplementary Tables 4 and 5).

Clones may be different in MLGs for reasons such as allele scoring error and somatic mutations. Somatic mutations, especially in perennial plants, can lead to differences between individuals with the same clonal genotype (Coughlan et al., 2017). Clonal variations were mostly detected in different varieties that do not form ecotypes within and between geographical regions/provinces. Clonal diversity detected among non-ecotype varieties is thought to be caused either by variations found in each geographical region/province accessions ('Mor Armudi' (172-Mediterranean, Adana), 'Kırmızı İncir' (174-Mediterranean, Adana), 'Kırmızı İncir' (187-Mediterranean, Adana)) or by the emergence of new clones, especially in case of other Aegean and/ or Marmara varieties ('Hamri' (182-Mediterranean, Adana), 'Siyah' (215-Marmara, Balıkesir), 'Siyah İncir' (216-Marmara, Balikesir)) grown in other ecologies (Black Sea, Mediterranean, etc.) (Supplementary Table 7).

In recent years, RPP analyses have been used by various researchers in figs for population structure groupings (Belttar et al., 2017; Teoman et al., 2017; Ikten et al., 2018).

In our study, overall RPP-based groupings showed correlations with genetic similarity relationships of the 310 accessions examined. Regardless of the geographical region/province, almost all 36 synonymous, 7 identical accession cases were included in the same RPP (RPP1 or RPP2) (Supplementary Tables 1, 5 and 6).

In addition, the finding that synonymous, identical accession are grouped with the same RPPs is an indication of their unique structures. Clonal cases except for a few clone groups (unnamed (306) – Sarı Bardak (227); Yediveren (249) – Dumanı Kara (218) and Mor İncir (200) – Kilis inciri (194)) have been found to be in the same RPPs groups (Supplementary Tables 5–7).

Common fig is a gynodioecious species where female and hermaphroditic trees are found together within a population. Male fig trees produce syconia containing both male and female flowers. In contrast, the syconia produced by female fig trees contain only female flowers. Because only male trees can produce pollen, the common fig is considered to be functionally dioecious (Boudchicha et al., 2018).

A total of 45 male accessions from Aegean-Aydın (37) and Aegean-İzmir (8) were included in this study. So far, the number of studies conducted on the structure distribution of male and female accessions in fig accessions has been limited. Teoman et al. (2017) reported that the structure analysis of 47 fig genotypes produced 2 RPPs without any clear male-female separation.

In contrast, in our study, caprifigs showed a distinct structure and mostly located in RPP1, although only five male accessions from the Aegean-Aydin male group ('Siyah İlek 48' (48), 'Kizilay 1' (58), ' Şeytan 1' (64), 'Taşlık' (73), 'Kızılburun' (74)) were also found in RRP2.

One of the reasons for these five male accessions to differ from the others could be due to their different genetic structures. Another reason why these five male accessions differed from others would be related to plant genetics as well as gender phenotype. An orthologue of RAN1 gene loci was reported to be associated with sex determination in fig (Mori et al., 2017). Mori et al. (2017) reported that mutational variations of the two SNP regions in RAN1, which is associated with sex determination in figs, caused heterozygous accessions in the 18 male fig accessions. In the current study, five accessions previously reported to be female (Ikten and Yilmaz, 2019) were identified as male based on RAN1associated cleaved amplified polymorphic sequences (CAPS) marker screenings. These heterozygous genome variations may be another reason for the fact that 5 of the 45 caprifigs accessions were found in different RPPs.

#### CONCLUSIONS

SSR primers used herein generated a significant number of alleles that enabled genetic characterisation of Anatolian figs and the identification of potentially redundant germplasm. Our findings presented here also suggest that cross-fertilisation might have played a significant role as a source of variability not only in wild fig populations but also in cultivated forms leading to homonymous accessions while the lack of phenotypic descriptions together with misnaming of accessions have resulted in synonymous and identical fig accessions. Another source of variation could be the clonal differences resulting from somaclonal variations among fig accessions. Together, these forces might have led to the development of a rich fig germplasm in Anatolia. Molecular characterisation of this germplasm will facilitate the utilisation and preservation of unique Anatolian fig accessions while generating useful data for future evolutionary studies on global figs populations.

#### FUNDING

This study was supported by the Scientific and Technical Research Council of Turkey (TUBITAK) (Grant No. 105 G 078).

#### AUTHOR CONTRIBUTIONS

AE designed and outlined the research. BPB, NA, SSA and CYÖ conducted the experiments. KK, NH, FY, CYÖ and MB analysed the data and drafted and edited the manuscript. NT, MÖ, İK and FÇ provided plant collections. All authors read and approved the manuscript.

#### **CONFLICT OF INTEREST**

The authors declare no conflict of interest.

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Received: December 13, 2020; accepted: February 13, 2021

## SUPPLEMENTARY MATERIALS



**Figure S1.** The UPGMA tree showing genetic relationships of six fig populations from Anatolia based on Nei's (1972) genetic distance.



**Figure S2.** Bayesian analysis of population structure of fig accessions. The structure where fig populations are shown in their heterogeneous, homogeneous or admixtured state is constructed based on their allele frequencies, using the BAPS software. In this figure, vertical bars correspond to individual genotypes. Black vertical lines are used to separate different populations.



**Figure S3.** A: The best *K* value (2) is shown in the graph, B: Population structure of fig populations based on K = 1-8. The best *K* value was calculated according to Evanno et al. (2005) and was K = 2.

