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EVALUATION OF PHENOTYPIC AND GENOTYPIC DIVERSITY OF SOME POLISH AND RUSSIAN BLUE HONEYSUCKLE (*Lonicera caerulea* L.) CULTIVARS AND CLONES

Jacek Gawroński, Jerzy Hortyński, Elżbieta Kaczmarska, Magdalena Dyduch-Siemińska, Wojciech Marecki, Agata Witorożec
University of Life Sciences in Lublin

Abstract. Blue honeysuckle due to the high health benefits of its fruit, early ripening (before the first strawberries cultivars) and high frost resistance of both plants and flowers has gained the great popularity both in cultivation and breeding. The implementation of the breeding program of new cultivars requires the knowledge of the characteristics that determine its direction in the selected material. Therefore, in this study the evaluation of the phenological phases, yield, fruit weight, number of seeds per fruit and pollen viability in the cultivars and breeding clones of this species was made. The tested cultivars and clones had different levels of the analysed qualities except the pollen viability which was high but did not differ significantly within the genotypes. The evaluation of such characteristics as yield potential and fruit weight indicates that cultivars 'Warszawa', 'Wojtek' and T2 clone which had higher values of these characteristics as compared to other genotypes are possible to be used in breeding programme. Obtainment of the forms with early fruit ripening can be realised through the use of the selected Russian cultivars. The objective of this study was also to characterise the blue honeysuckle germplasms using RAPD markers and to assess their genetic similarity. The analysed primers produced 61 fragments out of which 57 (93.44%) were polymorphic. The genetic similarity matrix was made on the basis of RAPD markers. The mean genetic similarity was calculated at 0.56. The presented study confirms that the use of RAPD markers is a practical and effective method to evaluate the genetic similarity of blue honeysuckle genotypes and to establish genetic relationships between these genotypes.

Key words: blue honeyberry, Random Amplified Polymorphic DNA (RAPD), genetic variability, pollen viability, flowering and ripening period, yielding

Corresponding author: Jacek Gawroński, Departament of Genetics and Horticultural Plant Breeding, University of Life Sciences in Lublin, Akademicka 15, 20-950 Lublin, Poland, e-mail: jacek.gawronski@up.lublin.pl

INTRODUCTION

The growing interest in the cultivation of blue honeysuckle will need to recognise the value of the currently available varieties in the direction of their use in breeding programs of this species. The breeding of this species was conducted primarily in Canada, the U.S., Russia and Japan [Plekhanova 2000, Thompson and Barney 2007, Bors 2009a, Miyashita and Hoshino 2010]. The evaluation of breeding materials also took place in Romania [Truta et al. 2013] and Estonia [Arus and Kask 2007].

Lonicera caerulea var. *kamtschatica* (also known as blue honeysuckle, haskap, blue honeyberry) belongs to Caprifoliaceae family and comprises more than 200 species [Hummer 2006, Svarcova et al. 2007, Miyashita et al. 2009, Sun et al. 2011]. Plants are either diploids ($2n = 18$) or tetraploid forms ($2n = 36$) [Miyashita et al. 2009]. Honeysuckle grows in cold – climate regions of Europe, Asia and North America. These long – lived plants (survive 25 – 30 years) grow from 0.8 to 3.0 m tall and 1.0 m wide [Svarcova et al. 2007]. Leaves are opposite, entire, dark green, lanceolate to elliptical. Yellow tubular flowers are about 2 cm. Haskap is self-incompatible and requires other genotypes for cross – pollination [Hummer 2006]. Bushes of this species are tolerant to low temperatures (-45°C). Flowers can withstand temperatures of even -8°C and are not injured by low temperature during flowering [Ochmian and Grajkowski 2007]. Flowering period of honeysuckle begins about mid-April and lasts until mid-May. Flowers are pollinated by insects – bees and bumblebees [Bożek and Wieniarska 2006, Hummer 2006]. Blue honeysuckle fruit ripen about two weeks earlier than strawberries (early June). The shapes of berry are variable depending on the species and can be cylindrical, ovoid or torpedo. Others may be pyriform, sickle – shaped or jug – shaped [Hummer 2006]. The dark purple fruit are covered by a wax coating. Haskap berries are a great source of ascorbicacid, β-carotene, catechol, macro and microelements and phenolic compounds, especially phenolic acids, anthocyanins, proanthocyanidins and other flavonoids [Frejnagel 2007, Gruia et al. 2008, Małodobry et al. 2010, Jurikova et al. 2012].

