Online journal ISSN - 1676-5680
GMR Genetics and Molecular Research
EVOLUTION AND TECHNOLOGY

Genetic characterization of heat tolerant tomato (*Solanum lycopersicon*) genotypes by SRAP and RAPD markers

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Genet. Mol. Res. 9 (4): 2263-2274 (2010)
Received July 12, 2010
Accepted September 8, 2010
Published November 23, 2010
DOI 10.4238/vol9-4gmr876

ABSTRACT. We employed RAPD and sequence-related amplified polymorphism (SRAP) markers to evaluate polymorphisms in 15 tomato (*Solanum lycopersicon*) genotypes that were obtained from a tomato breeding program. Four local tomato genotypes selected from the Sanliurfa province (Southeastern Anatolia Region of Turkey), 10 heat-tolerant tomato genotypes, received from the Asian Vegetable Research and Development Center, and a sample of *S. pimpinellifolium* were genotyped with RAPD and SRAP markers. Eleven SRAP primer combinations were used and 66 bands were scored. The number of bands scored per primer combination ranged from three to 12, with a mean of six alleles per primer combination. All fragments scored for each primer combination were polymorphic. The percentage of polymorphic products ranged from 25 to 80%. The 15 tomato genotypes were screened for RAPD markers using 50 primers in a PCR-based DNA amplification procedure; 46 primers produced clear and good amplification. Ten of these 46 primers amplified monomorphic

fragments in the tomato genotypes. A dendrogram was constructed by combining data from the RAPD and SRAP analyses. Similarity ratios of genotypes ranged from 0.87 to 0.99. The dendrogram was divided into two branches; the first main branch included only genotype CL 5915, and the second main branch included all the other genotypes.

Key words: *Solanum lycopersicon*; Heat tolerance; Molecular markers; Polymorphism; DNA fingerprinting; Genetic characterization

INTRODUCTION

Tomato (*Solanum lycopersicon*) is one of the most important and widely grown vegetable crops in both temperate and tropical regions of the world. In tropical and subtropical regions, heat stress may become a major limiting factor for the growth, reproduction and yield of tomato. Camejo et al. (2005) reported that the optimum temperatures for tomato cultivation are between 25° and 30°C during the photoperiod and 20°C during the dark period. However, a 2-4°C increase over the optimal temperature adversely affects gamete development and inhibits the ability of pollinated flowers to develop into seeded fruits and thus reduced crop yield (Peet et al., 1997; Sato et al., 2001; Firon et al., 2006). At high temperatures most tomato cultivars have problems with fruit set, pollen meiosis and germination, ovule development and viability and development of the embryo (Peet et al., 1988). Seed germination, seedling and vegetative growth, flowering, fruit set, and fruit ripening are adversely affected at a temperature of above 35°C (Thomas and Prasad, 2003; Wahid et al., 2007). Heat tolerance is a critical character of tomato varieties targeted for production in the tropics and sub-tropics. Heat-tolerant tomatoes are reported to have the ability to set fruit at higher temperatures than other tomatoes (AVRDC, 2001). Selection of crops for tolerance to high temperature stress is proposed as the best and easiest strategy for breeding (Warner and Erwin, 2005).

The most important aim of plant breeding includes high yielding varieties that are resistant to biotic and abiotic stress factors. Plant genetic sources are the main material in breeding of new varieties suitable for stress conditions, ever-changing consumer demands and changing ecologic conditions with the effects of global warming (Strauss, 1991). Classical plant breeding generally involves the stages of releasing genetic variations and selection from the populations that show variation (Gepts, 2002). Local populations, which naturally evolved in nature over many years, are of great importance for selection. With the development of better and more efficient species in numerous types of plants, domestic species with higher genetic diversity and lower yield are replaced by commercial varieties and genetic diversity is reduced. Average global temperatures are increasing by approximately 0.3°C a decade. It is estimated that by the middle of the 21st century, average temperatures will be 1.3-1.8ºC higher than current values and 3-6°C higher by the end of the century (IPCC, 2001; Meehl et al., 2007). Temperature is the most important environmental factor affecting plant growth and yield (Houghton and Yihui, 2001). Temperature affects physiological, biochemical, morphological, and agronomic properties of plants. When the average temperature increases by 1.5-2.5°C, 20-30% of plant species will be endangered (Meehl et al., 2007). To minimize the negative impacts of high temperature genetic improvements are of profound importance. Lower genetic diversity is required to develop new species (Heywood et al., 2007). Therefore,

