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PHENOTYPIC DIVERSITY IN A SAMPLE OF BLACKCURRANT (*Ribes nigrum* L.) CULTIVARS MAINTAINED IN THE FRUIT BREEDING DEPARTMENT AT THE RESEARCH INSTITUTE OF POMOLOGY AND FLORICULTURE IN SKIERNIEWICE, POLAND

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A B S T R A C T

In this paper assessment of the phenotypic diversity in 40 blackcurrant (*Ribes nigrum* L.) cultivars was presented. The cultivars were from the breeding (working) collection, and originated from over a large geographical range. Bushes of the genotypes in the working collection were planted in autumn of 2004 in the Experimental Orchard in Dąbrowice, near Skierniewice, belonging to the Fruit Breeding Department of the Research Institute of Pomology and Floriculture. Observations of 17 agronomical traits collected during the two years of 2007-2008 were analyzed. Two multivariate methods were used, i.e. principal component analysis (PCA) and cluster analysis (CA) using Ward's method and the square of the Euclidean distance. The first three PCs explained about 56% of the multi-trait variation among the cultivars, and the first two accounted for about 39% of the multi-trait variation. There was a high correlation of the two phenological traits, fruit size and firmness of fruit skin with PC1. This correlation represents the most important genetic common factor that could be called, "*Ripening time driving fruit size and firmness*". The PC2 was mostly correlated with number of basal shoots and fruit yield per plant. It represents the second common factor called, "*Plant architecture affecting fruit productivity*". Traits such as ripening time, fruit size and firmness, number of basal shoots, fruit yield per plant, as well as susceptibility to diseases and pests are the most discriminating pomological attributes that mainly contribute to overall phenotypic diversity of the blackcurrant cultivars. The cultivars were divided into five distinct clusters. Distribution of the cultivars in two PCs coordinates allowed us to find the existing rich diversity for the studied traits. Such diversity proves, that the characterized blackcurrant cultivar collection has high potential for specific breeding goals. The cultivars included in the diverse clusters could be promising parents with complementary levels of the most discriminating traits. They should be used for hybridization in order to obtain a high heterotic response. This response would substantially contribute to the blackcurrant breeding programs.

Key words: blackcurrant, *Ribes nigrum* L., working collection, cultivar diversity, pomological traits, principal component analysis, cluster analysis

INTRODUCTION

The blackcurrant (*Ribes nigrum* L.) is an important fruit crop cultivated in Poland and Northern and Central Europe. Presently, it is also commercially produced in moderate temperate regions encompassing many countries of the world. The Research Institute of Pomology and Floriculture (RIPF) in Skierniewice, Poland has been carrying out breeding programs oriented towards releasing new blackcurrant cultivars useful for the production of fruits for fresh consumption (desert cultivars) and fruits suitable for processing and freezing (industrial cultivars). It is required that new cultivars be winter hardy and tolerant to spring frosts, resistant to the main *Ribes* diseases and pests, as well as well adapted to the variable environments across Poland and across a large range of areas (Pluta and Żurawicz, 1993, 2002; 2009; Pluta, 1999; Żurawicz et al., 2000). To meet the challenges for crop improvement, efforts are required to widen the genetic base of the species. Enlarging the base may be done by collecting, conserving and characterizing germplasm throughout the world. This activity is very important because of the erosion of blackcurrant genetic diversity (as with all cultivated species), due to development of modern cultivars adapted to conventional production systems (Pluta and Żurawicz, 2002, 2009).

The blackcurrant germplasm (genetic resources) collections and working collections established during the last few decades in Europe include commercial cultivars, breeding selections, landraces and wild species (Pluta, 1999; Lanham et al., 1995; Grzyb, 2004; Hjalmarsson and Wallace, 2004). These collections are valuable sources of genes which are much needed in breeding programs performed in Poland and other countries (Pluta and Żurawicz, 1993, 2002, 2009; Lanham et al., 1995; Pluta, 1999; Brennan and Gordon, 2002; Kuras et al., 2002; Grzyb, 2004; Hjalmarsson and Wallace, 2004). On the other hand, there is limited information on the global evaluation of genetic and phenotypic diversity for pomological attributes in blackcurrant species (Lanham et al., 1995; Pluta, 1999; Kuras et al., 2002; Mądry et al., 2004). The collected germplasms need to be characterized for their genetic and phenotypic diversity which forms the perspective raw material of plant breeding (Lanham et al., 1995; Wiejacha et al., 2001; Brennan and Gordon, 2002; Kuras et al., 2002; Martinez-Calvo et al., 2008; Nikolic et al., 2010).

