

CHARACTERIZATION OF THE VINEYARD BYOTYP COLLECTION OF PEACH AS STEP IN PREBREEDING PROCESS

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In this research, morphological characterization of vineyard peach collection was conducted. In 78 accessions thirty qualitative traits of tree, flower, leaf, fruit and stone were analysed by using UPOV and ECPGR descriptors. Most of the studied traits showed a high degree of variability. The lowest variability obtained for the leaf traits, and highest for skin and flesh colour. Not only were the accessions sorted into a large number of categories by the most of their properties, but also there was a significant level of variability in the collection, reflecting in the fact that the traits were recombinant in a different way. Principal component analysis (PCA) and a dendrogram were performed to determine relationships among accessions and to obtain information on the usefulness of those characters for the discrimination. The PCA revealed that the first 4 principal components were able to represent 43.1% of total variance. Traits with high discriminating values comprised internal and external fruit colour, flower type and colour, flower bud density and stone shape. The cluster analysis showed that the accessions were placed in three main clusters. The greatest impact on the separation in clusters had fruit over colour and extent of fruit over colour. Moreover, the collection can also comprise some accessions with the preferred recombination of properties that might be interesting for further studies in breeding.

Key words: Morphological characterisation, multivariate analysis, vineyard peach

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INTRODUCTION

The peach [*Prunus persica* (L.) Batsch] is the third most important temperate fruit crop worldwide, after the apple and the pear. This species originates from China and is well adapted to temperate and subtropical regions, between 30° and 45° north and south latitudes. Peach breeding industry is one of the most dynamic of deciduous fruit species grown in the world (REIG *et al.*, 2013). Breeders continuously release new cultivars, creating about 100 commercial peach and nectarine cultivars per year (BYRNE, 2002). Modern peach cultivars have a narrow genetic base due to the limited number of genotypes used as parents in breeding programs (MYLES *et al.*, 2009). Recent studies have demonstrated a low level of genetic variation among peach cultivars from several breeding programs (ARANZANA *et al.*, 2010). Germplasm restrictions, genetic bottlenecks, and population shifts can be associated with changes in the germplasm genetic diversity (CHAVEZ *et al.*, 2014). Consequently, peach diversity has been drastically reduced by the use of modern cultivars that share a few common ancestors. Furthermore, due to the relatively narrow genetic base of the world's leading peach cultivars it becomes important to describe and use alternate genetic resources that may contribute to integrating genomes and widening world peach production areas or to increasing efficiency in traditional peach growing regions. Local peach germplasms could be a basis for genetic improvement of this species. One of them is the vineyard peach (*Prunus persica* spp. *vulgaris* Mill.), an indigenous peach population cultivated or grown spontaneously in Serbia.

The vineyard peach was originally cultivated in old vineyards, which it was named after. Propagation exclusively by seeds make this native population of the vineyard peach a great source of genetic variability that can improve economically most important traits of cultivars and rootstocks of peach grown nowadays. As cited by NIKOLI *et al.* (2010), within the native population of the vineyard peach, it is possible to find genotypes with valuable morphological traits that can be immediately distributed to farmers or breeders. The vineyard peach germplasm has been investigated very intensively in Serbia in the last thirty years. The evaluation has resulted in selecting genotypes resistant to plant pathogens, suitable for processing, for rootstock and fresh consumption (ZEC *et al.*, 2007; ZEC *et al.*, 2008; RAKONJAC *et al.*, 2008; OGNJANOV *et al.*, 2008; NIKOLIC *et al.*, 2013). Expanding cities, developing agriculture and intensive management in new vineyards have led to a significant reduction in the vineyard peach population. Thus, there is a need for protection and genetic conservation of the remaining vineyard peach as a source of germplasm, by establishing collection plantings as gene banks for developing new cultivars.

