

Morphological variability and genetic diversity within Latvian and Swedish sweet cherry collections

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Abstract

Forty nine sweet cherry accessions at the Latvia State Institute of Fruit-Growing (Dobele) and ninety one at the Division of Horticultural Genetics and Plant Breeding at Balsgård, Department of Crop Sciences, Swedish University of Agricultural Sciences (SLU-Balsgård) were used for the analysis of morphological variability and genetic diversity by means of multivariate statistic analyses. Both applied statistical approaches (cluster and principal component analysis) showed adequate grouping of accessions according to morphological characterization. Multivariate analysis showed the most important traits for sweet cherry accession grouping were tree architecture and fruit traits, which should therefore be considered in further sweet cherry genetic resource characterization. Multiple parameter analysis of sweet cherry traits increased the value of phenotypical data and created the basis for common analysis of phenotypical and genetical data.

Key words: genetic diversity, germplasm, multivariate statistics, *Prunus avium*.

Introduction

Sweet cherry (*Prunus avium* L.) is one of the most important fruit crops both in Latvia and Sweden (Trajkovski, Andersson 1996; Ruisa 1998). Many varieties of sweet cherry are found in small gardens, and these have growing commercial importance. Therefore sweet cherry is important in breeding programs and plant genetic resource (PGR) activities in both countries. Since 1996, coordinated breeding and PGR activities were established for evaluation and characterization of *Prunus* genetic resources, e.g. for sweet cherry.

The Latvia State Institute of Fruit-Growing (LIFG) and the Division of Horticultural Genetics and Plant Breeding at Balsgård, Department of Crop Sciences, Swedish University of Agricultural Sciences (SLU-Balsgård) hold wide and valuable genetic resource collections of fruit crops, including sweet cherry (Trajkovski 1996; Rashal, Lacis 1999). The origin of the collections and their variability differ because they were formed by different strategies. The largest part of the collection in the LIFG are local sweet cherry accessions acquired by Pēteris Upītis, famous Latvian horticulturist (Blukmanis et al. 1997). This material includes both samples from expeditions (mostly wild growing trees and landraces), as well as hybrids from breeding programs. Unfortunately, detailed information on breeding and

collection sources is not available. It is only known that mainly local plant material was used for both selection of advanced varieties and for hybridization (Ruisa 1998). Varieties and advanced hybrids created by other Latvian breeders using old cultivars from the Western Europe as well as sweet cherry varieties developed in the former USSR (Belarus, Russia, and Ukraine) are also included in the LIFG collection.

The cherry germplasm collection at SLU-Balsgård is the result of a long term breeding programme. The Swedish germplasm has been built through collaboration with plant breeders from the entire northern temperate zone, and includes (i) local (Scandinavian) material, (ii) introduced advanced cultivars from Western Europe and North America and (iii) wide diversity of selections developed at SLU-Balsgård during the breeding process (Trajkovski 1996).

The importance of genetic diversity in breeding is obvious. Therefore the recognition and measurement of such 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. Evaluation and characterization as well as estimation of diversity have been performed for various sweet cherry collections (Christensen 1970; Christensen 1977; Hjalmarsson, Ortiz 2000; Rodrigues et al. 2008).

Modern developments in biology allow wide utilisation of molecular markers in PGR research (IPGRI 1997). Unfortunately, the available molecular markers mostly cover only a small part of a target genome. In general, the developed markers mostly are random, not associated with a particular trait. Investigations of germplasm should include also morphological and agronomical characterization of traits having breeding value. The main problem is detection of complex traits, like winterhardiness, which are difficult to detect by a single gene or random marker analysis. Therefore a combined approach is the most preferable for description of genetic resources (Dias et al. 2008; Smýkal et al. 2008).

Characterization of plant genetic resources (PGR) usually contains a wide range of data, on both qualitative and quantitative traits. Such data are generally large and multivariate with a considerable number of descriptors measured on each of many accessions. Analysis of diverse data is complicated, especially if it is necessary to evaluate not only single trait, but 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. The advantages of PCA in horticultural studies have been widely discussed (e.g., Broschat 1979; Iezzoni, Pritts 1991; Lacis, Rashal 2000; Lacis, Rashal 2001). PCA allows to evaluate multicollinear data and to determine the traits most suitable for classification (Iezzoni, Pritts 1991). Cluster analysis allows to analyze simultaneously both quantitative and qualitative traits, and each entry is treated as an individual entity of equal weight. The most appropriate approach for classification purposes is the group average clustering method (Peeters, Martinelli 1989). PCA and cluster analysis based on descriptive data on genetic resources can be useful in classifying accessions in a germplasm collection. This is the only possibility to classify accessions with unknown origin, as in case of the Latvian material.

The goal of this work was to characterize and evaluate Latvian and Swedish sweet cherry genetic resources using multivariate statistic analysis. Assessment of genetic diversity based on morphological data and determination of the variation patterns in

both sweet cherries genetic resources collections were performed. The best accessions for breeding and PGR maintenance were selected.