Characterization of diversity for phenotypic traits in a plant germplasm collection or other sample of genetic entries involves 1) assessment of phenotypic structure and variation patterns, 2) identifying the traits which contribute the most to the total diversity in the collection of accessions and then, the most discriminative attributes in the set of genotypes 3) establishing groups of accessions with similar levels of studied traits (potentially heterotic groups), 4) describing homogenous group profiles for studied traits, focused on the most discriminative traits (Hillig and Iezzoni, 1988; Peeters and Martinelli, 1989; Iezzoni and Pritts, 1991; Badenes et al., 2000; Sieczko et al., 2004; Mądry, 2007; Martinez-Calvo et al., 2008; Ruiz and Egea, 2008; Nikolic et al., 2010). This could facilitate sustainable utilization of the genotype collection for hybridization in the breeding programs and also to establish a core collection.

The Fruit Breeding Department of the RIPF in Skierniewice, Poland has maintained the working collection of 100 blackcurrant genotypes, including cultivars and advanced breeding selections, in its field gene bank. These genotypes need to be characterized and evaluated for genetic and phenotypic diversity to assess their breeding value. Characterization and evaluation help facilitate further selection for hybridization in breeding programs with different goals.

The objective of the study was to assess the diversity for agronomic (pomological) traits in 40 blackcurrant cultivars maintained in the field collection. The objective includes the evaluation of the potential traits for the breeding of modern cultivars. There is a relatively high number of cultivars evaluated in the working collection. These cultivars come from different genetic and geographic origins They could provide valuable information on the breeding potential of blackcurrant species.

MATERIAL AND METHODS

Plant material. A working collection (*ex situ*) of 100 blackcurrant (*Ribes nigrum* L) genotypes was established in 2004 at the Fruit Breeding Department of the RIPF in Skierniewice, Poland. This collection includes cultivars and advanced breeding selections in its field collection. It is located in the Experimental Orchard at Dąbrowice near Skierniewice. Observations of pomological traits, being the subject of the studies reported in this paper, were recorded on 40 cultivars (Tab. 1). These were cultivars chosen on the basis of three criteria, i.e. differentiation of geographic origin, genetic (at DNA markers) and phenotypic diversity,

Table 1. List of the tested blackcurrant cultivars, their geographic origins and assigning to a homogenous group identified by cluster analysis

No.	Cultivar	Country of origin	Group number	No.	Cultivar	Country of origin	Group number
1	Almiai	Lithuania	1	21	Minaj Szmyriew	Russia	5
2	Ben Alder	UK	2	22	Nor de Bourgunde	France	4
3	Ben Connan	UK	3	23	Ojebyn	Sweden	1
4	Ben Gairn	UK	1	24	Ores	Poland	3
5	Ben Hope	UK	2	25	Pamiat Miczurina	Russia	5
6	Ben Lomond	UK	2	26	Pilieniai	Lithuania	1
7	Ben Sarek	UK	1	27	Pilot A. Mamkin	Russia	5
8	Ben Tirran	UK	2	28	Poezja	Russia	5
9	Consort	Canada	4	29	Ruben	Poland	3
10	Czereszniewa	Ukraine	1	30	Sanjuta	Ukraine	1
11	Dlinnokistnaja	Russia	4	31	Sjuta Kijewskaja	Ukraine	1
12	Docz Altaja	Russia	5	32	Sofijewskaja	Ukraine	1
13	Foxendown	UK	4	33	Szachalewskaja	Russia	5
14	Gofert	Poland	3	34	Tenah	Czech Rep.	4
15	Gołubka	Russia	5	35	Tiben	Poland	3
16	Joniniai	Lithuania	1	36	Tines	Poland	1
17	Jubilennaja Kopania	Ukraine	3	37	Tisel	Poland	3
18	Kasticiai	Lithuania	1	38	Titania	Sweden	3
19	Legenda	Russia	5	39	Triton	Sweden	1
20	Lentaj	Russia	1	40	Tsema	Czech Rep.	4

for the most important traits for breeding and cultivation (Badenes et al., 2000; Bekele et al., 2006). Therefore, these genotypes could be recognized as representative of the gene pool of *Ribes nigrum* L.