The development of new fruit cultivars is based on genetic resources. Germplasm collection and characterization are essential stages of breeding programs. The enhancement and utilization of genetic resources require a detailed knowledge on the morphological and genetic characterization of germplasm genotypes (DAY RUBESTEIN *et al.*, 2006; UPADHYAYA *et al.*, 2008). Characterization based on morphological parameters is commonly used to solve duplication problems within germplasm collections (ZAOUAY and MARS, 2011). Such analysis should be made before biochemical or molecular studies are carried out (KHADIVI-KHUB *et al.*, 2011). Morphological traits are useful for preliminary evaluation because they ensure a fast and simple evaluation and can be used as a general approach for assessing genetic diversity among morphologically distinguishable genotypes. It is a quick approach that does not require some sophisticated equipment or laborious procedures (OLI *et al.*, 2012). Furthermore, characterization based on the descriptors created by international organizations (UPOV and IPGRI) enable researchers to use common descriptive traits (YILMAZ *et al.*, 2012).

Characterization of plant genetic resources usually contains a wide range of data. Such data are generally large and multivariate with a considerable number of descriptors measured on each of the accessions, so the use of multivariate analysis is particularly well-adapted to this type of situation. Statistical methods, such as principal components analysis (PCA) and/or cluster analysis (CA), can be used as a tool for screening the genotypes of a collection (KHADIVI-KHUB *et al.*, 2013). PCA is mostly applied to reduce the number of input variables while CA is used to sort samples into groups (CROSSA and FRANCO, 2004).

The objective of this study was to describe and quantify the variability of morphological traits of 78 vineyard peach accessions, to identify the most useful variables for discrimination among accessions, to detect relationships among accessions, and to provide useful information to facilitate the choice of parental genotypes for crosses for peach breeding program. Some of the accessions would be a subject of further plant genetic resources maintenance.

MATERIAL AND METHODS

Germplasm collections derived from seeds from various types of the vineyard peach originating from different regions of Serbia. The *ex situ* collection was located 8 km North-East of Belgrade (44°45'N and 20°35'E, at 135 m altitude) at the "Radmilovac" Experimental Station of the Faculty of Agriculture. 78 vineyard peach accessions were selected for their vitality, health condition and phenotypic diversity. The trees were planted in 2008 and 2009, at 4 x 4 m distance and each tree was considered as a separate accession. Standard cultural practices were applied, with minimal pruning in order to allow natural growth habit expression. Irrigation was not applied. To minimize environmental effects, data were collected during three consecutive years (2012-2014).

Table 1. List of traits studied

Trait	Abbreviation	Code
Tree		
Tree vigour	TV	1 - Extremely weak, 2 - Very weak; 3 - Weak; 5 - Medium; 7 - Strong; 8 - Very strong; 9 - Extremely strong
Tree habit	TH	1 - Columnar; 2 - Upright; 3 - Semi upright; 4 - Standard; 5 - Open; 6 - Compact; 7 - Weeping
Flower		
Density of flower buds	DFB	1 - Extremely sparse; 3 - Very sparse; 5 - Medium, 7 - Very dense; 9 - Extremely dense
General distribution of flower buds	GDFB	1 - Isolated, 2 - in groups of two or more
Flowering shoot thickness	FST	3 - thin; 5 - medium; 7 - thick;
Flower type	FT	1 - rosaceous/showy; 2 - campanulate/non-showy
Position of the stigma compared to anthers	PS	1 - below anthers; 2 - same level as anthers; 3 - above anthers
Corolla predominant colour	CPC	1 - white; 2 - very light pink; 3 - light pink; 4 - medium pink; 5 - dark pink; 6 - violet pink; 7 - red