Collection cites (Geographical region-Provinces-Fig plant sex)	Accession no	Accession code	Accession name	RPP grouping (red: RPP1) (green: RPP2)
Aegean-Aydın-Female	1	1001	Göklop	
	2	1002	Bardakçı	
	3	1004	Kuşadası Bardakçı	
	4	1111	Mor Bardakçı	
	5	1006	Mor Güz	
	6	1007	Beyaz Güz	
	7	1106	Ak Güz	
	8	1008	Yeşil Güz	
	9	1039	Siyah Güz	
	10	1009	Mor 1	
	11	1020	Mor 2	
	12	1021	Mor 3	
	13	1022	Mor 4	
	14	1005	Şeker inciri	
	15	1011	Kış İnciri	
	16	1023	Kuş İnciri	
	17	1026	Siyah İncir	
	18	1003	Karahönü	
	19	1010	Kara Yaprak	
	20	1019	Karabakunva	
	21	1012	Sivah Orak	
	22	1013	Bevaz Orak	
	23	1014	Akca 1	
	24	1015	Akca 2	
	25	1016	Akça 3	
	25	1017	Bardak	
	20	1027	Asıl Bardak	
	27	1027	I ön	
	20	1030	Lop	
	29	1037	Lop	
	30	1018	Serencel	
	31	1025	Şaranpoi	
	32	1028	Kaya	
	33	1031	Alaca	
	34	1032	Devetabani	
	35	1034	Sakiz	
	36	1038	Lebi; Uzun	
	37	1040	Sıyıllı	
	38	1041	Sarı Dızılık	
	39	1042	Koca Ana	
	40	1043	Bektaşi	
	41	1044	Bağcılar	
	42	1104	Patlıcan	
	43	1098	Sarı Zeybek	
	44	1118	Unnamed	
	45	1100	Unnamed	
	46	1029	Sarı Lop	

Table S1. Collection cites, accession no, accession name of fig cultivars used in the study.

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			· · ·	
Collection cites (Geographical region-Provinces-Fig plant sex)	Accession no	Accession code	Accession name	RPP grouping (red: RPP1) (green: RPP2)
Aegean-Aydın-Male	47	28	Kara İlek	
	48	8	Siyah İlek	
	49	24	Ak İlek	
	50	36	Mor İlek	
	51	54	Sarı İlek	
	52	29	Kavun İlek	
	53	25	Elma İlek	
	54	53	Kaba İlek(Bozdoğan)	
	55	1	Kabaİlek(Ömerbeyli)	
	56	61	Körpe İlek	
	57	16	Hamza İlek	
	58	10	Kızılav 1	
	59	32	Kızılay-2	
	60	57	Yanako 1	
	61	59	Yanako 2	
	62	34	Büyük Konkur	
	63	38	Küçük Konkur	
	64	18	Sevtan 1	
	65	10	Şeytan 2	
	66	219	Çekin l	
	67	21a 21b	Çakın 2	
	68	60	Çaklı 2	
	69	23	Kıbrıslı	
	70	13	Gabalı	
	70	15	Abalı	
	71	15	Demortu	
	72	50	Dallialli	
	73	50	Taşıık Vazılbaran	
	74	52	Kiziloui uli	
	75	30	A from ou	
	76	35	Alyoncu Karah 1 (	
	77	37	Karabulut	
	78	17a	Mordemirtaş	
	/9	176	Çaçaron	
	80	12	Derviş Ali	
	81	14	Haci Yusuf	
	82	4	Bostanci	
A among İmmin Mala	83	/	Kuyucak	
Aegean-Izmir-Male	84	39	Hacı Abdullah	
	85	40	Kara Erkek	
	86	41	Ak Erkek 1	
	87	43	Ak Erkek 2	
	88	42	Çıçekli 2	
	89	44	Conkurt	
	90	46	Ayardolduran	
	91	49	Armut Ilek	

Collection cites (Geographical region-Provinces-Fig plant sex)	Accession no	Accession code	Accession name	RPP grouping (red: RPP1) (green: RPP2)
Aegean-İzmir-Female	92	TUR1081	Sarılop kim	
	93	TUR1082	Akça kim	
	94	TUR1047	Morgüz	
	95	TUR1045	Morgüz	
	96	TUR1035	Sarı çiçek	
	97	TUR1046	Mor	
	98	TUR1064	Mor	
	99	TUR1048	Ak sarılop	
	100	TUR1086	Mor lop	
	101	TUR1087	Unnamed	
	102	TUR1050	Boğmalı	
	103	TUR1051	Langav	
	104	TUR1053	Aydın inciri	
	105	TUR1054	Siyah	
	106	TUR1068	Siyah	
	107	TUR1055	Mor incir	
	108	TUR1056	Bardak lopu	
	109	TUR1057	Unnamed	
	110	TUR1059	Unnamed	
	111	TUR1060	Sarıca	
	112	TUR1061	Bal inciri	
	113	TUR1062	Eyyam bahur	
	114	TUR1065	Arap inciri	
	115	TUR1066	Yediveren	
	116	TUR1067	Gökçe	
	117	TUR1069	Kızgıt	
	118	TUR1070	Kasaba	
	119	TUR1071	Karabakunya	
	120	TUR1073	Beyaz Karabakunya	
	121	TUR1072	Unnamed	
	122	TUR1074	Midilli	
	123	TUR1058	Yeşil midilli 1	
	124	TUR1077	Yeşil midilli 2	
	125	TUR1075	Unnamed	
	126	TUR1076	Unnamed	
	127	TUR1078	Dibala	
	128	TUR1079	Yörük inciri	
	129	TUR1080	İzmir Bardacık 2	
	130	TUR1083	Unnamed	
	131	TUR1084	Unnamed	
	132	TUR1085	Lop yemiş	