Honeysuckle phylogeny and affinities are weakly explored. Suitable method to study phylogeny, genotyping and molecular selection is RAPD analysis. RAPD method is fast, inexpensive and does not require prior knowledge of the genome sequence. RAPD markers are widely used for phylogenetic analysis of various organisms, including blue honeysuckle [Fu et al. 2013, Naugžemys et al. 2007, Verma et al. 2009, Truta et al. 2013].

Therefore, in this study we tested genetic variation at the DNA level of *Lonicera caerulea* cultivars and clones planted in Department of Genetics and Horticultural Plant Breeding collection. The tested material was also evaluated at the phenotypic level examining dates of phenological phases, yield and fruit characteristics. In this way, the assessment of examined cultivars and breeding clones will facilitate the selection of the parental forms for breeding programs.

MATERIAL AND METHODS

Plant material and location. The study was carried out in 2010–2012 at University of Life Science in Lublin. The plantation of six blue honeysuckle cultivars: 'Czelabinka', 'Dlinnopłodna', 'Duet', 'Warszawa', 'Wołoszebnica', 'Wojtek' and three clones Nr 9, P, T2, was established in the spring in 2007 at the Felin Experimental station, eastern Poland (N 51º13', E 22º39'). These genotypes were taken from Experimental Station of The Research Institute of Horticulture in Brzezna. Experimental plots were established on the grey brown podsolic soil deposited on chalky clay soil. Bushes were planted at the spacing of 1.5 × 2 m. During the experiment no chemical protection of plants was used. The research was carried out on five bushes of each cultivar in three replications.

Field observations. During the 2010–2012 period, the flowering onset and the flowering termination were recorded in order to determine the timing and duration of flowering. Yields were recorded for each bush for 4 consecutive weeks starting from the third decade of May. The honeysuckle berries were collected fully ripened when fruits were uniformly coloured and softened and they were easily separated from stalk. Weight of the single fruit was calculated by weighing 100 individual fruit from each harvest. These fruits were also used to determine the number of seeds in one berry.

Examination of pollen viability. Pollen viability of 9 blue honeysuckle genotypes was measured on the basis of the grain colour. One day prior to flowering of each genotype, 20 flowers were randomly collected and microscopic preparations were made from them. Slides were coloured with 2% solution of acetocarmin and glycerin (1:1) and examined by use of the Olympus BX41 microscope under magnification 400×. There were analysed to 100 grains in 10 fields of vision in any combination (the microscopic slide). Pollen grains with 75–100% content of cytoplasm were taken as vital. The percentage data of pollen viability were transformed before analysis using the Bliss function $Y = \arcsin \sqrt{p}$.

The means were verified by Tukey test at a level of significance $\alpha = 0.05$.

DNA extraction. DNA was isolated from 5 plants (fresh young leaves) in two replications, for every above mentioned genotype and 'Atut' cultivar. DNA was extracted following the CTAB method described by Doyle and Doyle [1987].

RAPD amplification. RAPD-PCRs were carried out in volumes of 15 µl, containing 1× reaction buffer (10 mM Tris pH 8.8, 50 mM KCl, 0.08% Nonidet P40) (MBI Fermentas), 200 µM dNTP, 8 pM primer, 1.5 mM $MgCl_2$, 40 ng of DNA, 0.5 U *Taq* DNA polymerase (MBI Fermentas). The thermal cycler (TProfessional Basic Gradient Biometra GmbH) was programmed for one cycle of 4 min at 94ºC, followed by 44 cycles of 1 min at 94ºC, 1 min at 36ºC and 2 min at 72ºC and finally by one cycle of 5 min at 72ºC. Amplification products were separated by electrophoresis on 1.5% agarose gels containing 0.1% EtBr (Ethidium bromide). Fragments were visualized under UV transiluminator and photographed using GeneSnap ver. 7.09 (SynGene). Marker GeneRuler^{TM} DNA Ladder Mix (MBI Fermentas) was used to determine the size of the DNA fragments.

