ISSN 1644-0692
www.acta.media.pl

ACTA *Acta Sci. Pol. Hortorum Cultus, 14(2) 2015, 87-96*

GENETIC DIVERSITY IN TOMATO LANDRACES COLLECTED FROM TURKEY AND IRAN REVEALED BY MORPHOLOGICAL CHARACTERS

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Abstract. Ninety-seven tomato landraces collected from East Anatolian region of Turkey and North-West of Iran, along with three commercial cultivars were evaluated during two years. Experiment was carried out in an alpha lattice design at Agriculture and Natural Resources Research Center of West Azerbaijan, Iran. Analysis of variance revealed significant variation ($P \leq 0.01$) among genotypes for all the experimental characters. Yield showed a positive and significant correlation with length and width of cotyledon leaf, length and width of true leaf, fruit weight, fruit length and diameter, pericarp thickness and fruit peduncle length. In principal component analysis, the first three components explained for 71.6% of total variations among genotypes. Since the first component determined 50% of total variations and yield had high significant coefficient with this component, thus it might be used as s selection criteria to identify genotypes with high yield in breeding programs. Cluster analysis using Ward method classified genotypes into five groups. Groups included: early maturing genotypes in group I, genotypes with high yield in group II, genotypes with large fruit in group III, late maturing and high total soluble solids (TSS) genotypes in group IV and genotypes with high acidity in group V.

Key words: *Solanum lycopersicum* L., genetic variation, quantitative traits

INTRODUCTION

The cultivated tomato, *Solanum lycopersicum*, is the second most consumed vegetable worldwide and a well-studied crop species in terms of genetics, genomics and breeding [Foolad 2007]. Tomato has multipurpose uses in fresh as well as processed food

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industries and its production has increased in the world in recent decades. About 14% of the world's vegetable production is accounted for tomato [Osei et al. 2014]. Turkey and Iran are the main producers of tomatoes in the world. According to FAOSTAT [2012], tomato production in Turkey and Iran were 11,350,000 and 6,000,000 tonnes respectively, which are ranked as the fourth and sixth in the world.

Breeding of new tomato cultivars to improved characteristics started more than 200 years ago in Europe [Foolad, 2007]. There are more varieties of tomato sold worldwide than any other vegetable [Foolad 2007]. Today, fresh market and processing cultivars are quite distinct, largely as a result of the different quality requirements for intended use. The important goals of tomato breeding is increasing yield, disease resistance, earliness in maturity and improvement of fruit quality characteristics such as pH, total acidity and TSS [Foolad 2007].

The identification of variability among accessions is pivotal to the maintenance and utilization of germplasm resources [Mwirigi et al. 2009]. Systematic study and evaluation of germplasm is of great importance for current and future agronomic and genetic improvement of the crop [Reddy et al. 2013]. To identify and estimate the genetic diversity of plants, various methods can be used including morphological, biochemical and molecular markers. Morphological markers are used abundantly to study of genetic variation in plant species. Morphological traits are important diagnostic features for distinguishing genotypes [Osei et al. 2014]. Genetic variation in tomato by morphological characters has been the subject of many studies in regions of the world [Agong et al. 2001, Mazzucato et al. 2008, Al-Aysh et al. 2012, Osei et al. 2014].

Landraces are often heterogeneous and composed of different genotypes which are mostly homozygous and usually exhibit considerable genetic variation for quantitative and qualitative characteristics [Frankel et al. 1995]. Tomato landraces are still cultivated for local use and consumption in many regions of the world. They frequently have distinctive organoleptic traits (flavor and aroma) and nutritional value [Passam et al. 2007]. There are large numbers of tomato landraces in East Anatolian region of Turkey and North-West of Iran. As a result, many landraces were continuously replaced by modern tomato cultivars in these regions in recent years, therefore this germplasm has experienced an overall reduction of its genetic basis.

The objective of present study was collect, preserve of tomato germplasm of these regions and investigates the genetic variation in landraces collected in order to obtain suitable genotypes for fresh and processing industry use, improve tomato production and use in future breeding programs.