Collection cites (Geographical region-Provinces-Fig plant sex)	Accession no	Accession code	Accession name	RPP grouping (red: RPP1) (green: RPP2)
Aegean-Manisa-Female	133	TUR1049	Unnamed	
	134	TUR1107	Kadota	
	135	TUR1088	Siyah kış	
	136	TUR1089	Ufak yeşil	
	137	TUR1090	Esmer bal	
	138	TUR1091	Unnamed	
	139	TUR1092	Unnamed	
	140	TUR1093	Unnamed	
	141	TUR1094	Unnamed	
	142	TUR1095	Unnamed	
	143	TUR1096	Unnamed	
	144	TUR1097	Unnamed	
	145	TUR1108	Datça 1	
	146	TUR1110	Datça 2	
	147	TUR1112	Datça 3	
	148	TUR1114	Datça 4	
	149	TUR1102	Siyah incir	
	150	TUR1103	Beyaz incir	
	151	TUR1119	Unnamed	
	152	TUR1099	Unnamed	
	153	TUR1109	Şeker	
	154	TUR1113	Beyaz incir	
	155	TUR1115	Gökçe	
	156	TUR1116	Ada	
	157	TUR1117	Datça 5	
Central Anatolia-Eskişehir-Female	158	TUR708	Darpak	
	159	TUR709	Kızıl mor	
	160	TUR710	Ekși incir	
	161	TUR711	Beyaz incir	
	162	TUR712	Siyah incir	
	163	TUR701	Yabani(Mor)	
	164	TUR702	Yabani f	
	165	TUR704	Yabani f	
	166	TUR705	K.formu	
	167	TUR706	Çilci	
	168	TUR801	Kadota	

Collection cites (Geographical region-Provinces-Fig plant sex)	Accession no	Accession code	Accession name	RPP grouping (red: RPP1) (green: RPP2)
Mediterranean-Adana-Female	169	TUR 321	Mor Seyhan	
	170	TUR 322	Beyaz Seyhan	
	171	TUR 318	Mor İncir	
	172	TUR 311	Mor Armudi	
	173	TUR 312	Kızıl Mor	
	174	TUR 313	Kırmızı İncir	
	175	TUR 317	Aşı İnciri	
	176	TUR 314	Meyem İnciri	
	177	TUR 315	Kış İnciri	
	178	TUR 310	Armut Sapı	
	179	TUR 316	Yayladağ	
	180	TUR 323	Fahli	
	181	TUR 324	Şetvi	
	182	TUR 325	Hamri	
	183	TUR 326	Tarak	
	184	TUR 327	Lebi	
	185	TUR01I-01	Lop İnciri	
	186	TUR31-İ-08	Lop İnciri	
	187	TUR31-İ-04	Kırmızı İncir	
	188	TUR31-İ-02	Beyaz İncir	
	189	TUR31-İ-03	Siyah İncir	
	190	TUR31-İ-09	Kışlık İncir	
	191	TUR31-İ-06	Tarak İnciri	
	192	TUR31-İ-07	Fetike İnciri	
	193	TUR31-İ-11	Frenk İnciri	
	194	TUR31-İ-12	Kilis İnciri	
	195	TUR31-İ-10	Gök İncir	
	196	TUR31-İ-05	Kandamik	
Mediterranean-İçel (Mersin)-Female	197	TUR33-İ-01	Gök İncir	
	198	TUR 33-İ-02	Güzlük Mor İncir	
	199	TUR33-İ-03	Haziran İnciri	
	200	TUR33-İ-04	Mor İncir	
	201	TUR 306	Bodrum İnciri	
	202	TUR 307	Kalın Kabuk	
	203	TUR 308	Beyaz	
Mediterranean-Osmaniye-Female	204	TUR 319	Osmaniyeli	
	205	TUR 320	Unnamed	
Mediterranean-Antalya-Female	206	TUR 302	Mor İncir	
	207	TUR 305	Mor İncir	
	208	TUR 309	Mor İncir	
	209	TUR 301	Sarı İncir	
	210	TUR 303	Unnamed	
Marmara-Adapazarı-Female	211	TUR 249	Kavak	

Collection cites (Geographical region-Provinces-Fig plant sex)	Accession no	Accession code	Accession name	RPP grouping (red: RPP1) (green: RPP2)
Marmara-Balıkesir -Female	212	TUR 209	Mor İncir	
	213	TUR 210	Mor İncir	
	214	TUR 202	Siyah	
	215	TUR 255	Siyah	
	216	TUR 208	Siyah İncir	
	217	TUR 254	Midilli	
	218	TUR 220	Dumanlı Kara	
	219	TUR 205	Sarı Dizilik	
	220	TUR 206	Boğmalı Dizilik	
	221	TUR 207	Yemişi Lop	
	222	TUR 256	Yediveren	
	223	TUR 201	Istanbul	
Marmara-Bursa-Female	224	TUR 237	Bursa Siyahı	
	225	TUR 236	Bardak	
	226	TUR 238	Beyaz Bardak	
	227	TUR 242	Sarı Bardak	
	228	TUR 241	Gök Bardak	
	229	TUR 240	Lop	
	230	TUR 245	Sarı Yemiş	
	231	TUR 246	Gelin Yanağı	
	232	TUR 243	Susak	
	233	TUR 244	Kavak	
	234	TUR 247	Mor İncir	
	235	TUR 248	Siyah İncir	
	236	TUR 252	Löp İnciri	
Marmara-Çanakkale-Female	237	TUR 223	Yediveren	
	238	TUR 222	Kavak Yediveren	
	239	TUR 224	Beyaz İncir	
	240	TUR 213	Kara Yemiş	
	241	TUR 216	Siyah İncir	
	242	TUR 218	Siyah	
	243	TUR 225	Kabak Yemişi	
	244	TUR 212	Çiçek İncir	
	245	TUR 215	Midilli	
	246	TUR 214	Unnamed	
	247	TUR 219	Unnamed	