Experimental design. Bushes were planted in a density of 3.5 x 0.75 m with a space of 1.2 m between plots. Each genotype was represented by 3 plants on a plot. The collection occupied an area of about 350 m^2. The field was uniform in soil fertility and cultivation conditions.

Traits studied. In the studies, 17 traits such as morphological, phenological, productive value, fruit quality and resistance to diseases and pest characteristics were included (Tab. 2).

Table 2. Traits observed in the studied collection of 40 blackcurrant cultivars in 2007 and 2008, and the rating scale range

No.	Traits (Codes)	Rating scale
1	Time of beginning of flowering (**TBF**)	3 = early, 5 = medium, 7 = late
2	Time of fruit ripening (**TFR**)	3 = early, 5 = mid-season, 7 = late
3	No. basal shoots per plant (**BNS**)	3 = few, 5 = medium, 7 = many
4	Plant height (**PH**)	3 = short, 5 = medium, 7 = tall
5	Fruit size (**FS**)	3 = small, 5 = medium, 7 = large
6	Fruit weight (**FW**)	[g/fruit]
7	Firmness of fruit skin (**FSK**)	3 = soft, 5 = medium, 7 = firm
8	Length of truss (**LTR**)	1 = very short (1-2 berries); 2 = short (3-5 berries), 3 = medium (6-8 berries), 4 = long (9-12 berries), 5 = very long (>12 berries)
9	Vitamin C content in fruit (**CVC**)	[mg/100g]
10	Susceptibility to powdery mildew (**SPM**)	3 = low, 5 = medium, 7 = high
11	Plant vigour (**PV**)	3 = weak, 5 = medium, 7 = strong
12	Fruit yield per plant (**FY**)	3 = low, 5 = medium, 7 = high
13	Fruit yield observed per plant (**FYO**)	[kg/plant]
14	Susceptibility to leaf spot (**SLS**)	3 = low, 5 = medium, 7 = high
15	Susceptibility to white pine blister rust (**SWPBR**)	3 = low, 5 = medium, 7 = high
16	Susceptibility to gall mite (*Cecidophyopsis ribis* Westw.) (**SGM**)	3 = low, 5 = medium, 7 = high
17	Susceptibility to two-spotted spider mite (*Tetranychus urticae* Koch.) (**SSM**)	3 = low, 5 = medium, 7 = high

The traits are in nature quantitative but most of them were scored with three- or five-state ordered discrete variables (rating scale) according to the UPOV (International Union for the Protection of New Varieties of Plants) descriptors – TG/40/6 “Guidelines for the conduct of tests for distinctness, homogeneity and stability – Black currant, 1989”. The studied traits were recorded for two consecutive years 2007-2008 in 40 cultivars on 3 plants per cultivar. The observations of all pomological traits were done on individual plants and the mean scores from 3 plants were taken for further analysis. Fruit size was determined using a ranking scale, which corresponded to the fruit weight assessed as a weight of 100 berries (in grams) randomly picked from each plant. Fruit yield was first evaluated on a scale by rank, and the second time as a mean yield harvested from three plants per plot (kg/plant). The vitamin C content was measured in fruits harvested from each genotype and frozen immediately after harvest. In the autumn (October-November), fruits were refrozen and vitamin C content (mg/100 ml) was measured using the Reflectometer RQ-Easy and Merck’s ascorbic acid test strips.

