

Phenotypic Diversity of Apple (*Malus* sp.) Germplasm in South Serbia

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ABSTRACT

*To determine the overall degree of polymorphism, detect similarities among the accessions and collect highly valued genotypes of native apples, 21 characters of 18 autochthonous apple cultivars were studied for three years. Particular individual accessions were selected from the south region of Serbia according to economically valuable characters and tested in situ. Agronomic evaluation of germplasm accessions revealed considerable diversity among different accessions for all the characters studied. The analysis of variance revealed significant differences among the accessions and among years for some characters as well. Cluster analysis distinguished *Malus* sp. accessions into three distinct groups. Despite of the significant differences among the accessions, yield and fruit weight were a clear separation between the clusters. Among the germplasm of a small geographic area, it was possible to find the cultivars with valuable morphological traits that could be immediately distributed to the market or employed in breeding programs.*

Key words: apple, cluster analysis, diversity, genetic resources, Serbia

INTRODUCTION

The species belonging to the genus *Malus* are found in the wild almost continuously throughout the temperate Eurasia and North America. The primary centre of diversity appears to be within a region stretching from Asia Minor to the western provinces of China (Juniper et al. 1999). Archaeological evidence for the spread of apple from the central Asia is scanty, but the apple has doubtlessly spread by the travellers on the great trade routes, running from the central Asia to the Danube (Clement 2005). The genus *Malus* is characterized by a large diversity resulted from the accumulation of somatic mutations and fostered by the human activities during the long history of the cultivation (Muzher et al. 2007). The domestication of the apple started when wild genotypes are introduced into cultivation,

consciously by applying the selection in order to obtain certain traits, and unconsciously by automatic selection of the wild genotypes from their original wild environments (Ulukan 2009). Knowledge regarding the path of domestication is unclear and so far, various scenarios have been proposed for the origin of the today's apple (Evans 1993).

Normally, apple production focuses on regular plantations established with a few highly productive cultivars of extraordinary quality. However, great quantities of apples are produced in small orchards, established with local, stress resistant cultivars, having good pomological qualities that are superior to cultivated cultivars and form a huge reservoir of variability. These cultivars have been selected locally, but they also satisfy the acceptance of local consumers, having

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more flavours likely due to its less spraying (Pereira-Lorenzo et al. 2009).

Apple germplasm and the maintenance of genetic diversity are important to future breeding because genetic diversity gives species the ability to adapt to changing environments (Bull and Wichmann 2001) and provide the raw material to breed new cultivars *via* hybridization (Doebley et al. 2006) or selection (Dzhangaliev 2003). Some of the resistant local cultivars could be used in the breeding programs in order to transfer the polygenic resistance although many of them have undergone genetic erosion. It is estimated that, approximately, only 20-22% of the apple genetic resources survived gene pool decreasing (Avanzato and Raparelli 2005).

Presently, the public awareness about the worldwide loss of genetic diversity in the cultivated plant species has considerably increased in recent years. The knowledge in local apple cultivars is rising up, so this kind of a situation can serve to diversify the apple market (Itoiz and Royo 2003; Pereira-Lorenzo et al. 2007). There are numerous apple genetic resources conservation and utilization programs in different countries such as in Russia (Forsline 1993), Kazakhstan (Hokanson et al. 1998), New Zealand (Noiton 1998), China (Zhi-Qin 1999), Turkey (Ercisli 2004), Romania (Gradinariu et al. 2003), Spain (Pereira Lorenzo et al. 2003) and Denmark (Larsen et al. 2006) that are trying to establish the collections of germplasm *in situ*. However, these efforts have not been enough to compare the complete variability found in the world.

The standardization and globalization in apples marketing in Serbia have hardly reduced the number of cultivated autochthonous cultivars and the genetic base of the cultivated apples has greatly eroded over the time as regional cultivars have been replaced (Nenadović-Mratinić and Vulić 1988).

While important genetic diversity has been observed in the autochthonous apple cultivars regarding some quality parameters studied, research and utilization of apple genetic resources has a long tradition in Serbia. Various researchers and breeding stations have been gathering cultivars since the beginning of the last century, especially during the last 50 years, such as Jovančević (1959), Stanković and Mišić (1978), Vujanić-Varga et al. (1994), Miletić et al. (1997; 2003), Mratinić (2005).

