BIOLOGIJA. 2010. Vol. 56. No. 1–4. P. 1–8
DOI: 10.2478/v10054-010-0001-8

Phenotypical variability and genetic diversity within accessions of the Swedish sour cherry (*Prunus cerasus* L.) genetic resources collection

Gunars Lacis[1]*,

Viktor Trajkovski[2],

Isaak Rashal[3]

[1] *Latvia State Institute of Fruit-Growing, Graudu iela 1, Dobele, LV 3701, Latvia*

[2] *Swedish Pomological Science Centre, Stubbaröd 2818, SE 26023 Kågeröd, Sweden*

[3] *Plant Genetics Laboratory, Institute of Biology, University of Latvia, Miera iela 3, Salaspils, LV-2169, Latvia*

Multivariate statistic analysis was used to determine phenotypical variability and genetic diversity among 40 sour cherry accessions from the collection of the Division of Horticultural Genetics and Plant Breeding of the Swedish University of Agricultural Sciences. Both cluster and principal component analysis showed an adequate grouping of accessions according to phenotypical data and known pedigree data. The most important traits for sour cherry accession grouping were tree architecture and fruit traits, which should be taken into account in the further sour cherry genetic resource characterization and analysis of breeding material. The multivariate analysis of several sour cherry traits increased the value of phenotypical data as it provided comprehensive information about the genetic structure of the collection and relationships among the accessions, which is not possible by analysis of separate traits.

Key words: *Prunus cerasus*, germplasm, characterization, genetic diversity, multivariate statistics

INTRODUCTION

Sour cherry *Prunus cerasus* L. (2n = 4x = 32) is an allotetraploid species which originated from natural hybridization between sweet cherry (*P. avium* L.; 2n = 2x = 16) and ground cherry (*P. fruticosa* Pail.; 2n = 4x = 32) [1]. The distribution of European sour cherry comprises the territory from the Mediterranean islands to northern Russia, with a wide range of diversity as regards different plant habit and fruit characters [2–4].

Sweden is not a leader in sour cherry growing, but it is its traditional crop grown in home gardens and has a high potential for industrial processing. For these reasons, there is considerable experience in the collection, characterization and evaluation of its genetic resources, as well as in breeding. The Department of Crop Science of the Swedish University of Agriculture, Balsgård (SLU-Balsgård) holds a valuable collection of sour cherries, which is used in both research and breeding [4–6]. The collection contains germplasm from western and eastern sour cherry types designated by Kolesnikova [7] as well as hybrid material developed from these types. Focused breeding work on sour cherries has been conducted in Sweden, with introduction of wide genetic material from all over the northern hemisphere, hybridization and selection of new material [4, 5].

The importance of genetic diversity in breeding is obvious. Therefore, the estimation of the diversity and its nature and magnitude are beneficial or even crucial to a breeding programme. The availability and informative value of plant germplasm are becoming more and more important for the future preservation and sustainable use of genetic resources. Various sour cherry collections have been evaluated and characterized for various traits, including diversity [8–11].

Modern developments in biology allow a wide utilisation of molecular markers in PGR characterization and research [12]. Unfortunately, available molecular markers mostly cover only a small part of a target genome. In general, the developed markers are mostly random and not associated with a particular trait. Investigations of germplasm should

* Corresponding author. E-mail: gunars.lacis@lvai.lv

include also the morphologic and agronomic characterization of traits important for breeding. The main problem is detection of complex traits, such as winter-hardiness, which are difficult to detect by a single gene or random marker analysis. Therefore, a combined approach is most preferable for genetic resource description [13, 14].

Characterization of plant genetic resources (PGR) usually involves a wide range of data which include both qualitative and quantitative traits. Such data sets are generally large and multivariate, with a considerable number of descriptors measured for each of many accessions. Analysis of diverse data is complicated, especially when it is necessary to evaluate not only a single trait, but also such complex traits such as adaptivity, reproductivity or response to environmental or treatment conditions.

The most widely used multidimensional analysis methods in PGR characterization are principal component analysis (PCA) and cluster analysis. Advantages of PCA in horticultural studies have been widely discussed [see, for example, 15–18]. PCA is preferred because it allows evaluating multicollinear data; it does not require information about the dependence structure of variables and allows identifying those most suitable for classification [16]. Cluster analysis can be used to analyse quantitative and qualitative traits simultaneously, and each entry is treated as an individual entity of equal weight. The most appropriate approach for classification purposes has been suggested to be the group average clustering method [19]. The grouping capability of PCA and cluster analysis based on characterization data are useful for classifying accessions in a germplasm collection. This is the only way to classify accessions of unknown origin as in case of the Nordic landraces.

The goal of this work was to characterize and evaluate Swedish sour cherry genetic resources by the multivariate statistic analysis. To this end, assessment of genetic diversity based on morphological data, with the determination of variation patterns in the collection of sour cherry genetic resources was performed.