Statistical analyses. All statistical analyses were performed for the means of each trait, calculated on the basis of raw data from three plants across the two years. The method of analysis involved three stages (Badenes et al., 2000; Mohammadi and Prasanna, 2003; Sieczko et al., 2004; Mądry, 2007; Martinez-Calvo et al., 2008; Nikolic et al., 2010). First, descriptive statistics were used to describe distribution of the studied traits. Second, principal components analysis (PCA) was used to identify the patterns of multi-trait variation in the collection. PCA first looks for a linear combination of traits that extracts maximum variance. Then, PCA identifies a second linear combination to explain the remaining variance etc. leading to new uncorrelated variables called PCs or factors. The PC variation is measured by associated eigenvalues. Each PC is such a dimension (a factor), interpreted in the category of a subset of traits which are mostly correlated with the PCs. PCA is commonly used to study patterns of variation in a set of interrelated traits by identifying subsets of traits substantially correlated to each other. Then, each subset of such interrelated traits could be interpreted as observable expression of a common factor (here, genetic factor) simultaneously affecting these variables to a large extent. Usually, the first few PCs account for the majority of variation in tested units (here cultivars), as measured by Euclidean distance. Thus, they are the most important factors separating the units. Therefore, PCA allows visualization of the differences among units and distinguished homogenous groups by clustering. In the paper, PCA was used for the set of all 17 traits after they were standardized. This was done by extracting the means from a value of some trait for a given cultivar and dividing the result by the standard deviation. Varimax type rotation was made.

Next, cluster analysis (CA) using the Ward's method as agglomeration rule and the squared Euclidean distance as a measure of dissimilarity, was carried out to classify the genotypes into homogenous groups. Two multivariate methods, i.e. PCA and CA are complementary tools in within-collection diversity characterization. Data processing was performed using the PASW Statistics 18 (formerly SPSS) package (Gatnar, 1995; Anonim, 1999). The analyses used are also available in SAS, Statistica and StatGraphics packages.

RESULTS AND DISCUSSION

Summary characteristics. The tested blackcurrant cultivars were, on the average, rather early at ripening, but this attribute showed relatively high variation (coefficient of variability). They produced, on average, high plants with strong vigor and many basal shoots showing low coefficient of variability, i.e. narrow range of variation for these traits (Tab. 4). The cultivars showed, on average, low but substantially variable susceptibility to powdery mildew and moderate susceptibility to other diseases and pests. Means of the other studied traits were at the medium levels, while time of fruit ripening, fruit yield per plant and vitamin C content in fruit showed the relatively highest variation as measured by coefficient of variability.

Table 3. Correlations between the observed traits and the first five principal components (PCs) in the collection of 40 blackcurrant cultivars, and variation explained by these PCs

Traits	Principal Components (PCs)				
	PC1	PC2	PC3	PC4	PC5
Time of flowering	**0.89**	0.11	-0.03	0.01	0.11
Time of fruit ripening	**0.88**	0.01	-0.12	0.00	0.00
No. basal shoots per plant	0.00	**0.91**	0.09	-0.12	-0.07
Plant height	0.18	-0.02	0.07	**0.92**	0.10
Fruit size	**-0.67**	0.57	-0.03	-0.16	0.17
Fruit weight	**-0.67**	0.54	-0.19	-0.15	0.17
Firmness of fruit skin	**0.83**	-0.10	0.07	-0.13	0.03
Length of truss	-0.20	-0.29	-0.30	**0.53**	-0.27
Vitamin C content in fruit	0.19	0.30	**-0.54**	0.07	-0.38
Susceptibility to powdery mildew	0.02	-0.19	0.16	0.08	**0.78**
Plant vigour	0.07	-0.02	-0.03	**0.85**	0.18
Fruit yield per plant	-0.12	**0.91**	-0.20	-0.02	-0.15
Fruit yield observed per plant	-0.01	**0.80**	-0.41	0.02	-0.19
Susceptibility to leaf spot	0.08	-0.18	**0.88**	0.16	0.13
Susceptibility to white pine blister rust	-0.12	-0.10	**0.85**	-0.08	-0.25
Susceptibility to gall mite (*Cecidophyopsis ribis* Westw.)	0.09	0.01	**0.81**	0.03	0.28
Susceptibility to two-spotted spider mite (*Tetranychus urticae* Koch.)	-0.37	-0.04	0.23	**0.64**	-0.21
Eigenvalue	3.46	3.20	2.88	2.39	1.21
Proportion of total variance explained [%]	20.33	18.82	16.93	14.06	7.11
Cumulative Proportion of total variance explained [%]	20.33	39.15	56.08	70.14	77.25

Principal component analysis. Using eigenvalue greater than one, as a measure for significance of a principal component (PC), five PCs extracted about 77% of the total variance in the 40 blackcurrant cultivars (Tab. 3). Of these, the first three PCs explained about 56%, and the first two accounted for about 39% of the multi-trait variation.

