

Genetic diversity in Turkish eggplant (*Solanum melongena*) varieties as determined by morphological and molecular analyses

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In Turkey, local varieties of eggplant (*Solanum melongena* L.) occur in several types (including round, semi-long and long) and are a staple ingredient of the cuisine. Although Turkish eggplant varieties are morphologically distinct, little is known about their molecular genetic variation. In this study, the genetic variability of 67 Turkish eggplant accessions from the national germplasm collection was assessed with 30 morphological traits and AFLP markers. Morphological analysis indicated considerable variability especially for semi-long and round types. For molecular characterization, accessions of *S. macrocarpon*, *S. aethiopicum* and *S. linnaeanum* were included as outgroups. Ten primer combinations were used and yielded 488 polymorphic fragments with PIC values ranging from 0.03 to 0.50. Of the polymorphic fragments, 144 (29%) were specific to *S. melongena* accessions while 73, 49 and 16 fragments were specific to *S. macrocarpon*, *S. aethiopicum* and *S. linnaeanum*, respectively. UPGMA cluster analysis of the AFLP data resulted in a dendrogram which had a very high correlation ($r=0.97$) with the similarity matrix data. Genetic similarity in the dendrogram ranged from 0.30 to 0.95 with the related *Solanum* species located outside the *S. melongena* clusters, as expected. Genetic similarity of the *S. melongena* accessions ranged from 0.68 to 0.95 indicating good genetic diversity present in the Turkish national collection. It is hoped that this information, together with morphological data will help guide future germplasm collection and eggplant breeding efforts.

Keywords: AFLP, Genetic diversity, Germplasm, Genetic resources

INTRODUCTION

The Solanaceae is a very large plant family including the domesticated species tomato, pepper, potato, petunia, tobacco, and eggplant. Brinjal eggplant, *Solanum melongena*, is a member of the most crowded genus, *Solanum*, of the Solanaceae family (Knapp et al., 2004). *S. melongena* is only one of the three cultivated species referred to as 'eggplant.' The other two types of eggplant are scarlet eggplant, *S. aethiopicum*, and gboma eggplant, *S. macrocarpon*; however, *S. melongena* is, by far, the most important species in terms of economic and genetic significance. Brinjal eggplant (hereafter referred to as simply eggplant) is most widely grown in its primary

centers of diversity, India and China, as well as in the Mediterranean region. Turkey is considered to be a secondary area of eggplant domestication (Daunay et al., 2001; Kashyap et al., 2003) and this country produces as much eggplant as the rest of Europe combined, approximately 850,000 tons per year (Faostat, 2010).

As a staple of the national cuisine, eggplant is found as a wide variety of morphological types in Turkey. Small oblong or round fruited-types are stuffed or preserved; long cylindrical types are grilled, fried or stuffed; and large round or semi-long oblong types are stewed or fried. Thus, eggplant breeders in Turkey, and other Middle Eastern and Asian countries where diverse eggplants are in demand, are challenged by the necessity to improve multiple types. A similar challenge is also faced by germplasm repositories which must

maintain the genetic diversity of eggplant varieties grown in the country. Both breeders and germplasm managers rely on various tools to characterize plant germplasm including morphological and molecular genetic marker data. Each type of data has its own shortcomings and advantages, however, most experts will agree that both are indispensable resources for assessing plant genetic diversity.

The use of molecular genetic markers in eggplant has followed in the footsteps of the preeminent solanaceous model, tomato. Thus, initial research was performed using chloroplast DNA (Sakata et al., 1991; Sakata and Lester, 1994; Sakata and Lester, 1997) and isozyme markers (Isshiki et al., 1994a,b,c; Karihaloo and Gottlieb, 1995; Kaur et al., 2004) which were soon replaced by more abundant and polymorphic markers such as restriction fragment length polymorphism (RFLP; Isshiki et al., 1998; Isshiki et al., 2003; Doganlar et al., 2002a) and random amplified polymorphic DNA (RAPD; Karihaloo et al., 1995; Nunome et al., 2001; Kashyap et al., 2003) markers. More recently, microsatellite (SSR; Nunome et al., 2003a, b; Behera et al., 2006; Stigel et al., 2008; Munoz-Falcon et al., 2009; Nunome et al., 2009; Tumbilen et al., submitted) and amplified fragment length polymorphism (AFLP) markers were developed and applied in eggplant. Although AFLP is usually a dominant marker system and, thus, is less informative than codominant markers, this technique generates a large number of fragments with relatively high polymorphism (Vos et al., 1995; Staub and Serquen, 1996). Moreover, no prior sequence knowledge is needed for application of AFLP and the results are reproducible, thus, this method is preferred especially for taxonomic and mapping studies (Mohan et al., 1997; Ranade, 2003). AFLP was first applied to *S. melongena* and shown to be a suitable tool for assessing genetic diversity by Mace et al., (1999). In another study, Furini and Wunder (2004) combined morphological and AFLP data to evaluate the diversity and complexity of eggplant and its wild relatives. More recently, the genetic diversity of traditional Spanish cultivars, black and Spanish striped eggplants was assessed with both morphological traits and AFLP markers (Prohens et al., 2005; Munoz-Falcon et al., 2008; Munoz-Falcon et al., 2009). AFLP was also used for construction of linkage maps for eggplant (Nunome et al., 2001; Kashyap et al., 2003).