Collection cites (Geographical region-Provinces-Fig plant sex)	Accession no	Accession code	Accession name	RPP grouping (red: RPP1) (green: RPP2)
Marmara-İstanbul-Female	248	TUR 235	Yediveren	
	249	TUR 250	Yediveren	
	250	TUR 227	Yediveren	
	251	TUR 234	Siyah	
	252	TUR 230	Siyah	
	253	TUR 251	Dereköy	
	254	TUR 226	Kasım İnciri	
	255	TUR 228	İpek İnciri	
	256	TUR 231	Tüylü İncir	
	257	TUR 232	Koca Yemiş	
	258	TUR 253	Sultan Selim	
	259	TUR 233	Unnamed	
	260	TUR 229	Unnamed	
	261	TUR 211	Unnamed	
	262	TUR 203	Unnamed	
	263	TUR 204	Unnamed	
Black Sea-Artvin-Female	264	TUR 536	Beyaz İncir	
	265	TUR 542	Siyah Bukele	
	266	TUR 541	Sarı Kilis	
	267	TUR 540	Kilis İnciri	
Black Sea-Bartin-Female	268	TUR 505	Kara Sultani	
	269	TUR 506	Beyaz Sultani	
Black Sea-Giresun-Female	270	TUR 530	İpek İnciri	
	271	TUR 532	Kepek İnciri	
	272	TUR 531	Değirmen İnciri	
	273	TUR 534	Sarı İncir	
	274	TUR 533	Ağarsak	
Black Sea-Kastamonu-Female	275	TUR 507	Balduzdın	
	276	TUR 508	Baldıran	
Black Sea-Ordu-Female	277	TUR 528	Kara İncir	
	278	TUR 529	Könüs İnciri	
	279	TUR 523	Dilaver	
	280	TUR 524	Ham İncir	
	281	TUR 525	Ak İncir 1	
Black Sea-Sinop-Female	282	TUR 511	Şalgam İnciri	
	283	TUR 512	Istanbul İnciri	
	284	TUR 514	Deniz İnciri	
	285	TUR 515	Tabak İnciri	
	286	TUR 513	Filestos	
Black Sea-Samsun-Female	287	TUR 517	Mor İncir	
	288	TUR 522	Turna Boyu	
	289	TUR 519	Şeker İnciri	
Black Sea-Trabzon-Female	290	TUR 537	Kara İncir	
	291	TUR 538	Kabak İnciri	
	292	TUR 535	Horasan	

Collection cites (Geographical region-Provinces-Fig plant sex)	Accession no	Accession code	Accession name	RPP grouping (red: RPP1) (green: RPP2)
Black Sea-Zonguldak-Female	293	TUR 503	Ak İncir	
	294	TUR 501	Sarı İncir	
	295	TUR 504	Siyah İncir	
	296	TUR 502	Istanbul İnciri	
Southeast Anatolia	297	TUR 401	Mor Özer	
	298	TUR 402	Halebi	
	299	TUR 407	Halebi	
	300	TUR 403	Sultani	
	301	TUR 405	Kalazi	
	302	TUR 408	Azezi	
	303	TUR 404	Kış Hayrı	
	304	TUR 221	Yeşil İncir	
	305	TUR 217	Unnamed	
	306	TUR 239	Unnamed	
	307	TUR 304	Unnamed	
	308	TUR 07-I-0P5	Kızıl Yemiş	
	309	TUR 01-I-04	Unnamed	
Black Sea-Artvin-Female	310	TUR 539	Beyaz Bukele	