MATERIAL AND METHODS

Ninety-seven tomato landraces in East Anatolian region of Turkey and North-West of Iran were collected in 2011. Morphological markers such as size, form and color of fruit and plant size were used to identify and collect different genotypes. At the time of collection, fruits were harvested from each genotype and then seeds were gathered. Each genotype was coded based on the name of collected site (tab. 1).

Table 1. Geographical origins and genotype codes of tomato landraces

No	Origin	Genotype code	No	Origin	Genotype code	No	Origin	Genotype code
1.	Iran-Urmia	IR.U1	34.	Iran-Piranshahr	IR.P2	67.	Iran-Qaraziaediin	IR.Q5
2.	Iran-Urmia	IR.U2	35.	Iran-Piranshahr	IR.P3	68.	Iran-Qaraziaediin	IR.Q6
3.	Iran-Urmia	IR.U3	36.	Iran-Piranshahr	IR.P4	69.	Iran-Qaraziaediin	IR.Q7
4.	Iran-Urmia	IR.U4	37.	Iran-Piranshahr	IR.P5	70.	Iran-Qaraziaediin	IR.Q8
5.	Iran-Urmia	IR.U5	38.	Iran-Piranshahr	IR.P6	71.	Iran-Qaraziaediin	IR.Q9
6.	Iran-Urmia	IR.U6	39.	Iran-Piranshahr	IR.P7	72.	Iran-Khoy	IR.KH1
7.	Iran-Urmia	IR.U7	40.	Iran-Piranshahr	IR.P8	73.	Iran-Khoy	IR.KH2
8.	Iran-Urmia	IR.U8	41.	Iran-Piranshahr	IR.P9	74.	Iran-Salmas	IR.SA1
9.	Iran-Urmia	IR.U9	42.	Iran-Piranshahr	IR.P10	75.	Iran-Salmas	IR.SA2
10.	Iran-Urmia	IR.U10	43.	Iran-Naghadeh	IR.N1	76.	Iran-Sardasht	IR.SR1
11.	Iran-Urmia	IR.U11	44.	Iran-Naghadeh	IR.N2	77.	Iran-Sardasht	IR.SR2
12.	Iran-Urmia	IR.U12	45.	Iran-Miandoab	IR.MI1	78.	Iran-Sardasht	IR.SR3
13.	Iran-Urmia	IR.U13	46.	Iran-Miandoab	IR.MI2	79.	Iran-Sardasht	IR.SR4
14.	Iran-Urmia	IR.U14	47.	Iran-Miandoab	IR.MI3	80.	Iran-Sardasht	IR.SR5
15.	Iran-Urmia	IR.U15	48.	Iran-Miandoab	IR.MI4	81.	Iran-Sardasht	IR.SR6
16.	Iran-Urmia	IR.U16	49.	Iran-Miandoab	IR.MI5	82.	Iran-Sardasht	IR.SR7
17.	Iran-Urmia	IR.U17	50.	Iran-Miandoab	IR.MI6	83.	Iran-Sardasht	IR.SR8
18.	Iran-Urmia	IR.U18	51.	Iran-Miandoab	IR.MI7	84.	Turkey-Iğdır	TR.E1
19.	Iran-Urmia	IR.U19	52.	Iran-Bokan	IR.B	85.	Turkey-Iğdır	TR.E2
20.	Iran-Urmia	IR.U20	53.	Iran-Mahabad	IR.MA1	86.	Turkey-Iğdır	TR.E3
21.	Iran-Urmia	IR.U21	54.	Iran-Mahabad	IR.MA2	87.	Turkey-Iğdır	TR.E4
22.	Iran-Urmia	IR.U22	55.	Iran-Mahabad	IR.MA3	88.	Turkey-Iğdır	TR.E5
23.	Iran-Urmia	IR.U23	56.	Iran-Mahabad	IR.MA4	89.	Turkey-Iğdır	TR.E6
24.	Iran-Urmia	IR.U24	57.	Iran-Mahabad	IR.MA5	90.	Turkey-Iğdır	TR.E7
25.	Iran-Urmia	IR.U25	58.	Iran-Mahabad	IR.MA6	91.	Turkey-Iğdır	TR.E8
26.	Iran-Urmia	IR.U26	59.	Iran-Mahabad	IR.MA7	92.	Turkey-Iğdır	TR.E9
27.	Iran-Oshnavieh	IR.O1	60.	Iran-Mahabad	IR.MA8	93.	Turkey-Iğdır	TR.E10
28.	Iran-Oshnavieh	IR.O2	61.	Iran-Mahabad	IR.MA9	94.	Turkey-Iğdır	TR.E11
29.	Iran-Oshnavieh	IR.O3	62.	Iran-Mahabad	IR.MA10	95.	Turkey-Iğdır	TR.E12
30.	Iran-Oshnavieh	IR.O4	63.	Iran-Qaraziaediin	IR.Q1	96.	Turkey-Iğdır	TR.E13
31.	Iran-Oshnavieh	IR.O5	64.	Iran-Qaraziaediin	IR.Q2	97.	Turkey-Iğdır	TR.E14
32.	Iran-Oshnavieh	IR.O6	65.	Iran-Qaraziaediin	IR.Q3			
33.	Iran-Piranshahr	IR.P1	66.	Iran-Qaraziaediin	IR.Q4			