While the assessment of the level of diversity is necessary to help make the decision on management procedures (Oraguzie et al. 2001), the objective of the study was to investigate a diversity of apple autochthonous cultivars (*Malus* sp.) *in situ* from the South Serbia region not only for collecting and preserving a gene pool but for its use in apple breeding programs for creating new, better, resistant cultivars to most important diseases. Some of the selected accessions could be introduced for table consumption or for fruit processing industries.

MATERIAL AND METHOD

Eighteen autochthonous apple (*Malus* sp.) accessions from the south Serbia (municipalities Vranje, Bujanovac and Preševo) were analyzed in this study. Particular individual accessions, represented as solitary trees in numerous villages of the region, were selected according to economically valuable characters and tested *in situ*. Trees were not trained, having free canopy form, under non-irrigated, extensive cultural practice. All the accessions were examined for a set of 21 characters used as descriptors. Fruit characteristics were measured on the fruits harvested at full maturity stage. The samples of 50 fruits per tree were harvested randomly. All the qualitative properties were characterized and evaluated using the International Board for Plant Genetic Resources (I.B.P.G.R.) descriptor (Watkins and Smith 1982). To minimize the environmental effects, data from three years (2000–2002) were collected.

Following characters were studied:

1. Duration of flowering time (DFT) was the number of days between the beginning of flowering (10% flower opened) and end of flowering time (90% petals dropped).
2. Blooming time (BT) was represented as the number of days from April 20th
3. Period from the blooming time till the harvest time (FBHT) was represented as the number of days from full bloom till the full maturity.
4. Fruit weight (FW) was measured by scale in g.
5. Yield (Y) was presented as kg/tree.
6. Soluble solids content (SS) was determined by the refractometer (Atago, pocket PAL-1) in °Brix.
7. Total sugar content (TS) was determined by Luff-Schoorl method and presented in %.

8. Titratable acidity (TA) was measured by neutralization to pH 7.0 with 0.1 N NaOH; data were given as % of malic acid.

9. The mineral content was obtained by drying the samples at 550°C in a muffle furnace.

10. Tree vigour (TV): (1) Extremely weak, (3) Weak, (5) Intermediate, (7) Vigorous, (9) Extremely vigorous.

11. Tree habit (TH): (1) Extremely upright, (2) Extremely upright/ upright, (3) Upright, (5) Spreading, (6) Spreading/drooping, (7) Drooping, (9) Weeping

12. Susceptibility to *Venturia inaequalis* (scab) (SVEN): (3) Low susceptibility, (5) Medium susceptibility, (7) High susceptibility

13. Susceptibility to *Podosphaera leucotricha* (mildew) (SPOD): (3) Low susceptibility, (5) Medium susceptibility, (7) High susceptibility.

14. Susceptibility to pests (*Eriosoma lanigerum* - woolly aphid, *Cydia pomonella* - codling moth) (SPEST): (3) Low susceptibility, (5) Medium susceptibility, (7) High susceptibility.

15. Fruit shape (FS): (1.0) Globose, (1.1) Globose-conical, (1.2) Short-globose-conical, (2.0) Flat, (2.1) Flat-globose (oblate), (3.0) Conical, (3.2) Intermediate – conical, (4.0) Ellipsoid, (4.1) Ellipsoid-conical (ovate), (5.0) Oblong, (5.1) Oblong-conical.

16. Background colour (BC): (1) Red, (2) Orange, (3) Cream-white, (4) Yellow, (5) Green-yellow, (6) Green.

17. Over colour (OC): (1) Orange, (2) Pink, (3) Red, (4) Dark red, (5) Purple, (6) Brown.

18. Russet amount (RA): (1) 0%, (2) 12%, (3) 25%, (4) 37%, (5) 50%, (6) 62%, (7) 75%, (8) 87%, (9) 100%.

19. Fruit Attractiveness (FA): (1) Extremely poor, (3) Poor, (5) Intermediate, (7) Good, (9) Extremely good.

20. Texture (TX): (1) Extremely coarse, (3) Coarse, (5) Intermediate, (7) Fine, (9) Extremely fine.

21. Eating quality (EQ): (1) Extremely poor, (2) Very poor, (3) Poor, (4) Poor/intermediate, (5) Intermediate, (6) Intermediate/good, (7) Good, (8) Very good, (9) Extremely good.