The aim of this study was to assess genetic differences among Turkish local eggplant varieties using both morphological and AFLP markers. Three types of Turkish eggplants were included: long ('uzun'), semi-long ('beyli') and round ('topan') types as well as three related eggplant species. A total of 67 Turkish accessions were analyzed representing 30% of the national collection of eggplant (Mutlu, 2004). Results are discussed in terms of their usefulness for eggplant germplasm collection and breeding.

MATERIALS AND METHODS

Plant material

Seeds for 67 Turkish eggplant accessions were provided by Aegean Agricultural Research Institute (AARI), Menemen, Turkey. AARI houses the Turkish national germplasm collection. Two non-Turkish cultivars (Dusky and MM738, a Dutch breeding line) and three wild relatives (*S. linnaeanum*, *S. macrocarpon* and *S. aethiopicum*) were provided by Dr. Marie-Christine Daunay, French National Institute for Agricultural Research, Montfavet, France. Accessions are listed in Table 1 with type or species name as appropriate.

Morphological characterization

Plants were grown in the field in Menemen, Izmir, Turkey, in a random block design with two replications of each block and ten plants per replication. Because of field losses, only 61 of the 67 original accessions could be morphologically characterized. Thirty morphological descriptors were used for characterization with vegetative and fruit parameters of primary importance (Table 2). Evaluations were performed as described for eggplant by the International Plant Genetics Research Institute (currently Bioversity International) using the scale established for each descriptor (Table 2; IBPGR 1990).

AFLP characterization

For molecular analysis, plants were grown in the greenhouse with 10 seeds sown for each line. DNA was extracted from young leaves of each plant grown for the 70 accessions. For extraction, the Wizard Genomic DNA Purification Kit (Promega, Madison, WI, USA) was used. After rehydration of DNA, 5 µl DNA from each sample was combined in a new tube with the DNAs of the other individuals of the same accession. A NanoDrop ND-1000 Spectrophotometer (NanoDrop Technologies, Inc., Wilmington, DE, USA) was used to determine DNA concentrations of the pooled samples which were adjusted to 100 ng/µl.

Invitrogen AFLP Core Reagent and Invitrogen AFLP Starter Primer Kits were used for AFLP analysis. The protocol was the one defined in the user manual of AFLP Analysis System I, AFLP Starter Primer Kit, Version B, 2003 with a few modifications. The first change to the protocol was the use of 700 ng sample DNA for digestion with *EcoRI* and *Mse I*. After the first PCR amplification, samples were diluted 1:40 instead of 1:50. For the second, selective PCR amplification, the *Mse I* primers provided in the kit and specially synthesized fluorescent labeled *EcoRI* primers were used to allow detection in the CEQ 8800 Genetic Analysis System (Beckman-Coulter). Primer combinations that reportedly worked well for tomato, pepper and potato (as described in the user manual) were applied to two eggplant accessions. Of the 22 primer combinations that were tested in this way, the ten best primer pairs were selected for analysis on all of the Turkish eggplants (Table 3). The last step was preparation of the samples for the Genetic Analysis System. Selective PCR products were first diluted 1:5 with dH₂O then, a second 1:10 dilution with SLS (sample loading solution) was done: 3 µl DNA was mixed with 30 µl SLS and 0.5 µl size standard-600 (GenomeLab, Beckman Coulter, Inc., Fullerton, CA, USA). The Frag 4 method was used for fragment separation: capillary temperature 50°C, denaturation temperature 90°C for 120 sec., injection voltage 2.0kV for 30 sec. and a separation voltage of 4.8 kV for 60.0 min.

Data analysis

Morphological trait means, standard errors and ranges were calculated from the mean values for each accession. Principal components

Table 1. Turkish and other eggplant accessions used in this study.