Materials and methods

Plant material

Morphological and agronomical characterization were performed on a representative sample of both collections: 49 (LIFG) and 91 (SLU-Balsgård) sweet cherry accessions.

Characterization and evaluation

Evaluation of sweet cherry accessions in LIFG and SLU-Balsgård was carried out according to the methods accepted in each institution based on morphology and phenology, fruit quality, disease resistance and hardiness data.

Survey at LIFG was made in July - August for three successive years using 26 leaf and fruit traits, phenological characteristics, measures of susceptibility to diseases and hardiness (Table 1). Each year 25 random samples were evaluated (five samples per tree with five trees per accession). Leaf and fruit samples were collected according to Yushev (1975; 1977). Initially data were recorded as results of direct measurements. The acquired data were processed by descriptive statistics to determine data structure and variability for each year separately. A scoring system was developed for measurement. Scores (10-point scale) were estimated for each year separately and average values were determined for each accession.

The collection at the SLU-Balsgård was evaluated using 19 traits (Table 2) for three successive years. The characterization descriptor lists were based on UPOV (UPOV 1995) and IPGRI (IPGRI 1985) lists, supplemented by local reference cultivars. The measurements were expressed as points, based on IPGRI/UPOV rules.

Statistical analysis

Evaluation and characterization of the data from the collections at LIFG and SLU-Balsgård were analysed separately due to different growing conditions and rootstocks. Statistical analysis was performed using average values from three-year measurements.

Principal Component Analysis (PCA) and cluster analysis was used to evaluate relationships among accessions. Cluster analysis was performed using the Group Average Method and the Squared Euclidean distance measurement. Data analysis was performed using the Multivariate Statistics modules of Statgraphics for Windows Version 3.3 (Users Guide 1994).

Results

Analysis of Latvian plant material

The collection at the LIFG was characterized mostly by accessions with early to medium flowering season. The Latvian accessions had low fruit quality (average size – 4.29 g, which fits to the small fruit size group), and a high proportion of fruits were yellow with colourless juice. However, they had high resistance to diseases (7.44 points of 10 on average) and also high winterhardiness (7.91 points of 10 on average).

PCA was conducted on all of 26 traits (Table 1). In total, 74.17 % of the observed

Table 1. Component weights in Principal Component Analysis using morphological traits of accessions from the Latvia State Institute of Fruit-Growing sweet cherry collection

	Principal Components							
	1	2	3	4	5	6	7	8
Eigenvalues	5.1397	2.9088	2.5862	2.3735	2.1595	1.6033	1.3260	1.1873
Percent of variance	19.768	11.188	9.947	9.129	8.306	6.166	5.100	4.566
Fruit thickness	0.3271	-0.0059	-0.2695	0.0586	-0.1304	-0.0777	-0.1383	-0.1099
Fruit length	0.3751	0.0764	0.0819	0.0022	-0.0049	0.1011	-0.0096	0.0813
Fruit width	0.3796	0.1182	-0.0262	-0.0755	-0.1738	0.0046	0.0812	0.1142
Fruit weight	0.3932	0.0383	-0.1339	0.0750	-0.1271	-0.0212	0.0394	0.0114
Fruit skin colour	0.1166	0.2012	-0.1813	0.1850	0.0352	-0.3426	-0.2279	0.2054
Soluble solids	-0.1099	-0.0324	-0.3416	-0.1579	0.1038	-0.1960	0.2482	0.2797
Stone thickness	0.1481	-0.2939	-0.2489	0.2494	0.0603	-0.1164	-0.0366	-0.2753
Stone length	0.2642	-0.1424	0.2982	0.0357	0.1156	0.2593	0.1455	-0.0841
Stone weight	0.2464	-0.0767	-0.2491	0.1977	0.0656	0.1775	0.0882	-0.0477
Stone width	0.2989	-0.0619	-0.0268	-0.0283	-0.1759	0.0145	0.2970	0.1281
Length of fruit stalk	0.0636	0.0626	0.1169	0.2572	0.4061	-0.2725	0.0007	-0.0438
Yield	-0.0335	-0.0009	-0.1666	-0.2289	0.0397	0.2724	-0.2149	0.5036
Harvest maturity	-0.1829	0.0398	-0.1367	0.2537	0.0879	0.3012	-0.1485	0.0252
Leaf blade area	0.1753	0.2423	0.1849	-0.2457	0.2254	-0.1633	-0.0803	-0.0260
Leaf length	0.2305	-0.0662	0.0689	-0.3746	0.0937	-0.1166	-0.1180	-0.2536
Leaf blade width	0.0658	-0.0339	-0.1342	-0.3228	0.4158	-0.2034	-0.1135	-0.1281
Leaf vein angle (apex)	0.0249	0.4105	0.0132	0.2048	0.0191	-0.1068	0.1611	0.2009
Leaf vein angle (middle)	-0.0059	-0.2622	0.0904	0.4060	-0.0792	-0.2765	-0.0807	0.2361
Leaf vein angle (base)	0.0265	-0.4787	-0.0301	0.0179	-0.0678	0.0267	-0.3460	-0.0369
Leaf serration per cm	-0.0462	-0.1849	-0.0265	-0.1311	-0.2935	-0.3209	0.3500	0.1174
Petiole length	0.0830	-0.3697	0.2838	0.0433	0.1804	-0.1240	-0.0166	0.2623
Petiole thickness	0.0262	-0.1039	-0.1489	0.0456	0.4753	-0.0546	0.1480	0.2167
Gland number on the petiole	-0.0399	-0.2839	-0.2495	-0.3023	-0.0246	0.0331	0.1120	0.1375
Gland number on the basal leaf edge	0.0425	-0.1106	0.4967	-0.0522	-0.0709	-0.0881	0.0086	0.2274
Susceptibility to diseases	0.2071	-0.0107	0.0128	0.0356	0.1979	0.3629	-0.1236	0.2930
Winterhardiness	-0.0442	-0.1004	-0.0010	0.1066	0.2551	0.2091	0.5607	-0.1587