As indicators of characters variability, means value and coefficient of variation were determined.

An Analysis of variance (ANOVA) was done, and all ANOVAs were performed using the treatments as a statistical parameter at a significance level of $P \leq 0.05$. The least significant difference (LSD) when necessary was used to determine if the difference between the two accessions was large enough to be considered real at a fixed level of confidence (LSD 0.05 = 95% confidence and LSD 0.01 = 99% confidence). All the characters were used to perform the clustering of accessions into similarity groups using the method of an un-weighted pair group method with arithmetic mean (UPGMA). Data processing was performed using the program 'Statistica' (StatSoft, Inc., Tulsa, Oklahoma, USA). No matter the characterization was carried on during three cultivation seasons, only one cluster was developed.

RESULTS AND DISCUSSION

The scores for the 21 variables in 18 autochthonous apple accessions are shown in Tables 1 and 2. Genotypes with different trait composition were presented as the accessions studied. The duration of flowering time (DFT) of the accessions showed a narrow range (7 days), while the blooming time (BT) of examined genotypes showed a much wider (16 days). The ripening period of the selected accessions started from the last week of September till the first week of November, and varied for 45.66 days (Table 1). For TV (Table 2), about 5.56% showed extremely vigorous, 38.29% intermediate and 55.56% vigorous growth. Considering the disposition of the accessions over the classes of TH, 16.67% showed upright, 38.29% spreading, 33.34% spreading to drooping and only 11.11% showed drooping habit. The distribution curve revealed a predominance of the plants with intermediate to vigorous accessions having spreading canopy. This could be explained with the fact that the size of the plant was probably one of the first parameters to be considered as a goal of the selection in the local inhabitants. A high growing plant could assure a good yield potential even in low-inputs agriculture.

Table 1 - Means value and coefficient of variation (CV) for nine pomologic characters of 18 apple accessions from south Serbia.

Cultivar	Code	DFT ^a	BT	FBHT	FW	Y	SS	TS	TA	MC
Đulabija	G-1	7.33	17.33	140.67	133.33	223.00	19.20	10.78	0.31	0.30
Pečka Šerbetka	G-2	9.33	9.33	169.00	136.67	276.67	19.24	9.98	0.16	0.26
Laljče	G-3	8.33	10.33	168.33	76.67	300.00	18.43	12.00	0.82	0.29
Vizajka	G-4	10.00	10.67	186.33	145.00	253.33	18.61	11.06	0.65	0.24
Kuljača	G-5	8.00	9.00	182.00	126.67	82.67	18.91	11.53	0.21	0.24
Paša Šerbetka	G-6	7.00	20.67	161.33	106.67	257.67	17.68	9.80	0.17	0.27
Krupna Šerbetka	G-7	8.00	8.00	177.33	167.33	91.00	17.26	8.65	0.12	0.28
Buzlija	G-8	10.00	8.33	186.00	145.67	240.00	17.06	10.93	0.43	0.27
Hidži Sinan	G-9	9.00	12.67	177.00	177.33	96.00	12.55	11.46	0.22	0.12
Stambolka	G-10	8.33	4.67	168.33	70.00	366.67	17.57	11.64	0.08	0.24
Sitna Šerbetka	G-11	7.33	9.67	171.33	111.67	200.67	16.74	11.01	0.12	0.18
Avajlija	G-12	8.00	12.00	169.00	84.00	268.33	17.23	12.03	0.16	0.24
Uločanka	G-13	12.33	13.33	186.00	141.67	182.00	16.48	10.73	0.12	0.18
Budimka	G-14	10.67	12.33	167.33	86.67	132.67	17.99	12.01	0.16	0.26
Laknja	G-15	9.00	15.00	177.00	153.33	89.67	18.14	11.90	0.17	0.26
Demirka	G-16	12.00	13.67	162.67	142.67	83.00	18.81	11.50	0.27	0.28
Pašinka	G-17	10.33	10.00	173.00	193.33	81.33	18.27	12.18	0.17	0.27
Karapaša	G-18	9.00	9.33	154.00	123.33	353.33	17.99	10.59	0.10	0.30
Mean		9.11	11.46	170.93	129.00	198.78	17.68	11.10	0.25	0.25
CV		16.84	32.29	6.85	26.83	49.01	8.59	8.34	80.42	18.77
LSD	0.05	1.343	0.909	2.965	9.725	105.402	0.480	0.460	0.044	0.017
	0.01	1.945	1.315	4.293	14.080	152.610	0.695	0.665	0.063	0.024

^a For explanation of character symbols, see "Materials and methods"**Table 2.** Qualitative characters of 18 apple accessions from south Serbia.