MATERIALS AND METHODS

Plant material

The morphologic and agronomic characterization was performed on a representative part (40 sour cherry accessions) of the SLU-Balsgård collection. For characterization, mature sour cherry plants that had borne fruit for at least three seasons were chosen. Plants were grown in field trials according to the conventional fruit-growing practice.

Characterization and evaluation

The SLU-Balsgård collection was evaluated according to 21 morphological, phenological, fruit quality, disease resistance and hardiness traits (Table 1) for three successive years. The characterization was made using the UPOV [20]

Table 1. **Summary statistics of the phenotypical traits measured in sour cherry collection at the Division of Horticultural Genetics and Plant Breeding at Balsgård, Department of Crop Sciences, Swedish University of Agricultural Sciences, during a period of three years**

Trait	Mean	Standard deviation	Total variance	Range	Minimum	Maximum
Tree vigour	5.3 ± 0.7	2.266	5.133	6.2	2.3	8.5
Density of the head	5.8 ± 0.4	1.158	1.341	3.2	3.8	7.0
Tree habit	2.8 ± 0.4	1.323	1.749	3.5	1.5	5.0
Tree type	1.0 ± 0.0	0.063	0.004	0.2	1.0	1.2
Season of flowering	8.5 ± 0.3	0.933	0.871	3.0	6.0	9.0
Harvest maturity	4.5 ± 0.5	1.541	2.373	6.0	2.0	8.0
Fruit shape	2.5 ± 0.1	0.371	0.137	1.4	1.8	3.2
Fruit size	3.4 ± 0.4	1.275	1.624	3.5	1.0	4.5
Fruit firmness	1.3 ± 0.3	0.885	0.784	2.8	1.0	3.8
Fruit juiciness	7.0 ± 0.0	0.126	0.016	0.4	6.6	7.0
Fruit separation from stalk	6.4 ± 0.3	0.849	0.721	2.8	4.2	7.0
Stone shape	4.7 ± 0.3	1.070	1.145	3.2	3.0	6.2
Stone relative size in comparison with fruit	6.7 ± 0.2	0.483	0.233	1.5	5.5	7.0
Fruit skin colour	5.0 ± 0.1	0.260	0.068	0.9	4.4	5.3
Juice colour	7.7 ± 0.3	0.989	0.978	3.3	5.0	8.3
Susceptibility to fruit cracking	1.6 ± 0.3	0.846	0.716	2.3	1.0	3.3
Length of stalk	5.1 ± 0.3	0.930	0.865	3.1	3.4	6.5
Susceptibility to *Pseudomonas syringae*	2.7 ± 0.2	0.629	0.396	2.0	1.6	3.6
Susceptibility to *Monilia laxa*	6.3 ± 0.4	1.275	1.625	3.8	4.0	7.8
Susceptibility to *Monilia fructigena*	1.7 ± 0.3	0.798	0.637	2.3	1.0	3.3
Susceptibility to *Blumeriella jaapii*	1.2 ± 0.1	0.195	0.038	0.6	1.0	1.6

and IPGRI [21] descriptor lists modified by additional local reference cultivars. The measurements, based on the IPGRI / UPOV rules, were expressed in points.

Statistical analysis

Statistical analysis was performed using average values from three-year measurements. Cluster analysis and principal component analysis (PCA) were used to evaluate relationships among accessions. Cluster analysis was performed by Ward's method using squared Euclidean distances. Data analysis was conducted using the Multivariate Statistics modules of Statgraphics for Windows Version 3.3 [22].

RESULTS

The sour cherry collection at the SLU-Balsgård was characterised by accessions with a medium tree vigour and mostly semi-upright tree habit (Table 1). The collection in general flowered late to very late. The trees had small to medium fruits (with an average size of 3.6 points, which corresponds to about 3.5 g). Swedish accessions in general had soft fruits with medium to good separation from a stalk. The SLU-Balsgård collection contained mostly light red and red fruits. Susceptibility to diseases in the collection was low (1.3 to 2.6 points), except susceptibility to *Monilia laxa* (6.0 points on average) (Table 1).