Locus no	Locus name	Primer sequence $(5' \text{ to } 3')$	Kepeat motif	Expected range (hn)	Amplification temneratures (Tm)	GenBank accession numbers
L1	MFC1	f: ctagactgaaaaaacattgc, r:tgagattgaaaggaaacgag	(ct)13	174–192	55	AF333703
L2	MFC2	f: gcttccgatgctgctctta, r:tcggagacttttgttcaat	(ac)18(at)7	158-172	55	AF333697
L3	MFC3	f:gatattttcatgtttagtttg, r:gaggatagaccaacaacaac	(ac)15(tc)(ac)8(at)7	122–136	55	AF333698
L4	MFC8	f.gtggcgtcgtctctaataat, r.tattctatgctgtcttatgtca	(ca)9ta(ca)14(ta)6	170-174	57	AF333703
L5	FCUP008-2	f: catacactttcatggagcacaaa, r: cccagatgtttggtgaa	g (tg)22	158-184	53	EF198054
L6	FCUP027-4	f: aaccttttagtatgcctttggaa, r: tccaccatcaaatccttct	(ac)19	202-220	55	EF198058
L7	FCUP038-6	f.caatgtatcatttcatctcacgaa, r: agttcccatgtttggttac	ga (tg)23t(ag)11	170-193	58	EF198059
L8	FCUP066-7	f: ccctctcgaagaagaagca, r: ctacaggaaatgggcctcaa	(ca)14	162-182	58	EF198065
L9	FCUP068-1	f.ggaattaccgtccatggcta, r: cgccactctctctccact	(ag)14(gagagg)4	178-206	58	EF198066
L10	FCUP070-2	f:ttcaacttcaaccttcaccaa, r:tttgtctaaggaggcttattgtc	a (ag)15	183-195	58	EF198068
L11	LMFC23	f: tttcgtgtctaacgatcaaaaa, r: ctcccatctccaactccatc	(ag)20	132	53	AY545936
L12	LMFC25	f: gattctgattaaagggtattt, r: gctttccaaatctaaagtaac	(tc)11	216	55	AY545938
L13	LMFC30	f: ttgtccgtttcttatacaat, r: tctttttaggcagatgttag	(ct)18(ca)6	253	58	AY545942
L14	FM4-70	f.cagatgaggttgacgatgttattg, r: taaaccctcttcaaattc	ctctc (gaa)20–1	202-232	55	AJ854076
SSR, simple	sequence repeat.					
Table S3. G	fenetic distance	2/genetic similarity (%) between fig population	s based on Nei's (1972) gen	etic distance.		
Populations		Aegean Central	Anatolia Med	terranean	Marmara	Black Sea
Aegean		1				
Central Ana	utolia	0.107/89.3				
Mediterrane	an	0.149/85.1 0.20	5/79.4	Ι		
Marmara		0.055/94.5 0.06	5/93.5 0.1	26/87.4	Ι	
Black Sea		0.175/82.5 0.14	1/85.6 0.1	77/82.3	0.099/90.1	Ι
Southeast A	natolia	0.181/81.9 0.23	2/76.8 0.1	06/89.4	0.149/85.1	0.164/83.6

No	Homonymous-accession name (accessio	on no-geographical region, provinces)
	RPP1	RPP2
1	Kızılay 2 (59-Aegean, Aydın)	Kızılay 1 (58-Aegean, Aydın)
2	Şeytan 2 (65-Aegean, Aydın)	Şeytan 1 (64-Aegean, Aydın)
3	Çakın 1 (66-Aegean, Aydın) – Çakın 2 (67-Aegean, Aydın)	_
4	Datçal (145-Aegean, Manisa) – Datça 3 (147-Aegean, Manisa) – Datça 4 (148-Aegean, Manisa) – Datça 5 (157-Aegean, Manisa)	Datça 2 (146-Aegean, Manisa)
5	Ak Erkek 1 (86-Aegean, İzmir) – Ak Erkek 2 (87-Aegean, İzmir)	-
6	Morgüz (95-Aegean, İzmir) - Morgüz (5-Aegean, Aydın)	Morgüz (94-Aegean, Aydın)
7	Siyah (105-Aegean, İzmir) – Siyah (106-Aegean, İzmir) – Siyah (214-Marmara, Balıkesir) – Siyah (252-Marmara, İstanbul) – Siyah İncir (17-Aegean, Aydın) – Siyah İncir (241-Marmara, Çanakkale) – Siyah (215-Marmara, Balıkesir) – Siyah İncir (216-Marmara, Balıkesir)	Siyah (251-Marmara, İstanbul) – Siyah İncir (149-Aegean, Manisa) – Siyah İncir (162-Central Anatolia, Eskişehir) – Siyah İncir (189-Mediterranean, Adana) – Siyah İncir (235-Marmara, Balıkesir) – Siyah (242-Marmara, Çanakkale) – Siyah İncir (295 -Black Sea, Zonguldak)
8	Beyaz İncir (154-Aegean, Manisa) – Beyaz İncir (187-Mediterranean, Adana) – Beyaz İncir (238-Marmara, Çanakkale) – Beyaz İncir (263-Marmara, İstanbul)	Beyaz (203-Mediterranean, İçel ) – Beyaz İncir (150-Aegean, Manisa) – Beyaz İncir (161-Central Anatolia)
9	Akça 1 (23-Aegean, Aydın) – Akça 2 (24-Aegean, Aydın) – Akça 3 (25-Aegean, Aydın)	_
10	Mor 1 (10-Aegean, Aydın) – Mor 2 (11-Aegean, Aydın) – Mor 3 (12-Aegean, Aydın) – Mor 4 (13-Aegean, Aydın) – Mor (97-Aegean, İzmir) – Mor (98-Aegean, İzmir) – Mor İncir (107-Aegean, İzmir) – Mor İncir (206-Mediterranean, Antalya) – Mor İncir (207-Mediterranean, Antalya) – Mor İncir (234-Marmara, Bursa)	Mor İncir (171-Mediterranean, Adana) – Güzlük Mor İncir (198-Mediterranean, İçel) – Mor İncir (200-Mediterranean, İçel) – Mor İncir (208-Mediterranean, Antalya) – Mor İncir (212-Marmara, Balıkesir) – Mor İncir (213-Marmara, Balıkesir) – Mor İncir (287-Black Sea, Samsun)
11	Midilli (122-Aegean, İzmir) – Midilli (217-Marmara, Balıkesir) – Midilli (245-Marmara, Çanakkale) – Yeşil Midilli 2 (124-Aegean, İzmir)	Yeşil Midilli 1 (123-Aegean, İzmir)
12	Yabani F (165-Central Anatolia-Eskişehir)	Yabani F (164-Central Anatolia, Eskişehir) – Yabani (Mor) (163-Central Anatolia, Eskişehir)
13	-	Karabakunya (20-Aegean, Aydın) – Karabakunya (119-Aegean, İzmir) – Beyaz karabakunya (120-Aegean, İzmir)
14	Bardakçı (2-Aegean, Aydın) – Kuşadası Bardakçı (3-Aegean, Aydın) – Morbardakçı (4-Aegean, Aydın) – Bardak (26-Aegean, Aydın) – Bardak (225-Marmara, Bursa) – Gök Bardak (228-Marmara, Bursa)	Asıl Bardak (27-Aegean, Aydın) – Beyaz Bardak (226-Marmara, Bursa) – Sarı Bardak (227-Marmara, Bursa)
15	Yediveren (30-Aegean, Aydın) – Yediveren (115-Aegean, İzmir) – Yediveren (222-Marmara, Balıkesir) – Yediveren (248-Marmara, İstanbul)	Yediveren (237-Marmara, Çanakkale) – Kavak Yediveren (238 -Marmara, Çanakkale) –Yediveren (249-Marmara, İstanbul) – Yediveren (250-Marmara, İstanbul)
16	Şeker (153-Aegean, Manisa) – Şeker İnciri (14-Aegean, Aydın)	Şeker İnciri (289-Black Sea, Samsun)
17	Löp (28-Aegean, Aydın) – Lop (29-Aegean, Aydın) – Löp İnciri (236-Marmara, Bursa)	Lop İnciri (185-Mediterranean, Adana) – Lop İnciri (186-Mediterranean, Adana) – Lop (229-Marmara, Bursa)
18	Kaba İlek (Bozdoğan) (54-Aegean, Aydın) – Kaba İlek (Ömerbeyli) (55-Aegean, Aydın)	-
19	Büyük Konkur (62-Aegean, Aydın) – Küçük Konkur (63-Aegean, Aydın)	-
20	Frenk (75-Aegean, Aydın)	Frenk İnciri (193-Mediterranean, Adana)
21	_	Kış İnciri (15-Aegean, Aydın) – Kış İnciri (177-Mediterranean, Adana) – Kışlık İncir (190-Mediterranean, Adana)
22	_	Halebi (298 -Southeast Anatolia) – Halebi (299 -Southeast Anatolia)