Cultivar	Code	TV ^a	TH	SVEN	SPOD	SPES	FS	BC	OC	RA	FA	TX	EQ
Đulabija	G-1	7	5	3	3	3	3.2	5	2	3	7	3	7
Pečka Šerbetka	G-2	5	5	3	3	3	4	3	3	3	9	1	7
Laljče	G-3	9	5	7	3	3	1	5	5	1	7	1	5
Vizajka	G-4	7	5	3	3	3	3	5	3	1	5	5	4
Kuljača	G-5	5	3	7	3	3	1	3	3	1	9	3	4
Paša Šerbetka	G-6	7	6	3	3	3	1	3	2	1	5	3	6
Krupna Šerbetka	G-7	7	6	3	3	3	3.2	3	3	2	7	3	6
Buzlija	G-8	7	3	3	3	3	3.2	5	3	5	3	3	2
Hidži Sinan	G-9	5	6	3	3	3	2.1	5	4	2	7	5	4
Stambolka	G-10	7	5	3	3	3	3.2	4	3	2	7	3	3
Sitna Šerbetka	G-11	5	6	5	5	5	3.2	5	3	1	5	3	3
Avajlija	G-12	5	7	7	7	7	3.2	5	2	1	3	3	6
Uločanka	G-13	7	5	3	3	3	1	4	2	1	7	1	6
Budimka	G-14	7	6	7	3	3	2.1	3	2	4	5	3	3
Laknja	G-15	5	6	3	3	3	4.1	3	3	1	7	1	5
Demirka	G-16	7	5	3	3	3	1.2	5	3	2	7	7	7
Pašinka	G-17	5	3	7	5	5	2.1	3	2	2	3	3	6
Karapaša	G-18	7	7	3	3	7	1	4	2	1	9	3	5

^a For explanation of character symbols, see "Materials and methods"

FW (Table 1) varied between 70.00 (G1-10) to 193.33 g (G-17). Similar findings have been reported by Pirlak et al. (2003) for some local apple cultivars with FW values between 49.5 and 152.2 g. If genetics, environment and cultural practices interact to determine the eventual fruit size, and since the accessions in the present study had almost the same environmental conditions with almost no cultural practice, it could be concluded that the accessions G-7, G-9 and G-17 (with the average fruit weight 167.3, 177.3 and 193.3 g, respectively) had good genetic potential for this character.

Another character to be taken into consideration was the yield that varied from 81.33 to 366.67 kg/tree and showed big differences between the genotypes which was confirmed by the coefficient of variation (CV=49.01%). From 18 apple accession grown in the south part of Serbia (Table 1), 33.33% of them had yield below 100 kg/tree, 11.11% had 100-200 kg/tree, 38.89% yielded 200-300 kg/tree and the 16.67% over 300 kg/tree. The alternate bearing in the genotypes was present in all the accessions. Low chemical and fertilizer application due to a poor status of the agriculture could protect the environment; therefore, the performances of these accessions, especially in terms of yield efficiency, must be further evaluated.

Soluble solid content (SS) varied from 12.55 to 19.24%. TS were between 8.65 and 12.18%, while TA content was between 0.10 and 0.82% (Table 1). Similar findings have been reported for the local apple cultivars grown in Pakistan, with SS values varied from 11.80 to 14.25% and TA between 0.31 and 0.39% (Asif et al. 2004). Bostan (2009) reported SS values from 10.50 to 15.00%, which was in agreement with the present results.

Considering the fact that the apple cultivars with sugar/acid ratios lower than 20 are sharp and appropriate for processing and cider production (Lea 1995), only two accessions could be used for cider production (G-3 and G-4) and the others for direct consumption.