These genotypes and three commercial cultivars 'Peto Early CH', 'Rio Grande' and 'H-2274' were cultivated at the Kahriz Station of Agriculture and Natural Resources Research Center of West Azerbaijan during two years (2012 and 2013 design) in an alpha lattice design. The station locate at 45 km north of the city of Urmia (Iran) in latitude 45°, 0' east, longitude 37°, 53' north and 1325 m altitude. Soil texture of station is sandy loam soil with pH 7.8. To assess the genetic diversity of tomato genotypes, numbers of quantitative traits were studied based on UPOV descriptor. The studied characters included: length and width of cotyledon leaf, length and width of true leaf, number of days to flowering, to fruit maturity and to 50% fruit maturity, number of flowers per inflorescence, percentage of fruit set per cluster, number of fruits per plant, fruit weight, length and diameter of fruit, pericarp thickness, number of carpels per fruit, number of seeds per fruit, length of fruit peduncle, TSS, pH and acidity of fruit and yield per plant. To record these traits, 10 plants were randomly selected from each plot. After elimination of marginal effects in plot, characters were recorded.

Normality test of the data and combined analysis of variance were performed with SAS software. Correlation analysis was performed to assess relationship among characters. Principal component analysis was carried out in order to determinate the patterns of morphological variation. For grouping genotype, cluster analysis was achieved using the method of Ward based on squared Euclidean distance. Correlation, principal component and cluster analysis were performed using statistic program SPSS.

RESULTS AND DISCUSSION

Combined analysis of variance revealed significant difference ($P \leq 0.01$) among genotypes for all the experimental characters (tab. 2). Mean data shown high range for all the studied traits. For example percentage of fruit set per cluster ranged from 51.5 to 95, number of fruits per plant from 8 to 143.7, fruit weight from 8.8 to 232.4 g, number of days to 50% fruit maturity from 136.5 to 172.8, TSS from 3.4 to 6.8, pH from 4.07 to 4.5 and yield per plant from 1.4 to 3.3 kg. Coefficient of variation (CV%) varied from 1.2 for number of days to 50% fruit maturity to 17.43 for number of fruits per plant. In general, coefficient of variation value lower than 20% is considered to be good [Bernousi et al. 2011].

A negative significant correlation was observed between number of fruits per plant and yield per plant (tab 2). This association could be due to the large number of cherry tomatoes (small fruit) in germplasm studied. Although number of fruits per plant in cherry tomatoes was high, compared to most of the other genotypes and control cultivars, they had low yield. Similar results were also reported by Agong et al. [2001]. Yield per plant showed significant positive correlation with fruit weight. This finding was in consonance with Shafiei [2000]. With increase of number of days to 50% fruit maturity, yield decreased and this demonstrates that early maturing cultivars had higher yield than late maturing cultivars. A negative significant association was noticed between yield and TSS. This is in agreement with previous reports [Ibarbia and Lambeth 1971, Shafiei 2000 Foolad 2007]. This has limited breeder's success for increasing in fruit TSS with high yield [Foolad 2007].