Data analysis. RAPD products were scored as present (1) or absent (0) from the photographs. Only bright and reproducible products were scored. DNA fragments de-

tected not in all cultivars profiles were considered as polymorphic. Genetic pairwise similarities (SI-similarity index) between studied genotypes were evaluated according to Dice's formula after Nei and Li [1979]. A cluster analysis was conducted using the distance method UPGMA (Unweighted Pair-Group Method with Arithmetic Mean) in the program NTSYS [Rohlf 2001].

RESULTS AND DISCUSSION

During the analysed period the weather conditions permitted the early start of the plant vegetation. The average air temperature exceeded the long-term average in each of the analysed months (tab. 1). However, the rainfall was more variable. It was lower during the analysed period than the average long-term rainfall for the month of April. The average precipitation in the years of research in June was close to the average long-term precipitation in this month. Particularly high levels of rainfall were recorded in May 2010. Therefore, this month was considered extremely wet according to the scale estimated by the Skowera and Puła [2004].

Table 1. Mean monthly temperature and monthly precipitation in 2010–2012 compared to the multi-year average according to Laboratory of Agrometeorology, Department of Specific Plant Cultivation, University of Life Sciences in Lublin

Weather factor	Month	Years of research			The average temperature 2010–2012	The average precipitation 1951–2012
		2010	2011	2012		
Temperature (°C)	IV	9.4	10.2	9.5	9.7	7.4
	V	14.5	14.3	15.0	14.6	13.0
	VI	18.0	18.6	17.3	17.9	16.2
Precipitation (mm)	IV	24.5	29.9	34.0	29.5	40.2
	V	156.7	42.2	56.3	85.0	57.7
	VI	65.6	67.8	62.8	65.4	65.7

In the climatic conditions of Lublin blue honeysuckle blooming begun in the third decade of April (in the 'Wołoszebnica' cultivar a bit earlier) and even in some genotypes it extended until the first days of May (tab. 2). 'Wołoszebnica' cultivar was the first which began flowering and 'Dlinnopłodna' and 'Wojtek' cultivars started flowering a bit later. The temperature in the spring period has the decisive impact on the time of plants flowering [Thompson and Barney 2007] and it can vary up to 4 weeks at the particular location [Hummer 2006]. The length of the flowering period in the investigated genotypes was similar and it was about 3 weeks. This period is long enough to perform the planned crossing in the implementation of the breeding program. According to Thompson [2006] the period of time from the end of the flowering to the fruit ripening lasts for 6–8 weeks whereas Małodobry et al. [2010] indicate that in Poland this

period lasts for 35–63 days, depending on the weather conditions. In this study the ripening began in the third decade of May ('Wołoszebnica', 'Dlinnopłodna') and ran until the end of the first decade of June. Harvesting took place when the fruit are uniformly stained and easily separated from the stalk. At first, the harvest was small but it quickly increased as plants were reaching the full fruiting stage which took place in the first and second decade of June. The successive ripening of the fruit requires collecting berries several times (6–8×) [Małodobry et al. 2010]. Repeated fruit collection reduces also fruit dropping losses which in some cultivars can reach about 20% of the marketable yield [Ochmian and Grajkowski 2007, Ochmian et al. 2008]. Moreover, Ochmian at el. [2013], Szot and Lipa [2013], Skupień et al. [2009] indicate that the time of fruit harvest can affect the size and the quality characteristics of fruit. The diversified ripening period in the tested plants allows us to obtain a progeny which will have more diversified ripening period in comparison to the parental forms as Thompson and Barney [2007] observed.