The most dominant and harmful pathogens in apple production are scab (*Venturia inaequalis*) and powdery mildew (*Podosphaera leucotricha*), while the most common pests are woolly aphid (*Eriosoma lanigerum*) and codling moth (*Cydia pomonella*). By evaluation of data (Table 2), majority of examined accessions could be used as sources for scab, mildew and pests resistance, because it showed low susceptibility.

FS was controlled by both the climatic and non-climatic factors, and varied greatly. It was classified in eight groups ranging from short-globose-conical, conical, ellipsoid-conical and ellipsoid (all 5.56%, respectively) to flat-gobose (16.67%), globose (27.78%) and intermediated-conical (33.33%).

Skin colour has two components – background colour and over colour. BC varied from cream-white (38.89%), over yellow (16.67%) to green-yellow (44.44%), while OC ranged from red (50.0%) to dark red or purple (5.56%).

EQ depends upon the sweetness, acidity, astringency and aroma. No matter the fact that the traditional breeding practice has been to rely on the experience and opinions of one or two individuals to identify the tastiest accessions, these were classified them in six EQ categories. The majority of the accessions (27.77%) had intermediate to good EQ.

Looney (1993) suggested that large fruit size, attractive appearance and characteristic or distinctive flavour were amongst the most important fruit quality attributes. Considering this fact, accessions G-7, G-13 and G-16 could be placed in the quality group since had fruit weight over 140g, good fruit attractiveness and good eating quality. Link (2000) reported that quality components included the attributes such as size, colour, russet amount and chemical composition of the fruits, and in that case only accession G-16 could stayed in this group.

Agronomic evaluation of germplasm accessions revealed considerable diversity among different accessions for all the characters studied. The analysis of variance revealed significant differences among the accessions and among the years for some characters as well. The highest F value (Table 3) was obtained for TA (181.38), as a result of the particularly high acids content in the accession G-3 (0.82%). The acknowledgment of such large dissimilarity in TA was confirmed by the coefficient of variation that had the highest value among all the characters studied (CV=80.42%). Since inter-accession differences were highly significant, the local apple cultivars studied here could be considered to be statistically different. This was quite interesting because the accessions were not selected from various areas which were distinct in the environmental and agricultural parameters. On the other hand, these could be expected so, because the intention was to collect the largest diversity possible.

Table 3 - F-values obtained in the ANOVA for the studied quantitative factors.

Effect	df	MS	F-value	p-value
Duration of flowering time				
Cultivar	17	7.06**	7.53	0.00
Year	2	1.72	1.84	0.17
Error	34	0.94		
Blooming time				
Cultivar	17	41.10**	95.53	0.00
Year	2	2.02*	4.69	0.02
Error	34	0.43		
Period from blooming time till the harvest time				
Cultivar	17	411.16**	89.70	0.00
Year	2	2.07	0.45	0.64
Error	34	4.58		
Fruit weight				
Cultivar	17	3594.47**	72.96	0.00
Year	2	235.50*	4.78	0.01
Error	34	49.26		
Yield				
Cultivar	17	28477.88**	4.92	0.00
Year	2	222734.39**	38.49	0.00
Error	34	5786.60		
Soluble solid content				
Cultivar	17	6.92**	59.00	0.00
Year	2	0.02	0.15	0.86
Error	34	0.12		
Total sugar content				
Cultivar	17	2.57**	24.37	0.00
Year	2	0.06	0.52	0.60
Error	34	0.11		
Titratable acidity				
Cultivar	17	0.118**	181.38	0.00
Year	2	0.000	0.49	0.62
Error	34	0.001		
Mineral content				
Cultivar	17	0.007**	45.493	0.000
Year	2	0.000	1.178	0.320
Error	34	0.000		

Cluster analysis. The tree-plot obtained by the cluster procedure (UPGMA) showed the accessions grouped in the clusters with their respective distances. The determination of the 'true' number of the groups in a cluster analysis is difficult but a normalized maximum distance of 120 was used here as ultimate limit for clustering that was judged to best distinguish the accessions. Cluster analysis classified 18 *Malus* accessions into three distinct groups (Fig. 1). By this way, two of the three clusters included a large number of accessions, while the third one included only

two. Despite of the significance differences among the accessions, the yield and fruit weight were a clear separation between the clusters.