Cluster analysis identified four main clusters with different numbers of accessions (Fig. 1). Clusters 1 to 3 were further divided into two sub-clusters. Tree vigour, tree habit, harvest maturity, length of stalk and susceptibility to *Monilia laxa* showed the highest variability among clusters (Table 2). These traits had also the highest impact on the grouping of accessions. Low variability was found for tree type, fruit shape and juiciness, stone relative size in comparison with fruit, fruit skin colour and susceptibility to *Blumeriella jaapii*. Several traits had no distinguishable variability along the analysed accessions. Tree type was recorded as "normal" for all varieties, except the cultivar 'Meteor' characterized by "spur tree" type. The season of flowering was described as late for all accession groups. The only exception was observed in the sub-cluster 3b in which cv. 'Pamyat' Vavilova' had an early season of flowering. Fruit shape in most cases was described as flat-round (2 points) and round (3 points); only two varieties ('Pandy 8' and 'Nefris') had a kidney-shaped fruit (1 point). Most of the varieties had very soft fruits (1 point); exceptions were accessions of Cluster 4, which had soft (3 points) to firm (7 points) fruits. A low variation was observed also for fruit juiciness;

Table 2. **Characterization of sour cherry accession clusters in the sour cherry collection at the Division of Horticultural Genetics and Plant Breeding at Balsgård, Department of Crop Sciences, Swedish University of Agricultural Sciences**

Trait / Cluster	Average value per cluster*										Variance among clusters
	1	1a	1b	2	2a	2b	3	3a	3b	4	
Tree vigour	7.0	5.8	8.5	6.7	6.6	7.0	2.7	2.3	3.5	2.6	7.152
Density of the head	6.8	6.6	7.0	6.4	6.4	6.5	4.3	3.8	5.5	4.6	2.705
Tree habit	1.7	1.8	1.5	2.0	1.8	2.5	4.2	5.0	2.5	4.6	3.993
Tree type	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.2	0.021
Season of flowering	8.8	9.0	8.5	8.9	8.8	9.0	8.0	9.0	6.0	9.0	1.273
Harvest maturity	4.8	5.0	4.5	4.6	4.8	4.0	3.2	3.8	2.0	8.0	6.719
Fruit shape	2.4	2.6	2.3	2.8	3.2	1.8	2.4	2.4	2.5	2.8	0.858
Fruit size	1.7	2.2	1.0	4.4	4.4	4.5	3.8	3.8	4.0	4.2	2.035
Fruit firmness	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	3.8	1.154
Fruit juiciness	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0	6.6	0.492
Fruit separation from stalk	6.6	6.2	7.0	6.3	6.0	7.0	6.8	6.8	7.0	4.2	1.787
Stone shape	3.4	3.8	3.0	5.6	5.8	5.0	4.7	5.0	4.0	6.2	2.716
Stone relative size in comparison with fruit	7.0	7.0	7.0	6.9	6.8	7.0	6.3	6.8	5.5	7.0	0.562
Fruit skin colour	5.1	5.0	5.3	4.9	4.8	5.0	5.1	5.0	5.3	4.4	0.191
Juice colour	8.1	8.0	8.3	7.5	7.4	7.8	8.2	8.1	8.3	5.0	2.584
Susceptibility to fruit cracking	1.0	1.0	1.0	1.6	1.0	3.3	1.8	1.3	3.0	1.4	1.073
Length of stalk	4.8	3.4	6.5	5.3	5.0	6.0	5.0	4.5	6.0	4.2	3.042
Susceptibility to *Pseudomonas syringae*	1.9	1.6	2.3	2.8	2.7	3.0	3.2	3.6	2.3	3.2	1.644
Susceptibility to *Monilia laxa*	7.2	7.8	6.5	5.4	4.6	7.5	6.2	7.3	4.0	6.6	4.771
Susceptibility to *Monilia fructigena*	1.1	1.0	1.3	2.6	2.3	3.3	1.2	1.3	1.0	2.0	1.308
Susceptibility to *Blumeriella jaapii*	1.2	1.2	1.3	1.1	1.2	1.0	1.2	1.0	1.5	1.6	0.518

* Cluster numbers according to results of cluster analysis are represented in Fig. 1.

most varieties displayed strong juiciness (7 points), with the exception of cv. 'Ostheimer' characterized by medium juiciness (5 points). The majority of sour cherry accessions had a large stone relative to fruit size, but the varieties BPr 33487 and 'Nordia', located in the sub-cluster 3b, had a medium and a small stone as compared with fruit, respectively. The red fruit skin colour was most typical (82.5%); two accessions (5%) had black and five (12.5%) light red fruit skin colour. Most accessions had purple or brown red juice colour, but Cluster 4 contained accessions with red juice colour. A none to low susceptibility to *Pseudomonas syringae*, *Monilia fructigena* and *Blumeriella jaapii* was observed for all sour cherry accessions. All analysed sour cherry varieties showed a high susceptibility to *Monilia laxa*.

The accessions represented in Cluster 1 were characterized by a strong tree vigour, dense tree head, upright habit, and moderate harvest maturity, small, soft and juicy fruits with low susceptibility to fruit cracking, dark juice colour, and a high susceptibility to *Monilia laxa*. Sub-clusters 1a and 1b were characterized by tree vigour (medium in 1a, strong to very strong in 1b) and stalk length (short in 1a, medium to long in 1b).