it is important to characterize, conserve and utilize genetic sources (Barrero and Tanksley, 2004; Gepts, 2006). Since tolerance to abiotic stresses is complex, if the plant selection is made based on phenotypic conditions affected by environmental factors, this will result in a high level of misleading effects on breeding programs. Selection based on molecular markers is one of the most effective approaches in developing tolerance in plants (Foolad, 2007). Breeding studies should include plants with known genotypic properties, which are not affected by environmental conditions. Molecular marker techniques with high polymorphism can be used to identify similarity and differences between varieties and to identify parents, which can be used in breeding programs (Terzopoulos and Bebeli, 2008). The advantages and technological improvements recently offered by the new techniques should be used to conserve genetic resources and to use breeding activities in a more reliable, fast and efficient method. These techniques include molecular genetics, tissue culture and recombinant DNA technology.

DNA molecular marker technology provides powerful tools for cultivar identification in various crops with the advantages of being faster, less laborious and more efficient (Li-Wang et al., 2007).

Randomly amplified polymorphic DNA (RAPD) markers, resulting from the polymerase chain reaction (PCR) amplification of genomic DNA fragments using short oligonucleotides (usually 10-mers) of arbitrary sequence as primers, provide a fast and easy approach for many purposes in plant genetic analysis. For these reasons many fruit species have been successfully fingerprinted using RAPD markers (Aka-Kacar et al., 2005).

Sequence-related amplified polymorphism (SRAP) is a PCR-based marker system as described by Li and Quiros (2001). The SRAP is a simple and efficient marker system that can be adapted for a variety of purposes in different crops, including map construction, gene tagging, genomic and cDNA fingerprinting, and map-based cloning. It has several advantages over other systems. It is simple, has a reasonable throughput rate, discloses numerous co-dominant markers, targets open-reading frames (ORFs), and allows easy isolation of bands for sequencing (Uzun et al., 2009).

The aim of this study was to determine a genotypic characterization of tomato genotypes domestically planted in warm and arid climate conditions during tomato production season with RAPD and SRAP molecular marker programs, and to compare these with the genotypes resistant to heat provided by the Asian Vegetable Research and Development Center (AVRDC) to identify similarity of groups based on molecular markers with the aim of using them as a source of heat tolerance for the genetic improvement of tomato.

MATERIAL AND METHODS

Plant materials

Four local tomato (*S. lycopersicon*) genotypes (U-4-10, U-64-16, U-2-29, and U-117-2) selected from the Sanliurfa province, Southeastern Anatolia Region of Turkey (Soylu and Comlekcioglu, 2009), 10 heat tolerant tomato genotypes, CLN 2498 E, CLN 2001 A, CLN 1621 L, CLN 2418 A, CL 5915-93D4-1-0-3 (CL 5915), CLN 2413 R, BL 1173, BL 1174, BL 1175, BL 1176, received from the AVRDC and *S. pimpinellifolium* were used as plant materials in this study. Some morphological traits based on the Tomato Descriptors (IPGRI, 1996) are shown in Table 1.

Table 1. Selected characteristics in 14 tomato genotypes and *Lycopersicon pimpinellifolium*.

No.	Genotypes	Mean fruit weight (g)	Fruit size	Fruit shape	Plant growth type	Plant size	Foliage density	Fruit cross-sectional shape
1	U-4-10	308.5	Very large	Flattened	Semi-determinate	Large	Dense	Irregular
2	U-64-16	250.0	Large	Flattened	Semi-determinate	Large	Dense	Irregular
3	U-2-29	289.9	Large	Flattened	Semi-determinate	Large	Dense	Irregular
4	U-117-2	171.9	Large	Slightly flattened	Semi-determinate	Large	Dense	Irregular
5	CLN 2498 E	55.3	Small	Circular	Determinate	Small	Sparse	Round
6	CLN 2001 A	30.1	Small	High circular	Determinate	Small	Sparse	Round
7	CLN 1621 L	31.7	Small	Circular	Determinate	Small	Sparse	Round
8	CLN 2418 A	92.7	Medium	Circular	Determinate	Small	Sparse	Round
9	CL 5915	25.0	Small	Circular	Determinate	Small	Sparse	Round
10	CLN 2413 R	86.9	Medium	Circular	Determinate	Small	Sparse	Round
11	BL 1173	49.9	Small	Circular	Determinate	Small	Sparse	Round
12	BL 1174	69.1	Medium	Ovate	Determinate	Small	Sparse	Round
13	BL 1175	95.4	Medium	Ovate	Determinate	Small	Sparse	Round
14	BL 1176	71.5	Medium	Ovate	Determinate	Small	Sparse	Round
15	*L. pimpinellifolium*	1.0	Very small	Circular	Determinate	Medium	Sparse	Round