Factors / traits

variability was explained by the first eight components (eigenvalues for each was larger than 1). The highest loadings on PC1 were shown by fruit traits (weight, length, width, thickness) and on PC2 by leaf traits (length, vein angle on leaf base and stone thickness). PC3 was associated with stone traits: length, weight, content of soluble solids. Other agronomically important traits were found on PC6 (disease resistance, harvest maturity), PC7 (winterhardiness) and PC8 (yield). Therefore grouping along principal components were performed to identify the best grouping variables and to select distinct accessions.

Thus, PCA identified the following accessions with distinct traits: Kompaktnaya and PU-14646 – small stone, the largest number of glands on leaf basal edge, according to the scores on the third and fourth Principal Components (PC3-PC4); PU-14684 – large leaves (PC3-PC4); Dogan's Gelbe Knorpelkirsche and PU-14419 – large yield (PC6-PC8); Leningradskaya Czornaya – very small leaves, low yield (PC3-PC8); PU-300 – early harvest maturity (PC2-PC6); Agris, PU-18619 and PU-20923 – very short fruit stalk (PC5-PC6); PU-14419 and AM 24-10-22 – very good winterhardiness (PC7-PC8). Cultivar Aija showed a distinct position in all combinations of PC2, represented by leaf shape measurements.

Cluster analysis formed four main clusters of accessions (Fig. 1). Finer grouping inside some of the main clusters was also found; therefore some were divided into sub-clusters to better describe the variability.

The variability of traits among clusters was relatively low; therefore most of the traits had little informativity in the cluster discrimination (Table 3). The highest variability found was for leaf blade area, fruit length, fruit width, fruit weight, fruit stalk length, winterhardiness, resistance to diseases, harvest maturity season and fruit yield.

Since there is no pedigree information for the most of accessions in the Latvian sweet cherry collection, it is not possible to make any cluster interpretation based on the origin.

Cluster 1 was characterized, in general, by accessions with large fruits, high resistance to diseases, and large leaves. This cluster could be divided into two sub-clusters. Accessions in the sub-cluster 1a had large leaves and fruits. The sub-cluster 1b was characterized by the largest fruits in the whole collection and a specific yellow vermilion fruit skin color not observed in other groups.

Cluster 2 was the largest group, represented by a diversity of accessions with average fruit size, late flowering and maturing season, and good fruit yield. Sub-cluster 2a was distinct due to a high content of soluble solids; sub-cluster 2b – wide leaf blade, high fruit yield; sub-cluster 2c – small leaves, late flowering and harvest maturity season; high number of glands on petiole; 2d – short petiole, small fruit size, late maturing; 2e – the highest content of soluble solids among all clusters, the highest yield, small stone size. The sub-cluster 2f contained only one accession – cultivar Agris, which differed by having the smallest leaf blade size among all groups, late flowering and high yield.

Cluster 3 was characterised by a short, wide leaf blade with low serration per cm, long, thin petiole. Accessions of this cluster had the smallest fruit size of all accessions and low content of soluble solids.

Cluster 4 consisted only from one cultivar (Leningradskaya Czornaya), which was distinct because of very small leaf blade size.