Table 2. Time of plants flowering and fruit ripening of 9 genotypes of blue honeysuckle (average in the years of research)

Cultivar/clone	Time of florescence		Time of fruit ripening	
	beginning	end	beginning	full
Wołoszebnica	18–28 IV	10–15 V	21–24 V	1–5 VI
Dlinnopłodna	20–28 IV	12–16 V	21–25 V	1–5 VI
Wojtek	20–30 IV	12–16 V	23–29 V	3–8 VI
Duet	22 IV–1 V	13–17V	4–7 VI	12–15 VI
Czelabinka	23–30 IV	14–17 V	23–27 V	3–6 VI
Clone P	25 IV–1 V	16–18 V	6–9 VI	12–16 VI
Warszawa	26 IV–1 V	16–18 V	2–6 VI	11–16 VI
Clone nr 9	26 IV–1 V	16–19 V	2–6 VI	11–16 VI
Clone T2	26 IV–2 V	17–20 V	7–10 VI	13–18 VI

The results obtained during the experiment show that examined genotypes have differential yield potential (tab. 3). T2 clone and 'Warszawa' cultivar had the highest yield – more than 2 kg of fruit from a shrub. Such level of yield is considered by many authors [Golis 2007, Thompson and Barney 2007] as the average for 5–6 years old shrubs. However, there are also reports of a much higher potential yield reaching 5 kg per bush [Hummer 2006] and 8670 kg per 1 ha plantation [Pierzga 2001]. High-yielding cultivars allow an opportunity to use them in breeding programs aimed at obtaining forms with high fruitfulness as pointed out by Thompson and Barney [2007]. Two cultivars and two breeding clones belonged to the group of genotypes with the average yield in the range of 1300–1700 g. The 'Duet' cultivar yielded slightly higher than the same cultivar in Szot and Wieniarska [2012] studies. Its fruit yield was closer to that obtained in studies held by Małodobry et al. [2008]. In the case of the 'Wojtek' cultivar the yield of the

Table 3. Some characteristics of blue honeysuckle fruit (average in the years of research)

Cultivar/clone	The yield of fruit per bush (g)	Berry weight (g)	Number of seeds per fruit (pcs)
Clone T2	2216.7 a*	1.75 a	11.0 a
Warszawa	2000.3 ab	1.56 ab	11.0 a
Wojtek	1693.3 bc	1.24 c	8.7 ab
Duet	1560.0 cd	1.43 bc	11.3 a
Clone nr 9	1346.7 de	0.91 d	12.0 a
Clone P	1306.0 def	0.90 d	9.3 ab
Czelabinka	1262.3 def	0.58 e	7.3 ab
Dlinnopłodna	1052.7 ef	0.56 e	5.3 b
Wołoszebnica	977.3 f	0.74 de	7.7 ab

*Values in columns marked with the same letter do not differ significantly

3–4 years old shrubs ranged from 775 to 1118 g from the bush as defined by Ochmian et al [2008]. For example, Golis [2007] obtained the yield in the range of 2.3–2.7 kg per bush for the shrubs which were five years after planting. The lowest yields were obtained by the cultivars of the Russian selection ('Wołoszebnica', 'Dlinnopłodna', 'Czelabinka'). Golis [2007] points out that their yield potential is low in Poland. In the United States (Oregon) it is also low according to Thompson and Barney [2007]. The tested cultivars of Russian origin had the lowest berry weight. Gwozdecki and Golis [2006] also report about the low single berry weight of these cultivars but Plekhanova [2000] states that the newer cultivars of the Russian selection can have the weight in the range of 0.70–1.32 g. In this study, the value of this quantitative parameter was greatly exceeded by the genotypes of Polish selection (clone T2 and the 'Warszawa' and 'Duet' cultivars) in the relation to the Russian cultivars. The 'Duet' cultivar was also characterized by a high berry weight in other authors' studies. [Małodobry et al. 2010, Szot and Wieniarska 2012]. In addition, Thompson and Barney [2007] state that the weight of the berries of this species is in the range of 0.50–2.70 g. Bors [2009b] indicates that one of the main breeding purposes should be the obtaining of varieties with large fruit which are suitable for mechanised harvesting. He also notices that varieties which produce large fruit other then ovoid and elongate can be useful for hand picking for amateur fruit growers. Blue honeysuckle genotypes require pollination of foreign pollen in order to produce a high yield of fruits but this is not a rule as there have been selected cultivars which produce fruits as a result of self-pollination. Thompson [2006] states that the appropriate pollination leads to a larger amount of seed and thus to larger fruits. One large fruit can contain up to 22 seeds. The indicated phenomenon was also noticed in this work, as fruits with the highest weight contained a greater number of seeds.