Due to substantial high correlation of the two phenological traits, fruit size and firmness of fruits with PC1, this principal component represents the most important genetic common factor, affecting the two phenological traits of fruit size and firmness of fruit skin (Tab. 3). This factor could be called “ripening time driving fruit size and firmness”.

Table 4. Summary of characteristics of the observed traits in the collection of 40 blackcurrant cultivars and the means for these traits in 5 distinguished groups by cluster analysis

Traits	Codes	All cultivars			Cluster means				
		means	standard deviations	CV	1	2	3	4	5
Time of flowering	TBF	4.13	1.51	36%	3.14	7.00	4.13	5.67	3.25
Time of fruit ripening	TFR	4.30	1.54	36%	3.29	6.50	4.50	6.33	3.25
No. basal shoots per plant	BNS	6.20	1.04	17%	5.86	6.50	6.00	6.67	6.50
Plant height	PH	5.85	1.21	21%	6.00	7.00	7.00	4.50	4.88
Fruit size	FS	5.18	1.39	27%	6.29	4.75	5.63	3.00	4.63
Fruit weight	FW	1.08	0.29	27%	1.30	0.93	1.22	0.69	0.90
Firmness of fruit skin	FSK	5.10	1.35	27%	4.29	6.50	4.88	6.33	5.13
Length of truss	LTR	3.05	0.55	18%	3.04	2.50	3.13	3.42	3.00
Vitamin C content in fruit	CVC	86.35	33.72	39%	70.88	87.73	127.68	82.90	73.98
Susceptibility to powdery mildew	SPM	3.60	1.22	34%	3.29	4.00	3.00	4.00	4.25
Plant vigour	PV	6.23	1.03	16%	6.07	6.00	6.00	6.67	6.50
Fruit yield per plant	FY	5.58	1.17	21%	5.93	6.00	7.00	4.33	4.25
Fruit yield observed per plant	FYO	1.49	0.60	40%	1.47	1.64	2.36	0.96	0.99
Susceptibility to leaf spot	SLS	4.95	1.20	24%	5.14	6.00	3.50	4.67	5.75
Susceptibility to white pine blister rust	SWPBR	5.08	1.38	27%	5.79	6.50	3.25	4.33	5.50
Susceptibility to gall mite (*Cecidophyopsis ribis* Westw.)	SGM	5.10	1.19	23%	5.07	6.50	4.13	4.33	6.00
Susceptibility to two-spotted spider mite (*Tetranychus urticae* Koch.)	SSM	5.33	1.19	22%	5.43	5.00	5.25	4.50	6.00

Negative and positive correlations of these traits with PC1 show that later ripening cultivars produced predominantly smaller fruits and their fruits were more firm. The smaller fruits produced by later ripening cultivars was not related to fruit yield – the yield of small-fruit and large-fruit could be both higher and lower. Smaller (negative) values in Figure 2 for PC1 indicate earlier cultivars producing larger and softer fruits. Larger (positive) PC1 values indicate later cultivars producing smaller and more firm fruits. The second principal component was mostly correlated with number of basal shoots and fruit yield per plant. These two traits relate to plant architecture and fruit productivity. PC2 represents the second important common genetic factor called "plant architecture affecting fruit productivity". Smaller values in Figure 2 for PC2 indicate cultivars with lower productivity because of lower number of basal shoots per plant. Larger PC2 values indicate more productive cultivars with more basal shoots per plant. The third PC was mostly due to vitamin C content in fruit in contrast to leaf spot susceptibility, white pine blister rust and gall mite. The PC3 expresses another common factor called "susceptibility to diseases and pests negatively related to vitamin C content in fruit ". PC4 was positively related to plant height and vigor, truss length and susceptibility to two-spotted spider mite. This PC determines a factor being less important for affecting variability among the cultivars which could be called "plant and truss architecture favoring susceptibility to two-spotted spider mite".

