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Original scientific article

DIVERSITY OF THE GENUS *Rosa* POMOLOGICAL TRAITS IN ECOLOGICAL CONDITIONS OF CONTINENTAL CROATIA

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Rosaceae family is characterized by the large number of genus and species which are of great importance for horticulture. The main goal of this research was to analyze pomological traits in order to determine biodiversity existence between five genotypes (G) of genus *Rosa* belonging to four different taxons (G1 - *Rosa canina* L., G2 - *Rosa corymbifera* Borkh., G3 - *Rosa canina* L. var. *squarrosa* A. Rau *Rosa squarrosa* (A. Rau) Boreau, G4 - *Rosa subcanina* (Christ.) Vuk., G5 - *Rosa corymbifera* Borkh) in continental part of Croatia during two years. Genotype had significant effect on all pomological traits, while year and interaction between year and genotype affected the majority of pomological traits. Multivariate discriminant analysis successfully explained 77.48% of total variability. It achieved separation of genotypes G5 and G1 from genotypes G2 and G4 using canonical axis 1 (Can1) (46.74% of total variability mostly influenced fruit length, width, volume, surface, and shape index). Likewise, genotype G2 was separated from genotype G3 by the Can2 axis (30.74% of total variability mostly influenced by fruit mass). Since genotypes G2 and G5 were of the same species (*Rosa corymbifera*), their separation by Can1 axis indicates notable effect of ecological factors on pomological traits, which was not the case for *Rosa canina* genotypes (G1 and G3) where no separation occurred, indicating major effect of hereditary factors on studied pomological traits on this species.

Key words: biodiversity, ecology, genetics, pomology, *Rosa* spp

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INTRODUCTION

Rosaceae family is characterized by the large number of genus and species that are of great importance for agriculture. The genus *Rosa* is the most important genus in floriculture, but in addition to its ornamental value its nutritional, medical and cosmetic values are also recognized (JOUBLAN and RIOS, 2005; ÇELIK *et al*., 2009). The importance of *Rosa* genus is indicated by its historical background. Cultivation of *Rosa rubiginosa* L. began in the Nordic countries as early as 1551, followed by *Rosa canina* L. in 1737 and *Rosa dumalis* Bechst. in 1872 (UGGLA, 2004; according to GUSTAVSSON, 1998). Rose cultivation as a fruit-bearing plant in southern Europe, Asia and South America began in the 18th and 19th centuries. This is the period when the species *Rosa canina*, *Rosa villosa* L., *Rosa blanda* Aiton, *Rosa majalis* Herrm., *Rosa pendulina* L. and *Rosa rugosa* Thunb. were introduced into cultivation (PORPÁCZY and KOLLÁNYI, 2009). Today *Rosa canina ΄Laxa΄* (*Rosa corymbifera ΄Laxa΄*; according to WERLEMARK, 2009), the most widespread rootstock in Europe for garden roses, is commonly used in fruit production. In recent years, Croatia has seen a significant increase in production areas under this crop, which can be explained by small initial investments for establishing plantations (cheap planting material) and state incentives received by producers. However currently only several varieties and hybrids of species from the genus *Rosa* are present in cultivation in Europe and Turkey, but they are mostly of local importance (BUNDESSORTENAMT, 1999; UGGLA, 2004; PORPÁCZY and KOLLÁNYI, 2009; WERLEMARK, 2009; WERLEMARK and NYBOM, 2010; TOMLJENOVIĆ *et al.*, 2016; GÜNEŞ *et al*., 2017). Hence today numerous studies are directed towards the selection of *Rosa* spp. genotypes with favorable agronomic and pomological characteristics. In the breeding process of the genus *Rosa* spp., the greatest attention is paid to pomological traits, which are the main key to greater market expansion.

However, genus *Rosa* is characterized by complex relationships between species which are not fully genetically and taxonomically separated. In several studies (MATSUMOTO *et al*., 1998; WISSEMAN and RITZ, 2005; SMULDERS *et al*., 2011 according to BRUNEAU *et al*., 2007), extremely low levels of DNA sequences divergence were found in the genus *Rosa*, suggesting that it is a young genus in which many speciations have occurred since the last Glacial period. Although fossil evidence suggests a fairly ancient origin of the genus *Rosa*, the spread and diversification process is recent. As a diversification center for roses SU *et al.* (2016) state China. Approximately half of the *Rosa* species occur in Asia while Europe and North America have approximately a quarter of the species each (FOUGÈRE-DANEZAN *et al*., 2015). Among the approximately 200 species of roses widespread in the temperate and subtropical regions of the northern hemisphere, 95 are native to China of which 65 are endemic (SU *et al*., 2016 according to FAVRE *et al*., 2015). Recent molecular studies reveal that complex topography and climate in southwest China played a key role in diversification of many plant groups which may also have been an evolutionary scenario in *Rosa* species and led to great diversity at that area (SU *et al*., 2016). High CO_2 levels were one of the important climatic factors which could also increase evolutionary and selective pressures on plants due to induction of abiotic stress (DE BODT *et al*., 2005). Significant polymorphism between and within species of this genus was influenced by hybridization, polyploidy and the asymmetric type of meiosis (so-called canina meiosis) (DE COCK *et al*., 2008; WROŃSKA-PILAREK, 2010). The genus *Rosa* is taxonomically very complex with unclear boundaries between species and therefore difficulties are present in their

determination. Despite intensive study of this genus in the last 200 years, with the use of morphological, anatomical, micromorphological and palynological tools and as well various molecular markers a better insight into the relationships between species and sections has been created, although final solution is still not present (TOMLJENOVIĆ and PEJIĆ, 2018).