Leaf		
Leaf blade colour	LBC	1 - greenish yellow; 2 - green; 3 - purplish red
Presence of nectaries	PN	1 - absent; 2 - present
Shape of nectaries	SN	1 - reniform; 2 - globose (round)
Predominant number of nectaries	NN	1 - two; 2 - more than two
Fruit		
Fruit shape	FS	1 - flat; 3 - oblate ; 5 - round; 7 - ovate; 9 - elliptic
Fruit ground colour	FGC	1 - green ; 2 - greenish-white; 3 - cream-green; 4 - cream-white; 5 - cream; 6 - pink white; 7 - greenish yellow; 8 - light yellow; 9 - yellow; 10 - orange yellow; 11 - not visible
Fruit over colour	FOC	1 - absent; 2 - orange red; 3 - pink; 4 - pink red; 5 - light red; 6 - medium red; 7 - dark red; 8 - blackish red
Extent of fruit over colour	EFOC	1 - none (0%); 2 - very slight (10-15%); 3 - slight (15-30%); 4 - slight to medium (30-45%); 5 - medium (45-60%); 6 - medium to widespread (60-75%); 7 - widespread (75-90%); 8 - very widespread (90-100%); 9 - hiding ground colour
Flesh firmness	FF	1 - very soft; 3 - soft; 5 - medium; 7 - firm; 9 - very firm
Flesh colour	FC	1 - greenish white; 2 - white; 3 - cream white; 4 - greenish yellow; 5 - light yellow; 6 - yellow; 7 - orange yellow; 8 - orange
Anthocyanin coloration of the flesh	ACF	1 - absent; 2 - weak; 3 - only under the skin ; 4 - under the skin and around the stone ; 5 - only around the stone; 6 - in the whole flesh, faint; 7 - in the whole flesh, intense
Flesh to stone adherence	FSA	1 - freestone; 2 - semi-freestone; 3 - clingstone
Fruit flesh fibre	FFF	1 - absent or weak; 2 - moderate; 3 - strong
Fruit prominence of suture	FPS	3 - weak ; 5 - medium; 7 -strong
Fruit density of pubescence	FDP	1 - very sparse; 3 - sparse ; 5 - medium; 7 - dense; 9 - very dense
Fruit thickness of skin	FTS	3 - thin; 5 - medium; 7 - thick
Fruit adherence of skin to flesh	ASF	1 - absent or very weak; 3 - weak; 5 - medium; 7 - strong; 9 - very strong
Stone		
Stone shape	SS	1 - oblate; 2 - round; 3 - elliptic; 4 - obovate
Stone relief of surface	SRS	1 - only pits; 2 - predominantly pits; 3 - pits and grooves; 4 - predominantly grooves; 5 - only grooves
Stone size compared to fruit	SSCF	1 - extremely small; 3 - small; 5 - medium; 7 - large ; 9 - extremely large
Stone intensity of brown colour	IBCS	3 - light; 5 - medium; 7 - dark
Stone tendency of splitting	STS	1 - absent or very low; 3 - low; 5 - medium ; 7 - high; 9 - very high

Thirty qualitative traits were analysed. The accessions were evaluated for tree, flower, leaf, fruit and stone traits (Table 1). Tree vigour, tree habit, density of flower buds, presence of nectaries, shape of nectaries, flower type, position of the stigma compared to the anthers, fruit

shape, fruit ground colour, fruit over-colour, extent of fruit over-colour, flesh firmness, flesh colour, anthocyanin coloration of the flesh, flesh to stone adherence, stone shape, stone relief of surface, fruit flesh fibre and stone size compared to fruit, were evaluated according to the ECPGR priority descriptors for peach (GIOVANNINI *et al.*, 2013). General distribution of flower buds, flowering shoot thickness, leaf blade colour, predominant number of nectaries, corolla predominant colour, fruit prominence of suture, fruit density of pubescence, fruit thickness of skin, fruit adherence of skin to flesh, stone intensity of brown colour and stone tendency of splitting, were evaluated according to the UPOV (1995) descriptor for peach.

On the basis of the morphological categorisation of the accessions the frequency distribution of 30 variable traits was presented with histograms. The collected data were also analysed by the multivariate analysis, using the principal component analysis (PCA) and clustering analysis (CA). PCA was performed to summarize the manifold data in the first principal component containing the highest possible variability of the data. As a criterion for extracting the main principal components, an eigenvalue greater than 1 was taken, and to determine which of the PC scores accounted for the greatest amount of variation, the eigenvalues of these components were compared for each trait. CA was applied to classify the accessions into homogenous groups. Ward's method was used as an agglomeration rule and the Euclidean distance as a measure of dissimilarity. Statistical analyses were performed using Statistica for Windows, version 5.0 (StatSoft Inc., Tulsa, OK) statistical package.

RESULTS AND DISCUSSION

Frequency distribution of the 78 vineyard peach accessions are shown on the Figure 1. In all accessions absent or very low stone tendency of splitting has been observed. Regarding flesh to stone adherence all 78 accessions were freestone.