Genotype	Accession	Type	Genotype	Accession	Type	Genotype	Accession	Type
1	TR 66688	long	30	TR 61564	round	56	TR 66584	long
3	TR 66572	long	32	TR 61518	long	57	TR 66587	long
4	TR 43010	semi-long	33	TR 61493	long	58	TR 66589	long
5	TR 40300	semi-long	34	TR 61766	long	59	TR 66597	long
6	TR 37266	semi-long	35	TR 61856	semi-long	60	TR 66672	long
7	TR 66013	round	36	TR 62049	long	61	TR 66667	long
8	TR 43306	semi-long	37	TR 62043	round	62	TR 66687	semi-long
10	TR 66012	semi-long	39	TR 62073	semi-long	63	TR 66695	semi-long
11	TR 66559	semi-long	40	TR 62072	long	65	TR 66701	semi-long
12	TR 62668	long	41	TR 62139	semi-long	66	TR 66709	semi-long
13	TR 68530	long	42	TR 62101	long	68	TR 66728	semi-long
14	TR 70633	long	43	TR 62100	long	69	TR 66730	long
15	TR 50591	long	44	TR 61956	long	70	TR 43768	semi-long
17	TR 62004	long	45	TR 66009	semi-long	72	TR 55976	semi-long
18	TR 52348	semi-long	46	TR 66014	semi-long	73	TR 56029	long
19	TR 62430	semi-long	47	TR 66011	semi-long	74	TR 61540	long
20	TR 62423	semi-long	48	TR 66018	semi-long	75	TR 61620	long
21	TR 62491	semi-long	49	TR 66334	semi-long	76	TR 61892	long
23	TR 62581	semi-long	50	TR 66331	semi-long	78	MM 0738	semi-long
24	TR 62667	semi-long	51	TR 55852	long	79	Çamlıca	long
25	TR 62736	round	52	TR 52522	round	80	Dusky	semi-long
26	TR 62776	semi-long	53	TR 43134	long	81	MM 0195	<i>linnaeanum</i>
28	TR 61593	long	54	TR 43919	long	82	MM 0232	<i>aethiopicum</i>
29	TR 61563	long	55	TR 66579	semi-long	83	MM 0150	<i>macrocarpon</i>

analysis (PCA) was performed using JMP 7.0 software (SAS Institute Inc., Cary, NC, USA). For analysis of AFLP data, the samples were genotyped for the presence and absence of peaks (bands) as 1 and 0, respectively. The polymorphism information content of each AFLP marker (fragment) was calculated as $PIC_i = 2 f_i (1 - f_i)$ where f_i is the frequency of band presence for marker i (Roldan-Ruiz et al., 2000). The data were also used to draw a dendrogram. NTSYS-pc version 2.2j, (Applied Biostatistics Inc, Setauket, NY, USA) was used to generate a matrix determining similarity and dissimilarity among samples according to Dice's method (Dice, 1945). The similarity matrix was then used to draw a dendrogram with the clustering method UPGMA via the SHAN module in the software. To determine the efficiency of clustering, the cophenetic correlation coefficient was calculated with the Mantel method (Mantel, 1967). A correlation matrix of the data was calculated with the SIMINT module of the software. Eigen values were calculated with the Eigen module and principle coordinates analysis (PCoA) was done.

RESULTS

Morphological characterization

The Turkish eggplant varieties were classified by type based on their shape (Table 1). Of the accessions used in the morphological analysis, 3 were round, 30 were semi-long (longer than broad) and 29 were long (several times longer than broad). The accessions were

characterized for 30 morphological traits (Table 2). No variation was observed for five parameters: cotyledon color (green), anthocyanin in hypocotyl (present), leaf prickles (absent), fruit position (pendant) and seed color (brownish yellow). In contrast, fruit shape and color traits showed considerable variation. Fruit shape (length/breadth ratio) varied from oblate (broader than long) to very long with generally very little curvature. Fruit color ranged from milk white to black at commercial ripeness and from deep yellow to light brown at physiological ripeness. Vegetative characters showed less variation.

Multivariate PCA of the morphological data indicated that the first, second and third components accounted for 16.1, 13.3 and 7.7% of the variance among accessions, respectively. Thus, the first three components explained 37.05% of variance. The most important parameters separating accessions in the first component were fruit shape traits including length/breadth ratio, cross-section, widest part, tip shape, breadth and curvature. Fruit length/breadth ratio and curvature were negatively correlated with the first component ($r = -0.383$ and -0.242 , respectively) while the other traits were positively correlated with the first component ($r = 0.378$ to 0.296). The most important parameters separating accessions in the second component were leaf, seed and fruit traits.

Table 2. Scales, means and ranges for the morphological traits measured in Turkish eggplants.