Analysis of Swedish plant material

The collection at SLU was characterised by accessions with medium to strong tree vigour,

Table 2. Component weights in Principal Component Analysis using morphological traits of accessions from the Division of Horticultural Genetics and Plant Breeding at Balsgård, Department of Crop Sciences, Swedish University of Agricultural Sciences sweet cherry collection. * - average measurement of susceptibility to *Pseudomonas syringae*, *Monilia laxa* and *Monilia fructigena*

	Principal Components						
	1	2	3	4	5	6	7
Eigenvalues	2.8590	2.4014	1.9909	1.6272	1.4890	1.1848	1.0728
Percent of variance	15.047	12.639	10.478	8.564	7.837	6.236	5.646
Tree vigour	-0.1743	0.4572	-0.0018	0.2744	0.0218	0.1500	0.1097
Tree habit	0.1589	-0.4976	-0.0228	-0.1206	0.0018	-0.2979	0.1040
Tree type	0.0253	0.1885	0.0628	-0.1557	-0.6214	-0.2104	-0.0955
Density of the head	-0.0960	0.4802	0.1841	0.1559	-0.0925	-0.1740	0.1448
Season of flowering	-0.0907	-0.0544	-0.4628	-0.2325	-0.1296	-0.1113	-0.0714
Fruit shape	0.2902	0.1119	0.2457	-0.0649	0.4027	-0.2975	-0.0228
Fruit size	-0.3094	-0.0567	-0.2606	0.2284	0.1486	-0.3403	0.2606
Fruit firmness	-0.4176	0.0932	0.1921	-0.2944	-0.1544	-0.1465	-0.0789
Fruit juiciness	0.4266	0.0175	-0.1646	0.3763	-0.0015	0.0859	0.0115
Fruit separation from stalk	0.2498	0.1457	-0.1796	0.2573	-0.1136	-0.1123	-0.3773
Fruit skin colour	0.3197	0.1933	-0.2398	-0.4172	-0.0007	-0.0257	0.0327
Juice colour	0.2708	0.2769	-0.3278	-0.2518	-0.1636	0.0146	0.1864
Susceptibility to fruit cracking	-0.2312	0.1027	-0.1573	-0.3258	0.3046	0.0540	0.1437
Length of fruit stalk	0.2268	0.0495	0.1930	0.0031	-0.0598	-0.3025	0.6862
Stone shape	0.0758	0.2474	0.1221	-0.1492	0.3636	-0.4354	-0.4261
Stone relative size in comparison with fruit	0.1955	0.0425	0.3911	-0.2995	0.0608	0.4775	0.0585
Susceptibility to diseases *	-0.0568	0.1958	-0.3580	-0.0342	0.3286	0.2075	0.1119

Factors / traits

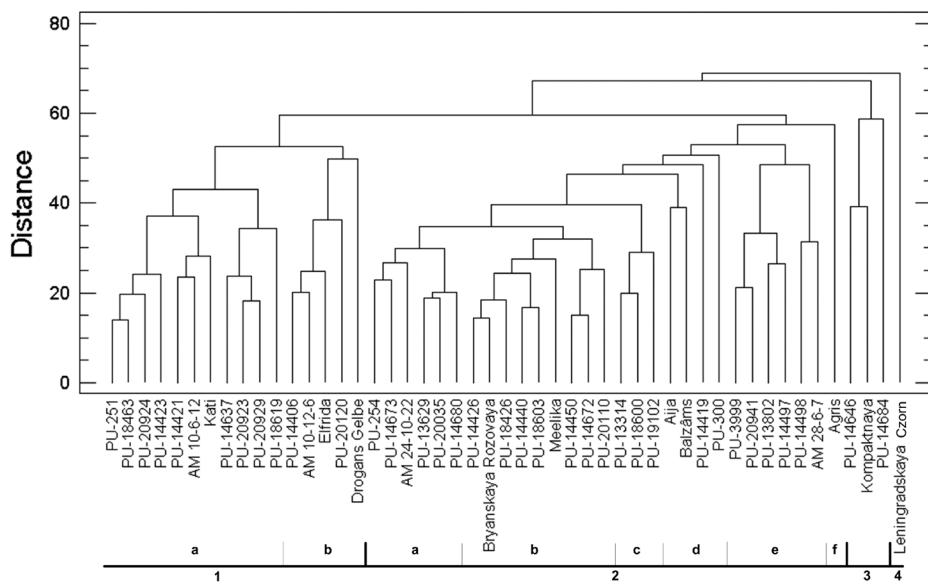


Fig. 1. Hierarchical analysis dendrogram obtained by Group Average Method (Squared Euclidean) using morphological traits of sweet cherry accessions of the Latvia State Institute of Fruit-Growing.

mostly semi-upright tree habit. The collection in general was characterized by medium to late season of flowering. Sweet cherry accessions in the Swedish collection had large fruits (with an average size of 6.36 points, which corresponds to about 7 g).

Swedish accessions in general had medium fruit firmness with good separation from a stalk. The collection at SLU contained mostly red and dark red colored fruits. Swedish sweet cherry genetic resources contained mostly accessions with intermediate susceptibility to diseases (4.30 points). Susceptibility to *Pseudomonas syringae* was an exception (5.57 points in average).

PCA analyses were performed on 19 measured traits (Table 2). Seven components with eigenvalues larger than 1.0 were extracted. They described 66.5 % of the variability of the original traits. The highest loadings on PC1 were by factors fruit size, shape, firmness and juiciness, on PC2 – tree traits. PC3 was associated with mostly season of flowering, fruit juice colour, and disease resistance. PC1 and PC3 were chosen to display accession variability pattern in the collection, as they represented the most important breeding criteria: fruit quality and disease resistance. These traits are used for selection of accessions with outstanding value in breeding.