Species of the genus *Rosa* are xeromesophytes (GHIORGHIȚĂ *et al*., 2012a) and are found on all continents (except Antarctica). The genus *Rosa* is distributed throughout the temperate zones of the entire northern hemisphere, spreading to the south in the regions with a Mediterranean climate or even to mountainous parts of tropical latitude. In the area of Republic of Croatia, 37 species with a large number of synonyms in Croatian and Latin terminology (NIKOLIĆ, 2018) have been determined, which makes their determination difficult. Spontaneous populations and ecotypes of species of this genus are considered cosmopolitan and are therefore present in all regions in diverse ecological conditions.

Previous research in Croatia (ŠINDRAK *et al*., 2012; TOMLJENOVIĆ *et al*., 2016; TOMLJENOVIĆ *et al*., 2019) and in the world (UGGLA *et al*., 2003 according to NYBOM *et al*., 1996; DE COCK *et al*., 2008; WERLEMARK, 2000; ERCIŞLI and EŞITKEN, 2004;) suggests the existence of variability of morphological and pomological traits, which is a good basis for the selection process of quality genotypes among species of this genus. Accordingly, it can be assumed that in Croatia, as well as in the investigated area of the continental part of Croatia, there is a significant *in situ* biodiversity between the species of the genus *Rosa*. It should also be noted that in Croatia no systematic research on botanical and agrobiological traits of genus *Rosa* was conducted, nor has the agrobiodiversity of these species has been used for breeding.

The main goal of this research was with the analysis of pomological traits to determine biodiversity existence between four different taxons or five genotypes of genus *Rosa* on continental par of Croatia.

MATERIALS AND METHODS

Plant material

To estimate pomological variability of native genus *Rosa* populations, five genotypes from four locations of mainland Croatia areas were selected and sampled. Genotypes were labeled from G1 to G5 and their origin is stated in Table 1.

Table 1. Origin and taxonomy mark of studied Rosa spp. genotypes

Genotype	Taxon	Origin
G1	*Rosa canina* L.	Pitomača
G2	*Rosa corymbifera* Borkh.	Grabovac
G3	*Rosa canina* L. var. *squarrosa* A.Rau *Rosa squarrosa* (A.Rau) Boreau	Đakovo
G4	*Rosa subcanina* (Christ.) Vuk.	Đakovo
G5	*Rosa corymbifera* Borkh.	Velika Ludina

Botanical analyses

Botanical analyses of selected genotypes were conducted at Department of environmental biology, University of Sapienza, Rome, by professor E. Lattanzi. Taxonomy of studied genotypes is stated in Table 1. According to BAKKER *et al*. (2011), all listed species belong to the *Caninae* section and the *Caninae* subsection.

Pomological measurements

Fruits were harvested at optimum harvest date in year 2010 and 2012. Afterwards, fruits were transferred to laboratory of Department of Pomology, Division of Horticulture and Landscape Architecture, University of Zagreb Faculty of Agriculture where measurements were conducted. Following pomological parameters were measured: fruit length (mm), fruit width (mm), middle geometrical fruit diameter (mm), fruit sphericity (%), fruit volume (mm^3), fruit surface (mm^2), fruit mass (g), fruit flesh mass (g), fruit flesh ratio (%), shape index and total dry matter (%). For each trait (except for total dry matter) from each genotype 20 fruits were analyzed per year. Regarding analysis of total dry matter trait 3 joint samples per year were analyzed (60 fruit in each year since 1 joint sample consisted of 20 fruits). Fruit length and width (mm) were measured by digital scrolling scale Prowin HMTY0006. Fruit mass (g) and fruit flesh mass (g) were measured by analytical balance OHAUS Adventurer AX2202. Fruit flesh ratio (%) was calculated by equation: (fruit mass / fruit flesh mass) x 100). Sphericity, volume, middle geometric fruit diameter (Md) and fruit surface were calculated by equations reported by DEMIR and KALYONCU (2003) according to JAIN and BAL (1997) and MC CABE *et al*. (1986). Analysis of total dry matter was conducted according to GHIORGHIȚĂ *et al*. (2012a) and GÜNEŞ (2010) and samples were dried by Dryer Binder ED115.

Statistical analysis

Data were statistically analyzed using SAS statistical software ver. 9.4 (SAS Institute, NC) using ANOVA, Tukey's HSD test ($P \leq 0.05$) and discriminant multivariate analysis.