Table S4. Reconstructed panmictic population (RPP) grouping of homonymous identified based on SSR analysis.

SSR, simple sequence repeat.

Table S5. RPP	grouping of s	ynonymous ident	tified based on	SSR analysis.
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No	Synonymous-accession name (acces	sion no-geographical region provinces)
110	RPP1	RPP2
1	Gök Lop (1-Aegean, Aydın) – Löp (28-Aegean, Aydın) – Yediveren (30-Aegean, Aydın) – Alaca (33-Aegean, Aydın) – İstanbul (223-Marmara, Balıkesir) – Çiçek	_
	Incir (244-Marmara, Çanakkale)	
2	Mor (98-Aegean, Izmir) – Dibala (127-Aegean, Izmir)	-
3	Ada (156-Aegean, Manisa) – Yemişi Lop (221-Marmara, Balıkesir) – Balduzdın (275 -Black Sea, Kastamonu) – Könüş İnciri (278-Southeast Anatolia)	_
4	Bağcılar (41-Aegean, Aydın) – Unnamed (45-Aegean, Aydın) – Sarı Lop (46-Aegean, Aydın)	-
5	Sarilop Kim (92-Aegean, İzmir) – Ak Sarilop (99-Aegean İzmir) – Unnamed (138-Aegean Manica)	-
6	Unnamed (126-Aegean, İzmir) – İzmir Bardacık 2 (129-Aegean, İzmir)	-
7	Mor 4 (13-Aegean, Aydın) – Unnamed (142-Aegean, Manisa)	-
8	Sarı Zeybek (43-Aegean, Aydın) – Siyah (252-Marmara, İstanbul)	_
9	Kara İlek (47-Aegean, Aydın) – Kavun İlek (52-Aegean, Aydın)	_
10	Lop Yemiş (132-Aegean, İzmir) – Kadota (134-Aegean, Manisa) – Kadota (168-Central Anatolia, Eskişehir)	-
11	Darpak (158-Central Anatolia, Eskişehir) – Löp İncir (236-Marmara, Balıkesir)	-
12	Beyaz Güz (6-Aegean, Aydın) – Ak Güz (7-Aegean, Aydın)	-
13	Siyah Güz (9-Aegean, Aydın) – Datça (145-Aegean, Manisa)	-
14	Yediveren (222-Marmara, Balıkesir ) – Unnamed (263-Marmara, İstanbul)	-
15	Unnamed (259-Marmara, İstanbul)	Unnamed (260-Marmara, İstanbul)
16	Mor Güz (5-Aegean, Aydın) – Bektaşi (40-Aegean, Aydın) – Mor Güz (95-Aegean, İzmir) – Mor İncir (107-Aegean, İzmir)	_
17	Lop (29-Aegean, Aydın) – Sarıca (111-Aegean, İzmir) – Unnamed (133-Aegean, Manisa) – Esmer Bal (137-Aegean, Manisa)	-
18	Gökçe (116-Aegean, İzmir) – Kızgıt (117-Aegean, İzmir)	-
19	Boğmalı (102-Aegean, İzmir) – Langav (103-Aegean, İzmir)	_
20	Şeker (153-Aegean, Manisa) – Beyaz İncir (154-Aegean, Manisa)	-
21	Siyah İncir (17-Aegean, Aydın) – Fahli (180 -Mediterranean, Adana)	-
22	_	Mor Armudi (172-Mediterranean, Adana) – Kırmızı İncir (174-Mediterranean, Adana) – Kırmızı İncir (187-Mediterranean, Adana)
23	-	Kara Yaprak (19-Aegean, Aydın) – Patlıcan (42-Aegean, Aydın)
24	_	Beyaz (203-Mediterranean, İçel) – Unnamed
		(205-Mediterranean, Osmaniye) – Kara Yemiş (240-Marmara, Çanakkale) – Kış Hayrı (303 -Southeast Anatolia)
25	_	Asıl Bardak (27-Aegean, Aydın) – Gök İncir (197-Mediterranean, Adana)