Descriptor	Scale	Mean $\pm$ SE	Range
Cotyledon color	3-7 (3 = green, 7 = violet)	3.00 $\pm$ 0	3-3
Anthocyanin in hypocotyl	0-1 (0 = absent, 1 = present)	1.00 $\pm$ 0	1-1
Plant growth habit	3-7 (3 = upright, 7 = prostrate)	4.13 $\pm$ 0.13	3-5
Leaf blade length	3-7 (3 = short, 7 = long)	5.06 $\pm$ 0.08	3-7
Leaf blade width	3-7 (3 = narrow, 7 = wide)	5.32 $\pm$ 0.09	5-7
Leaf blade size	3-7 (3 = small, 7 = large)	5.10 $\pm$ 0.10	3-7
Leaf blade lobing	1-9 (1 = very weak, 9 = very strong)	5.10 $\pm$ 0.05	5-7
Leaf blade tip angle	1-9 (1 = very acute, 9 = very obtuse)	3.45 $\pm$ 0.13	1-5
Leaf prickles	0-9 (0 = none, 9 = very many)	0 $\pm$ 0	0-0
Plant height	1-9 (1 = very short, 9 = very tall)	6.58 $\pm$ 0.10	5-7
Plant breadth	1-9 (1 = very narrow, 9 = very broad)	6.81 $\pm$ 0.08	5-7
Start of flowering	3-7 (3 = early, 7 = late)	5.19 $\pm$ 0.08	5-7
Days to 50% flowering	Number of days	43.61 $\pm$ 0.64	35-56
Corolla color	1-9 (1 = greenish white, 9 = bluish violet)	6.29 $\pm$ 0.14	5-9
Days to 50% fruit set	Number of days	55.69 $\pm$ 0.46	48-65
Fruit length	1-9 (1 = very short, 9 = very long)	8.10 $\pm$ 0.13	7-9
Fruit breadth	1-9 (1 = very small, 9 = very large)	7.10 $\pm$ 0.09	5-9
Fruit length/breadth ratio	1-9 (1 = broader than long, 9 = several times longer than broad)	8.03 $\pm$ 0.21	1-9
Fruit curvature	1-9 (1 = none, 9 = U-shaped)	2.95 $\pm$ 0.23	1-8
Fruit cross section	1-9 (1 = circular, 9 = very irregular)	1.77 $\pm$ 0.22	1-9
Fruit widest part	3-7 (3 = widest $\frac{1}{4}$ from base, 7 = widest $\frac{3}{4}$ from base)	5.19 $\pm$ 0.08	5-7
Fruit apex shape	3-7 (3 = protruded, 7 = depressed)	4.55 $\pm$ 0.20	3-7
Fruit color at commercial ripeness	1-9 (1 = green, 9 = black)	7.24 $\pm$ 0.13	2-9
Fruit color at physiological ripeness	1-9 (1 = green, 9 = black)	6.35 $\pm$ 0.34	2-8
Fruit flesh density	1-9 (1 = very loose, 9 = very dense)	5.87 $\pm$ 0.22	3-9
Fruit calyx length	1-9 (1 = very short, 9 = very long)	3.68 $\pm$ 0.14	1-5
Fruit calyx prickles	0-9 (0 = none, 9 = very many)	3.71 $\pm$ 0.23	1-7
Fruit position	1-9 (1 = erect, 9 = pendant)	9.00 $\pm$ 0	9-9
Number of seeds/fruit	0-9 (0 = none, 9 = very many)	7.55 $\pm$ 0.11	7-9
Seed color	1-9 (1 = white, 9 = black)	4.00 $\pm$ 0	4-4

Leaf breadth had the highest correlation with the second component ($r = 0.345$) while the other traits: seed number, fruit length, leaf lobing and leaf size were also positively correlated ($r = 0.312$ to 0.291). When plotted in two dimensions, the PCA showed some separation of the accessions based on type (Figure 1). Long types formed the tightest cluster while semi-long types were more loosely associated among themselves. Round types seemed to be morphologically distinct from the other types, however, only three round accessions were examined in this study. Interestingly, several of the semi-long types were morphologically quite similar to the long types. For example, genotypes 41 and 42 which are long and semi-long, respectively, were very similar to each other.

Molecular characterization

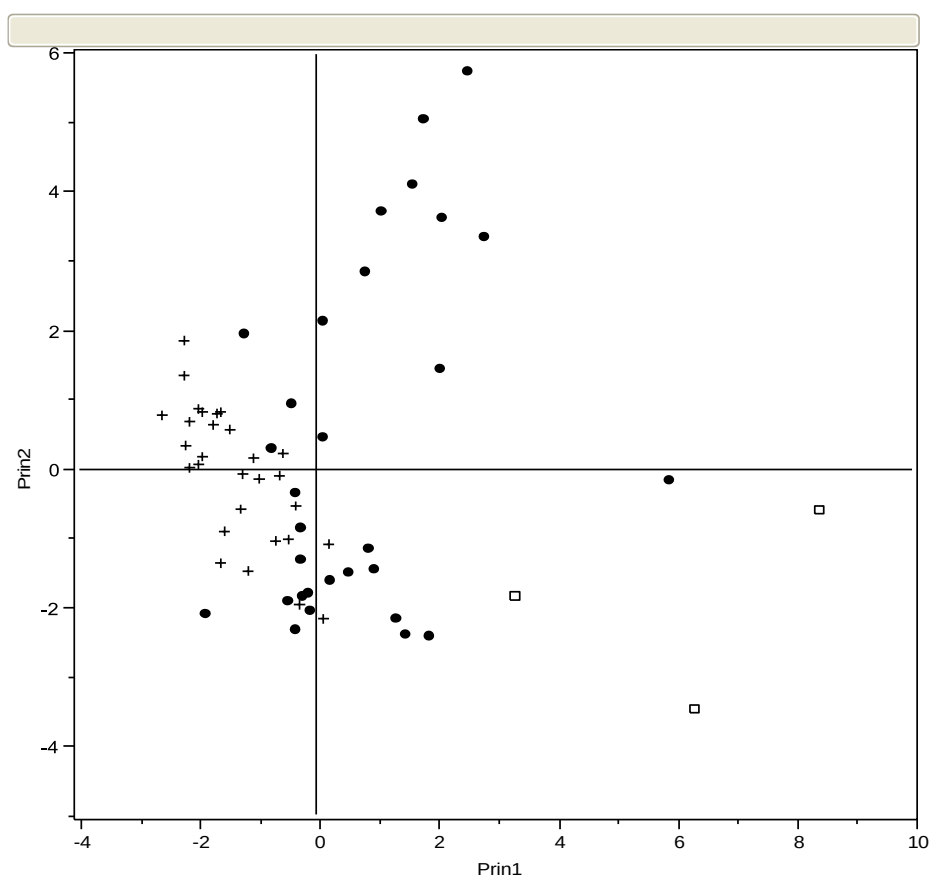
Ten AFLP primer combinations were used with three pairings (E-ACT/M-CAG, E-AAC/M-CAG, E-AGC/M-CAA) the same as previously published eggplant AFLP primer combinations (Mace et al., 1999; Munoz-Falcon et al., 2008). A total of 484 polymorphic fragments (markers)