RESULTS AND DISCUSSION

According to ANOVA table (Table 2) year had significant effect on all pomological traits ($P \leq 0.001$) except sphericity, shape index and fruit flesh ratio. Genotype had significant effect on all pomological traits ($P \leq 0.001$). Interaction of year with genotype had significant effect on all pomological traits except sphericity and shape index. Significance of interaction was very high ($P \leq 0.001$) in most cases, except for total dry matter ($P \leq 0.05$). Due to the significant effect of year on majority of studied pomological traits the results were additionally analyzed separately for each year (Tables 2, 3 and 4). In 2010 and 2012 genotype had significant effect on all studied pomological traits with $P \leq 0.01$ level of significance for total dry matter trait and $P \leq 0.001$ for all other traits (Table 1). Significant effect of year on majority of studied traits was probably due to less favorable ecological conditions (less precipitation) in 2012 (data not shown) when average values from majority of studied traits were reduced in comparison to 2010. Likewise, UGGLA *et al*. (2003) in three-year research of *Rosa* spp. reported that in one year fruit mass values were reduced (except for *Rosa villosa*) as a result of smaller precipitation amount and difference in its distribution during fruit ripening.

According to Table 3 in 2010, genotype G1 had significantly higher fruit length than genotypes G2, G3 and G4. Genotype G2 had significantly smaller fruit length than all other genotypes with exception of genotype G3 where no significant difference was recorded. In 2012 genotypes G1 and G4 had significantly higher fruit length than genotypes G2, G3 and G5. According to SOARE *et al*. (2015) fruit length is a trait with high variability which is in agreement with results obtained in this study.

Table 2. ANOVA table of pomological traits of Rosa spp. genotypes

Source	Length	Width	Md	Sphericity	Volume	Surface	Shape index	Fruit mass	Flesh mass	Fruit flesh ratio	Total dry matter
Year (Y)	$<.0001^{***}$	$<0.0001^{***}$	$<0.0001^{***}$	$0,6538^{n.s.}$	$<0.0001^{***}$	$<0.0001^{***}$	$0.5138^{n.s.}$	$<0.0001^{***}$	$<0.0001^{***}$	$0.4820^{n.s.}$	$<0.0001^{***}$
Genotype G)	$<0.0001^{***}$	$<0.0001^{***}$	$<0.0001^{***}$	$<0.0001^{***}$	$<0.0001^{***}$	$<0.0001^{***}$	$<0.0001^{***}$	$<0.0001^{***}$	$<0.0001^{***}$	$<0.0001^{***}$	$<0.0001^{***}$
Y x G	$<0.0001^{***}$	$<0.0001^{***}$	$<0.0001^{***}$	$0,0623^{n.s.}$	$<0.0001^{***}$	$<0.0001^{***}$	$0.1444^{n.s.}$	$<0.0001^{***}$	$<0.0001^{***}$	0.0003^{***}	0.0118^{*}
Year 2010											
Genotype	$<0.0001^{***}$	$<0.0001^{***}$	$<0.0001^{***}$	$<0.0001^{***}$	$<0.0001^{***}$	$<0.0001^{***}$	$<0.0001^{***}$	$<0.0001^{***}$	$<0.0001^{***}$	$<0.0001^{***}$	0.0067^{**}
Year 2012											
Genotype	$<0.0001^{***}$	$<0.0001^{***}$	$<0.0001^{***}$	$<0.0001^{***}$	$<0.0001^{***}$	$<0.0001^{***}$	$<0.0001^{***}$	$<0.0001^{***}$	$<0.0001^{***}$	$<0.0001^{***}$	0.0026^{**}

', *, **, ***: nonsignificant or significant at P≤ 0.05, P≤ 0.01, P≤ 0.001, respectively

Table 3. Length, width, medium diameter (Md), sphericity, volume, surface and shape index of fruits of Rosa spp. genotypes (mean and standard deviation)