The investigated genotypes of blue honeysuckle had high pollen viability (tab. 4). There were no differences in terms of this trait in the evaluated genotypes in individual years whereas there were differences between the years of research. Pollen viability of

this species was similar to gooseberry cultivars pollen viability (85.3–95.3) which was observed by Golis et al. [2001]. In contrast, pollen viability of blackcurrant cultivars ranged from 30 to 88.7% [Golis et al. 2001], pollen viability of cranberries varied from 9.8 to 82.1% [Kaczmarska 2009] and pollen viability of strawberries ranged from 33.8 to 70.8% [Kaczmarska et al. 2008].

Table 4. The percentage of viable pollen grains in the studied cultivars and clones of blue honeysuckle

Cultivar/clone	Pollen viability (%) in particular years of research			Mean pollen viability of cultivars/clones
	2010	2011	2012	
Czelabinka	99.0a*	91.7a	85.1a	91.9a
Wojtek	98.3a	97.7a	94.3a	96.8a
Duet	98.1a	97.7a	99.3a	98.4a
Clone nr 9	98.0a	96.0a	94.1a	96.1a
Clone T2	98.1a	96.0a	89.3a	94.5a
Clone P	97.9a	95.3a	84.5a	92.6a
Dlinnopłodna	97.7a	96.7a	94.8a	96.4a
Warszawa	97.7a	94.5a	91.7a	94.6a
Wołoszebnica	95.7a	95.4a	92.9a	94.7a
Mean for years	97.8a	95.6ab	91.8b	

*Values in columns and last row marked with the same letter do not differ significantly

Table 5. Characteristics of banding patterns obtained with six selected oligodeoxynucleotide primers used for RAPD analysis of *Lonicera caerulea*

No.	RAPD Primer (Sigma)	Sequence 5'-3'	Total bands	Polymorphic bands	%P[a]	Size range of DNA fragments (bp)
1.	RJ2	ATGCCGCGAT	8	7	87.5	772–3791
2.	RJ3	TAGCGCCAAT	11	10	90.9	700–4151
3.	RJ6	ATGTGCCGTA	9	8	88.9	876–3791
4.	RJ7	TGGCGCAATA	9	9	100	772–4000
5.	RJ8	ACAACGCCPC	12	12	100	481–3500
6.	RJ9	GACCGCTTTG	12	11	91.7	387–2966
Total			61	57	93.44	387–4151

[a] – Percentage of polymorphism

Of the 20 primers tested for their capacity to differentiate among 10 blue honeysuckle cultivars and clones, the best 6 primers showed a polymorphism between accessions and gave reproducible banding patterns. Table 5 shows the characteristics of band-

ing patterns obtained with selected primers. These 6 primers amplified 61 loci and 57 of them were polymorphic (93.44% polymorphism). Naugžemys et al. [2007] characterised genetic variation and relationships among 39 *Lonicera caerulea* accessions representing four subspecies, three cultivars, six genetic lines and one native *L. xylosteum* L. using the random amplified polymorphic DNA (RAPD) method. A total of 105 DNA fragments were scored after amplification of all DNA samples with 11 selected random primers; 83.9% of scored bands were polymorphic. Blue honeysuckle accessions were also genotyped by Lamoureux et al. [2011] with five intersimple-sequence repeat markers, yielding more than 1100 polymorphic fragments across the 194 accessions. Statistical analysis of these data showed that the subspecies level was key in explaining blue honeysuckle diversity.