PCA discriminated several distinct accessions based on particular traits. The following accessions were identified as distinct: Kaiser Franz and BPr 37239 – high fruit firmness, low tree vigour, low density of head, according to scores on the first and second Principal Components (PC1-PC2); Heinrich Riesen – high fruit firmness (PC1); BPr 36781 and 4570D – upright tree habit, low tree vigour (PC1); Regina – spur type of tree (PC5) in combination with all other PCs, large fruit size (PC1-PC6 and PC2-PC6), dark fruit skin colour, low susceptibility to fruit cracking (PC2-PC4); 13-116-76 – soft, juice fruits (PC1);

Table 3. Characterization of sweet cherry accession clusters in the Latvia State Institute of Fruit-Growing sweet cherry collection. * - cluster and sub-cluster numbers according results of cluster analysis presented in the Fig. 1

Trait / cluster	Average value per cluster and sub-cluster*										Total average	Variance		
	1a	1b	1	2a	2b	2c	2d	2e	2f	2			3	4
Fruit length	3.8	4.4	4.0	2.6	2.6	2.5	2.1	2.9	2.8	2.5	3.8	2.2	3.1	0.803
Fruit skin colour	1.0	3.4	1.8	1.0	1.7	1.6	1.0	2.0	1.0	1.4	1.0	1.0	1.5	0.131
Fruit thickness	4.8	5.6	5.1	3.8	4.1	4.1	3.1	4.4	3.3	3.9	2.4	3.2	4.1	1.291
Fruit weight	4.9	5.8	5.2	3.2	3.1	3.4	2.3	3.9	3.2	3.1	2.1	2.6	3.7	1.880
Fruit width	6.3	6.7	6.4	5.2	4.7	4.8	4.7	5.5	5.7	4.9	4.9	3.6	5.4	1.333
Gland number on the basal leaf edge	1.3	1.2	1.2	1.2	1.2	1.2	1.2	1.1	1.1	1.2	1.5	1.2	1.2	0.024
Gland number on the petiole	1.3	1.2	1.3	1.5	1.3	1.5	1.3	1.3	1.5	1.4	1.2	1.2	1.3	0.008
Harvest maturity	4.1	5.8	4.6	6.3	5.9	6.4	6.6	6.0	9.0	6.3	5.7	7.0	5.7	1.026
Leaf blade area	3.5	4.1	3.7	2.9	3.5	2.6	3.8	3.7	1.7	3.2	4.0	2.7	3.4	0.344
Leaf blade width	4.6	4.8	4.7	4.8	5.1	4.5	4.6	4.9	3.9	4.7	4.9	4.8	4.7	0.007
Leaf length	6.5	6.2	6.4	5.8	6.2	5.8	6.0	6.3	5.5	6.0	6.1	5.6	6.1	0.109
Leaf serration per cm	2.0	1.8	1.9	2.0	1.9	2.0	1.9	2.0	1.9	2.0	1.9	2.0	1.9	0.003
Leaf vein angle (apex)	4.8	5.9	5.2	4.3	4.6	4.8	5.7	4.9	4.9	4.8	4.8	5.5	4.9	0.114
Leaf vein angle (base)	5.4	4.9	5.2	5.4	5.7	6.0	4.8	4.6	6.1	5.5	5.5	5.2	5.4	0.029
Leaf vein angle (middle)	5.6	5.3	5.5	5.2	6.2	6.6	4.3	4.3	7.2	5.7	5.8	7.6	5.7	0.936
Length of fruit stalk	4.1	5.4	4.5	4.1	4.7	4.0	3.5	4.4	3.0	4.1	5.4	6.2	4.4	0.846
Petiole length	4.9	4.1	4.7	4.2	5.3	4.9	3.3	2.9	3.8	4.4	5.6	5.0	4.6	0.256
Petiole thickness	4.0	4.0	4.0	4.1	4.4	3.7	3.7	3.7	4.0	4.0	3.9	4.0	4.0	0.002
Soluble solids	5.0	5.4	5.2	6.5	5.8	6.2	6.2	6.5	3.6	6.1	4.0	5.9	5.6	0.900
Stone length	5.8	4.4	5.3	3.4	4.0	3.9	2.8	2.8	4.4	3.6	5.6	4.4	4.3	0.833
Stone thickness	5.1	4.0	4.7	4.2	5.4	5.0	2.8	3.7	3.1	4.4	1.9	6.4	4.4	3.511
Stone weight	4.6	4.2	4.5	3.9	4.0	3.9	2.3	3.7	3.4	3.6	2.9	3.1	3.9	0.488
Stone width	5.8	4.8	5.5	4.4	3.9	3.8	3.6	3.5	5.8	3.9	3.3	2.5	4.4	1.643
Susceptibility to diseases	7.8	9.0	8.2	5.8	7.7	7.5	6.5	6.2	10	7.0	8.0	5.0	7.4	2.084
Winterhardness	8.0	7.7	7.9	8.6	7.8	8.0	8.0	4.2	5.5	7.7	7.6	9.0	7.9	0.409
Yield	6.5	6.8	6.6	7.2	7.6	7.1	7.4	8.0	8.0	7.4	7.0	2.5	7.0	5.174