Genotype	Fruit length (mm)	Fruit width (mm)	Md (mm)	Sphericity (%)	Volume (mm^3)	Surface (mm^2)	Shape index
				Year 2010			
G1	22.95 ± 2.98 a	11.26 ± 0.65 c	14.38 ± 1.09 b	0.60 ± 0.05 c	401.25 ± 51.35 c	651.35 ± 101.83 b	2.04 ± 0.20 a
G2	18.26 ± 1.24 c	13.29 ± 0.82 b	14.76 ± 0.75 b	0.81 ± 0.05 a	556.49 ± 67.09 b	686.16 ± 68.98 b	1.38 ± 0.11 d
G3	20.13 ± 1.82 bc	14.24 ± 1.02 a	15.97 ± 1.12 a	0.80 ± 0.04 a	639.79 ± 92.14 a	804.96 ± 112.65 a	1.42 ± 0.10 d
G4	20.65 ± 1.80 b	13.05 ± 1.05 b	15.20 ± 1.07 ab	0.74 ± 0.05 b	538.50 ± 88.12 b	728.78 ± 104.57 ab	1.59 ± 0.15 c
G5	21.96 ± 2.54 ab	11.64 ± 0.80 c	14.37 ± 1.10 b	0.66 ± 0.04 c	427.87 ± 57.21 c	652.78 ± 96.38 b	1.88 ± 0.17 b
				Year 2012			
G1	21.77 ± 3.25 a	11.10 ± 0.62 b	13.83 ± 1.07 ab	0.64 ± 0.06 d	393.70 ± 44.99 c	618.96 ± 91.81 ab	1.95 ± 0.29 a
G2	16.84 ± 2.06 b	12.43 ± 1.40 a	13.73 ± 1.38 ab	0.82 ± 0.07 a	491.08 ± 111.10 a	597.68 ± 118.46 ab	1.36 ± 0.18 c
G3	17.54 ± 1.18 b	11.48 ± 1.12 ab	13.21 ± 1.02 b	0.75 ± 0.05 b	417.44 ± 76.01 bc	550.96 ± 81.37 b	1.54 ± 0.16 bc
G4	20.04 ± 2.05 a	12.15 ± 0.91 ab	14.34 ± 1.06 a	0.72 ± 0.05 bc	466.04 ± 68.17 ab	649.30 ± 93.52 a	1.65 ± 0.16 b
G5	15.85 ± 2.21 b	8.45 ± 1.19 c	10.38 ± 1.14 c	0.66 ± 0.09 cd	228.59 ± 61.32 d	342.37 ± 72.22 c	1.91 ± 0.39 a

[1]means followed by the same letter with the same year are not significant according to Tukey's HSD test at P≤0.05 significance level

In Turkey (Van region) ÇELIK *et al.* (2009) reported that fruit length of *Rosa* spp. ranged from 15.28 to 33.83 mm. In a two-year study EKINCIALP and KAZANKAYA (2012) reported that in the Turkey (Hakkari region) average fruit length values of *Rosa* spp. ranged from 19.01 to 27.52 mm. In Montenegro (Bijelo Polje region) ŠEBEK *et al*. (2019) reported that fruit length of *Rosa canina* L. ranged from 15.60 to 24.50 mm. In a three-year study in Turkey (Erzurum province) ERCIŞLI and EŞITKEN (2004) reported that average fruit length values of 12 *Rosa* spp. genotypes ranged from 22.48 to 36.42 mm. ERSOY and ÖZEN (2016), in the Turkish province of Bolu, reported that fruit length values of *Rosa* spp. ranged from 18.92 to 24.13 mm. In the pomological analysis of the *Rosa* spp. in northeastern Romania, ROSU *et al.* (2011) determined that average fruit length values of *Rosa canina* (seven genotypes), *Rosa subcanina* (two genotypes) and *Rosa corymbifera* (five genotypes) ranged from 16.8 to 24.0 mm, 19.3 to 22.0 mm and 15.4 to 21.5 mm (respectively). In the spontaneous flora of the Romanian region of Oltenia, SOARE *et al.* (2015) reported that the magnitude of fruit length variation of the *Rosa canina* biotypes was between 14.20 and 24.90 mm, with a small to medium variability. ŠINDRAK *et al*. (2012) reported that fruit length of eight *Rosa canina* seedlings in Croatia varied from 20.40 to 25.30 mm. Fruit length values of *Rosa* spp. genotypes recorded in this study coincide with values obtained in other countries or are slightly lower.

According to Table 3 in 2010 genotype G3 had significantly highest value of fruit width while lowest genotypes G1 and G5. In 2012 genotype G5 had significantly lowest fruit width value while genotype G2 had significantly higher than G1. According to these results a notable variation in fruit width of *Rosa* spp. genotypes is evident which is also confirmed by a few studies conducted in Turkey and other countries. The average fruit width of *Rosa* spp. selection obtained by ERCIŞLI and EŞITKEN (2004) ranged from 15.04 to 19.69 mm. According to DOGAN and KAZANKAYA (2006) fruit width of six *Rosa* species from Lake Van Basin (Eastern Anatolia Region, Turkey) ranged from 13.10 to 14.40 mm. ÇELIK *et al*. (2009) reported that fruit width of *Rosa* spp. ranged from 13.11 to 19.26 mm, while according to EKINCIALP and KAZANKAYA (2012) from 11.35 to 17.20 mm. Study in Tunisia on four *Rosa* spp. conducted by BEN CHEIKH-AFFENE *et al*. (2013) showed that fruit width values ranged from 10.50 to 14.10 mm. In Montenegro (Bijelo Polje region) ŠEBEK *et al*. (2019) reported that fruit width of *Rosa canina* L. ranged from 9.20 to 14.40 mm. ŠINDRAK *et al.* (2012) reported that fruit width of eight *Rosa canina* seedlings ranged from 13.10 to 16.00 mm. In the pomological analysis of the 10 species of *Rosa* genus ROSU *et al.* (2011) determined that average fruit width values of *Rosa canina* (seven genotypes), *Rosa subcanina* (two genotypes) and *Rosa corymbifera* (five genotypes) ranged from 11.4 to 14.8 mm, 12.8 to 14.1 mm and 10.7 to 16.2 mm (respectively). As fruit length and width affect fruit mass and thus yield, these traits are of significant agronomic importance.