were reliably scored from the ten combinations; thus, each primer pair provided an average of 48.4 ± 3.8 (SE) polymorphic fragments. Primer combinations E-ACT/M-CAT and E-ACC/M-CAT produced the most polymorphic markers with 63 and 62 fragments, respectively (Table 3). Combination E-AAC/M-CAG amplified the fewest polymorphic fragments, 26. PIC (polymorphism information content) values for the AFLP markers ranged from 0.03 to 0.50 with mean and median PIC values of 0.17 and 0.08, respectively. Based on primer combination, the highest average and median PIC values were obtained with E-ACT/M-CAT and E-AGG/M-CAA (Table 3). When only *S. melongena* accessions were considered, the mean and median PIC values for all of the markers were 0.24 and 0.22, respectively. Of the polymorphic fragments, 144 (29%) were specific to *S. melongena* accessions while 73, 49 and 16 fragments were specific to *S. macrocarpon*, *S. aethiopicum* and *S. linnaeanum*, respectively. Thus, 350 (72%) of the AFLP fragments were useful for separating *S. melongena* accessions.

UPGMA cluster analysis of the AFLP data resulted in a dendrogram (Figure 2) which had a very high correlation ($r=0.97$) with the similarity matrix data as determined by a

Table 3. Selective AFLP primer combinations applied to Turkish eggplants.

<i>EcoRI</i> primer	<i>MseI</i> primer	Total polymorphic fragments	# Average PIC $\pm$ SE (median)
E - ACA	M - CAC	56	0.189 ± 0.022 (0.129)
E - ACC	M - CAT	62	0.145 ± 0.020 (0.067)
E - ACT	M - CAC	41	0.089 ± 0.016 (0.055)
E - ACT	M - CAT	63	0.223 ± 0.023 (0.192)
E - ACT	M - CAG	37	0.157 ± 0.026 (0.084)
E - AAC	M - CAG	26	0.111 ± 0.027 (0.057)
E - AGC	M - CAA	58	0.171 ± 0.021 (0.117)
E - AGC	M - CTA	58	0.134 ± 0.020 (0.061)
E - AGG	M - CAG	36	0.208 ± 0.034 (0.056)
E - AGG	M - CAA	47	0.223 ± 0.024 (0.227)

**Figure 1.** Two dimensional PCA plot of relationships among Turkish eggplant accessions based on 30 morphological parameters; + = long-fruited types, • = semi-long-fruited types, □ = round-fruited types.

Mantel test. Genetic similarity in the dendrogram ranged from 0.30 to 0.95. As expected, the outgroups were located outside of the *S. melongena* clusters. Among the outgroups, *S. linnaeanum* was closest to *S. melongena* with a genetic similarity of 0.48 while *S. aethiopicum*

(genetic similarity 0.34) and *S. macrocarpon* (genetic similarity 0.30) were more dissimilar.

Molecular genetic similarity of the *S. melongena* accessions ranged from 0.68 to 0.95. The topology of the dendrogram revealed two main clusters (A and B) of

Turkish eggplants with a smaller, more distantly related group containing just three accessions: MM738, a non-Turkish breeding line, and two Turkish accessions (TR56029 and TR66728). The two main clusters of eggplant had genetic similarity of 0.78. Cluster A contained 37 accessions while cluster B contained 29 accessions. Interestingly, the only other non-Turkish variety used in the study, 'Dusky,' grouped with cluster B of Turkish material. Cluster A had lower genetic diversity than cluster B; 68% of the accessions had genetic similarities of 0.90 or higher. In cluster B, only 27% of the accessions had such low genetic diversity. Genotypic clustering of the eggplants was not associated with their collection locations or with their type.