Table 2. Summary of statistic parameters for studied characters in tomato genotypes

Character	Mean Square	Range	Standard Deviation	CV%	Correlation with yield	Correlation with TSS	Correlation with days to 50% maturity
Cotyledon leaf length (cm)	0.854**	3.1–5.2	0.46	3.63	0.248*	-0.089	-0.068
Cotyledon leaf width (mm)	1.548**	4.6–7.2	0.62	2.53	0.372**	-0.251*	-0.182
Leaf length (cm)	95.297**	11.3–30.9	4.85	2.86	0.518**	-0.386**	-0.379**
Leaf width (cm)	43.769**	6.3–22.1	3.29	4.03	0.513**	-0.388**	-0.401**
Days to flowering	40.623**	72–86	3.19	3.39	0.194	0.081	0.042
Flowers/inflorescence	1.995**	3.7–7.2	0.71	6.26	-0.413**	0.233*	0.231*
Fruit set/cluster (%)	376.902**	51.5–95	9.71	9.36	-0.513**	0.227*	0.344**
Fruits/plant	3423.38**	8–143.7	29.11	17.4	-0.475**	0.281**	0.282**
Fruit weight (gr)	14904.1**	8.8–232.4	60.74	5.32	0.446**	-0.090	-0.154
Days to fruit maturity	126.134**	113.3–143.8	5.58	2.76	0.198*	0.118	0.158
Fruit diameter (cm)	9.963**	2.1–9	1.57	5.52	0.425**	-0.096	-0.132
Fruit length (cm)	7.066**	2.5–7.5	1.32	5.49	0.576**	-0.348**	-0.393**
Days to 50% fruit maturity	203.07**	136.5–172.8	7.06	1.20	-0.404**	0.565**	1
Pericarp thickness (mm)	7.851**	2.7–8.8	1.39	6.03	0.540**	-0.448**	-0.381**
Carpels/fruit	16.551**	2–12.4	2.02	8.85	0.119	0.157	0.136
Seeds/fruit	10674.9**	40.4–244.5	51.40	9.03	-0.067	0.294**	0.190
Fruit peduncle length (cm)	0.636**	1.7–3.6	0.40	7.32	0.378**	-0.169	-0.197*
TSS	1.586**	3.4–6.8	0.62	3.80	-0.442**	1	0.565**
pH	0.045**	4.07–4.5	0.11	1.48	0.032	-0.021	0.066
Acidity	0.147**	0.34–1.17	0.19	11.09	-0.508**	0.347**	0.434**
Yield/plant (kg)	0.760**	1.4–3.3	0.43	10.45	1	-0.442**	-0.404**

Note: *, ** – significant at 5% and 1% probability level respectively

The principal component analysis identified three important components. These components analysis explained 71.6% of total variations among genotypes (tab. 3). For each main component, greater positive coefficients were considered as a significant factor. In the first component which described 50% of total variation, characters length and width of cotyledon leaf, length and width of leaf, number of days to flowering and fruit maturity, fruit weight, length and diameter of fruit, pericarp thickness, length of fruit peduncle and yield had high coefficients. Since these traits have a positive significant correlation with yield, thus the first component can be named as yield component. Selection of genotypes based on this component can increase the yield. The second component illustrated 15% of the total variance and characters with higher scores were number of days to 50% fruit maturity, number of carpels, number of seeds and TSS. Because these characters have a significant correlation with TSS, thus this component

can be entitled as TSS-related. Selection based on second component will access to genotypes with high TSS. The third component includes number of days to 50% fruit maturity, TSS, pH, number of flowers per inflorescence and percentage of fruit set per cluster. Since these traits have a positive relationship with number days to 50% fruit maturity, therefore third component can be considered as fruit maturity and selection made based on this component lead to obtain late maturing genotype. Bernousi et al. [2011], in study of twenty five tomato cultivars using 19 characters in Iran, concluded that first seven components state more than 91% of the total variability. Variables with higher scores on first component were: fruit weight, fruit length, fruit diameter, pericarp thickness, number of carpels, pH, number of days to flowering and number of days to fruit production. Second component included pH, plant height, number of node on stem and number of tillers.