Molecular analysis

DNA isolation

Young leaves were collected from tomato genotypes and immediately frozen in liquid nitrogen and stored at -80°C. High molecular weight genomic DNA was extracted from the leaf samples following the protocol for minipreps by using CTAB (Edwards et al., 1991). DNA concentration was measured using a NanoDrop, ND 100 spectrophotometer (NanoDrop Technologies, Inc.) and gel electrophoresis. DNA was diluted in water to a final concentration of 50 ng/µL and stored at -20°C.

SRAP analysis

All SRAP primer combinations were initially screened with the genotypes (Table 2). The 11 primers that produced scorable polymorphic bands were used to amplify the rest of the accessions (Table 3). Amplification reactions were done in volumes of 22 µL containing 2X PCR Mastermix (Fermantas K0171), 1 U Taq DNA polymerase (Fermentas EP0402), $MgCl_2$, 25 mM of each primer and 125 ng tomato DNA. The mixtures were assembled at 0°C, and then transferred to thermal cycler, precooled to 4°C. The amplification was carried out in a model Master Gradient thermal cycler (Eppendorf) using a program consisting of an initial denaturation step of 5 min at 94°C, and then 5 cycles of 1 min at 94°C, 1 min at 35°C, 2 min 72°C, and then 35 cycles of 1 min at 94°C, 1 min at 50°C, 2 min at 72°C, followed by a 10-min elongation step at 72°C. PCR products were stored at 4°C before analysis.

Table 2. The forward and reverse sequence-related amplified polymorphism primer information for this study.

Forward primers	Reverse primers
Me1: TGAGTCCAAACCGGATA	Em1: GACTGCGTACGAATTAAT
Me2: TGAGTCCAAACCGGAGC	Em2: GACTGCGTACGAATTTGC
Me8: TGAGTCCAAACCGGACT	Em3: GACTGCGTACGAATTGAC
Me10: TGAGTCCAAACCGGAAA	Em4: GACTGCGTACGAATTTGA
	Em5: GACTGCGTACGAATTAAC
	Em13: GACTGCGTACGAATTCTG
	Em14: GACTGCGTACGAATTCTT
	Em15: GACTGCGTACGAATTGAT
	Em16: GACTGCGTACGAATTGTC

The amplification products were separated by electrophoresis on 2.5% agarose gels and 0.5 g/mL ethidium bromide in 1X TAE buffer (40 mM Tris-acetate, 1 mM EDTA, pH 8.0) for 3.5 h at 110 V. The fragment patterns were photographed under UV light for further analysis. A 100-bp DNA ladder was used as the molecular standard in order to confirm the appropriate SRAP markers.

RAPD analysis

Fifty RAPD primers (from sets of OPA, OPAE, OPAF, OPAI, OPAJ, OPAK, OPE, and OPX; Operon Technologies, Almeda, CA, USA) were used initially on accessions (Table 4). Primers that produced polymorphic bands were used to amplify all 15 genotypes studied. Thirty-six 10-mer primers found to be polymorphic (Table 4) were used to generate RAPD markers.

Amplification reactions were done in 9-µL volumes containing 2X PCR Mastermix

(Fermantas K0171), 1 U Taq DNA polymerase (Fermentas EP0402), $MgCl_2$, (25 mM) 30 ng of the primer and 15 ng tomato DNA. The mixtures were assembled at 0°C, and then transferred to a thermal cycler, precooled to 4°C. The amplification was carried out in a model Master Gradient thermal cycler (Eppendorf) using a program consisting of an initial denaturation step of 2 min at 94°C, and then 45 cycles of 2 min at 94°C, 1 min at 37°C, 2 min at 72°C, followed by a 10-min elongation step at 72°C. PCR products were stored at 4°C before analysis.