No	Synonymous-accession name (acce	ssion no-geographical region, provinces)
	RPP1	RPP2
26	_	Beyaz İncir (188-Mediterranean, Adana) – Mor İncir (200-Mediterranean, İçel)
27	-	Meyem İncir (176-Mediterranean, Adana) – Fetike İnciri (192-Mediterranean, Adana)
28	-	Kışlık İncir (190-Mediterranean, Adana) – Kandamik (196-Mediterranean, Adana)
29	-	Lop (229-Marmara, Balıkesir) – Unnamed (306-Southeast Anatolia)
30	-	İpek İnciri (270-Black Sea, Giresun) – Sarı İncir (273 -Black Sea, Giresun)
31	Siyah (242-Marmara, Çanakkale)	Beyaz İncir (239-Marmara, Çanakkale) -Siyah İncir (295-Black Sea, Zonguldak)
32	Ekşi İncir (160-Central Anatolia, Eskişehir) – Dereköy (253-Marmara, İstanbul) – Sarı Kilis (266-Black Sea, Artvin) – Kilis İnciri (267-Black Sea, Artvin)	_
33	_	Siyah İncir (149-Aegean, Manisa) – Unnamed (210-Mediterranean, Antalya)
34	Yediveren (115-Aegean, İzmir) – Karabakunya (119-Aegean, İzmir)	Kış İnciri (15-Aegean, Aydın)
35	_	Haziran İnciri (199-Mediterranean, İçel) – Beyaz Sultani (269-Black Sea, Bartın )
36	-	Lop İnciri (185-Mediterranean, Adana) – Kilis İnciri (194-Mediterranean, Adana)

SSR, simple sequence repeat.

No	Identical-accession name (accession no-geographical region, provinces)		
	RPP1	RPP2	
1	Yanako 1 (60-Aegean, Aydın) – Yanako 2	-	
	(61-Aegean, Aydın)		
2	Siyah (215-Marmara, Balıkesir) – Siyah İncir	_	
	(216-Marmara, Balıkesir)		
3	_	Tarak (183-Mediterranean, Adana) – Tarak İnciri	
		(191-Mediterranean, Adana)	
4	Morgüz (5-Aegean, Aydın) – Morgüz (95-Aegean, İzmir)	-	
5	_	Kırmızı İncir (174-Mediterranean, Adana) – Kırmızı İncir	
		(187-Mediterranean, Adana)	
6	_	Siyah (242-Marmara Çanakkale) – Siyah İncir (295-Black	
		Sea, Zonguldak)	
7	Kadota (134-Aegean, Manisa) - Kadota (168-Central	_	
	Anatolia, Eskişehir)		

Table S6. RPP grouping of identical identified based on SSR analysis.

SSR, simple sequence repeat.

