

TOMATO (*L. ESCULENTUM* MILL.) GENOTYPES VARIABILITY OF FRUIT TRAITS

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Tomato (*Lycopersicum esculentum* Mill.) is vegetable which could be produced and consumed in a many different ways, due to its variability, made by breeding programs. Variability of analyzed genotypes was determined for further fruit traits: average mass, fruit shape, locules number and dry matter content. Variability source structure was determined using principal components analysis (PCA). Three main components, which explain 94,2 % of total variability, were chosen for further analysis. The biggest part of the first main component has fruit shape and locule number. The second component is determined by dry

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matter content, and the third by the fruit mass. For more precisely perception of homology and divergence between analyzed genotypes, nonhierarchical grouping analysis (k-means) was performed, and genotypes were divided into three groups. Divergency was determined for fruit mass and locule number, while for index shape and dry matter content analyzed genotypes are homologous. The aim of this study is to examine tomato genotypes variability for fruit traits.

Key words: fruit traits, PCA, tomato, variability

INTRODUCTION

Success in plant breeding, depends on genetic variability in the initial breeding material. Determining the degree of relationship and divergence within tomato germplasm collection represents one of the essential conditions for its successful exploitation during the selection process (SUŠIĆ *et al.*, 1999). Divergent initial breeding material of tomato consider presence of semi-wild and wild forms, old cultivars, local populations, breeding lines and new cultivars and hybrids. Even this populations and cultivars are very important source of desirable genes (diseases resistance, higher dry matter content, and better quality), commercialization of vegetable production put the most yielded and the most profitable cultivars and hybrids in the first plan. Possibilities to obtain new superior genotypes are smaller, due to the lack of genetic variability. Many of these local populations and old cultivars are very different from each other and due to their good agroecological adaptation, attractive design and good fruit quality, they have been conserved in the collections of Institutes and Gene Banks (TAKAČ *et al.*, 2005). The Institute of Field and Vegetable Crops, in Novi Sad, since its establishment, until today, has been working on collecting, researching and maintaining, of tomato collection. Results of analysis, of a part of the collection, are presented in this paper in order to determine the genetic variability of tomato fruit traits.

MATERIALS AND METHODS

This paper presents the results obtained by analysis of 34 genotypes of tomato (5 local populations, 14 old cultivars, 4 new cultivars, 10 breeding lines and 1 hybrid), tab. 1. Genotypes were raised in a randomized block design with three replications, with space between rows 1,4 m and between plants in row 0,5 m, at the experimental field Rimski Šančevi (GLOGOVAC and TAKAČ, 2010). Further fruit traits were analyzed: average mass, index shape, locule number and dry matter content. In order to determinate variability source structure and to evaluate contribution of particular fruit traits in total variability, principal component analysis (PCA) was performed. The principal components were formed based on the correlation matrix (Pearson coefficient correlation). The Varimax method (Kaiser and Wilkins, 1990) was used for the rotation of principal components. The percentage part of three main components in total variability was shown, and also the traits which were decisive for components defining. PCA analysis is widely used in evaluations of genetic collections of other vegetable species, also (GVOZDANOVIĆ-VARGA 2002; 2003;

2005). For more precisely perception of homology and divergence between analyzed genotypes nonhierarchical analysis (k-means) was performed. The statistical package SYSTAT 11 for Windows, Inc. 2004, module Cluster was used for statistical data calculation.

RESULTS

Results of analysis are shown in table 1.

Table 1 Analyzed tomato genotypes and average values of fruit traits

Local populations	Fruit mass (g)	Index shape	Locule number	Dry matter content (%)
Bitoljski kasni	98	0,8	3,9	6,2
Bitoljski rani	49	0,8	2,8	4,9
Devdelijski	65	1,0	2,0	5,9
Skopski rani	95	0,7	4,5	5,9
Tetovski	54	1,0	2,8	5,5

Old cultivars	Fruit mass (g)	Index shape	Locule number	Dry matter content (%)
Novosadski rani	118	0,5	10,2	5,4
Novosadski export	91	0,9	2,2	5,4
Debrecinski	96	0,7	6,1	6,5
Golden jubilej	170	0,9	4,7	5,9
Gloria di Milano	150	0,9	4,3	5,8
Sunny Brok	240	0,7	6,5	5,8
Valiant	145	0,9	4,2	6,0
Saint Pierre	150	0,9	4,8	5,9
Rutgers	200	0,8	6,5	6,3
Belgijski orijaš	205	0,9	4,8	6,0
Moran	172	0,9	5,8	6,3
Kečkemeti torpe	55	1,1	3,5	4,9
Hode	142	0,9	4,2	5,6
Novosadski jabučar	125	0,9	3,9	6,1

