P R O G R A M

in the frame of COST Action FA1104 on

Sustainable production of high-quality cherries for the European market

of the WG 1 meeting on

Use of Molecular Markers for Diversity Studies

03 – 05 Marc 2014. Budapest

A program helyszíne: Danubius Hotel Flamenco, 1113. Budapest, Tas vezér u. 3-7.

03. 03. 2014.

14.00 Ildikó Balla: Welcome and meeting information

14.05 Kasztovszky Zoltán: Opening

14.15 Margit Laimer: Functional genomics in cherries

15.15. Gregorio Lopez-Ortega: Introduction to the use of molecular genotyping techniques

15.30 Coffee break

16.00 Emma Skipper - DJ Sargent – FF Fernandez: Linkage map development using the cherry6k whole genome genotyping array and the identification of a novel locus controlling flesh colour

16.20 Sezai Ercisli: Molecular studies on cherries in Turkey so far

16.40 Jose Quero-Garcia: Horizon 2020 call

17.00 – 17.30 Discussion

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09:00 Halász Júlia: Genetic fingerprinting of Hungarian sour cherry cultivars

09.20 Gunars Lacis: Charachterisation of Latvia cherry genetic resources by application of molecular markers

09.40 Larisa Gustavsson: Genetic diversity in Swedish cherry collections estimated with SSR markers

10.00 – 10.30 Discussion

10.30 Coffee break

11.00 Teresa Barreneche: Genetic diversity studies in sweet cherry

11.20 Haibo Xuan: Identification of Sweet (*Prunus avium*) and Sour Cherry (*Prunus cerasus*) Cultivars using the SSRs as proposed by the ECPGR

11.40 Goran Barać: Genotypic and phenotypic diversity in cherry species collected in Serbia

12.00 Jose Quero-Garcia: Horizon 2020 call

12.10 - 13.00 Discussion and poster presentation

Posters:

1. Békefi Zs. [1] - Papp M. [2] - Simon G. [3] - Timon B. [3] *SSR marker analysis of cultivated and wild sweet cherry genotypes originated from different geographical places*

2. Kiss E. – Veres A.: Microsatellite fingerprinting of sweet and sour cherry varieties in Hungary.

13.00 – 14.00 Lunch break

04. 03. 2014.

14:00 Mirela Kajkut: Using molecular markers for germplasm identification in Bosnia and Herzegovina

14.20 Elisabeth Schüller: Comparing results of phenotypic characterization and genetic fingerprints for traditional sweet cherry varieties

14.40 Aleš Vokurka: Case studies about authenticity of planting material in nurseries

15.00 – 15.30 Discussion

15.30 Coffee break

16.00 Henryk Flachowsky: German National Fruit Genebank

16.20 Daniela Giovannini: Prioritise the characterisation of the most promising genetic resources for breeders: progress of the task

16.40 – 17.30 Discussion

20.00 Meeting diner

05. 03. 2014. 9.00

Visit to the Faculty of Horticulture of the Corvinus University of Budapest

Welcome speech of the dean, Prof. Károly Hrotkó

Short presentations on the sweet and sour cherry research activities of the Faculty

Visiting departments

A B S T R A C T S

of the WG 1 meeting on

Use of Molecular Markers for Diversity Studies

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03. 03. 2014. 14:00

Ildikó Balla: Welcome and meeting information

Kasztovszky Zoltán: Opening

Margit Laimer: **Functional genomics in cherries**

Gregorio Lopez-Ortega: **Introduction to the use of molecular genotyping techniques.**
G. López-Ortega, A. Bayo-Canha, E. S. Skipper and F. Fernández-Fernández.