According to Table 3 in 2010 genotype G3 had significantly higher middle geometrical fruit diameter than all other genotypes with exception of genotype G4. In 2012 genotype G5 had significantly smallest middle geometrical fruit diameter, while genotype G4 had significantly higher than G3. According to Table 3 in 2010 highest fruit sphericity had genotypes G2 and G3 while lowest genotypes G1 and G5. In 2012 significantly highest fruit sphericity had genotype

G2, while genotype G3 had significantly higher than G1 and G5. According to Table 3 in 2010 significantly highest fruit volume had genotype G3 and lowest genotypes G1 and G5. In 2012 genotype G2 had higher fruit volume than all other genotypes with exception of genotype G4. Significantly lowest fruit volume had genotype G5. According to Table 3 in 2010 genotype G3 had significantly higher fruit surface than all other genotypes with exception of genotype G4 while between all other genotypes no significant difference was recorded. In 2012 genotype G4 had significantly higher fruit surface than genotypes G3 and G5. Significantly lowest fruit surface had genotype G5. To the best of our knowledge, there is scarcity of published data on the above mentioned pomological traits of the *Rosa* spp. Therefore, it was not possible to make comparison with previously published results.

According to Table 3 in 2010 significantly highest value of fruit shape index had genotype G1 and lowest genotypes G2 and G3. In 2012 significantly highest value of fruit shape index had genotypes G1 and G5. Genotype G2 had significantly lower value of fruit shape index than all other genotypes with exception of genotype G3. For the most part, the average values of the shape index ranged between values of 1 and 2, and thus the fruits were more or less elongated. DOGAN and KAZANKAYA (2006) reported that among six *Rosa* spp. fruit shape index varied between 1.11 and 2.05. EKINCIALP and KAZANKAYA (2012) reported that fruit shape index among *Rosa* spp. genotypes varied from 1.32 to 2.41, while according to ERSOY and ÖZEN (2016) from 1.23 to 1.81. In Hungary, KOVÁCS *et al.* (2000) reported that fruit shape index among *Rosa* spp. ranged from 1.18 to 2.14, whereas *Rosa canina* had fruit shape index from 1.82 to 1.52 (in 1996 and 1997 year, respectively) and *Rosa corymbifera* from 1.37 to 1.45 (in 1996 and 1997 year, respectively). In Romania *Rosa canina* genotypes obtained a shape index values between 1.16 and 1.72 (GHIORGHIȚĂ *et al*., 2012b). ŠINDRAK *et al*. (2012) reported significant difference between fruit shape index values of eight *Rosa canina* seedlings which ranged from 1.48 to 1.86. The values obtained in this study are comparable to the values obtained in other studies.

According to Table 4 in 2010 genotype G3 had significantly higher fruit mass than all other genotypes with exception of genotype G4. Genotype G4 had significantly higher fruit mass than genotypes G1 and G5. In 2012 significantly highest fruit mass had genotype G4 while lowest genotype G5. EKINCIALP and KAZANKAYA (2012) reported that fruit mass among *Rosa* spp. ranged from 1.55 to 3.92 g and according to ERCIŞLI and EŞITKEN (2004) from 3.15 to 4.80 g. Among six *Rosa* spp. genotypes BEN CHEIKH-AFFENE *et al*. (2013) reported that fruit mass varied from 0.90 to 1.90 g. ERSOY and ÖZEN (2016) determined that the average fruit mass of *Rosa* spp. genotypes ranged from 1.40 to 2.77 g. In Montenegro (Bijelo Polje region) ŠEBEK *et al*. (2019) reported that fruit mass of *Rosa canina* L ranged from 1.25 to 2.76 g. According to ŠINDRAK *et al*. (2012) the average fruit mass of eight *Rosa canina* seedlings ranged from 1.88 to 2.96 g. Obtained values in this study are in agreement or are slightly lower than the ones obtained in other countries. These results also indicate a large variation of this trait with a notable influence of environmental factors.

According to Table 4 in 2010 genotypes G3 and G4 had significantly higher fruit flesh mass than genotypes G1 and G5. In 2012 genotype G4 had significantly higher fruit flesh mass than all other genotypes with exception of genotype G2. Genotype G5 had significantly lowest fruit flesh mass. BEN CHEIKH-AFFENE *et al*. (2013) reported that average fruit flesh mass of four *Rosa* species ranged from 0.69 to 1.20 g. ŠINDRAK *et al*. (2012) reported significant difference

between fruit flesh mass of eight *Rosa canina* seedlings while average values varied from 1.31 to 1.94 g.