Table. 1(continued) Analyzed tomato genotypes and average values of fruit traits

Breeding lines	Fruit mass (g)	Index shape	Locule number	Dry matter content (%)
O2	157	0,9	4,6	5,9
O3	190	0,9	5,3	5,8
O10	144	0,9	4,7	6,0
O13	79	0,9	3,2	6,1
O14	147	0,9	5,1	6,6
O15	138	0,9	4,1	6,1
V2	152	0,8	5,3	5,6
V9	180	0,8	5,4	6,1
V18	121	1,1	3,8	6,1
V21	118	0,9	4,5	6,0

New cultivars	Fruit mass (g)	Index shape	Locule number	Dry matter content (%)
Alparac	90	1,2	3,7	5,1
Knjaz	130	0,9	4,9	6,2
Bačka	160	0,9	6,2	5,2
Pegaz	127	1,0	3,9	6,5

Hybrid	Fruit mass (g)	Index shape	Locule number	Dry matter content (%)
NS - 6	100	0,9	4,5	5,2
X	130,9	0,9	4,6	5,9
C.V. %	35,3	14,5	32,9	7,9

O- indeterminate breeding lines with yellow (O13) and orange fruit colour

V- indeterminate breeding lines with red fruit colour

Decisive traits for genotype differentiation, were determined by principal component analysis. The first three main components were analyzed (tab. 2). Number of components which would be included in further analysis was determined based on percentage of explained variability. The main components were also shown through the rotated values of trait correlation with the main axes. Rotation was performed to avoid grouping of all traits effect in one main component. Percentage part of particular main components in total variability for the first main component was higher, with amount of 38,5 % , and for the second and the third were 25,5 % and 30,07 %, respectively.

Table 2 Rotated principal components of tomato cultivars characteristics

Characteristics	Main components		
	PCA 1	PCA 2	PCA 3
Fruit mass (g)	0,153	0,229	0,939
Dry matter content (%)	0,044	0,980	0,174
Locule number	0,767	-0,050	0,537
Index shape	-0,963	-0,093	-0,042
Latent roots	2,099	1,055	0,613
% of total variability explained	38,52	25,57	30,07
Cumulative variation	38,52	64,09	94,16

The biggest part of the first main component had index shape and locule number. The results obtained by DIMOVA and KRASTEVA (2007), indicated variability of locule number, also. Fruit shape represents horizontal and vertical fruit diameter ratio (ZDRAVKOVIĆ *et al.*, 1999). Index shape and locule number are negatively correlated traits with each other. Index shape 1 is characteristic for round fruits, < 1 for flattened fruits, while elongated fruits have index shape > 1. For manual harvesting of industrial tomato, round fruits shape and equable size are desired, while round and elongated fruits are suitable for mechanical harvesting. In despite of different consumer's requirements of fresh tomato, most of them prefer round shape and equable fruit size tomato. Percentage of total variability that was explained by the second main component was 25,57. The biggest part of the second main component, had a main quality indicator, dry matter content. Tomato belongs to low-calorie vegetables, but it is characterised by high quality because of its vitamin contents (B1, B2, B3, B5, B6, C, folic acid, K, E, PP, β -carotene), MARKOVIĆ *et al.*, (2002). Tomato and its products are the main sources of lycopene (compound with antioxidative effects) and important sources of β -carotene in human nutrition (TOMLEKOVA *et al.*, 2007). For industrial processing, as well as for fresh fruit consumption, higher dry matter content is desirable. The biggest part in the third main component had fruit mass. This trait, also, greatly influenced the tomato divergence in analysis of SEKHAR *et al.*, 2008; SINGH *et al.*, 2008. For more precisely perception of homology and divergence between analyzed genotypes, nonhierarchical analysis (k-means) was performed, and genotypes were divided into three groups.

Tab. 3. k-means splitting

Trait	Variation sources				F-ratio
	between groups		within groups		
	df.	MS	df.	MS	
Index shape	2	0,1205	31	0,0091	13,262**
Locule number	2	28,3845	31	0,5165	54,953**
Dry matter content	2	2,7165	31	0,0278	97,500**
Fruit mass	2	29056,9	31	335,195	86,687**

According to the index shape and locule number, genotypes were divided into three groups (tab. 4). Index shape values, for all analyzed genotypes, ranged from 0,5-1,2. The first group consisted of 14 genotypes (5 old cultivars, 4 local populations, 2 colored breeding lines, 1 high breeding line and 2 new cultivar), tab. 4. In this group, the highest average value of index shape (1,2) had new cultivar Alparac, while the smallest average value of index shape (0,8), had two local populations, Bitoljski kasni and Bitoljski rani. Average value, in the first group, was 1,0 with coefficient of variation 12,5 % (tab. 4)