The aim of this work was the introduction to the use of molecular identification and characterization of the S-alleles in sweet cherry cultivars. For varietal identification two multiplex PCR were used which included 10 SSR-markers recommended for ECPGR to cherry genotyping and two more markers linked with fruit size. All the microsatellites for fingerprinting amplified successfully. The segregation of this set of primers provided us the fingerprinting of ten varieties cultivated in IMIDA (Murcia) unknown until now. Additionally, data obtained by the markers related with fruit size in a F1 population allows us the opportunity to check the use of these markers in breeding programs. On the other hand, S-Allele analysis identification was made with two pairs of labelled primers but it was not possible to find all the S-alleles for the ten varieties due to the complexity of this analysis.

15.30 Coffee break

Emma Skipper: **Linkage map development using the cherry6k whole genome genotyping array and the identification of a novel locus controlling flesh colour**

Emma Skipper[2] - DJ Sargent[1] – FF Fernandez[2]
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[2]*East Malling Research, New Road, East Malling, Kent, UK*

The publication of the genome of *Prunus persica* has greatly facilitated molecular genetics investigations in the genus *Prunus* and the subsequent development of whole genome genotyping (WGG) arrays for a number of species within the genus has revolutionised the development of linkage maps, population genetics studies, genetic fingerprinting and genome-wide association studies for those species. Utilising the cherry 6k Infinium WGG array, a linkage map was developed for a segregating sweet cherry progeny derived from a cross between the varieties Colney and Lapins. The progeny comprised 138 seedlings, and the resultant linkage map contained a total of 480 mapped loci distributed across the expected eight *Prunus* linkage groups. The male and female linkage maps spanned a total of 581.5 and 632.8 cM respectively. The genetic positions of the majority of the mapped molecular markers were concordant with their physical positions on the peach genome sequence, highlighting the conservation of synteny between peach and cherry, however, a number of clear translocations were identified. Mapping of a single major gene controlling flesh colour in the progeny revealed a previously unreported genetic locus controlling the trait. Characterisation of the locus showed it contained 31 predicted genes, one of which is a potential candidate gene warranting further investigation. The development of the linkage map using Infinium technology, including the scoring of loci with GenomeStudio, the characterization of the cherry genome and its comparison with the peach genome sequence, along with the mapping of the new cherry flesh colour locus will be discussed in this talk.

Sezai Ercisli: **Molecular studies on cherries in Turkey so far**

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Turkey is origin center of cherries and the country has long history on cultivation of cherries. The cherries are an important part of Turkish people's life. Introduction of molecular methods in plant science opened a new horizon for scientists working on cherries as well. So far molecular methods have been applied on cherries including *Prunus avium, Prunus cerasus, Prunus laurocerasus, Prunus mahaleb, Prunus angustifolia* and *Prunus microcarpa* in Turkey. The main point to use molecular methods in cherries in Turkey is to determine
- Diversity within specie
- Genetic relationships between species
- *S* genotyping of local cultivars and finally to characterize of important germplasm properly.

The molecular studies included to use AFLP and SSR markers. Results showed that there were interesting relationships among species and also there were differences within species as well. Investigation of S-genotypes of Turkish cultivars by PCR based method After 1st and 2nd intron analyses, the fragment sizes of standard cultivars corresponded to individual alleles as described. Cultivars in the same incompatibility group are cross-incompatible. The cultivars then had been assigned to incompatibility groups. New S alleles are also determined.

Discussion

04. 03. 2014. 09:00

Halász Júlia: **Genetic fingerprinting of Hungarian sour cherry cultivars**

Júlia Halász*[1], Attila Hegedűs[1]