Principal coordinates analysis showed similar clustering (Figure 3) with the first eigen vector accounting for 69.8% of the genotypic variation and the first three vectors accounting for a total of 78.4% of the variation. The two-dimensional plot of accessions revealed two primary clusters of Turkish eggplant accessions with lower genetic diversity in cluster A. Clustering in the PCoA plot was not related to accession type and a Mantel test indicated no significant correlation between molecular and morphological distance matrices.

DISCUSSION

Only a handful of recent studies have analyzed eggplant genetic diversity at both the morphological and molecular levels (Behera et al., 2006; Prohens et al., 2005; Munoz-Falcon et al., 2008; Munoz-Falcon et al., 2009). Such studies are, however, imperative for the information that they supply for germplasm management and breeding efforts using collected genetic material. In this study we examined Turkish eggplant varieties for their morphological and molecular diversity. The examined varieties represent approximately one-third of the national eggplant collection and the results indicate that characterization of the rest of the collection is merited.

Analysis of morphological diversity in Turkish eggplants indicated that separation of accessions was strongly associated with traits related to fruit appearance such as fruit shape and length. Thus, long and semi-long types tended to form different clusters in PCA analysis. Such separation based on eggplant type was also observed by Prohens et al., (2005) who studied morphological variation in Spanish eggplants. Despite the tendency of the accessions to cluster by fruit type, several of the semi-long types were morphologically quite similar to the long types. This result was not surprising considering that type classification was based on only fruit shape while the PCA plot was the result of analysis of 30 variables. The results of trait analysis also suggested that long types have lower morphological diversity than semi-long (and perhaps round) types. Similar results were also shown in Spanish eggplants with round and

semi-long types having more morphological variation than long eggplants (Prohens et al., 2005). This information indicates that further eggplant germplasm collection efforts in Turkey should focus primarily on semi-long and round types as these types are expected to represent morphologically more diverse materials.

Genetic diversity analysis of the Turkish eggplants using AFLP markers revealed that these markers are highly suitable for such work as they were highly polymorphic on the tested material (all tested primer combinations were polymorphic) and a majority of the markers (72%) showed polymorphism among *S. melongena* accessions. In contrast, Stigel et al. (2008) found that only 28% of microsatellite markers were informative within 38 *S. melongena* accessions. This difference in marker polymorphism probably reflects the fact that AFLP and microsatellite markers may sample different portions of the genome. The SSRs used by Stigel et al., were identified using gene sequences and are, therefore, expected to map to coding regions. In contrast, AFLP markers do not specifically target genic regions. As a result, such sequences may be less conserved and more polymorphic than gene-based markers.

AFLP markers positioned the eggplant outgroups as expected from previous studies. Thus, *S. linnaeanum* was closest to *S. melongena* (Furini and Wunder, 2004 and Levin et al., 2006) while *S. aethiopicum* and *S. macrocarpon* were more dissimilar. The greater genetic similarity between eggplant and *S. linnaeanum* is also revealed in their taxonomy. *S. melongena* and *S. linnaeanum* both belong to *Solanum* section *Melongena* while *S. aethiopicum* and *S. macrocarpon* belong to section *Oliganthes* (Furini and Wunder, 2004).

Dendrogram analysis based on the AFLP data revealed that Turkish eggplants have moderate molecular genetic diversity with genetic similarity ranging between 0.30 and 0.95. Moderate genetic diversity was also observed in the *S. melongena* accessions studied by Mace et al. (1999) and Furini and Wunder (2004) using AFLP data. Behera et al. (2006) found broader diversity in 92 South Asian *S. melongena* accessions (genetic similarity between 0.37 and 0.90) using microsatellite markers. However, such greater variation was expected because South Asia is a primary center of eggplant diversity. Spain, like Turkey, is a secondary center of diversity and Spanish eggplants have also been shown to harbor considerable morphological and molecular genetic variation (Prohens et al., 2005; Munoz-Falcon et al., 2008; Munoz-Falcon et al., 2009). When AFLP markers were used to assess the molecular diversity of 28 Spanish and four non-Spanish varieties, the Spanish eggplants were not molecularly distinct from other countries' accessions, however, they were quite variable (Prohens et al., 2005). The authors attributed this diversity to several factors: Spain's position as a bridge between North Africa and Europe during eggplant's dispersal by the Arabs starting in the 7th century; the