Analysed vineyard peach germplasm is rich in diversity for tree vigour and habit. Tree vigour varied from very weak to extremely strong while tree habit ranged from upright to open (Figure 1). This variability allows selection for different training and growing systems (from low to high density), and cultivation technology. Regarding density of flower buds, fifteen accessions were characterized by extremely density which, suggests their good potential for high and regular yields. The general distribution of flower buds in groups of two or more was dominant, and only for three accessions it was isolated (Figure 1). Regarding flowering shoot thickness, most of the accessions (57) were with medium type. The majority of vineyard peach accessions (63) had a rosaceous flower type, while fifteen accessions had a campanulate flower type. Regarding the position of the stigma compared to the anthers, it was observed that the predominant was the one in which the stigma was the same level as anthers (67 accessions), while the position where the stigma was below and above anthers was detected in seven and four accessions, respectively. This was expected having in mind the fact that the peach is an inbred species. Great differences observed for flower colour, so 19 accessions had very light pink, 38 had light pink, 4 accessions had medium pink, 9 accessions had dark pink, 7 had violet pink and only one had red flower colour. The variation in tree habit and flower colour can be particularly interesting from the aspect of the vineyard peach as a decorative species.

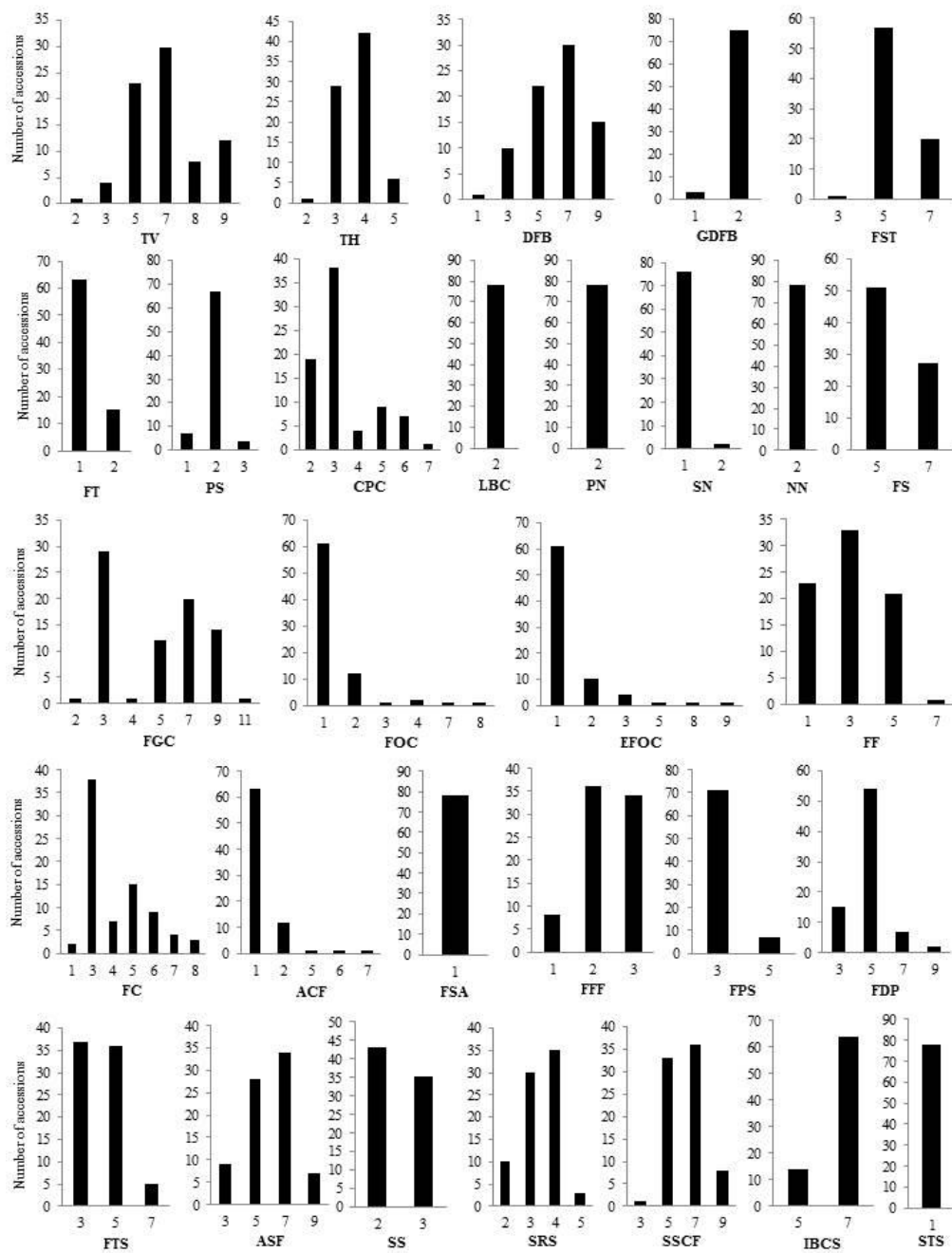


Figure 1. Frequency distribution of the 78 vineyard peach accessions for tree, flower, leaf, fruit and stone traits studied (For an explanation of traits and code symbols, see Table 1)

Accessions showed low variability for leaf characteristics (Figure 1). All 78 analysed accessions had green leaf blade coloration and showed the presence of more than two nectaries. The greatest proportion of accessions (97.44%) had reniform nectaries, while only two accessions expressed a round shape of nectaries.

Analysed vineyard peach germplasm showed high level of morphological variation for fruit traits. Fruit shape is an important fruit quality attribute, since it influences consumers' acceptance and post-harvest handling. In peach, round shapes without protruding tips are preferred by consumers (CANTIN *et al.*, 2010). In studied germplasm of the vineyard peach collection rounded fruit shape was present in 51 accessions, while the remaining 27 accessions had ovate fruit shape (Figure 1). Moreover, most of the accessions (71 accessions) had weak fruit prominence of suture. Great differences were found for skin colour of the fruits. Cream-green skin had a 37.18% of accessions, cream skin 15.38%, greenish yellow skin 25.64%, yellow skin 17.95% of accessions, while one was with a greenish white skin, one with