Table 3. Values of three principal components for characters of tomato genotypes

Character	1	2	3
Cotyledon leaf length	0.664	0.130	0.165
Cotyledon leaf width	0.686	0.025	-0.006
Leaf length	0.853	-0.271	0.064
Leaf width	0.801	-0.308	0.017
Days to flowering	0.708	0.406	0.179
Flowers/inflorescence	-0.751	-0.171	0.226
Fruit set/cluster	-0.839	-0.045	0.225
Fruits/plant	-0.893	-0.068	0.172
Fruit weight	0.907	0.278	-0.042
Days to fruit maturity	0.730	0.439	0.249
Fruit diameter	0.890	0.351	-0.175
Fruit length	0.863	-0.317	0.172
Days to 50% maturity	-0.319	0.630	0.417
Pericarp thickness	0.819	-0.371	0.140
Carpels/fruit	0.573	0.645	-0.194
Seeds/fruit	0.148	0.719	-0.351
Fruit peduncle length	0.804	0.009	0.156
TSS	-0.302	0.669	0.315
pH	0.268	-0.024	0.677
Acidity	-0.692	0.438	-0.297
Yield/Plant	0.572	-0.382	-0.282
Eigen values	10.475	3.134	1.423
Percent of variance	49.879	14.92	6.776
Cumulative percentage	49.879	64.80	71.580

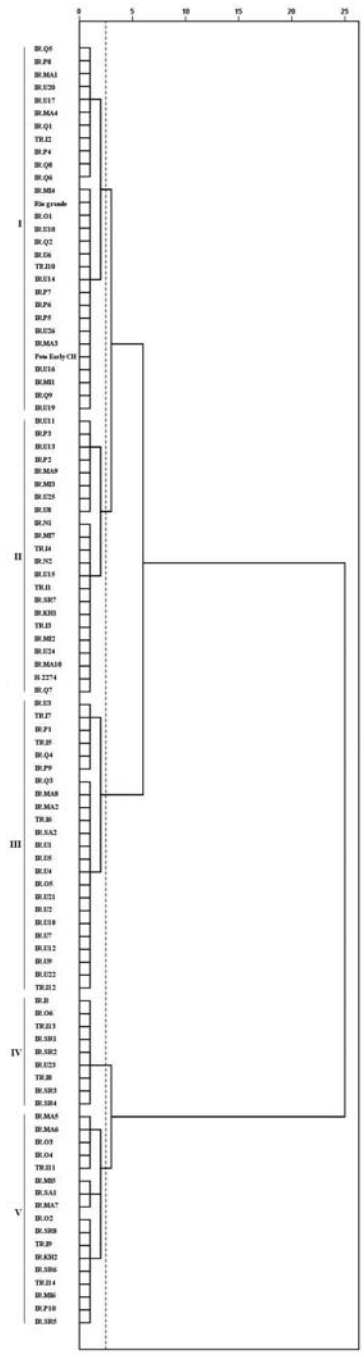

Fig. 1. Dendrogram of tomato landraces and control cultivar constructed with Ward's method based on morphological characters

Table 4. Mean comparison of characters for each cluster

Character	Group I	Group II	Group III	Group IV	Group V
Cotyledon leaf length	4.05	4.2	4.55	3.59	3.73
Cotyledon leaf width	5.99	6.16	6.5	5.14	5.55
Leaf length	26.2	24.78	25.47	14.66	16.8
Leaf width	15.7	15.09	14.76	8.32	9.47
Days to flowering	79.9	79.86	83.3	76	77.18
Flowers/Inflorescence	4.81	4.49	4.38	6.31	5.06
Fruit set/Cluster	69.79	68.5	66.09	91.89	81.53
Fruits/Plant	21.42	18.91	11.19	108.4	45
Fruit weight	116.8	139.9	187.1	14.54	47.28
Days to fruit maturity	129.5	130.7	135.9	124.1	124.2
Fruit diameter	5.8	6.67	7.57	2.83	4.43
Fruit length	6.5	5.69	6.13	3.02	3.95
Days to 50% maturity	151.6	153.6	157.9	163.2	158.4
Pericarp thickness	7.16	6.24	6.53	3.24	4.75
Carpels/Fruit	4.17	5.43	7.11	2.61	3.72
Seeds/Fruit	83.9	142	169.6	100	145.3
Fruit peduncle length	2.82	2.82	2.98	2.04	2.37
TSS	4.66	4.77	5.34	5.64	5.25
pH	4.32	4.18	4.34	4.28	4.24
Acidity	0.504	0.655	0.594	0.859	0.871
Yield/Plant	2.38	2.49	2.08	1.53	1.85