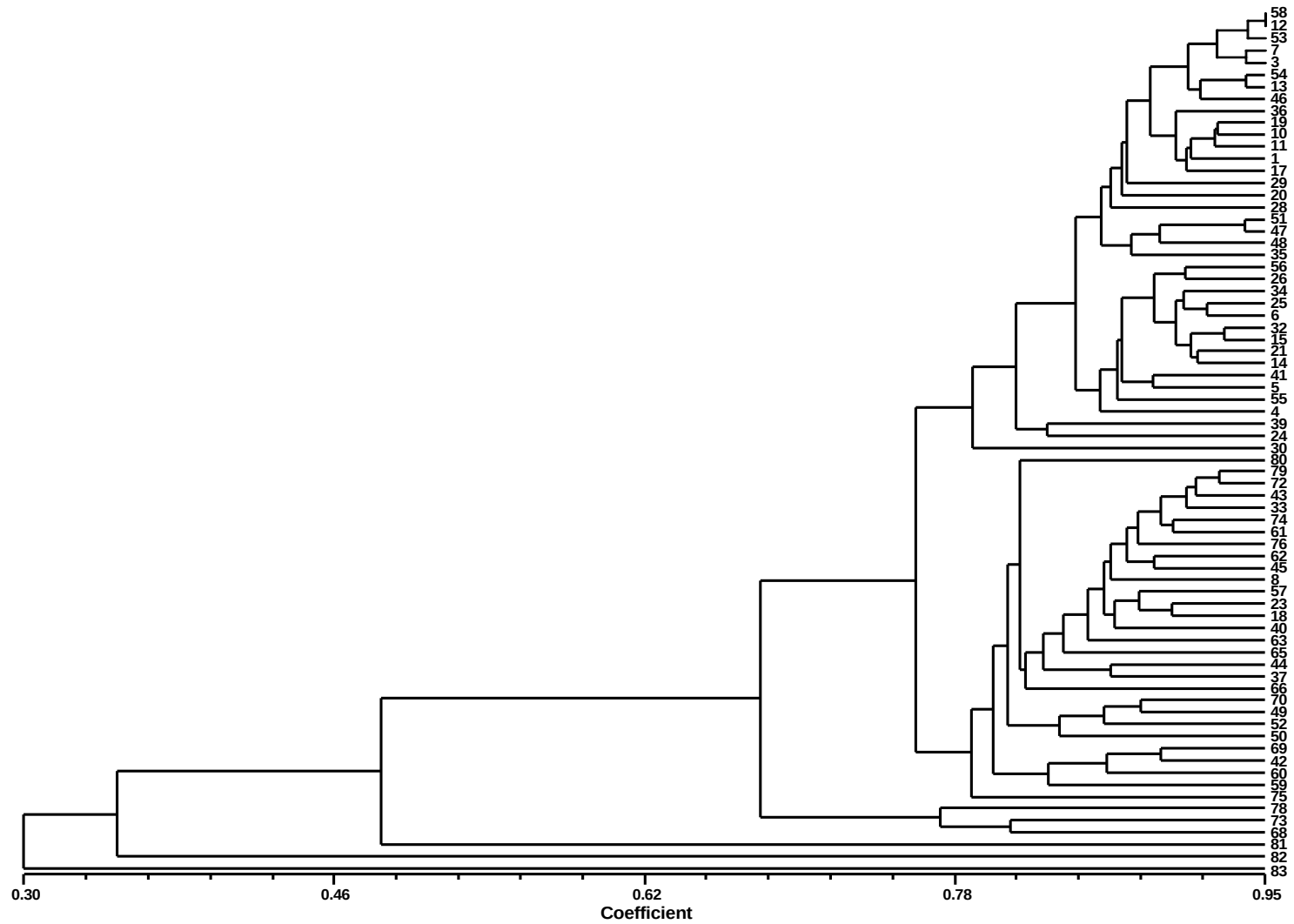


Figure 2. UPGMA dendrogram of 67 Turkish eggplant varieties based on 484 AFLP loci from ten primer combinations. Outgroups are labeled on branches.