Matched	Accession name (accession no-geographical region, province)	Matches at $T = 2$
number		(accession no-geographical region, province)
1	Ak Güz (7-Aegean-Aydın)	Beyaz Güz (6-Aegean-Aydın)
2	Karabakunya (20-Aegean-Aydın), Yediveren (115-Aegean- İzmir), Karabakunya (119-Aegean),	Kış Inciri (15 Aegean-Aydın)
3	Löp (28 Aegean-Aydın), Yediveren (30-Aegean-Aydın), Alaca (33-Aegean-Aydın), Devetabanı (34-Aegean-Aydın), Istanbul (223-Marmara-Balıkesir), Cicek İncir (244-Marmara-Bursa)	Göklop (1-Aegean-Aydın)
4	Sakız (35-Aegean-Avdın)	Göklop (1-Aegean-Aydın)
5	Bektasi (40-Aegean-Aydın), Morgüz (95-Aegean-İzmir)	Mor Güz (5-Aegean-Avdın)
6	Patlican (42-Aegean-Avdin)	Karavaprak (19-Aegean-Avdın)
7	Unnamed (45-Aegean-Avdın), Unnamed (46-Aegean-Avdın)	Bektasi (41-Aegean-Avdın)
8	Kavun İlek (52-Aegean-Avdın)	Kara İlek (47-Aegean-Avdın)
9	Yanako 2 (61-Aegean-Avdın)	Yanako 1 (60-Aegean-Avdın)
10	Ak sarilon (99-Aegean-İzmir). Unnamed (138-Aegean-Manisa)	Bağcılar (41-Aegean-Avdın)
10	Boğmalı (102-Aegean İzmir) Langay (103-Aegean İzmir)	Sivilli (37-Aegean-Avdın)
12	Mor İncir (107-Aegean-İzmir)	Mor Güz (5-Aegean-Avdın)
12	Sarica (111-Aegean-İzmir) Unnamed (133-Aegean-Manisa)	Lon (29-Aegean-Aydın)
15	Esmer Bal (137-Aegean-Manisa)	Lop (2) riegoun riyani)
14	Kızgıt (117-Aegean-İzmir)	Gökçe (116-Aegean-İzmir)
15	Beyaz Karabakunya (120-Aegean-İzmir)	Beyaz Orak (22-Aegean-Aydın)
16	Dibala (127-Aegean-İzmir)	Beyaz Orak (22-Aegean-Aydın)
17	İzmir Bardacık 2 (129-Aegean-İzmir)	Unnamed (126-Aegean-İzmir)
18	Kadota (134-Aegean-Manisa)	Lop Yemiş (132-Aegean-İzmir)
19	Unnamed (142-Aegean-Manisa)	Mor 4 (13-Aegean-Aydın)
20	Datça 1 (145-Aegean-Manisa)	Siyah Güz (9-Aegean-Aydın)
21	Beyaz İncir (154-Aegean-Manisa)	Şeker (153-Aegean-Manisa)
22	Şeker (153-Aegean, Manisa)	Kadota (134-Aegean-Manisa)
23	Kırmızı İncir (174-Mediterranean-Adana), Kırmızı İncir (187-Mediterranean-Adana)	Mor Armudi (172-Mediterranean-Adana)
24	Fahli (180-Mediterranean-Adana)	Siyah İncir (17-Aegean-Aydın)
25	Tarak inciri (191-Mediterranean-Adana)	Tarak (15-Mediterranean-Adana)
26	Fetike İnciri (192-Mediterranean-Adana)	Meyem İnciri (176-Mediterranean-Adana)
27	Kilis İnciri (194-Mediterranean-Adana)	Lop İnciri (185-Mediterranean-Adana)
28	Kandamik (196-Mediterranean-Adana)	Kışlık İncir (190-Mediterranean-Adana)
29	Gök İncir (197-Mediterranean-İçel)	Asıl Bardak (27-Aegean-Aydın)
30	Mor İncir (200-Mediterranean-İcel)	Kilis inciri (194-Mediterranean-Adana)
31	Unnamed (205-Mediterranean-Osmanive)	Bevaz (203-Mediterranean-İcel)
32	Unnamed (210-Mediterranean-Antalya)	Sivah incir (149-Aegean-Manisa)
33	Sarı Kilis (266-Black Sea-Artvin), Kilis İnciri (267-Black	Asıl Bardak (27-Aegean-Aydın)
	Sea-Artvin), Dereköy (253-Marmara-İstanbul)	
34	Beyaz Sultani (269-Black Sea-Bartın)	Dumanı Kara (218-Marmara-Balıkesir)
35	Sarı İncir (273-Black Sea-Giresun)	İpek İnciri (270-Black Sea-Giresun)
36	Siyah (242-Marmara Çanakkale)	Siyah İncir (295-Black Sea, Zonguldak)
37	İpek İnciri (270-Black Sea, Giresun)	Sarı İncir (273 -Black Sea, Giresun)
38	Yemişi Lop (221-Marmara, Balıkesir)	Balduzdın (275 -Black Sea, Kastamonu)
39	Balduzdın (275-Black Sea-Kastamonu), Könüs İnciri (278-Black Sea-Ordu)	Ada (156-Aegean-Manisa)
40	Sivah İncir (295-Black Sea-Zonguldak)	Bevaz İncir (239-Marmara-Canakkale)
41	Sivah (215-Marmara-Balikesir). Sivah İncir	Hamri (182-Mediterranean-Adana)
	(216-Marmara-Balıkesir)	
42	Yemişi Lop (11-Aegean-Aydın)	Ada (156-Aegean-Manisa)
43	Kara Yemış (240-Marmara-Çanakkale)	Dumanı Kara (218-Marmara-Balıkesir)
44	Löp Inciri (236-Marmara-Bursa)	Siyah Orak (21-Aegean-Aydin)
45	Yediveren (249-Marmara-Istanbul)	Dumanı Kara (218-Marmara-Balıkesir)
		(Continued)

**Table S7.** Accessions and individuals assigned to different accession at T = 2 threshold value based on MLLs analyses.

Matched	Accession name (accession no-geographical region, province)	Matches at $T = 2$
number		(accession no-geographical region, province)
46	Siyah (252-Marmara-İstanbul)	Sarı Zeybek (43-Aegean-Aydın)
47	İpek İnciri (255-Marmara-İstanbul)	Siyah Orak (21-Aegean-Aydın)
48	Unnamed (260-Marmara-İstanbul)	Unnamed (259-Marmara-İstanbul)
49	Unnamed (261-Marmara-İstanbul)	Beyaz Karabakunya (120-Aegean-İzmir)
50	Unnamed (263-Marmara-İstanbul)	Yediveren (222-Marmara-Balıkesir)
51	Kalazi (301-Southeast Anatolia)	Mor Özer (297-Southeast Anatolia)
52	Kış Hayrı (303-Southeast Anatolia)	Unnamed (205-Mediterranean-Osmaniye)
53	Unnamed (306-Southeast Anatolia)	Sarı Bardak (227-Marmara-Bursa)
54	Unnamed (309-Southeast Anatolia)	Siyah Orak (21-Aegean-Aydın)

MLLs, multilocus lineages.