Cluster 2 was characterised by a moderate tree vigour, dense tree head, upright habit, moderate fruit size with intermediate stone shape and moderate to high susceptibility to *Monilia laxa*. Sub-clusters 2a and 2b were distinguished by several traits: fruit shape (2a – flat-round to elongate, 2b – kidney-shape and flat-round), susceptibility to fruit cracking (2a – none, 2b – very low to low), length of stalk (2a – medium, 2b – medium to long), and susceptibility to *Monilia laxa* (2a – low to intermediate, 2b – high to extremely high).

Accessions in Cluster 3 had a weak tree vigour, medium density of head, a semi-upright to spreading tree habit, early harvest maturity, small to medium fruits with good separation from stalk, low susceptibility to fruit cracking, and an intermediate to high susceptibility to *Monilia laxa*. Two sub-clusters (3a and 3b) were distinguished by tree habit (3a – spreading, 3b – upright, semi-upright), season of flowering (3a – very late, 3b – medium to late), susceptibility to fruit cracking (3a – none to very low, 3b – low), and susceptibility to *Monilia laxa* (3a – high, 3b – low to intermediate).

Cluster 4 was most distantly separated, characterized by a weak tree vigour and open tree head. This cluster contained only one variety ('Meteor') which was of a spur-tree type. Accessions of Cluster 4 had a late season of flowering and harvest maturity, medium fruit size, medium soft fruits with bad separation from stalk, light red to red fruit skin colour and red juice colour, as well as medium susceptibility to *Pseudomonas syringae* and *Monilia laxa*.

The results of PCA analysis are presented in Table 3. Nine components with eigenvalues larger than 1.0 were extracted, which described 80% of the variability of the original traits. The PCA ordination showed that the sour cherry traits most useful for characterization (Table 3) were fruit skin colour, fruit separation from stalk, harvest maturity, fruit firmness, juice colour, tree vigour head density, tree habit, and susceptibility to *Pseudomonas syringae* and *Blumeriella jaapii*. The traits with the highest load on PC1

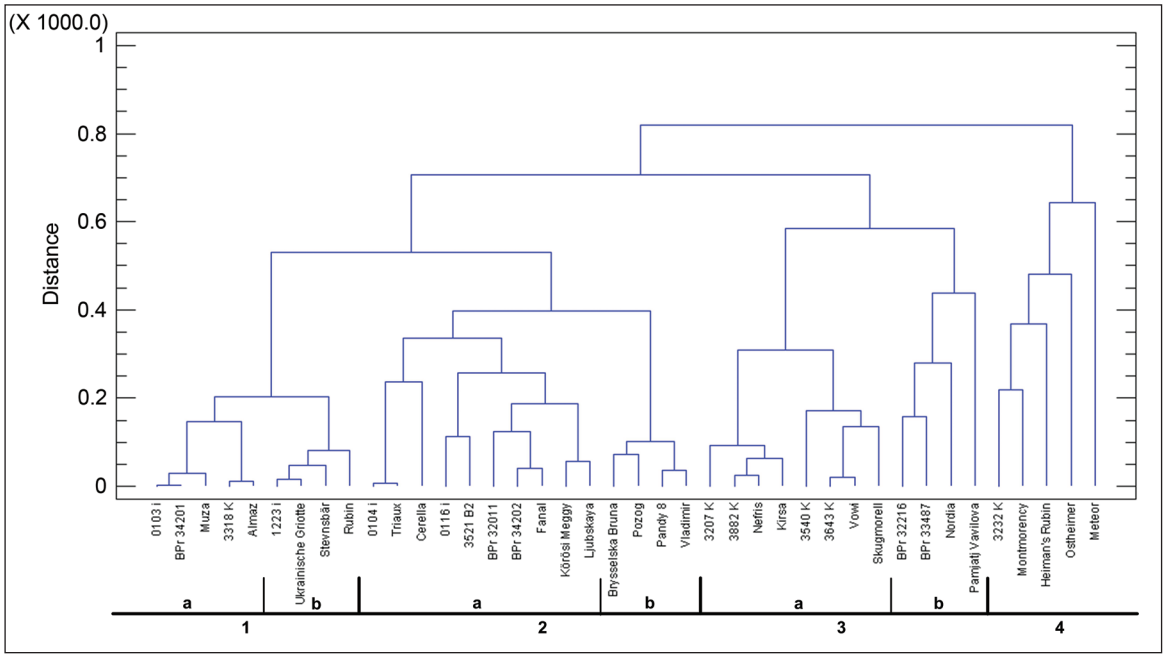

Fig. 1. Hierarchical analysis dendrogram obtained by Ward's method (squared Euclidean) using morphological traits of sour cherry accessions of the Division of Horticultural Genetics and Plant Breeding at Balsgård, Department of Crop Sciences, Swedish University of Agricultural Sciences