cream white skin and for one fruit ground colour was not visible. Fruit over-colour in most of the analysed accessions (61 accessions) was absent. In the remaining seventeen accessions, fruit over-colour differed from orange-red to blackish red. In most of the analysed accessions, the extent fruit over-colour varied from 10-60%, except for two accessions, one with hiding ground colour and one with very wide spread fruit over-colour. This is in line with FATHI *et al.* (2013), who found that a percentage of skin blush in local peach cultivars varied from 20 to 45%. Besides the shape of the fruit, fruit color is also positively related to consumer acceptance and sales of peaches fresh market (IGLESIAS and ECHEVERRÍA, 2009) because consumers associate an intense fruit colour with better quality (BYRNE *et al.*, 2011).

All accessions had a pubescent skin, 15 of them had sparse pubescence, 54 medium, 7 dense, and only two very dense pubescence. Most of the accessions had thin and medium fruit thickness of skin: 47.44% and 46.15% respectively. Fruit adherence of skin to flesh varied from weak to very strong, while strong was predominant. Flesh colour showed variation from greenish-white to orange, but cream white flesh colour (38 accessions) was predominant.

The blood-flesh trait in peach is due to the accumulation of anthocyanin. Anthocyanins possess a wide range of biological activities that promote human health and thus represent one of the important aspects of fruit quality (MARTIN *et al.*, 2011). Based on anthocyanin presence in the flesh, vineyard peach accessions were classified into 5 groups, where the largest one (63 accessions) was without coloration. Regarding flesh firmness, 23 accessions had very soft, 33 accessions soft, 21 accessions medium, and only one accession had firm flesh firmness. Most of the analysed accessions had moderate or strong fruit flesh fibre (36 and 34 accessions, respectively), while only 8 accessions had absent or weak fruit flesh fibre.

The largest variability of the studied fruit traits, in terms to skin and flesh colour is in accordance with previous studies conducted by GASIC *et al.* (2011) and MILOSEVIC and MILOSEVIC (2010) who also detected the presence of a large number of categories of variations in skin colour and flesh colour of the different vineyard peach accessions.

The majority of the analysed accessions had medium and large stone size compared to fruit, (33 accessions and 36 accessions, respectively). The predominant shape of vineyard peach stones in the accessions was rounded (55.13%), followed by elliptic stone shape (44.87%). Stone relief of surface varied from predominantly pits to only grooves, while the highest number of accessions characterised predominantly grooves. As for the intensity of brown colour of stones,

the stones of 64 accessions were predominantly dark, whereas the stones of 14 accessions were medium brown (Figure 1).