The amplification products were separated by electrophoresis on 1.5% agarose gels and 0.5 g/mL ethidium bromide in 1X TAE buffer (40 mM Tris-acetate, 1 mM EDTA, pH 8.0) for 3 h at 70 V. The fragment patterns were photographed under UV light for further analysis. A 1-kb DNA ladder was used as the molecular standard in order to confirm the appropriate RAPD markers.

Data analysis

Reproducible SRAP and RAPD profiles were scored manually in the binary mode with 1 indicating the presence, and 0 indicating the absence of a band. SRAP and RAPD analysis results were combined. The unweighted pair-group method using the arithmetic average clustering procedure (UPGMA) was employed to construct the clustering dendrograms based on the genetic distance matrix using the NTSYS-PC program (version 2.02i) (Rohlf, 1998). The representativeness of the dendrogram was evaluated by estimating the cophenetic correlation for the dendrogram and comparing it with the similarity matrix, using Mantel's matrix correspondence test (Mantel, 1967). The result of this test is a cophenetic correlation coefficient, indicating how well the dendrogram represents similarity data.

RESULTS AND DISCUSSION

SRAP analysis

A total of 11 SRAP primer combinations were used and a total of 66 bands were scored. The number of bands scored per primer combination ranged from 3 (Me8Em1, Me8Em13, Me8Em16) to 12 (Me1Em4, etc.), with a mean of 6 alleles per primer combination. All fragments scored for each primer combination were polymorphic. The percentage of polymorphic products ranged from 25% (Me10Em5) to 80% (Me10Em16) (Table 3).

Table 3. Sequence-related amplified polymorphism (SRAP) primers with the number of amplified products.

SRAP primer combinations	Size range (bp)	Total number of bands	Polymorphic bands	Polymorphism (%)
Me1Em4	220-1050	12	5	41.6%
Me2Em3	500-1050	5	2	40.0%
Me8Em1	510-790	3	2	66.6%
Me8Em13	350-500	3	2	66.6%
Me8Em15	300-1050	9	3	33.3%
Me8Em16	150-800	3	2	66.6%
Me10Em2	250-1000	5	2	40.0%
Me10Em5	210-580	4	1	25.0%
Me10Em14	220-1010	10	5	50.0%
Me10Em15	250-1050	7	2	28.5%
Me10Em16	210-800	5	4	80.0%
Total	150-1050	66	28	42.42%

RAPD analysis

Fifteen tomato genotypes were screened for RAPD markers using 50 primers in a PCR-based DNA amplification procedure. Forty-six primers produced a clear and good amplification. Ten of the remaining forty-six primers amplified monomorphic fragments for the tomato genotypes studied (OPA-04, OPA-13, OPA-19, OPE-09, OPAK-14, OPX-07, OPX-12, OPX-13, OPX-15, and OPX-18). Therefore, these primers were uninformative for distinguishing among the tomato genotypes.

Thirty-six 10-mer primers, which produced polymorphic bands were used to generate RAPD markers with all genotypes (Table 4). Among 208 bands generated by 36 selected RAPD primers, 55.3% were monomorphic, i.e., present in all individuals. The remaining 44.7% of variable bands were selected as RAPD markers. The mean number of polymorphic bands per primer was lower than that obtained by other researchers (Carelli et al., 2006). The low degree of polymorphisms indicated that there is low divergence between the genotypes studied.

Table 4. Random amplified polymorphic DNA (RAPD) primers with the number of amplified products.