Table 3. **Component weights of the principal component analysis using morphological traits of accessions from the sweet cherry collection at the Division of Horticultural Genetics and Plant Breeding at Balsgård, Department of Crop Sciences, Swedish University of Agricultural Sciences**

		Principal components								
		1	2	3	4	5	6	7	8	9
Eigenvalues		4.02195	2.48434	2.03044	1.90391	1.48203	1.41508	1.31604	1.13695	1.0003
Percentage of variance		19.152	11.83	9.669	9.066	7.057	6.738	6.267	5.414	4.763
Factors / traits	Tree vigour	0.2263	0.4503	–0.1152	0.2560	0.1027	–0.1134	0.0028	–0.0168	–0.0098
	Density of the head	0.2220	0.4450	0.04919	–0.0296	0.1719	0.0457	–0.0355	–0.2666	–0.1162
	Tree habit	–0.2698	–0.3667	0.0868	–0.2373	0.1806	0.1158	0.0713	0.0791	–0.1132
	Tree type	–0.1517	0.1267	0.1759	–0.4742	0.3186	0.2303	0.0200	–0.0591	–0.1651
	Season of flowering	–0.1445	–0.0258	–0.3891	0.0134	0.2553	0.0239	0.2874	–0.4280	–0.0196
	Harvest maturity	–0.3103	0.2162	–0.1794	–0.0242	0.0776	–0.1150	0.2469	0.0529	–0.2106
	Fruit shape	–0.1304	0.0901	0.0814	0.3134	–0.1821	0.3337	0.3518	–0.0125	0.3146
	Fruit size	–0.1701	–0.0514	0.3686	0.2305	0.1714	–0.2723	–0.2978	0.0050	0.2183
	Fruit firmness	–0.3177	0.0195	–0.0101	–0.1708	–0.1763	–0.2015	–0.1076	–0.0248	0.1296
	Fruit juiciness	0.1736	–0.0666	0.0354	–0.0622	0.4372	–0.2197	0.1942	0.3470	0.3371
	Fruit separation from stalk	0.3206	–0.0444	0.1290	0.0149	0.1506	0.3969	–0.0707	0.0185	–0.3451
	Stone shape	–0.2846	0.1473	0.1263	0.1884	0.1129	0.2597	–0.3088	0.1464	0.1364
	Stone relative size in comparison with fruit	–0.1236	0.1955	–0.3535	–0.0084	0.1746	0.0474	–0.3077	0.4223	–0.1002
	Fruit skin colour	0.3338	–0.1760	–0.1049	–0.2424	0.1442	0.1242	–0.1956	0.1361	0.1551
	Juice colour	0.3045	–0.2476	–0.2202	0.1655	–0.0789	0.1184	–0.2712	–0.1774	0.1325
	Susceptibility to fruit cracking	0.0927	–0.1633	0.3785	0.1258	0.0491	–0.4079	–0.03741	–0.2120	–0.4187
	Length of stalk	0.0945	–0.0010	0.2093	0.3154	0.1350	0.0426	0.3813	0.4383	–0.2217
	Susceptibility to *Pseudomonas syringae*	–0.2097	–0.2842	–0.0194	0.3448	0.0273	0.3621	–0.0711	–0.0523	–0.2061
	Susceptibility to *Monilia laxa*	–0.0838	–0.0483	–0.3469	0.1347	–0.1522	–0.2046	–0.1946	0.2327	–0.4010
	Susceptibility to *Monilia fructigena*	–0.1893	0.0779	0.0201	0.2384	0.4665	0.0181	–0.2571	–0.2507	0.0534
	Susceptibility to *Blumeriella jaapii*	–0.0454	0.3402	0.3052	–0.1847	–0.3388	0.1795	–0.1593	0.0694	–0.0678

were fruit harvest maturity, fruit firmness, fruit separation from stalk, stone shape, fruit skin colour, juice colour, and on PC2 tree vigour, head density, tree habit, as well as traits of disease resistance (susceptibility to *Pseudomonas syringae* and *Blumeriella jaapii*). PC3 was related best with the season of flowering, fruit size, stone relative size in comparison with fruit (correlate with fruit size), susceptibility to fruit cracking and to *Monilia laxa*. PC1 and PC2 were chosen to describe the pattern of accession variability in the collection, because they represented the most important breeding criteria: fruit traits and tree traits, as well as disease resistance. Further, these traits were used for selection of accessions with an outstanding value in breeding.

The ordination of sour cherry accessions according to the first two principal components is presented in Fig. 2. In general, the distribution of accessions means agreement with results of the cluster analysis. PCA highlighted one distinct accession group 3232 K, 'Heiman's Rubin', 'Ostheimer', 'Meteor' and 'Montmorency'. All of them were separated in the Cluster 4 by cluster analysis. These varieties share in common a very late season of flowering and a large stone size in comparison with fruit. This group could be further separated into two subgroups based on the value of PC1 which is related to the density of a tree head: 3232 K and 'Heiman's Rubin' have an open tree head, whereas 'Meteor', 'Montmorency', 'Ostheimer' have a medium and dense tree head.