The average accession distance (AD) among the apple cultivars based on phenologic, quantitative and qualitative traits was AD = 128, ranging from AD = 14 (the most relate accessions, G-7 and G-9) to 311 (the most distantly related, G-10 and G-17). *Cluster I.* This group included nine accessions (G-1, G-2, G-3, G-4, G-6, G-8, G-11, G-12 and G-13) which were mainly characterized by high yields that varied from 182.0 kg/tree (G-13) up to 300.0

kg/tree (G-3) and medium fruit size. Attending to its morphological characteristics, this group displayed intermediate pomological characters between the clusters II and III. Apples from this cluster had larger fruits and lower yields than the accessions from cluster II, but smaller fruits and

higher yields than in cluster III. This cluster was split off into two distinct sub-groups, defined as cluster IA and IB. Sub-group (IA) consisted of three accessions (G-1, G-11 and G-13) with lower yields than the accessions G-2, G-3, G-4, G-6, G-8 and G-12 that formed sub-group (IB).

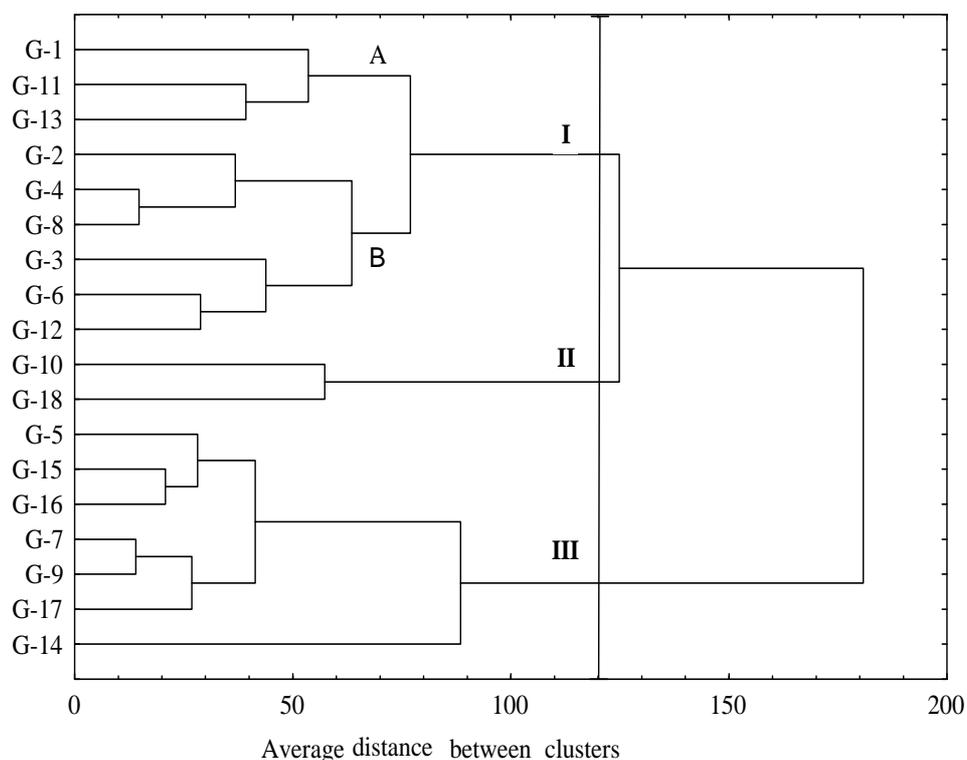


Figure 1 - Cluster resulting from the hierarchical classification of 18 autochthonous apple cultivars (Euclidean distances on the averages of the characters).

Cluster II. The second group was created by two apple accessions (G-10 and G-18). Those two had the highest yield (353.33- 366.67 kg/tree) and the lowest fruit weight (70.00 - 123.33 g) of all the cultivars examined. Actually, they shared important traits such as low mineral content, yellow ground colour, red to pink over colour and almost no russet.

Cluster III. The third cluster was created by seven accessions (G-5, G-7, G-9, G-14, G-15, G-16 and G-17). All of them had very low yields but very high fruit weight. Accessions G-5 and G-14 acted as a barrier of the cluster. This was particularly referred to G-14 because while reviewing the fruit weight and yield, it looked like that this accession was by a mistake classified in this cluster.