Cluster analysis. Dividing the tested cultivars into five clusters (groups) is justified by the dendrogram (Fig. 1) which shows level similarity at all agglomeration steps. This decision to cut branches off the dendrogram is a compromise between reasonable number of clusters received and similarity within- and between-clusters variation. Assigning cultivars to each of the five groups is given in Table 1. Cultivars comprising Cluster 1 originated predominantly from Lithuania, the Ukraine and Sweden. The smallest Cluster 2, included only UK cultivars. Predominantly Polish cultivars were assigned to Cluster 3. Cluster 4 includes cultivars which are heterogeneous with respect to country origin; bred in Canada, Russia and other European countries. Eight Russian cultivars were assigned to Cluster 5. This study confirmed the existing geographical diversity of the cultivars chosen also on the basis of origin.

Characterizing cultivar groups and evaluation of their potential for breeding cultivars. In Figure 2 approximated similarities and relations among 40 tested cultivars for the 17 traits are presented in the coordinate axis of the first two principal components accounting for 39% of the total variation. The approximation of the real multivariate diversity of the cultivars is generally moderate, but it is quite acceptable for the most important discriminating (contributing) traits as revealed by PC1 and PC2. Projection of the genotypes

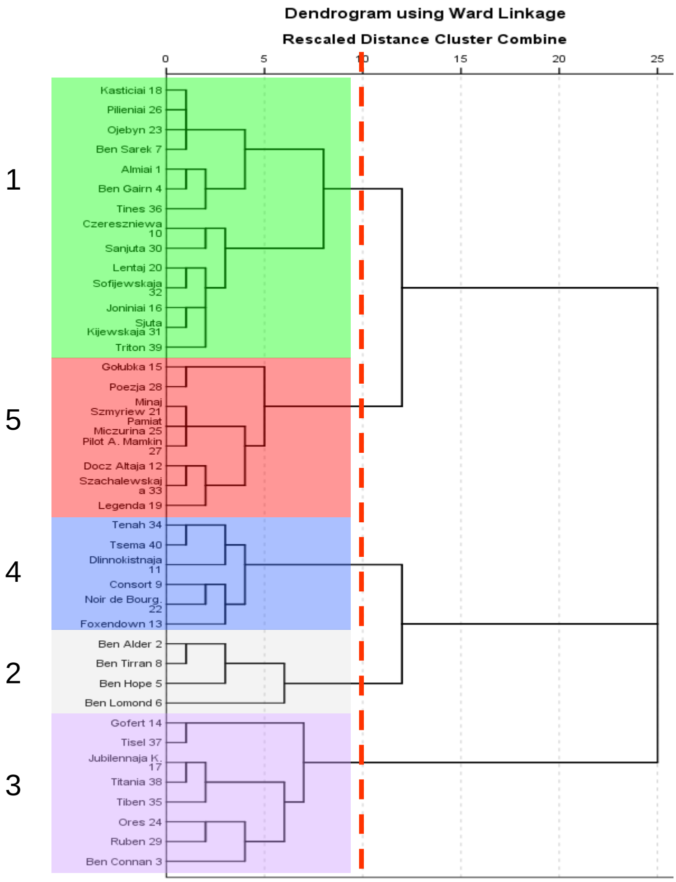

Figure 1. Dendrogram relating the 40 blackcurrant cultivars for 17 pomological traits using Ward's clustering method and the squared Euclidean distance as a measure of dissimilarity

on a two-dimensional plane, based on the first two principal components, substantially confirmed the results of the cluster analysis. This is true, even though some members of the clusters overlap.