Table 2. Eigenvalues, proportion of total variability and correlation between the original variables and the first six principal components (PCs) for 78 vineyard peach accessions evaluated

Variable	PC1	PC2	PC3	PC4	PC5	PC6
TV	-0,228	-0,341	0,301	0,318	-0,080	-0,363
TH	-0,128	0,225	0,031	0,183	0,037	-0,019
DFB	-0,254	-0,012	0,461	-0,090	0,064	0,262
GDFB	-0,088	0,003	0,412	-0,202	0,323	0,230
FST	-0,167	-0,344	0,473	-0,194	-0,272	-0,044
FT	0,047	-0,722	-0,125	0,142	-0,381	0,096
PS	-0,009	-0,169	0,165	-0,531	-0,095	0,070
CPC	0,330	-0,675	0,039	0,036	-0,300	0,301
SN	-0,061	0,344	-0,174	0,465	0,114	0,010
FS	0,486	-0,119	-0,475	-0,286	-0,203	0,099
FGC	0,920	0,090	0,229	-0,020	0,024	-0,078
FOC	0,926	0,031	0,213	0,023	0,064	-0,111
EFOC	-0,081	0,571	0,117	-0,072	-0,307	0,059
FF	0,360	-0,150	-0,654	-0,166	0,043	0,216
FC	0,889	0,016	0,192	0,110	0,035	-0,109
ACF	0,016	-0,132	-0,098	0,648	-0,278	0,126
FFF	0,117	0,093	0,195	0,166	-0,030	0,602
FPS	0,222	-0,051	0,220	0,526	0,280	0,352
FDP	0,158	0,371	-0,435	0,149	-0,251	0,092
FTS	-0,128	0,183	-0,155	-0,057	0,295	0,316
ASF	0,543	0,095	0,116	0,016	0,177	-0,421
SS	0,243	0,482	0,366	-0,021	-0,287	0,196
SRS	-0,005	0,468	0,304	-0,031	-0,629	0,022
SSCF	0,115	0,398	-0,234	-0,232	-0,076	0,142
IBCF	0,239	-0,185	0,175	-0,141	0,238	0,343
% Variance	14.7	10.5	8.8	6.8	5.9	5.7

For an explanation of variable symbols, see Table 1, Bold values indicate correlation coefficients with value greater than 0.6 in absolute value

Principal component analysis (PCA) was used to determine the number of main factors and reduce the number of effective parameters in order to discriminate accessions (Table 2). Only 25 traits were analysed in PCA, i.e. only the traits that expressed some variability in the investigated collection. The ten principal components (PCs) had an eigenvalue greater than 1 and accounted for 74.8 % of the total variance. Using the correlation between the original variables and PCs and an absolute value greater than 0.60 as criteria, it was found that these values were present in the first six PCs. These components are enough to explain 52.4% of the total variability

observed, with PC1, PC2, PC3, PC4, PC5, and PC6 accounting for 14.7%, 10.5%, 8.8%, 6.8%, 5.9% and 5.7% on the variance, respectively.

The percentage of variation explained by the first six components is much lower than those of reported by WU *et al.* (2003), NIKOLI *et al.* (2010), MILOSEVIC and MILOSEVIC (2010) and LI *et al.* (2014). According to REIM *et al.* (2012) this results revealed a great morphological variation indicating a high genetic diversity within the vineyard collection.

The first component explains 14,7 % of the total variance. Traits with higher scores on PC1 are related to skin and flash colour (FGC, FOC and FC) (Table 2). The FT and CPS were more important in the second PC, accounting for 10.5 % of the variance.

Traits with higher scores on PC1, which explains the largest proportion of variability, are related to skin and flash colour (FGC, FOC and FC). PC2, that represents the second most important factor, was strongly correlated to the FT and CPC ($r = -0.722$ and -0.675 , respectively). PC3 was correlated only with FF ($r = -0.654$), PC4 only with ACF ($r = 0.648$), PC5 only with SRS ($r = -0.654$), and PC6 only with FFF ($r = 0.648$) suggesting that this trait was genetically affected by independent genes.