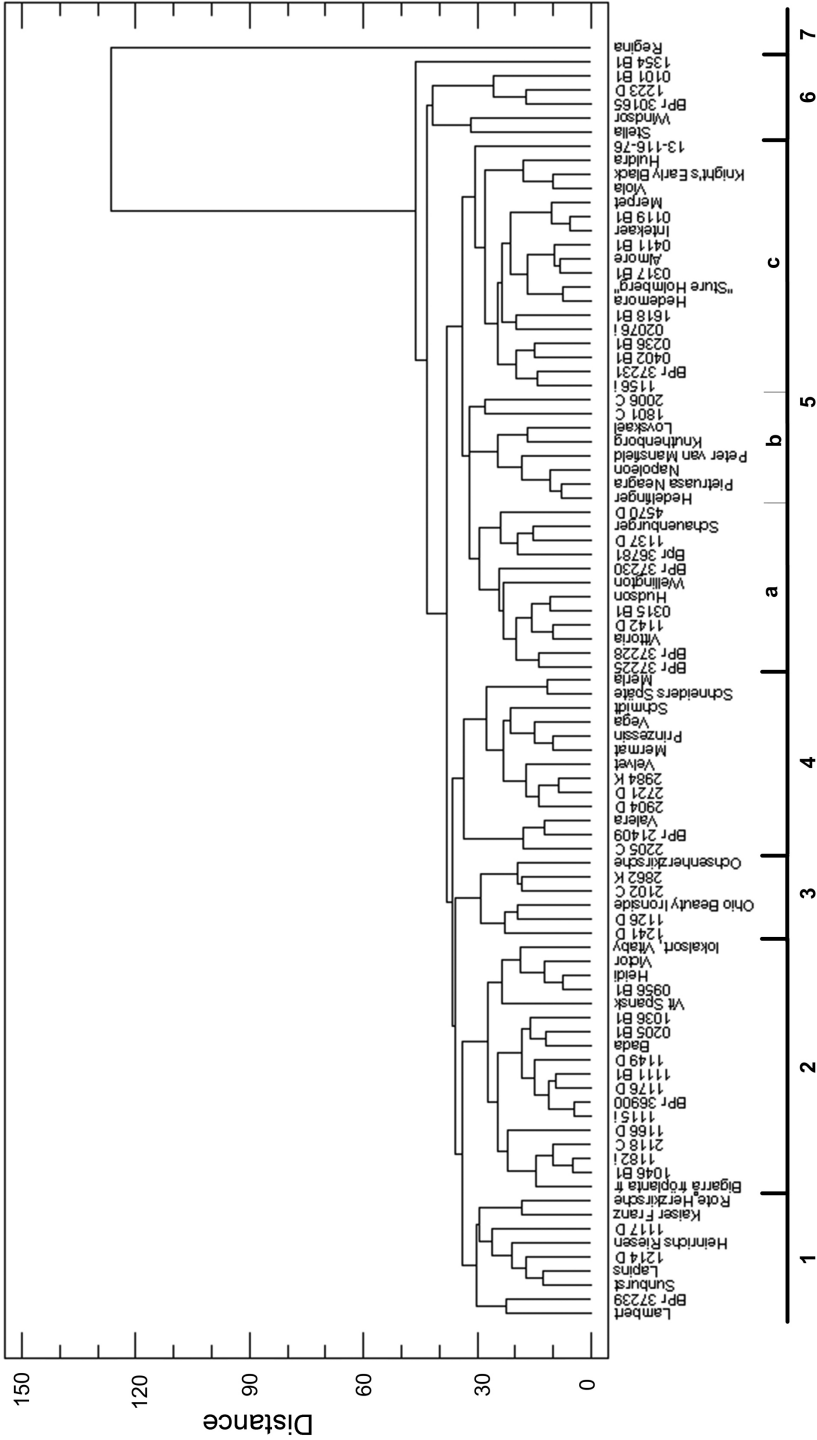


Fig. 2. Hierarchical analysis dendrogram obtained by Group Average Method (Squared Euclidean) by using morphological traits of the sweet cherry accessions of the Division of Horticultural Genetics and Plant Breeding at Balsgård, Department of Crop Sciences, Swedish University of Agricultural Sciences sweet cherry accessions.