RAPD primer[a]	Sequence	Size range (bp)	Total number of bands	Polymorphic bands	Products detecting polymorphism (%)
OPA-09	GGGTAACGCC	300-1200	8	4	50.0%
OPA-14	TCTGTGCTGG	600-1600	4	3	75.0%
OPA-15	TTCCGAACCC	650-1250	4	1	25.0%
OPA-17	GACCGCTTGT	350-1500	5	3	60.0%
OPA-18	AGGTGACCGT	375-1220	8	1	12.5%
OPAE-10	CTGAAGCGCA	500-1200	5	3	60.0%
OPAE-17	GGCAGGTTCA	750-1500	4	2	50.0%
OPE-10	CACCAGGTGA	700-1700	5	2	40.0%
OPE-15	ACGCACAACC	480-1300	6	2	33.3%
OPE-17	CTACTGCCGT	375-1400	3	1	33.3%
OPE-20	AACGGTGACC	470-1050	6	1	16.7%
OPAF-04	TTGCGGCTGA	400-1900	7	6	85.7%
OPAF-07	GGAAAGCGTC	240-1700	10	2	20.0%
OPAF-09	CCCCTCAGAA	250-2100	8	7	87.5%
OPAJ-03	AGCACCTCGT	600-1550	5	3	60.0%
OPAJ-11	GAACGCTGCC	350-1250	5	3	60.0%
OPAK-05	GATGGCAGTC	380-1000	6	4	66.7%
OPAK-09	AGGTCGGCGT	675-1260	6	2	33.3%
OPAK-12	AGTGTAGCCC	250-1050	6	1	16.7%
OPAK-17	CAGCGGTCAC	500-1020	5	1	20.0%
OPAK-19	TCG CAG CGAG	250-1250	7	3	42.9%
OPAI-18	TCGCGGAACC	800-1100	3	1	33.3%
OPAI-20	CCTGTTCCCT	750-1100	4	3	75.0%
OPX-02	TTCCGCCACC	480-1000	6	3	50.0%
OPX-04	CCGCTACCGA	580-1500	6	1	16.7%
OPX-05	CCTTTCCCTC	510-1255	5	2	40.0%
OPX-06	ACGCCAGAGG	450-1170	5	2	40.0%
OPX-08	CAGGGGTGGA	400-1230	7	4	57.1%
OPX-09	GGTCTGGTTG	530-1250	6	2	33.3%
OPX-10	CCCTAGACTG	675-1400	6	2	33.3%
OPX-11	GGAGCCTCAG	750-1100	4	2	50.0%
OPX-14	ACAGGTGCTG	400-1200	8	4	50.0%
OPX-16	CTCTGTTCGG	450-1600	5	2	40.0%
OPX-17	GACACGGACC	500-1400	7	4	57.1%
OPX-19	TGGCAAGGCA	400-1450	6	1	16.7%
OPX-20	CCCAGCTAGA	400-1450	7	5	71.4%
Total		240-1900	208	93	44.7%

[a]Marker notation refers to the kit (last letter) and the primer (-number) purchased from Operon Technologies (OP).

The number of amplified DNA products depended on genotype primers. Although the number of bands for each primer varied from 3 (OPE-17, OPAI-18) to 10 (OPAF-07) with an average of 5.47 bands per primer, the sizes of the amplified DNA bands ranged from 240 (OPAF-07) to 2100 (OPAF-09) bp. Primers differed in their capacity to detect polymorphism (Figure 1). The percentage of polymorphic products ranged from 12.5% (OPA-18) to 85.7% (OPAF-04) (Table 4).

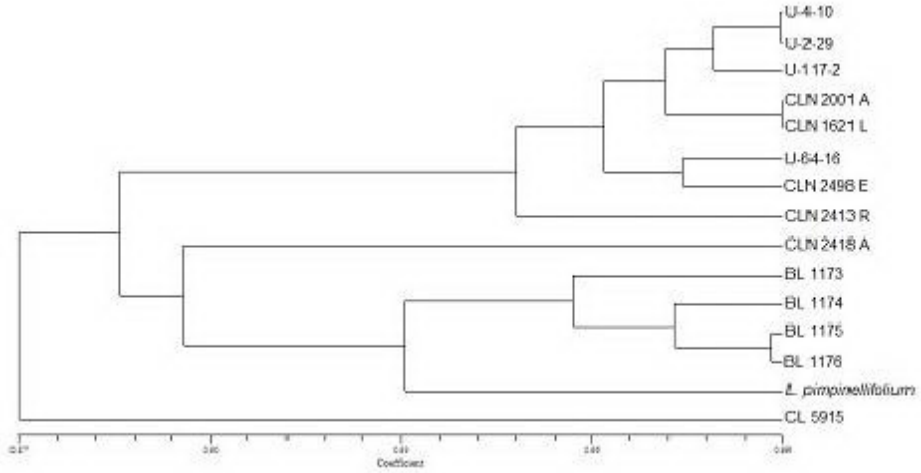

Figure 1. UPGMA dendrogram of 15 tomato genotypes from SRAP and RAPD data. Similarity values are shown at the bottom of the dendrogram.