Table 4. Fruit mass, flesh mass, fruit flesh ratio and total dry matter of fruits of Rosa spp. genotypes (mean and standard deviation)

Genotype	Fruit mass (g)	Flesh mass (g)	Fruit flesh ratio (%)	Total dry matter (%)
		Year 2010		
G1	1,44 ± 0,29 c	0,98 ± 0,21 b	68,65 ± 3,21 b	31,25 ± 0,73 a
G2	1,56 ± 0,25 bc	1,15 ± 0,17 ab	74,07 ± 3,49 a	32,61 ± 1,47 a
G3	2,15 ± 0,45 a	1,31 ± 0,29 a	60,79 ± 2,74 c	31,72 ± 2,08 a
G4	1,87 ± 0,38 ab	1,36 ± 0,30 a	72,72 ± 5,13 a	26,96 ± 1,77 b
G5	1,45 ± 0,30 c	1,00 ± 0,21 b	69,06 ± 4,51 b	31,76 ± 0,92 a
		Year 2012		
G1	1,32 ± 0,27 b	0,87 ± 0,18 bc	66,82 ± 6,17 b	23,56 ± 0,58 abc
G2	1,33 ± 0,37 b	0,99 ± 0,27 ab	75,17 ± 3,81 a	29,56 ± 3,19 a
G3	1,29 ± 0,29 b	0,75 ± 0,15 c	58,71 ± 5,95 c	27,06 ± 1,30 ab
G4	1,68 ± 0,34 a	1,12 ± 0,22 a	66,80 ± 3,42 b	21,18 ± 1,55 bc
G5	0,66 ± 0,23 c	0,49 ± 0,16 d	74,75 ± 12,77 a	19,53 ± 1.29 c

[1]means followed by the same letter with the same year are not significant according to Tukey's HSD test at P≤0.05 significance level

According to Table 4 in 2010 genotypes G2 and G4 had significantly highest fruit flesh ratio while genotype G3 lowest. In 2012 genotypes G2 and G5 had significantly highest fruit flesh ratio while genotype G3 again lowest. According to GÜNEŞ (2010), fruit flesh ratio presents economically important trait since fruits are usually used for processing. ÇELIK *et al*. (2015), citing a number of other authors (UGGLA, 1991; KAZANKAYA *et al*., 2001; KIZILCI *et al.*, 2007; DOLEK, 2008; ÇELIK, 2007; GÜNEŞ and DÖLEK, 2010), reported that fruit weight (and thus fruit flesh ratio) depends on variety, genotype, growing conditions, altitude, and genetic structure. DOGAN and KAZANKAYA (2006) (according to YAMANKARADENIZ, 1983) claim that the fruit flesh ratio of fruits from natural populations of *Rosa* spp. ranges from 56 to 80%. EKINCIALP and KAZANKAYA (2012.) reported that average fruit flesh ratio values of *Rosa* spp. ranged from 59.33 to 76.69%, ERCIŞLI and EŞITKEN (2004.) from 63.11% to 71.13% and ERSOY and ÖZEN (2016.) from 64.92 to 82.83%. According to GÜNEŞ (2010.) fruit flesh ratio from natural populations of *Rosa* spp. in Tokat region of northern Anatolia (Turkey) ranged from 66.00 to 80.20%. In Montenegro (Bijelo Polje region) ŠEBEK *et al*. (2019) reported that fruit flesh ratio of *Rosa canina* L. ranged from 50.20 to 64.40%. According to KOVÁCS *et al*. (2000) studied *Rosa* spp. had fruit flesh ratio that ranged from 46.07 to 69.24% whereas for *Rosa canina* it was 62.66% and for *Rosa corymbifera* 62.12%. SOARE *et al.* (2015) reported that fruit flesh ratio values, expressed as a percentage of pulp per 100 g of fruit weight, ranged from 49.20 to 66.50%. ANCU *et al*. (2012) reported that in Romania fruit flesh ratio of *Rosa pendulina* L. accounted 89.91%. On four *Rosa* species (six genotypes), BEN CHEIKH-AFFENE *et al.* (2013) reported that fruit flesh ratio ranged from 63.60 (*Rosa pomifera* J. Herrmann) to 73.70% (*Rosa canina*). According to

ŠINDRAK *et al*. (2012) among eight *Rosa canina* seedlings fruit flesh ratio ranged from 65.40 to 74.70%, and differences between genotypes were significant. Results in this study are in agreement with results obtained in above cited literature.

According to Table 4 in 2010 significantly smallest percentage of total fruit dry matter had genotype G4, while between all other genotypes no significant difference was recorded. In 2012 genotype G2 had significantly higher total fruit dry matter than genotypes G4 and G5. ÇELIK *et al*. (2015) reported that in the Turkish region of Van content of total dry matter of *Rosa* spp. varied from 45.70 to 53.26%. The data obtained by DEMIR and ÖZCAN (2001) show considerably lower total fruit dry matter amount of *Rosa canina* genotypes from Konya (Hadim) and Kastamonu province (Turkey) which ranged from 20.50 to 23.47%. ERCIŞLI and EŞITKEN (2004) reported that among *Rosa* spp. selections average values of total fruit dry matter ranged from 34.82 to 40.15%. According to DOGAN and KAZANKAYA (2006) total fruit dry matter among *Rosa* species ranged from 34.34 to 66.70 %. In Erzurum (Turkey) ERCIŞLI (2007) reported that among *Rosa* spp. average values of total fruit dry matter ranged from 33.85 to 40.35%. EKINCIALP and KAZANKAYA (2012) recorded that among *Rosa* spp. values of fruit, total fruit dry matter ranged from 43.63 to 59.39% and according to ERSOY and ÖZEN (2016) from 32.44 to 56.94%. Research conducted by ŠINDRAK *et al*. (2012) showed significant difference in fruit dry matter content of eight *Rosa canina* seedlings, which according to average values varied from 22.90 to 28.60%. In the research conducted by ROSU *et al*. (2011) average total fruit dry matter amounted from 27.53 to 49.90% for *Rosa canina* (seven genotypes), 32.93 to 33.00% for *Rosa subcanina* (two genotypes) and 31.09 to 38.87% for *Rosa corymbifera* (five genotypes).