Among the 25 traits, 9 of them proved to have the most discriminating effect of vineyard peach accessions. Fruit traits (FGC, FOC, FF, FC, ACF, and FFF) were prevalent and contributed to the most of the total variation, indicated that these traits have the highest variability between the studied accessions and the greatest impact on separation of the accessions. Two flower traits (FT and CPC) and one seed trait (SRS) also have a significant impact on the first six components. Our results correspond with those of MILOSEVIC and MILOSEVIC (2010), who found that the flesh colour, ground colour and red over-colour are variables that had high correlations to first tree PC in the vineyard peach.

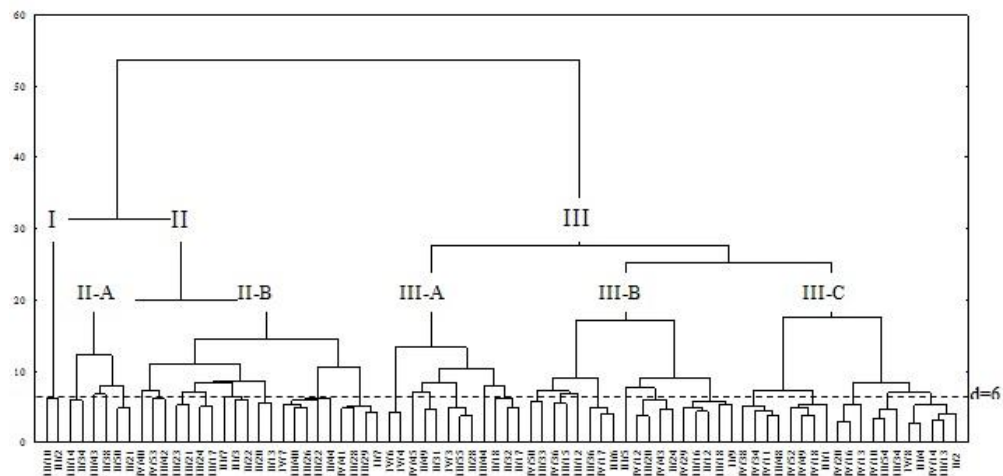


Figure 2. Hierarchical cluster analysis dendrogram obtained by Ward's method using 25 traits of 78 vineyard peach accessions

A hierarchical cluster analysis allowed the assessment of similarity or dissimilarity and clarified some of the relationships among vineyard accessions. Accessions are connected in different ways, which show existence of numerous hierarchical levels. Dissimilarity level (d) ranged from 5.38 to 53.69, which is a considerably higher value than the one received by NIKOLI *et al.*, (2010), who analysed the variability of traits in vineyard peach accessions selected from natural populations. This indicates that the generative propagation, applied when forming the collection that is the subject-matter of this paper, significantly increased the levels of variability within vineyard gene pool.

The cluster analysis showed high degree of diversity in the germplasm. The dendrogram obtained by Wards procedure separated the studied vineyard accessions in tree main clusters (Figure 2). Cluster I included only two accessions. Cluster II had 27 accessions and was divided into sub-groups II-A and II-B, with 6 and 21 accessions, respectively. Cluster III consisted of the largest number of accessions (49) and was split off into three distinct sub-groups, defined as cluster III-A, III-B, and III-C. Sub-group III-A included 12, sub-group III-B 18 and sub-group III-C 19 accessions.

It was not possible to extract traits that are clearly responsible for vineyard accessions grouping in clusters and sub-clusters. Overall, the greatest impact on the separation in clusters had FOC and ACF. Two accessions in Cluster I (III/2 and III/10) that were most diverse from each other were characterized by dark red and blackish red complementary colour that covered almost the entire surface of the fruit and by presence of anthocyanin coloration of whole flesh. The classification of accession to the other two clusters was mainly done on the basis of skin colour and flesh colour. Thus, Cluster II consisted of accessions with yellow fruit skin and flesh, and Cluster III of accessions with white fruit skin and flesh. Sub-clustering in Cluster I was further done according to DFB and FDP, whereas the accessions from II-A had extremely sparse to medium density of flower buds and skin pubescence and the accessions from sub-cluster II-B had very to extremely dense flower buds and pubescence of skin. Flower bud density was a trait that had the biggest impact on creating sub-cluster A within Cluster III. These accessions were characterised by lower density of flower buds than the density of flower buds in the other two sub-clusters. The difference between sub-clusters III-B and III-C reflects primarily in the intensity of fruit skin hairiness.