Thorough description of the homogenous groups of the studied traits of the divided cultivars may be effectively limited to those traits recognized as the most important (contributing) to the overall variation of the cultivars and to those traits which distinguish the cultivars the most. To meet this task one can use cluster means for these significant traits (also other traits) given in Table 4. Fig. 2 also needs to be taken into account, as it presents an approximate visualization of similarity among 40 cultivars along the first two principal axes related accordingly to the

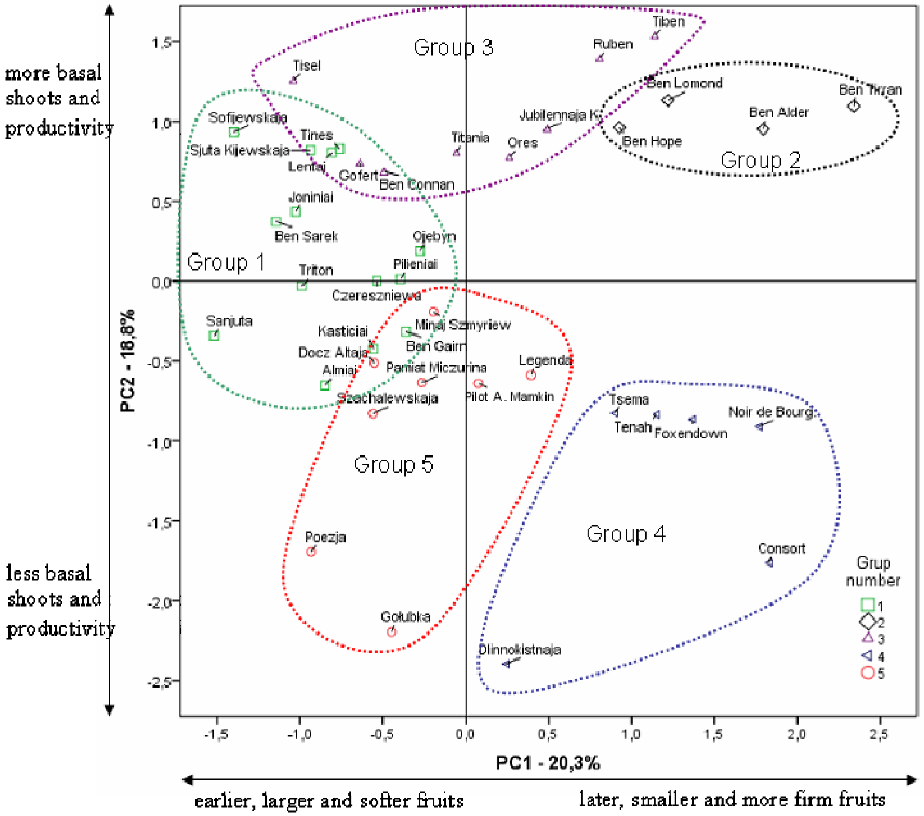

Figure 2. Visualization of similarity among 40 blackcurrant cultivars along the first two principal axes, accounting for 39, 1% of the total variation; symbols of the 5 groups obtained by Ward's cluster method

significant traits. Information results showed, that cultivars in Group 1 were early ripening, produced a moderate amount of fruit yield per plant, had relatively large and soft fruit, contained a low amount of vitamin C and showed moderate susceptibility to important diseases and pests. Substantially different (with opposite levels of the significant traits) in relation to those cultivars from Group 1, were the cultivars from Group 4. They were late ripening, producing very low fruit yield per plant (in spite of very tall plants) with the smallest, most firm fruits, containing more vitamin C and showing rather lower susceptibility to important diseases and pests. Cultivars from Group 5 were similar to those from Group 4 though they differed in earliness, fruit size and firmness. Groups 2 and 3 include very productive cultivars while they differed for earliness, produced fruits of moderate size and firmness, but had fruits which contained much vitamin C. These groups differed also for susceptibility to important diseases and pests – cultivars in Group 2 showed the highest susceptibility and those in Group 3, the lowest susceptibility.

The distribution of cultivars on Figure 2 showed the rich diversity (profiles) in the studied traits. It confirms that the characterized blackcurrant cultivar collection has high potential for specific breeding goals. However, there was a lack of cultivars located in Figure 2, in the area of the plot between Groups 2 and 4. From this, a conclusion may be drawn that such lacking genotypes should show moderate fruit productivity, earliness, fruit size and firmness. From the breeding point of view, such genotypes with moderate levels of significant traits are not much needed. The complementary profiles of the traits of potential parental genotypes existing in the working collection are quite satisfying. It makes this collection, a source of genes for desirable combinations of trait profiles in new blackcurrant cultivars.