Hierarchical cluster analysis allowed the assessment of similarity or dissimilarity and clarified some of the relationships between the cultivars. The accessions clustered in the first two groups revealed relatively closer genetic relationships than those in cluster III. The reason of a low dissimilarity could be explained with the fact that the population of apple cultivars included the genotypes from relatively small area of dissemination and those one gone through the selection. Also, the fragmentation and reduction in the habitat size as well as isolation of population could increase the inbreeding depression which could lead to little differentiation between the local populations (McKay and Latta 2002). But, on the other hand, high dissimilarity between some accessions could be explained by the apple

polymorphism (Pereira-Lorenzo et al. 2003, 2007) or by continuous accession introduction from other part of Balkan Peninsula or even whole Europe.

Hybridization can be a key for both low and high dissimilarity level. If hybridization between the cultivars and their wild progenitor occurred, where both types of materials had remained in close contact for a long time (Allendorf et al. 2001), the individuals with intermediate phenotypes occurred (Coart et al. 2003). Also, it could be speculated that outcrossing and a self-incompatibility system in apple would result in higher levels of heterozygosity and continuous diversity of the accessions. But, it was, however, more apparent that the hybridization had led to the reduction of the population fitness (Lynch 1991) as well as the extinction of some cultivars (Rhymer and Simberloff 1996).

Recent observations had determined that some accessions growing in different villages had similar morphology and slightly different names. That was why a strong similarity was expected between the four accessions (G-2, G-6, G-7 and G-11) that were collected in the same part of the region, and with the similar local name (having word `Šerbetka` in its local name which means `too sweet`), but they were placed in two different clusters. The accessions from cluster I (G-2, G-6 and G-11) were virtually identical and were grouped in the same cluster, especially G-2 and G-6 that were in the same sub-cluster. Accession G-7 from cluster III was different from the previous and did not correspond to the mentioned accessions description because it had larger fruits, lower yield, and different phenology. It seemed that these accessions were probably the same cultivar in the past, but accession G-7 separated earlier and developed independently under the selection of Serbian conditions.

No matter the fact that cluster analysis separated the apple accessions from each others, it was difficult to say how many of these accessions were really originated from this area, undergone human selection or obtained from the seedlings. It was hard to assume how many of them could be a single plant imported from other part of Serbia or neighbour countries and later domesticated.

Royo and Itoiz (2004) classified apple cultivars in the clusters according to its morphological characterization and found that the fitness of the dendrogram obtained using the morphological data was poor. Forte et al. (2002) constructed dendrogram of the morphological traits for the

analysis of the phylogenetic relationships among the wild and cultivated apple cultivars. Also, Damyar et al. (2007) showed that the classification of apple genotypes in the clusters, based on several quantitative and qualitative traits, had good segregation on the population.

CONCLUSION

Morphological and agronomic data analyses using the analysis of variance and cluster analysis revealed the existence of a wide variability of genus *Malus* in a very small area such as south Serbia. This study demonstrated that the numerical analysis of apple morphological traits could be used as a rapid and comprehensive method to establish accessions classification within the germplasm collections. Based on these results, it could be concluded that all apple cultivars of cluster I were the best sources of genotypes having high fruit weight and yield and with the longest period from the flowering till the harvest time. Genotypes G-3 and G-4 could be used for cider production. Accessions grouped into cluster II appeared to be industrial one because of the enormously high yields. Cluster III had accessions that could be used for table consumption, especially G-16 as the most quality one. Further accumulation of data across the years and across the country might result in an increase of the precision of accessions assessment. It was interesting that in each cluster, accessions could be found with low susceptibility to diseases and pest, so the cultivars could be used in future breeding program for apple improvement in all the directions. Obviously, the multiplication of representative accessions of these clusters will be given priority.

Present study confirmed the necessity of preserving these unique genetic resources and continuing its study no matter the fact that in practice. However, it was difficult to determine whether a specific genetic variant would be of future value. For this reason, all the collected accessions were transferred to the Experimental Station `Radmilovac` of the Faculty of Agriculture in Belgrade for further study. The main goal was to ensure the conservation of a wide range of genetic variability and progress in long-term breeding program because greater genetic diversity would be desirable for future development of innovative, market-driven cultivars (Noiton 1998).

Since the value of genetic resources can be expressed as an ecological, economical or ethical value, it should be also considered to promote the accession's come back to main markets of Serbia or surrounded countries in order to create an economical opportunity for the local farmers.

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