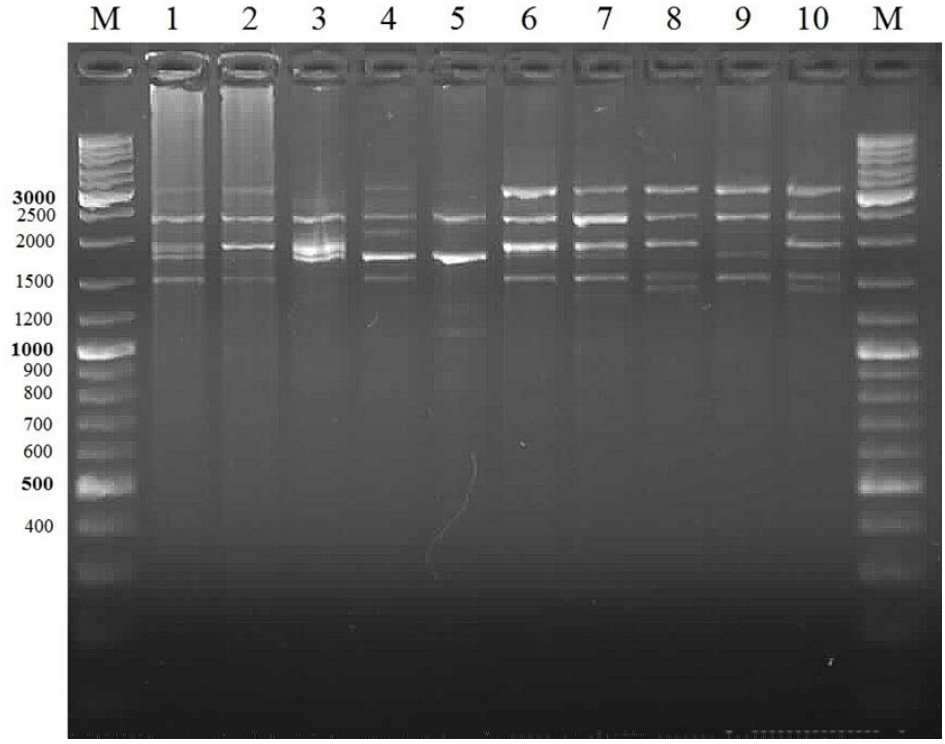

Fig. 1. RAPD analysis with RJ6 primer of *Lonicera caerulea* – standard of DNA fragment size GeneRuler^{TM} DNA Ladder Mix (100–10000 bp) (M). The arabic numerals on the top of the picture indicate the code number of the individuals: 1 – 'Warszawa', 2 – clone T2, 3 – 'Dlinnopłodna', 4 – 'Wołoszebnica', 5 – 'Czelabinka', 6 – 'Wojtek', 7 – 'Duet', 8 – clone nr 9, 9 – 'Atut', 10 – clone P

The number of RAPD bands scored per primer in this work varied from 8 (primer 2) to 12 (primer 8 and 9). An average of 10.2 bands was obtained per primer and their size ranged from 387 to 4151 bp. Examples of typical RAPD banding patterns produced by

primer RJ6 are shown in fig. 1. The results obtained in this study are the same as those of Naugžemys et al. [2007], where the number of RAPD markers identified per primer ranged from 6 to 11. Huo and Dong [2012] assessed the genetic diversity of wild blue honeysuckle native to northeastern China by RAPD technology. In their study the total number of bands for each primer in all samples varied from 3 to 11 with an average of 6.9 bands per primer. The size of the amplified fragments ranged from 80 to 3200 bp.