Phylogenetic analysis

A dendrogram was formed by combining the data obtained from RAPD and SRAP analyses. Similarity ratio of the genotypes varied between 0.87 and 0.99 in the dendrogram (Figure 1). Variation was found to be low among genotypes under study. The most important reason for this is that except for *S. pimpinellifolium*, all genotypes belonged to the same species (*S. lycopersicon*) and were selected as heat-resistant genotypes. The dendrogram was numbered as 1 and 2 and was divided into two branches. While main branch No. 1 included only genotype CL 5915, main branch No. 2 included all the other genotypes used in the study. It was found that genotype CL 5915 in main branch No. 1 genetically resembled all other genotypes in main branch No. 2 at a ratio of 87% and deviated from those genotypes at a ratio of 13%. Tomato line CL 5915 (CL 5915-93D4-1-0-3) was determined to be a valuable source of heat tolerance genes for tomato genetic improvement at AVRDC by evaluating the fruit-set characters (AVRDC, 2001). Except for *S. pimpinellifolium*, CL 5195 had the lowest fruit weight among all genotypes in the study. Branch No. 2 was further divided into two branches: 2.1 and 2.2. Branch 2.1 included CLN 2418 A, BL 1173, BL 1174, BL 1175, BL 1176, and *S. pimpinellifolium*; branch 2.2 included U-4-10, U-64-16, U-2-29, U-117-2, CLN 2498 E, CLN 2001 A, CLN 1621 L, and CLN 2413 R genotypes. Since genotypes U-4-10, U-64-16, U-2-29, and U-117-2 were selected from the same area, it was an expected result for them to have the same genotypic characteristics and to be included in the same group. The genotypes in 2.1 and 2.2 branches were found to be approximately 89% similar to each other. *S. pimpinellifolium*, on the 2.1 branch, was different from other genotypes in this group. This was an expected result

since this genotype was a different species. However, although this genotype is a different species, it resembled other genotypes in this group by 93%. This might have occurred for two reasons. The first one is that there is low genetic variation in tomato (Alvarez et al., 2001) and the second one is that the marker systems used in the study might have failed to amplify the different regions. Our findings are consistent with those of Alvarez et al. (2001). Higher levels of genetic diversity in the self-incompatible species (*S. peruvianum*, *S. hirsutum*, *S. pennellii*, and *S. chilense*) than the self-compatible species (*S. esculentum*, *S. pimpinellifolium*, *S. cheesmanii*, *S. parviflorum*, and *S. chmielewskii*) have been reported (Miller and Tanksley, 1990; Breto et al., 1993). *S. lycopersicon* is self-compatible and inbreeding. *S. pimpinellifolium* populations are self-compatible and although some populations are autogamous and highly uniform in morphological terms, some populations have varying rates of outbreeding. Although fruit seeds were smaller than *S. lycopersicon*, they are morphologically very similar. *S pimpinellifolium* can be reciprocally hybridized with *S. lycopersicon* and it is the only species showing natural introgression with *S. esculentum* (Taylor, 1986). DNA markers are derived from a small region of DNA that shows sequence polymorphism between individuals within or between species and they often do not allow detection of polymorphism within the cultivated species or between the cultivated species and closely related species such as *S. pimpinellifolium* (Miller and Tanksley, 1990; Saliba-Colombani et al., 2000).