Varieties from Clusters 3a and 3b also formed well distinguishable groups as a result of ordination according to PC1 and PC2 (Fig. 2). The only exception was cv. 'Pamyat' Vavilova' which was located more close to the varieties of Cluster 1 and 2. Cultivar 'Pamyat' Vavilova' has a strong tree vigour, early season of flowering and an extremely early harvest maturity as well as a low susceptibility to *Blumeriella jaapii*.

On the contrary, varieties structured in Clusters 1 and 2 by the cluster analysis did not form distinguishable groups by PC1 and PC2 ordination. Varieties of Cluster 1 were located among sour cherry accessions of Cluster 2 which formed a widely dispersed group according to PCA (Fig. 2).

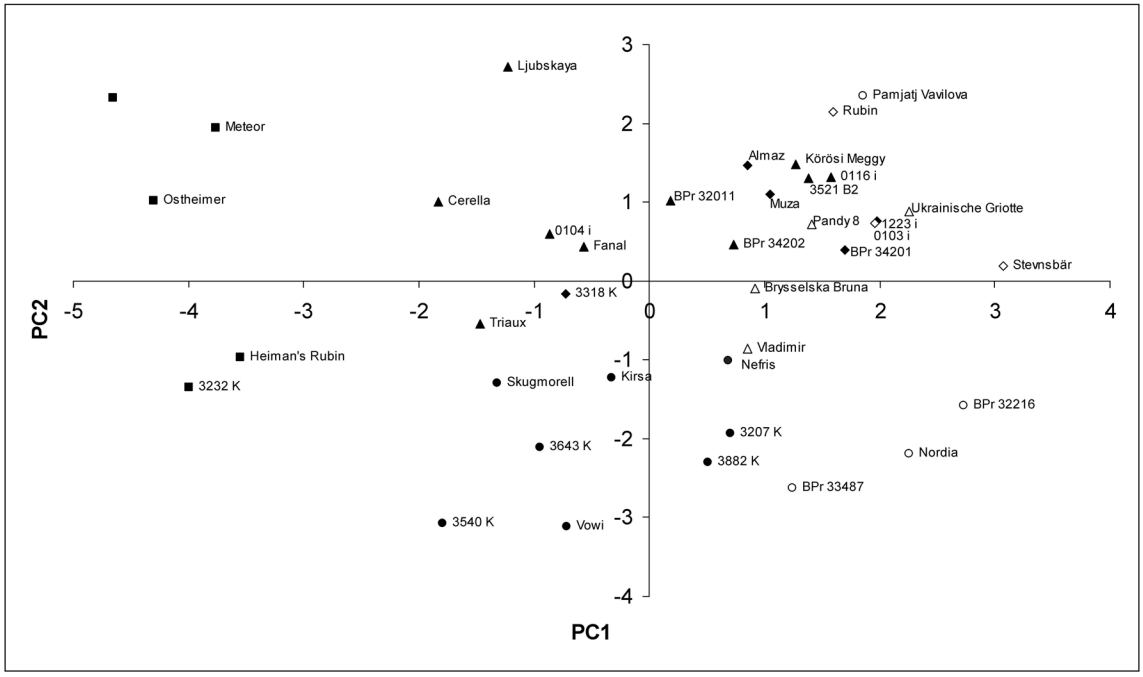

Fig. 2. Principal component analysis based on morphological traits of the collection of the Division of Horticultural Genetics and Plant Breeding at Balsgård, Department of Crop Sciences, Swedish University of Agricultural Sciences sour cherry accessions

Accession groups according to results of cluster analysis (Fig. 1): ◆ – cluster 1a, ◇ – cluster 1b, ▲ – cluster 2a, △ – cluster 2b, ● – cluster 3a, ○ – cluster 3b, ■ – cluster 4

Sour cherry accessions of Clusters 1 and 2 had similar characteristics of traits, important in the PC1–PC2 ordination: mid-season harvest maturity, very soft fruits with a good fruit separation from the stalk, red fruit skin colour and brown red juice colour, a strong tree vigour, the upright tree habit.

DISCUSSION

A detailed description of the Swedish collection of sour cherry genetic resources makes a valuable contribution to establishing a targeted management and evaluation programme. The evaluation can serve also as a base for the further utilization of available genetic resources in breeding, since a detailed plant material description makes it easier to identify interesting properties and to ensure that the whole spectrum of variation is preserved.