Table 6. Matrix of genetic similarity among 10 *Lonicera caerulea* cultivars and clones based on RAPD markers calculated by Dice's coefficient

Cultivar/clone	Warszawa	clone T2	Dlinnopłodna	Wołoszebnica	Czelabinka	Wojtek	Duet	clone nr 9	Atut
Warszawa									
Clone T2	0.51								
Dlinnopłodna	0.43	0.43							
Wołoszebnica	0.59	0.51	0.43						
Czelabinka	0.52	0.51	0.43	0.52					
Wojtek	0.59	0.51	0.43	0.70	0.52				
Duet	0.59	0.51	0.43	0.70	0.52	0.71			
Clone nr 9	0.63	0.51	0.43	0.59	0.52	0.59	0.59		
Atut	0.59	0.51	0.43	0.70	0.52	0.71	0.74	0.59	
Clone P	0.59	0.51	0.43	0.70	0.52	0.71	0.85	0.59	0.74

The genetic similarity matrix was produced on the basis of RAPD markers using the Dice's coefficient (tab. 6). RAPD based genetic similarity was estimated between 0.43 ('Dlinnopłodna' to other genotypes) and 0.85 (between clone P and cultivar 'Duet'). The mean genetic similarity was calculated at 0.56. Smolik at al. [2010] estimated genetic similarity among 14 Polish and Russian blue honeysuckle accessions using ISSR markers. They identified level of similarity ranged from 0.44 to 0.95. Random polymorphic DNA analysis was also used to assess the genetic variation of 51 accessions of blue honeysuckle, including 19 elite cultivars and 32 genetic lines derived from seeds collected in wild populations [Naugžemys et al. 2011]. The pairwise genetic distance (GD_{xy}) values among studied accessions ranged from 0.054 to 0.479, the mean GD_{xy} was 0.283. The UPGMA dendrogram based on GD_{xy} estimates genetic relationships (derived from RAPD analysis) among the studied accessions. The UPGMA analysis grouped all accessions into two main clusters.

In this study the genetic similarity matrix was applied for cluster analysis through UPGMA method (fig. 2). The generated dendrogram of ten accessions showed exactly two clusters. The largest cluster included seven accessions: 'Warszawa', Nr 9, 'Wołoszebnica', 'Wojtek', 'Duet', P clone, 'Atut'. The smallest cluster consisted of three samples – 'Czelabinka', T-2 clone and 'Dlinnopłodna'. The phylogenetic similarity between 'Atut ' and 'Wojtek' cultivars was relatively high (0.71) therefore they were classified in common group. On the basis of the analysis conducted by Smolik at al. [2010] these two accessions constituted a separate group 'c'.