Tab. 4 Grouping of tomato genotypes according to the analyzed traits

Trait	Group	<i>X</i>	<i>Min</i>	<i>Max</i>	<i>% C.V.</i>	Genotype
Index shape and locule number	I	1,0 3,44	0,80 2,0	1,2 4,2	12,5 21,5	Bitoljski kasni, Bitoljski rani, Devdélijski, Tetovski, Novosadski export, Valiant, Kečkemeti torpe, Hode, Pegaz, O13, O15, V18, Novosadski jabučar, Alparac Skopski rani, Debrecinski, Golden jubilee, Gloria di Milano, Sunny Brok, Saint Pierre, Rutgers, Belgijski orijaš, Moran, O2, O3, O10, O14, V2, V9, V21, Knjaz, Bačka, NS-6
	II	0,8 5,2	0,70 4,4	0,90 6,5	9,4 13,5	Moran, O2, O3, O10, O14, V2, V9, V21, Knjaz, Bačka, NS-6
	III	0,50 10,2	0,50 10,2	0,50 10,2	...	Novosadski rani
Dry matter content	I	5,9	5,6	6,1	2,5	Devdélijski, Skopski rani, Golden jubilei, Gloria di Milano, Sunny Brok, Valiant, Saint Pierre, Belgijski orijaš, Hode, O2, O3, O10, O13, O15, V2, V9, V18, V21, Novosadski jabučar
	II	5,2	4,9	5,5	4,2	Bitoljski rani, Tetovski, Novosadski rani, Novosadski export, Kečkemeti torpe, Alparac, Bačka, NS-6
	III	6,4	6,2	6,6	2,3	Bitoljski kasni, Debrecinski, Rutgers, Moran, Pegaz, O14, Knjaz
Fruit mass	I	79,3	49	100	24,9	Bitoljski kasni, Bitoljski rani, Devdélijski, Skopski rani, Tetovski, Novosadski export, Debrecinski, Kečkemeti torpe, O13, Alparac, NS-6
	II	139	118	160	10,1	Novosadski rani, Gloria di Milano, Valiant, Saint Pierre, Hode, O2, Pegaz, O10, O14, O15, V2, V18, V21, Novosadski jabučar, Knjaz, Bačka

Locule number, for all analyzed genotypes, amounted from 2-10. The highest averaged locule number in the first group (4,2) had old cultivar Valiant, while the smallest locule number (2) had old cultivar Đevdelijski (this is the smallest locule number between all analyzed genotypes, also). Average locule number in this group was 3,44 with coefficient of variation 21,5 % (tab. 4). The second group consisted of 19 genotypes: 9 old cultivars, 4 colored breeding lines, 3 high breeding lines, 2 new cultivars and 1 hybrid (tab. 4). The highest average value for index shape, in this group, was 0,9 and in the same time, it was the most frequent value in this group, since it was determined in 13 genotypes. The smallest index shape value (0,7) was determined in three genotypes: local population Skopski rani, and two old cultivars Debrecinski and Sunny Brok. Average value of index shape, in the second group, was 0,8 with coefficient of variation 9,4 % (tab. 4). The highest locule number (6,5), among genotypes of the second group, had old cultivar Sunny Brok, while the smallest locule number (4,4) had old cultivar Gloria di Milano. Average value of locule number in the second group was 5,2 with coefficient of variation 13,5 % (tab. 4). Genotype with the largest deviation from average values, in this group, was old cultivar Sunny Brok, since it had the smallest index shape (0,7) and the highest locule number (6,5). In the third group there was only one genotype, old cultivar Novosadski rani, since it had the highest locule number (10,2) and the smallest index shape (0,5) among all analyzed genotypes (tab. 4).

Dry matter content (expressed in percentage) is the main indicator of fruit quality. Determined values among all analyzed genotypes ranged 4,9-6,6 %. According to the average values, analyzed genotypes were divided into three groups. The first one is the most numerous and consisted of 19 genotypes: 10 old cultivars, 5 colored breeding lines and 4 high breeding lines (tab. 4). The highest dry matter content in this group (6,1) had breeding lines O13 and V18. The smallest dry matter content (5,6) and also the largest deviation from average value, had high breeding line V2. Average value of dry matter content, in this group was 5,9 with coefficient of variation 2,5 % (tab. 4). The second group consisted of 8 genotypes: 5 old cultivars, 2 new cultivars and 1 hybrid (tab. 4). The highest average value in this group (5,5) had local population Tetovski. The smallest average value (4,9) was determined in local population Bitoljski rani. Average value of dry matter content for this group was 5,2 with coefficient of variation 4,2 % (tab. 4). The third group consisted of 7 genotypes with the highest dry matter content: 4 old cultivars, 2 colored breeding lines and 1 new cultivar (tab. 4). The highest dry matter content in this group and also among all analyzed genotypes (6,6) had breeding line O14. The smallest average dry matter content in this group (6,2) had local population Bitoljski kasni. Average value in this group was 6,4% with coefficient of variation 2,3 % (tab. 4). The results obtained by TAKAČ *et al.*, 2005; 2003, also indicated that local populations and old cultivars collected in gene bank of Institute of field and vegetable crops, represent an excellent starting point in breeding, for increasing fruit quality in tomato.