Table 4. Characterization of sweet cherry accession clusters in the Division of Horticultural Genetics and Plant Breeding at Balsgård, Department of Crop Sciences, Swedish University of Agricultural Sciences sweet cherry collection. * - cluster and sub-cluster numbers according results of cluster analysis represented in the Fig. 3. ** - average measurement of susceptibility to *Pseudomonas syringae*, *Monilia laxa* and *Monilia fructigena*

Trait / cluster	Average value per cluster and sub-cluster*										Total average	Variance
	1	2	3	4	5	5a	5b	5c	6	7		
Density of the head	5.7	4.3	6.7	4.8	4.5	4.0	3.3	5.3	5.3	7.0	5.09	1.352
Fruit firmness	6.8	4.8	5.3	5.0	4.0	5.2	3.8	3.3	6.0	7.0	5.11	1.507
Fruit juiciness	3.9	5.2	5.0	5.3	5.8	5.0	5.8	6.4	4.7	5.0	5.21	0.489
Fruit separation from stalk	4.6	6.3	6.3	6.2	6.5	6.0	6.8	6.8	6.7	7.0	6.32	0.472
Fruit shape	1.9	3.1	4.3	2.6	3.7	3.3	4.5	3.6	2.3	3.0	3.23	0.694
Fruit size	7.2	6.7	7.0	7.3	5.4	5.0	6.3	5.3	7.0	3.0	6.02	1.832
Fruit skin colour	4.1	3.3	5.5	5.2	5.7	5.3	6.6	5.6	6.0	6.0	5.34	0.950
Juice colour	3.2	1.2	4.7	6.3	7.0	6.2	6.1	7.9	6.8	9.0	5.84	5.157
Length of stalk	5.0	4.8	6.3	5.6	5.7	6.5	6.0	5.1	3.7	7.0	5.57	0.944
Season of flowering	5.7	5.7	5.7	7.9	5.9	6.2	6.8	5.4	6.0	7.0	6.22	0.604
Stone relative size in comparison with fruit	5.0	4.4	4.7	4.1	5.8	6.3	4.5	6.1	5.3	5.0	5.13	0.576
Stone shape	3.2	4.0	6.3	4.1	4.1	3.8	5.0	3.9	5.3	5.0	4.48	0.843
Susceptibility to diseases **	4.2	3.8	2.9	4.9	4.6	4.1	5.8	4.5	5.3	3.7	4.39	0.723
Susceptibility to fruit cracking	4.9	2.8	4.7	6.1	3.1	3.4	3.5	2.8	4.0	3.0	3.83	1.162
Tree habit	1.9	3.8	3.0	2.4	3.9	5.7	4.8	2.3	1.7	1.0	3.04	2.156
Tree type	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	2.0	1.10	0.100
Tree vigour	6.6	5.6	4.3	7.6	4.8	3.7	3.3	6.3	6.3	7.0	5.55	2.158

2862K and Ochsenherzkirsche – large fruit size (PC1-PC6, PC2-PC6); 1618 B1 – small fruit size (PC2-PC6, PC3-PC6); Ohio Beauty Ironside – dark juice colour, late flowering season, low susceptibility to diseases, specific fruit shape (PC3-PC5, PC3-PC6); Vit Spansk, 1354 B1 – short stalk, bad fruit separation from stalk (PC3-PC7).

Cluster analysis found seven clusters of different size (Fig. 2). Because a high number of accessions was found in cluster 5, it was divided in to three sub-clusters.

The highest variability among clusters was shown by traits such as tree vigour, density of head, tree habit, fruit size, fruit firmness, fruit skin colour, juice colour, and susceptibility to fruit cracking and susceptibility to diseases (Table 4). These traits had also the highest impact on grouping of accessions.

Accessions represented in Cluster 1 were characterized by early season of flowering, round shape of fruits, large to very large size of fruits, firm fruits with weak juiciness. The fruits were characterized by light fruit skin and juice colour, high susceptibility to cracking.

Accessions in cluster 2 were characterized by early flowering (approximately the same as cluster 1) and mostly round, medium fruit size. This cluster was associated with very light fruit skin and juice colour, very low susceptibility to fruit cracking and very short length of stalk.

Cluster 3 was distinguished by high density of head, and very low susceptibility to diseases. It was characterized by early flowering, good fruit separation from stalk, and more elongate fruit shape.

Cluster 4 was separated based on strong tree vigour, late flowering season and low stone relative size in comparison with fruit. The cluster was also characterised by large fruits, high susceptibility to cracking, and intermediate susceptibility to diseases. However, it was highly susceptible to *Monilia fructigena*.

Cluster 5 could, in general, be characterised by comparatively small soft, juicy fruits, small tree size and low density of head. This cluster showed quite distinguishable subdivision in smaller clusters with some specific traits. Sub-cluster 5a was distinguished by large stone relative size in comparison with fruit and long length of stalk. This sub-cluster was characterized by weak tree vigour, low density of head, tree habit mostly dropping and weeping. Sub-cluster 5b differed from sub-cluster 5a by weaker tree vigour, more elongated fruit shape, very soft fruits with dark juice colour and small stone relative size. This sub-cluster had also high susceptibility to diseases. Sub-cluster 5c differed from 5a and 5b by early flowering season, very soft and juicy fruits with very dark juice colour and large stone relative size. This sub-cluster showed very low susceptibility to *Blumeriella jaapii*.