According to the dendrogram formed by the comparison of RAPD and SRAP analysis data, no genetic difference was identified between U-4-10 and U-2-29, and CLN 2001 A and CLN 1621 L genotypes. U-4-10 and U-2-29 genotypes are two separate genotypes selected from the domestic population. These genotypes were found to be very similar in terms of fruit characteristics. Genotype No. U-117-2 in the dendrogram was different from genotypes U-4-10 and U-2-29. As indicated in the table, this genotype is slightly different from the other two genotypes in terms of morphology. Since genotype U-117-2 was selected from the same population as genotypes U-4-10 and U-2-29, it was an expected result for these genotypes to be in the same branch. Genotypes CLN 2001 A and CLN 1621 L were both taken from the gene bank as genotypes that are resistant to heat; they show slight differences in terms of fruit weight and form. Autogamous domestic populations are a mixture of pure lines in terms of agriculture, pathology and quality. These are expected to be more heterogeneous than the breeding varieties. Genetic diversity decreased with the replacement of new breeding varieties and conventionally cultivated domestic varieties and this caused the genotypes in the population to become genetically and morphologically uniform. Molecular characterization of breeding materials is essential for breeders, germplasm collections and the commercial sector, such as nurseries. The identification of genotypes provides a standardizable reference for the identification of any genotype, regardless of any factors that limit or influence phenotypic characterization, such as environmental factors, the time of year or the age of the plant material. Furthermore, the possibility of studying the genetic diversity among different cultivars and populations will benefit tomato breeding programs by helping to take decisions on parental genotypes for crosses, and germplasm management to maximize diversity. This is becoming increasingly important to conserve the existing variability in the wild stands of this species scattered throughout most European and some Asian countries, especially due to the progressive narrowing of the genetic base. In this study, we employed RAPD and SRAP markers to evaluate polymorphisms among tomato genotypes, which were obtained from our breeding program (Figure 2). Our results indicated that RAPD and SRAP markers are useful tools for tomato variety

identification. The advantages of RAPD and SRAP molecular techniques include the ability to detect extensive polymorphisms, simplicity, rapidity and without the need for radioisotopes.

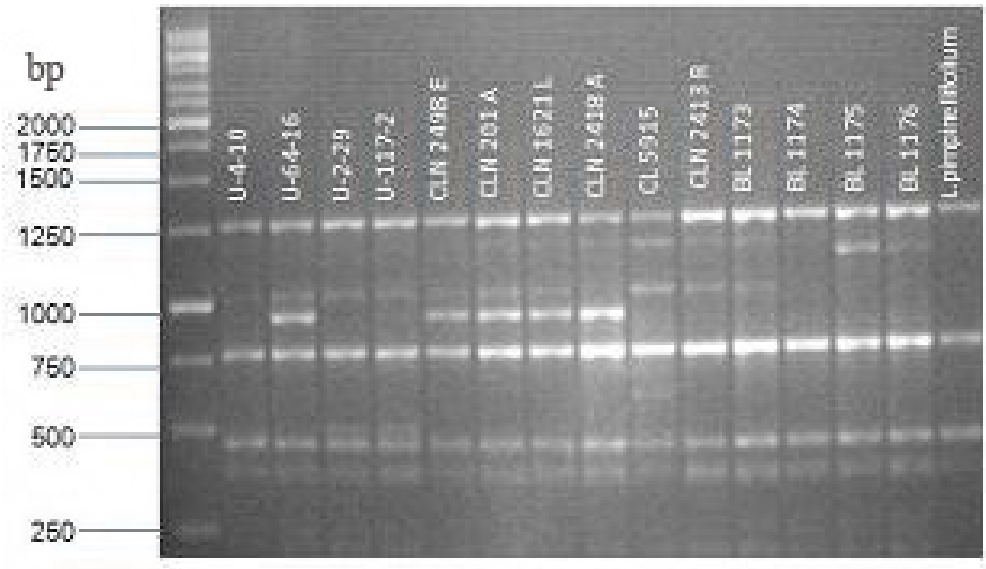

Figure 2. Polymorphic RAPD-agarose gel image.

The same group of tomato lines (except for *S. pimpinellifolium*) were characterized and evaluated by means of the pollen performances and fruit-set characters at high temperature in our previous studies and similarity among genotypes differed depending on traits (Soylu and Comlekcioglu, 2009; Comlekcioglu and Soylu, 2010). Although genotypes characterized in this study exhibited a great deal of morphological variation, they seem to have a relatively limited polymorphism level of RAPD and SRAP primers. There may indeed be limited genetic variation among those genotypes. The results of this study show that similarity ratio of the genotypes studied is high and varied between 0.87 and 0.99 based on molecular markers. We believe that both morphological-agronomic traits and molecular characterization are needed in the quantification of diversity and discrimination. The domestic genotypes could be a valuable source of heat tolerance genes for the genetic improvement of tomato.

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