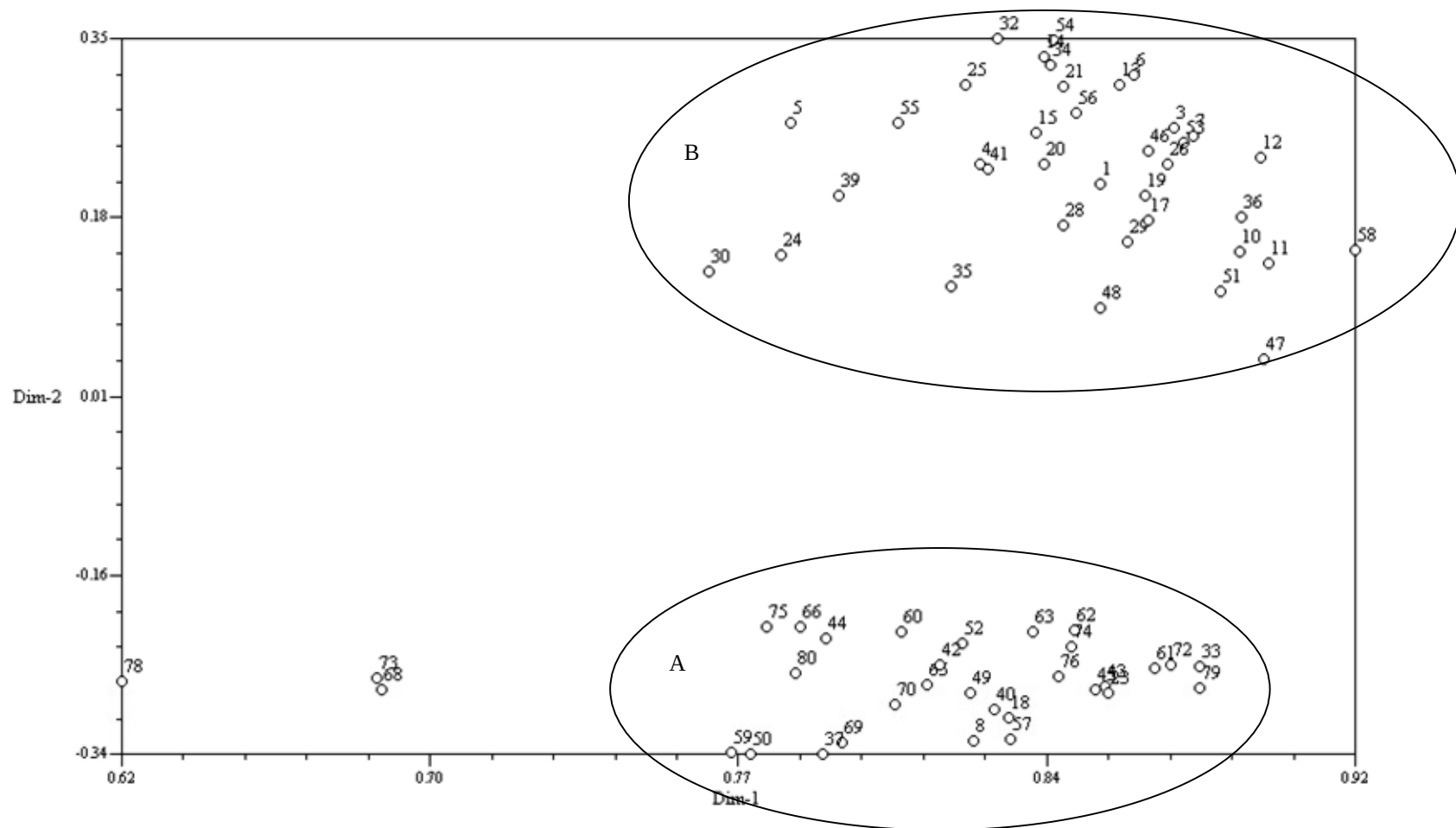


Figure 3. Two dimensional PCoA plot of relationships among Turkish eggplant accessions based on molecular data. Outgroups are not included to increase resolution of Turkish eggplant genotypes.

diversity of types used in Spanish cuisine and the diversity of environmental conditions (Prohens et al., 2005). Turkey also served as a bridge between the Middle East and North Africa (M-C. Daunay, INRA, France, personal communication) during eggplant's dispersal and many morphological types are in common use in the country. Thus, these factors may have also contributed to the molecular variation observed in Turkish eggplants.

Clustering analysis of the Turkish eggplants based on molecular data showed no relationship with eggplant type (long, semi-long, round). In contrast, Spanish long and semi-long types showed clustering in PCoA based on AFLP data (Prohens et al., 2005). A relationship was also seen between grouping based on AFLP data and the presence/absence of striping on Spanish eggplants (Prohens et al., 2005; Munoz-Falcon et al., 2008). These results indicated a relationship between molecular and morphological diversity measurements; however, such an association was not apparent for Turkish varieties.

Assessment of genetic diversity in germplasm collections provides information that is useful for both germplasm management and breeding. Effective, efficient and economic germplasm management requires both morphological and molecular characterization of material. These data allow establishment of core, nonredundant germplasm collections and help to guide future germplasm collection efforts. In addition, these data are valuable for breeders who wish to use germplasm resources for eggplant improvement. Although molecular characterization is quite expensive, it provides information about genetic diversity that is not provided by morphological data. For example, it is known that many morphological traits associated with the domestication of solanaceous crops are controlled by one or a few genes (Frery et al., 2000; Doganlar et al., 2002b; van der Knapp and Tanksley, 2003; Cong et al., 2008; Xiao et al., 2008). Thus, collection and retention of germplasm based solely on morphology can be misleading as morphologically disparate accessions may differ by only one or two alleles. Similarly, consideration of only molecular genetic data is not rational for either germplasm management or breeding as it is nearly impossible to molecularly tag all relevant agronomic traits. Therefore, a combination of both molecular and morphological approaches, as demonstrated in this study, should be used to guide conservation and breeding efforts in Turkish eggplant.

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