CONCLUSIONS

Traits such as ripening time, fruit size and firmness, number of basal shoots, fruit yield per plant as well as susceptibility to diseases and pests are the most important for discriminating pomological attributes in our studied cultivars. These attributes mainly contribute to overall phenotypic diversity of blackcurrant cultivars originating from a large geographical range. The genotypes included in the diverse clusters could be used as promising and complementary parents for hybridization. Such an inclusion would be done in order to obtain a high heterotic response and thus, contribute to blackcurrant breeding purposes. The considerable diversity in plant morphology, phenology, yielding and resistance to important diseases and pests observed within the collection of 40 blackcurrant cultivars shows the agronomic potential of the species as a valuable fruit crop. These findings provide an important step to assess the diversity of a wide range of *Ribes nigrum*, including collections from cultivars. The clustering of the blackcurrant cultivar collection identified groups of similar genotypes with appropriate characteristics for different uses in breeding programs. All or some, of the genotype groups could be targeted for further testing. This would be testing in multi-environment trials replicated not only over years but also over locations, to clarify the potential of those cultivars which seems to be promising within this study. The findings have significance for blackcurrant breeding programs, conservation and future collecting strategies.

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ZMIENNOŚĆ FENOTYPOWA KOLEKCJI ROBOCZEJ ODMIAN PORZECZKI CZARNEJ W ZAKŁADZIE HODOWLI ROŚLIN SADOWNICZYCH INSTYTUTU SADOWNICTWA I KWIACIARSTWA W SKIERNIEWICACH

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STRESZCZENIE

W pracy przedstawiono ocenę zmienności i różnorodności fenotypowej 40 odmian porzeczki czarnej (*Ribes nigrum* L.) w hodowlanej (roboczej) kolekcji, pochodzących z różnych rejonów geograficznych. Krzewy genotypów w kolekcji roboczej Zakładu Hodowli Roślin Sadowniczych Instytutu Sadownictwa i Kwiaciarstwa (ISK) posadzono jesienią 2004 roku w Sadzie Doświadczalnym w Dąbrowicach k. Skierniewic. Obserwacje 17 cech użytkowych (pomologicznych), zebrane w dwóch latach (2007-2008), opracowano z użyciem analizy składowych głównych (PCA) i analizy skupień (CA), stosując metodę Warda i kwadrat odległości Euklidesa. Pierwsze trzy składowe główne wyjaśniły około 56%, a pierwsze dwie składowe, około 39% wielocechowej (ogólnej) zmienności badanych odmian. Ze względu na silną korelację dwóch cech fenologicznych, wielkości i jędrności owocu z pierwszą składową (PC1), reprezentuje ona najważniejszy wspólny czynnik genetyczny, nazwano "*Termin dojrzewania powiązany z wielkością i jędrnością owocu*". Druga składowa (PC2) była głównie skorelowana z liczbą pędów nasadowych i plonem owoców na roślinie, zatem reprezentuje ona drugi wspólny czynnik genetyczny, nazwany "*Architektura rośliny warunkująca jej plonowanie*". Termin dojrzewania, wielkość i jędrność owocu, liczba pędów nasadowych, plon owoców na roślinę, jak również podatność na choroby i szkodniki są najważniejszymi cechami dyskryminacyjnymi i mają największy udział w ogólnej zmienności fenotypowej cech użytkowych odmian porzeczki czarnej. Badane odmiany zostały podzielone na pięć jednorodnych grup (skupień), które wskazywały na bogatą zmienność zgromadzonej kolekcji roboczej pod względem badanych cech roślin. Potwierdza to, że scharakteryzowana kolekcja odmian porzeczki czarnej ma duże znaczenie dla konkretnych celów hodowlanych. Odmiany należące do różnych grup (skupień) mogą być wartościowymi formami rodzicielskimi, ze względu na uzupełniający poziom najbardziej dyskryminujących cech. Powinny one być używane do krzyżowań w programach hodowlanych dla uzyskania dużej zmienności potomstwa i znaczącego postępu w hodowli porzeczki czarnej.

Słowa kluczowe: porzeczka czarna, *Ribes nigrum* L., robocza kolekcja odmian, zmienność odmianowa, cechy pomologiczne, analiza składowych głównych, analiza skupień