Table 5. Wilks' Lambda test (Rao's approximation) for selected pomological traits of Rosa spp. Genotypes

Lambda	0.060
F (Observed value)	21.274
F (Critical value)	1.434
DF1	36
DF2	684
p-value	< 0.0001

Among *Rosa* spp. (*Rosa dumalis*, *Rosa rubiginosa*, *Rosa spinosissima* L.), UGGLA (2004) reported significant increases in fruit dry matter during ripening and significant differences in the percentage of fruit dry matter among seedlings. However, author showed data only for *Rosa spinosissima* where in 36 days (at the time of fruit ripening) the percentage of dry matter increased from 18.80 to 23.40%. GÜNEŞ *et al*. (2016) also confirm that the amount of total dry matter increases with fruit ripening. In this study differences in the amount of fruit total dry matter can be attributed to the uneven maturation time of the studied genotypes or as DEMIR and ÖZCAN (2001) suggested to the differences in growing conditions, ecological factors and fruit size. Studies of total dry matter at different localities in Turkey obtained considerably higher values of fruit total dry matter, which could be attributed to the influence of ecological and growing conditions, fruit size, and probably genetic potential. UGGLA *et al*. (2003) stated existence of a highly significant positive correlation between fruit weight and fruit flesh weight, which are moderately negatively correlated with the percentage of dry matter.

High variability of majority of studied pomological traits of *Rosa* spp. genotypes can be due to numerous reasons. According to SMULDERS *et al.* (2011) quantitative (morphometric) characters of *Rosa* species show a continuous variation and are likely to be polygenically controlled. In a study of fruit growth properties of *Rosa dumalis* and *Rosa jundzillii* BESSER, DÖLEK and GÜNEŞ (2016) conclude that fruit development can be affected by ecological factors, genetics and breeding conditions. ŠINDRAK *et al*. (2012) assumed that high variations in fruit mass among *Rosa canina* seedling were as a result of the influence of agro-ecological conditions and genetic variability. SOARE *et al*. (2015) noted that fruit mass variations were due to divergence in site altitude and climatic conditions.

Discriminant analysis showed significant difference between genotypes (Table 5) and revealed two significant canonical axes (Can1 and Can2, respectively) having eigenvalues higher than 1, comprising 77.48% of total variability (Fig. 1, Table 6). Can1 (46.74% of total variability) positively correlated with fruit width, sphericity, volume, fruit mass, fruit flesh mass; and negatively with fruit length and fruit shape index (Table 6). Can2 (30.74% of total variability) positively correlated with fruit flesh ratio and negatively with fruit mass. However, RENCHER (1992) stated that correlation coefficients do not contribute to the explanation of multivariate space but only indicate how much original variables are correlated with canonical axis for themselves and, hence, standardized coefficients are better for explanation of the influence of original variables to multivariate space. Standardized coefficients of Can1 had high positive values for fruit width, surface, flesh mass and shape index and negative values for fruit length and volume. Standardized coefficients for Can2 had high positive values for fruit surface and fruit flesh mass, and high negative values for fruit volume and fruit mass. Although fruit surface and fruit volume were positively correlated with Can1 and negatively correlated with Can2, only Can1 was considered because the standardized coefficient for the above traits was more than twice that for Can2. Can1 and Can2 showed positive values of standardized coefficients for fruit flesh mas, but the difference was not so pronounced and therefore this trait was considered unimportant for explanation.

Table 6. Correlation coefficient and standardized canonical discriminant function coefficients (CCDF) for canonical axes (Can1 and Can2) for pomological traits of Rosa spp. Genotypes

	Correlation coefficient		CCDF	
Trait	Can1	Can2	Can1	Can2
Fruit length	-0.45	0.02	-8.11	-0.27
Fruit width	0.61	-0.240	11.47	0.60
Sphericity	0.85	-0.15	0.16	0.94
Volume	0.62	-0.26	-12.10	-1.31
Surface	0.281	-0.21	5.48	2.15
Fruit mass	0.35	-0.36	-0.20	-5.28
Flesh mass	0.43	-0.07	2.09	3.88
Fruit flesh ratio	0.17	0.82	-0.05	-0.16
Shape index	-0.85	0.20	3.77	0.93
Variance explained (%)			46.74	30.74
Eigenvalue			2.12	1.40