Characterization also provided data for multivariate statistical analyses (cluster analysis and PCA), which allowed to obtain a general view on plant material variability in the collection, based on the complete range of described traits. Cluster analysis of sour cherry accession groups showed that the most important traits for grouping were tree architecture and fruit traits (Table 2). Thus, these traits should be used in the further characterization of sour cherry genetic resources. The same traits were also found to be most important for sweet cherries [23].

The PCA revealed the main gradients of complex trait factors among the accessions. The main traits associated with the first two PCs were fruit quality, tree architecture and susceptibility to diseases (Table 3). Therefore, these traits are important in breeding, and more attention should be paid to them during the further evaluation of sour cherry collections. The high heritability and usefulness of fruit traits was also noted for sweet cherries [23, 24]. The PCA ordination of morphological traits did not show good applicability in finding complex factor gradients of accessions in the sour cherry collection, as the first four PCs explained only 50% of the total variation. This might be due to a common gene pool of accessions. A high degree of relatedness of accessions in this collection was confirmed by pedigree data (unpublished observations). The phenotypical similarity of breeding material is defined mostly by breeding work targeted towards valuable traits. However, PCA was useful in selecting accessions and their groups based on a complete trait set characterization, which would have been difficult by analysing separate traits.

Comparison of both used multivariate analyses identified common traits important for characterization of accession groups: fruit harvest maturity, tree vigour, head density, and tree habit. PCA identified susceptibility to *Blumeriella jaapii* as an additional trait which had a low variability within clusters. Since both analyses mainly identified the same traits, the methods supplement each other and could

be combined for a more accurate analysis of sour cherry accession diversity and relatedness.

Cluster analysis provided an objective grouping of accessions, which showed a high continuity of traits. Clustering of sour cherry accessions according to the evaluated phenotypic traits was quite clear, and four distant clusters were detected. The clustering results did not reveal a good separation of sour cherry accessions on the basis of West-European and Middle-Russian sour cherry types, as designated by Kolesnikova [7]. However, varieties from Russia and Eastern Europe, as well as hybrids developed using these varieties, were located mostly in Clusters 1 and 2, while the most typical Western-European cultivars (e. g., 'Heiman's Rubin', 'Montmorency', 'Ostheimer') were located in Cluster 4 (Fig. 1). Clustering according to a particular ecogeographical group of sour cherries did not occur possibly because several varieties and hybrids in the SLU-Balsgård collection had been acquired by crosses between representatives of the groups. Also, the correspondence between accession clustering results and known pedigrees was assessed, and some interrelations between clustering and pedigree data were found (Fig. 1). Some varieties are located in the same cluster as their parent, but several varieties of the same parent were found in other clusters. The SLU-Balsgård sour cherry collection contained groups of accessions bred using cultivars 'Brysselska Bruna', 'Heiman's Rubin', 'Körösi Meggy' and 'Skugmorell' as parents. Varieties developed using 'Brusselska Bruna' as a parent were located in Clusters 1, 2 and 3, but the parent variety belonged to Cluster 2. Varieties bred using 'Heiman's Rubin' as a parent were located in Clusters 3 and 4, but the parent variety belonged to Cluster 4. Similarly, accessions developed using 'Körösi Meggy' as a parent were located in Clusters 2 and 3, but the parent variety belonged to Cluster 2. Finally, varieties bred using 'Skugmorell' as a parent were located in Clusters 1, 2 and 3, but the parent variety was located in Cluster 3. Some regularity was found for cases where both parents were known and analyzed together with offspring. In some cases, offspring was located in the same cluster as one of parent cultivars: 3232 K ('Heiman's Rubin' × 'Korosi Meggy'), 3643 K ('Skugmorell' × 'Heiman's Rubin'). In both cases, the female parent variety was located in the same cluster as the offspring, showing a closer genetic relatedness. In the case of cv. 'Kirsa' ('Brysselska Bruna' × 'Heiman's Rubin'), the parent varieties were located in different clusters than the offspring. Cluster analysis adequacy to pedigree data was confirmed also by cv. 'Meteor' which was located in the same cluster as its parent cv. 'Montmorency' (Fig. 1). In contrast, cv. 'Nefris' showed a relatively high dissimilarity to its parent clone 'Fanal'. As suggested by Peeters and Martinelli [19], cluster analysis is useful for grouping accessions to increase the understanding of the internal structure of germplasm collections. Since the cluster analysis of sour cherry germplasm at the SLU-Balsgård showed a correspondence between clustering results and pedigree data, it can likely also be used to estimate the relatedness of accessions to plant material of unknown origin. This is particularly important for Nordic sour cherry landraces, as there is little information on their origin.