In general, grouping of the accessions according to the cluster analysis is in line with the results of PCA. Traits that had high values of correlation coefficients with PCs had the greatest impact on the formation of the clusters and sub-clusters in the cluster analysis. Moreover, corresponds with a research of PETRUCCELLI *et al.* (2013), who recorded that traits with a high degree of variation were more discriminating and therefore could be reliable markers for the classification. This result also indicates that flash and skin colour combined with skin pubescence and flower bud density are traits that could be sufficient for reliable characterisation of different vineyard peach germplasm collections. This is supported by the fact that these traits are caused by major genes and as such they are less affected by environmental factors.

It should be pointed out that the multivariate analysis singled out a relatively small number of properties and divergent groups in terms of large number of accessions (78) and properties (30) covered by this research. The reason may lie in the fact that the qualitative traits exhibit discontinuous variability (1 to 7 categories). Hence, the main variability of the collection can be seen in the fact that these traits are recombined on different way in individual accessions. Accordingly, from the aspect of diversity it is not enough to take into account only individual traits

but to set aside the accessions with different recombination traits for further collection. As a criterion for further collection in gene bank, it is recommended to take distance $d = 6$ obtained by cluster analysis (Figure 2) as the limit. In this way, the number of accessions would be reduced but the genetic variability present in the collection of germplasm would still be preserved. Furthermore, germplasm collections can comprise some accessions with a large number of positive traits that can be implemented in future breeding programmes.

Our results show that traditional descriptive methods, based on tree, flower, leaf, fruit and stone traits, have a great role in establishing the identity of accessions, because each accession has a unique combination of scores for the studied traits. This indicates that morphological characterisation is necessary to describe, and it is very important for the characterization of accessions in the gene bank. The vineyard peach accessions varied least in leaf traits, and most in skin colour and flesh colour. This variability may be due to the out-crossing recombination, combined with generative propagation. PCA determined the properties with the highest discriminatory effect, whereas CA resulted in different connections between accessions, indicating their genetic relatedness. Within the vineyard peach germplasm, it is possible to find accessions with valuable morphological traits that can be implemented in some future breeding programmes. Moreover, the obtained results may serve as a significant reference for the comparison of genetic resources and the characterisation of peach accessions. This study should also include agronomical and molecular evaluations to confirm the usage and genetic distances among accession.

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KARAKTERIZACIJA BIOTIP KOLEKCIJE VINOGRADSKJE BRESKVE KAO KORAK U PREDOPLEMENJIVA KOM PROGRAMU

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Izvod

U ovom istraživanju, sprovedena je morfološka karakterizacija kolekcije vinogradarske breskve. U 78 uzoraka trideset kvalitativnih osobine drveta, cveta, lista, voća su analizirani pomoću UPOV i ECPGR deskriptora. Većina ispitivanih svojstava pokazala su visok stepen varijabilnosti. Najniža varijabilnost dobijena je za osobine lista, a najviša za boju. Ne samo da su uzorci sortirani u velikom broju kategorija na osnovu većine njihovih osobina, nego je značajniji nivo varijabilnosti u kolekciji ukazao na činjenicu da su se osobine rekombinovale na drugačiji način. Analiza glavnih komponenti (PCA) i dendrogram su izvedeni za određivanje odnosa između uzoraka i da se dobiju informacije o korisnosti tih karaktera za diskriminaciju. PCA je otkrio da prve 4 glavne komponente predstavljaju 43,1% ukupne varijanse. Osobine sa visokim diskriminirajućim vrednostima obuhvataju interna i eksterna boju ploda, tipa cveta i boje, gustine pupoljaka. Klaster analiza je pokazala da su uzorci grupisani u tri glavna klastera. Najveći uticaj na odvajanje u klasterima imala je boja ploda i veličina ploda preko boje. Osim toga, kolekcija možda sadrži i neke uzorke sa željenom rekombinacijom svojstava koja bi mogla biti interesantna za dalje studije u oplemenjivanju.

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