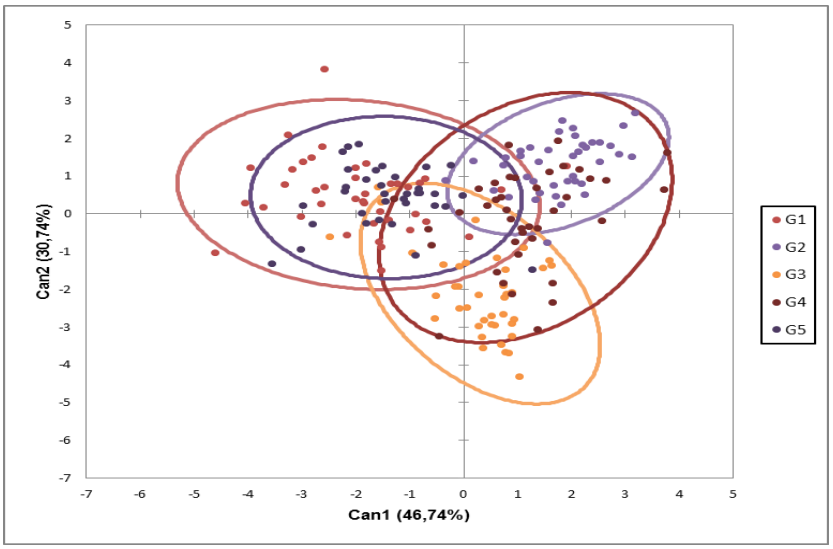

Figure 1. Canonical Plot for a linear discriminant analysis of the pomological traits of genus Rosa spp. Genotypes (G1-G5) obtained during two seasons

Fig. 1. showed that genotypes G5 and G1 distinguish themselves between genotype G2 and partly G4 by the Can1 axis. Since genotypes G2 and G5 are of the same species, their separation by Can1 axis indicate notable effect of ecological factors on following pomological traits of *Rosa corymbifera* (Borkh): length, width, surface, volume, shape index. Although geographical distance between *Rosa canina* genotypes was similar as for *Rosa corymbifera* genotypes (Table 1), the same distinction for studied traits was not evident for *Rosa canina* genotypes. Such results indicate that hereditary factors have stronger impact on studied pomological traits of *Rosa canina* genotypes than ecological factors.

CONCLUSIONS

The analysis of pomological properties highlighted existence of notable variability of studied *Rosa* spp. genotypes as a result of the influence of ecological and hereditary factors. The highest values for most pomological important traits in both studied years had genotypes G2, G3 and G4, while the lowest genotypes G1 and G5. According to multivariate analysis, certain pomological traits of *Rosa corymbifera* genotypes were influenced stronger by ecological factors than hereditary factors, while for *Rosa canina* genotypes the opposite was true. Consequently, this research highlighted the fact that in continental Croatia there is a huge *Rosa* spp. biodiversity which could be used for further breeding process.

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DIVERZITET POMOLOŠKIH OSOBINA RODA *ROSA* U EKOLOŠKIM USLOVIMA KONTINENTALNE HRVATSKE

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Izvod

Porodica *Rosaceae* se karakteriše velikim brojem rodova i vrsta koji su od velike važnosti za hortikulturu. Glavni cilj ovog istraživanja je bio utvrditi postojanje biološke raznolikosti između pet genotipova (G) roda *Rosa* koji pripadaju različitim taksonima (G1 - *Rosa canina* L., G2 - *Rosa corymbifera* Borkh., G3 - *Rosa canina* L. var. *squarrosa* A. Rau *Rosa squarrosa* (A. Rau) Boreau, G4 - *Rosa subcanina* (Christ.) Vuk., G5 - *Rosa corymbifera* Borkh). Istraživanje je provedeno tokom 2010 i 2012 godine u kontinentalnom delu Republike Hrvatske. Genotip je imao signifikantan uticaj na sve pomološke osobine, dok je godina i interakcija između godine i genotipa imala signifikantan uticaj na većinu pomoloških osobina. Multivarijantna diskriminacijska analiza uspešno je objasnila 77,48% ukupne varijabilnosti. Ostvarila je razdvajanje genotipova G5 i G1 od genotipova G2 i G4 pomoću osi Can1 (46,74% ukupne varijabilnosti na koju je najviše uticala daljina, širina, volumen i površina ploda te indeks oblika ploda). Slično, genotip G2 je bio razdvojen od genotipa G3 pomoću osi Can2 (30,74% ukupne varijabilnosti na koju je najviše uticala masa ploda). S obzirom da genotipovi G2 i G5 pripadaju istoj vrsti (*R. corymbifera*), njihovo razdvajanje putem Can1 osi indicira izrazit uticaj ekoloških faktora na pomološke osobine navedene vrste. Navedeno nije bio slučaj za *R. canina* genotipova (G1 i G3) koji nisu bili razdvojeni, što indicira izrazit uticaj genetskih faktora na istraživane pomološke osobine navedene vrste.

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