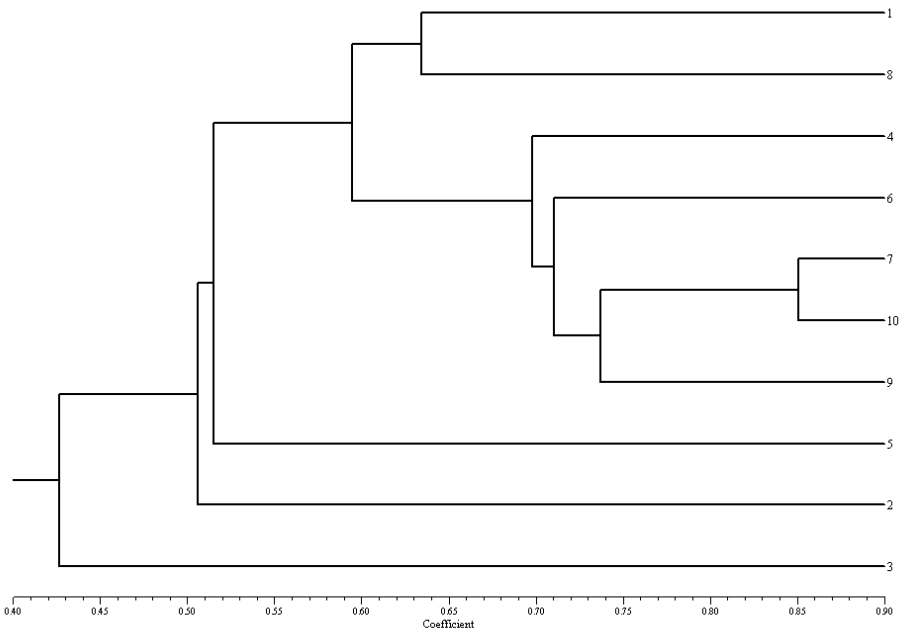

Fig. 2. Dendrogram of genetic similarity among ten blue honeysuckle cultivars and clones, obtained from RAPD markers using the UPGMA method. The arabic numerals on the right side of the picture indicate the code number of the individuals: 1 – 'Warszawa', 2 – clone T2, 3 – 'Dlinnopłodna', 4 – 'Wołoszebnica', 5 – 'Czelabinka', 6 – 'Wojtek', 7 – 'Duet', 8 – clone nr 9, 9 – 'Atut', 10 – clone P

The study demonstrated that RAPD analysis is efficient for genotyping blue-berried honeysuckle accessions and that DNA polymorphism significantly exceeds the morphological diversity of the studied samples.

On the basis of the obtained results it can be stated that high-yielding T2 clone with a high weight of one berry can be used in the breeding programs with such promising cultivars as 'Warszawa', 'Wojtek' and 'Duet', which due to its genetic analysis were classified to a separate clusters.

CONCLUSIONS

1. The investigated phenotypic diversity in the tested honeysuckle genotypes provides the opportunity to use them in the breeding programs of this species.

2. The undertaken DNA analysis allowed us to characterise the investigated cultivars and breeding clones and to determine their genetic similarity.

3. The 'Warszawa' and 'Wojtek' cultivars and T2 clone are regarded as the most valuable for breeding because of their high yield and fruit weight.

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OCENA ZRÓŻNICOWANIA FENOTYPOWEGO I GENOTYPOWEGO WYBRANYCH POLSKICH I ROSYJSKICH ODMIAN I KLONÓW JAGODY KAMCZACKIEJ (*Lonicera caerulea* L.)

Streszczenie. Jagoda kamczacka, ze względu na właściwości prozdrowotne owoców, wczesny termin ich dojrzewania (przed pierwszymi odmianami truskawek) oraz wysoką mrozoodporność zarówno roślin, jak i kwiatów, zyskuje coraz większą popularność nie tylko w uprawie, ale także hodowli. Realizacja programu hodowli nowych odmian wymaga znajomości wartości cech determinujących wybrany jej kierunek w materiale wyjściowym. Dlatego też w pracy dokonano oceny przebiegu faz fenologicznych, plonowania, masy owocu, liczby nasion w owocu oraz żywotności pyłku u odmian i klonów hodowlanych tego gatunku. Badane odmiany i klony cechowały się zróżnicowanym poziomem analizowanych właściwości poza żywotnością pyłku, która była wysoka, ale nie różniła się istotnie w obrębie genotypów. Ocena potencjału plonowania oraz masy owocu wskazuje na możliwe do wykorzystania w programie hodowli odmiany 'Warszawa' i 'Wojtek' oraz klon T2, ze względu na większe wartości tych cech w porównaniu z pozostałymi genotypami. Formy o wczesnej porze dojrzewania owoców można uzyskać poprzez wykorzystanie odmian selekcji rosyjskiej. Ponadto na podstawie metody RAPD dokonano charakterystyki tych genotypów, a także określono ich podobieństwo genetyczne. Analizowane startery produkowały 61 fragmentów, z czego 57 (93,44%) było polimorficznych. Wykorzystując markery RAPD, utworzono matrycę podobieństwa genetycznego. Średnia wartość podobieństwa analizowanych genotypów wynosiła 0,56. Przeprowadzone badania potwierdzają przydatność metody RAPD do oceny podobieństwa genetycznego jagody kamczackiej.

Słowa kluczowe: jagoda kamczacka, losowo wzmocnione polimorficzne DNA (RAPD), zróżnicowanie genetyczne, żywotność pyłku, termin kwitnienia i owocowania, plonowanie

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