The cluster analysis placed genotypes into five groups (fig. 1). Group I contained 29 genotypes. Genotypes in this group had length and width of leaf, length of fruit and pericarp thickness more than other genotypes and most early maturing genotypes were in this group (tab 4). In geographical regions with cold climatic conditions, early maturing genotypes should be cultivated. In group II with 22 genotypes, the yield was higher than other groups. Genotypes of third group in 50% of the traits studied were dominant compared with other groups. Most genotypes with large fruit were observed in this group. In fresh market tomato, fruit size has significant effect on its marketability. High amount of traits such as the number of flowers per inflorescence, fruit set per cluster, number of fruits per plant, number of days to 50% fruit maturity and TSS was viewed for genotypes in group IV. All genotypes of this group were cherry tomates. Fruit TSS is particularly important to the processing industry and has received more attention than any other fruit trait. The acidity of the fifth group was more than other groups. Acidity influences the storability of processed tomato. Higher acidity and lower pH reduces the risk of pathogen growth in tomato products by contributing to heat inactivation of thermophilic organisms [Foolad 2007]. Fruit flavor is a major consumer demand and one that attracts much attention based on high acidity.

CONCLUSIONS

The results of present work revealed that based on morphological traits, high genetic variation was observed in tomato landraces of Iran and Turkey. A number of genotypes had quantitative and qualitative characteristics better than the commercial cultivars. Because the genotypes of same geographical region were in different group, thus it can be concluded that the genotypes present in same region are genetically distant together. It seems that superior genotypes of each group with genetically distant should be crossed together for increasing hetrosis in breeding programs.

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RÓŻNORODNOŚĆ GENETYCZNA MIEJSCOWYCH ODMIAN POMIDORA ZEBRANYCH W TURCJI I IRANIE WEDŁUG CECH MORFOLOGICZNYCH

Streszczenie. W czasie dwóch lat oceniono 97 miejscowych odmian pomidora zebranych w anatolijskim regionie Turcji i północno-zachodnim Iranie oraz trzy odmiany handlowe. Eksperyment przeprowadzono w układzie alpha lattice w Centrum Badawczym Rolnictwa i Zasobów Naturalnych w Zachodnim Azerbejdżanie w Iranie. Analiza wariancji ukazała zmienność ($P \leq 0.01$) wśród genotypów w odniesieniu do wszystkich cech doświadczenia. Plon wykazał pozytywną, istotną korelację z długością i szerokością liścienia, długością i szerokością liścia, masą owocu, długością i średnicą owocu, grubością owocni oraz długością szypułki owocu. W analizie głównych składowych, pierwsze trzy składowe odpowiadały za 71.6% wszystkich różnic między genotypami. Ponieważ pierwszy komponent określał 50% wszystkich różnic, a plon był istotnie skorelowany z tym komponentem, może on być używany jako kryterium selekcji do identyfikowania genotypów o wysokim plonie w programach hodowlanych. Analiza skupień przy użyciu metody Warda klasyfikowała genotypy w trzy grupy obejmujące wczesnodojrzewające genotypy w grupie I, genotypy o wysokich plonach w grupie II, genotypy o dużych owocach w grupie III, późno dojrzewające genotypy oraz genotypy o wysokiej całkowitej zawartości rozpuszczalnych składników (TSS) stałych w grupie I oraz genotypy o wysokiej kwasowości w grupie V.

Słowa kluczowe: *Solanum lycopersicum* L., różnorodność genetyczna, cechy ilościowe

Accepted for print: 18.02.2015

For citation: Henareh, M., Dursun, A., Mandoulakani, B.A. (2015). Genetic diversity in tomato landraces collected from Turkey and Iran revealed by morphological characters. Acta Sci. Pol. Hortorum Cultus, 14(2), 87–96.