Accessions of Cluster 6 had upright or semi upright tree habit, very low juiciness, very short fruit stalk and very high susceptibility to diseases. Fruits of accessions in this cluster had mostly elongated stone shape.

Cluster 7 was represented only by one accession – Regina. The main trait determining the distinct location of this cultivar was tree type: Regina was the only accession of the collection with a spur tree type. This cultivar was also characterized by strong tree vigour, high density of head, and high firmness of fruits. It also showed low susceptibility to diseases.

Discussion

Since both sweet cherry collections have different historical and geographical origin and, therefore genetic background, they showed clear differentiation of important breeding traits. The Latvian collection represents locally well adapted accessions, which showed comparatively high uniformity in traits suited to local environmental conditions: high disease resistance, winterhardiness, but comparatively low fruit quality. The Swedish collection includes mostly accessions which produce high quality fruits. Combining of both gene pools may favour development of locally well adapted, high quality cultivars. This may promote extension of harvesting season, since most of accessions in Latvian collection have early to medium harvest season, whereas Swedish accessions – medium to late. The detailed description of Latvian and Swedish sweet cherry genetic resources collections is valuable input for establishment of a targeted management and evaluation programme. It could serve also a base for further utilization of available genetic resources in breeding, because better plant material description allows to more easily identify interesting properties and make sure that the whole spectra of variation is preserved.

Characterization also provided data for further analyses of material, including multivariate statistical analyses (PCA and cluster analysis), which allowed to obtain an overall view of the existing plant material variability, based on the complete range of described traits. PCA showed the overall variability in collections and revealed traits with high impact on determination of similarity and relatedness. In this investigation it was not possible to make direct comparison of particular principal components between collections, since the used sets of traits differed. Therefore only general trend of trait groups were compared. From this point of view the most useful for both collections were fruit and tree architecture traits, which were associated with the first PC with a high percent of variability (Tables 1 and 2). As those traits are also important in breeding, more attention should be paid to them during further evaluation activities in sweet cherries collections. Fruit traits are especially important as they have high heritability (Hjalmarsson, Ortiz 2000). Leaf traits should be excluded from further evaluation due to low informativity and high dependence on environmental conditions (Lacis, Rashal 2000).

PCA based on morphological traits did not show good applicability in determining relationships between accessions in both sweet cherry collections, especially in the Swedish collection. This might be due to a common gene pool of accessions. A high degree of relatedness of accessions in this collection is confirmed by pedigree data (Lacis et al., 2008). Phenotypical similarity of breeding material is defined mostly by targeted breeding work towards valuable traits. However, PCA showed good usability in selection of distinct accessions based on a complete trait set for characterization, which is not possible to perform accurately by analysis of separate traits.

Cluster analysis was performed to classify accessions. The level of similarity discovered by cluster analysis was relatively high, especially for the Swedish collection. Nevertheless, cluster analysis discovered grouping of accessions within the collections. Although analysis was based only on phenotypical data, results could be supported by pedigree, which was available for the sweet cherry collection in Sweden (Lacis et al. 2008). There was some similarity of grouping based on morphological data on pedigree data. Many accessions or their parents in Group 1 and 2 had a cultivar Kaiser Franz as an ancestor. Kaiser Franz as a progenitor was ancestor of many accessions of Groups 5a and 6, but

not of Groups 5b and 5c, where the common ancestor of many accessions was cultivar Smidt. Accessions of Group 3 have no common ancestor. Several accessions in Group 4 have cultivar Windsor as an ancestor, while Windsor itself is located in Group 6. Cultivar Lambert, which is located in Group 1, is in the pedigree of several accessions from Group 6. Particular accessions showed distinctive separation from the other groups (Fig. 1 and 2), such as cultivar Regina, characterized by a spur tree type. Cultivars Leningradskaya Czornaya from the Latvian collection showed separation based on small leaf size. Cluster analysis is useful for grouping of accessions to obtain understanding of internal structure of germplasm collections (Peeters, Martinelli 1989). This was particularly informative for the Latvian sweet cherry collection, because of the lack of information on origin of most of accessions.

Comparison of sweet cherry accession groups by cluster analysis revealed the most important traits for grouping. For both collections tree architecture and fruit traits differed most between clusters (Table 3 and 4), which is in agreement also with the PCA analysis (Table 1 and 2). This should be taken into account in further characterization of sweet cherry genetic resources.

Combined application of PCA and cluster analysis of sweet cherry accession data revealed the most useful traits for further accession description and provided comprehensive information about the collection's genetic structure and internal relatedness of accessions, which was not possible by analysis of separate traits. Application of multivariate statistics increased the value of phenotypical data and created the basis for combined analysis with genetic data.

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