For the fruit mass, greatest variability was observed. This trait, for all analyzed genotypes, ranged from 49-240g. According to the average values of fruit

mass, analyzed genotypes were divided into three groups. The first group, consisted of 11 genotypes: 8 old cultivars, 1 colored breeding line, 1 new cultivar and 1 hybrid (tab. 4). The highest average value (100g), within this group, was observed in hybrid NS-6. This hybrid is intended for production in greenhouses and early, open field production (TAKAČ and GVOZDENOVIĆ, 2004). The smallest fruit mass (49g) in this group, and also among all analyzed genotypes, had Bitoljski rani. Average value for fruit mass in the first group was 79,3g with coefficient of variation 24,9 % (tab. 4). The second group consisted of 16 genotypes: 6 old cultivars, 5 colored breeding lines, 3 high breeding lines and 2 new cultivars (tab. 4). The highest average value in this group (160g) had new cultivar Bačka. Since it is known that fruit mass is one of the factors which determine cultivar purpose, cultivar Bačka can be used for industrial processing and for the fresh consumption, also (TAKAČ, *et al.*, 2001). The smallest fruit mass (118g) was observed in old cultivar Novosadski rani and high breeding line V21. Average value for fruit mass in the second group was 139g with coefficient of variation 10,1 % (tab. 4). There were 7 genotypes in the third group : 5 old cultivars, 1 colored breeding line and 1 high breeding line (tab. 4). The biggest average value in this group (240g), and among all analyzed genotypes, had old cultivar Sunny Brok. This cultivar was also characterized by the largest Euclidean distance within this group. Old cultivar Golden jubilei had the smallest average fruit mass (170g), in this group. Average fruit mass in the third group was 193,9g with coefficient of variation 12,5 % (tab. 4).

CONCLUSION

According to the presented results, variability for all analyzed fruit traits was determined. Fruit mass ranged from 49-240g, with coefficient of variation 10,1-24,9%. The smallest fruit mass (49g) was measured in local population Bitoljski rani. Old cultivar Sunny Brok had the highest fruit mass (240g). Locule number varied from 2-10 with coefficient of variation 13,5-21,5%. Smaller values of this trait (2-4), were determined in old cultivars and local populations, in most cases. The highest locule number, above 10, had old cultivar Novosadski rani. Values of dry matter content varied from 4,9-6,6%, with coefficient of variation 2,3-4,2%. All breeding lines, except V2, had dry matter content over 6 %. The highest dry matter content (6,6%) had breeding line O14, while the smallest dry matter content (4,9%) was measured in local population Bitoljski rani. Index shape varied from 0,5-1,2, with coefficient of variation 9,4-12,5%. The smallest index shape (0,5) had old cultivar Novosadski rani, while the highest index shape (1,2) had new industrial cultivar, Alparac. According to these values, fruit shape varied from flattened, and slightly flattened to elongated, but most of the genotypes had round fruit shape.

The results of analysis indicate the possibility of using those genotypes for different purposes, and also, as a source of variability, in tomato breeding programs.

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**VARIJABILNOST PLODA KOD RAZLIČITIH GENOTIPOVA
PARADAJZA (*L. esculentum* Mill.)**

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I z v o d

Paradajz (*Lycopersicum esculentum* Mill.) se odlikuje raznolikošću načina proizvodnje i upotrebe, zahvajući varijabilnosti koju čovek stvara oplemenjivanjem. Varijabilnost ispitivanih genotipova paradajza analizirana je za sledeće osobine ploda: prosečna masa, oblik, broj komora i sadržaj suve materije. Struktura izvora varijabilnosti određena je primenom metode glavnih komponentata (PCA). Za dalju analizu odabrano je tri glavne komponente, kojima je objašnjeno 94,2% ukupne varijabilnosti. Najveći udeo u prvoj glavnoj komponenti imaju oblik ploda i broj komora. Druga glavna komponenta definisana je sadržajem suve materije dok je masa ploda izdvojena u treću glavnu komponentu. U cilju jasnijeg sagledavanja sličnosti i razlika između genotipova paradajza, primenjena je nehijerarhijska analiza grupisanja (k-means), sa podelom genotipova u tri grupe. Utvrđeno je da se ispitivani genotipovi razlikuju u masi ploda i broju komora, dok su po obliku ploda i sadržaju suve materije sličniji. Cilj rada je ispitivanje varijabilnosti genotipova paradajza za osobine ploda.

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