In general, grouping of varieties according to first two principal components (Fig. 2) are in good agreement with the results of cluster analysis. Accessions of Clusters 3 and 4 are very well separated from other varieties; the only exception is the variety 'Pamyat' Vavilova'. In both cases, the varieties 3232 K, 'Meteor', 'Montmorency' and 'Ostheimer' showed a high dissimilarity with the other accessions (a separate group in the left side of PCA in Fig. 2 and Cluster 4 in Fig. 1), indicating the phenotypical distinctiveness of these varieties in the SLU-Balsgård sour cherry collection. Cluster 3 was also distinguished as a group in the PCA ordination, except cv. 'Pamyat' Vavilova', which in the PCA ordination showed a closer similarity to Clusters 1 and 2 (Figs. 1 and 2). Cluster analysis showed a clear separation of accessions in Cluster 1 and 2 (Fig. 1). There were also some overlaps between accessions from Clusters 1a and 1b. PCA (Fig. 2) did not differentiate between these clusters of accessions and formed one disperse group with a random distribution. This suggests that Clusters 1 and 2 might be merged into one group. Some discrepancy between sour cherry accession grouping in cluster analysis and PCA could be explained by the fact that PCA takes into account PC1 and PC2 ordination which represents only 31% of variability, whereas the cluster analysis uses the whole variability.

Combined application of cluster analysis and PCA to sour cherry accession characterization data revealed the most useful traits for the further description of sour cherry germplasm. The analysis also provided comprehensive information about the genetic structure and internal relatedness of accessions, which would not be possible by analysis of separate traits. Application of multivariate statistics increased the value of phenotypical data and created the basis for a common analysis with genetic data.

ACKNOWLEDGEMENTS

This research was possible with support from the Royal Swedish Academy of Agriculture and Forestry, the Swedish Institute (SI), the Swedish Council for Forestry and Agricultural Research (SJFR) and the Knut and Alice Wallenberg Foundation.

Received 21 June 2010
Accepted 8 July 2010

References

1. Iezzoni AF. Temperate Fruit Crop Breeding. In: Hancock JF (ed.). Temperate Fruit Breeding: Germplasm to Genomics. Springer Science, 2008: 151–75.
2. Krahl KH, Lansari A, Iezzoni AF. Euphytica 1991; 52: 47–55.
3. Beaver JA, Iezzoni AF, Ramm CW. Theor Appl Genet 1995; 90: 847–52.
4. Trajkovski V. Acta Hortic 1996; 410: 387–8.
5. Trajkovski V, Andersson G. Verksamhetsberattelse 1994–96. Report SLU – Balsgård 1996: 26–9.
6. Lacis G, Rashal I, Trajkovski V. Proc Latvian Acad Sci; Sect B 2010 (in press).
7. Kolesnikova AF. Breeding and some biological characteristics of sour cherry in the Central Russia zone of the RSFSR. Oriol, Russia, 1975 (in Russian).
8. Christensen JV. Tidsskr Planteavl 1986; 90: 339–47.
9. Christensen JV. Tidsskr Planteavl 1990; 94: 51–63.
10. Budan S, Stoian I. Acta Horticult 1996; 410: 81–6.
11. Rodrigues LC, Morales MR, Fernandes AJB, Ortiz M. Genet Resour Crop Evol 2008; 55: 593–601.
12. IPGRI. Molecular tools in plant genetic resources conservation: a guide to the technologies. Rome, Italy: International Plant Genetic Resources Institute, 1997.
13. Dias PMB, Julier B, Sampoux JP, Barre P, Dall'Agnol M. Euphytica 2008; 160: 189–205.
14. Smýkal P, Hýbl M, Corander J, Jarkovský J, Flavell AJ, Griga M. Theor Appl Genet 2008; 117: 413–24.
15. Broschat TK. HortScience 1979; 14: 114–7.
16. Iezzoni AF, Pritts MP. HortScience 1991; 26: 334–8.
17. Lacis G, Rashal I. Proc Int Conf "Fruit Production and Fruit Breeding", Polli, Estonia, 2000: 147–51.
18. Lacis G, Rashal I. Hortic Veget Grow 2001; 20: 211–21.
19. Peeters JP, Martinelli JA. Theor Appl Genet 1989; 78: 42–8.
20. UPOV. Guidelines for the Conduct of Tests for Distinctness, Uniformity and Stability, TG/35/6, Cherry (*Prunus avium* (L.) L., *Prunus cerasus* L.). UPOV, Geneva, Switzerland, 1995.
21. IPGRI. Cherry Descriptor List. Schmidt H, Vittrup-Christensen J, Watkins R, Smith RA (eds). Rome: IBPGR Secretariat, 1985.
22. Users Guide. Statgraphics Plus for Windows Version 3.3. Manugistics Inc., 1994.
23. Lacis G, Kaufmane E, Rashal I, Trajkovski V. Acta Universitatis Latviensis 2009; 753: 19–32.
24. Hjalmarsson I, Ortiz R. Scient Horticult 2000; 85: 37–49.