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Hungary is considered as a secondary gene centre of sour cherry (*Prunus cerasus* L.). An amazing level of genetic variation is displayed by the native germplasm due to the seed propagation that has been carried out by village people through centuries in the country. Several cultivars including the well-known 'Újfehértói fürtös' have become popular in many countries due to their favourable fruit characteristics and ecological adaptability and have been widely used in breeding programs. More recently, genotypes providing increased quantities of health-promoting compounds have been also identified. Our work aims to use a DNA-based fingerprinting assay that might be eligible and reliable for the discrimination of the most important genotypes. We have analysed 24 sour cherry genotypes (cultivars, clones and advanced selections) using 10 polymorphic SSR and *S*-locus specific markers. We determined length variations among microsatellite alleles and determined the DNA sequences of specific *S*-alleles. 'Pipacs 1' is a perspective cultivar due to its specific polyphenolic composition; however this cultivar cannot be reliably discriminated based on morphological characters and hence mixing in nursery gardens is a real threat. We have identified a set of markers that can be used efficiently to differentiate between the two. In addition, we compared their genetic fingerprints to other phenotypically similar accessions like 'Montmorency' and have drawn conclusions regarding the genetic relationships among the amarelle-type sour cherries. We have also confirmed the identity of some accessions that have been supposed to be clones by the breeder. In addition, we identified a *Prunus*-specific miniature inverted-repeat transposable element (MITE) that may be used for marker development in future.

Gunars Lacis: **Charachterisation of Latvia cherry genetic resources by application of molecular markers**

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A diversity of sweet and sour cherry varieties is available in Latvia, which consists of landraces and selections of local breeding as well as germplasm that result from years of plant material exchange among different countries and breeding institutes. Main feature of this germplasm is adaptability to the local climate and growing conditions. Base collection of all fruit crop genetic resources, including cherries, is maintained at the Latvia State Institute of Fruit-Growing. Presently this collection comprises about 170 sweet and 62 sour cherry; 40 and 33, accessions respectively, are designated as national genetic resources, as well as breeding material developed at the institute. Conservation of germplasm itself has a little value without characterization and further utilization of the stored plant material. To intensify these activities DNA based fingerprinting has been implemented in the characterization of germplasm. In general, two main groups of molecular markers have been utilized for cherry genetic resources characterization: markers for identification of accessions, detection of the structure of genetic resources collection and relatedness of available plant material, and gene specific markers, subsequently applicable for Marker Assisted Selection (MAS). At the moment genotyping methods based on SSR (microsatellite) markers have been implemented for use in the plant material identification, True-to-Type verification as well as evaluation of genetic diversity and internal collection structure. These marker sets have been harmonized with ECPGR Prunus WG recommended ones to ensure data compatibility with international data bases. Presently 262 varieties of sweet and 50 varieties of sour cherries have been genotyped. Gene specific molecular markers have been applied for 226 sweet cherry varieties, ensuring essential information for germplasm utilization in MAS and breeding.

Key words: cherry, molecular markers, MAS, SSR, S-gene, self-incompatibility

10.30 Coffee break

Larisa Gustavsson: **Genetic diversity in Swedish cherry collections estimated with SSR markers**

Larisa Garkava-Gustavsson, Jasna Sehic and Hilde Nybom

Department of Plant Breeding, Swedish University of Agricultural Sciences, Sweden

In Sweden, preservation of genetic resources in fruit crops is organized within ‘National Program for Diversity of Cultivated Plants’, which has defined a set of mandate cultivars for publically funded conservation. These mandate cvs are old and presumably indigenous. The trees are maintained in numerous clone archives as part of the Swedish cultural history. In addition, many of these cultivars are also included in a more research and breeding oriented germplasm collection at Balsgård, Swedish University of Agricultural Sciences.
Origin of these cultivars is often uncertain, which leads to potential mistakes with identification. SSR (Simple Sequence Repeats) markers were used to provide mandate cultivars with ‘molecular profiles’, to detect duplicates and mis-labellings in germplasm collections (Balsgård and clone archives around Sweden), In total, 23 sour and sweet cherry cultivars were analyzed with 7 SSR markers, 13 of them were found at at least two collections. About 35% of analysed genotypes had problematic identification.

Teresa Barreneche: **Genetic diversity studies in sweet cherry**

The Cherry Genetic Resources Collections of INRA are maintained in the *Prunus* Genetic Resources Center (GRC) located near Bordeaux. This collection counts nearly 600 cherry accessions of which 30% belong to the French National Cherry Collection. The task of the *Prunus* GRC is to collect, preserve, evaluate and distribute the genetic resources of *Prunus* species and especially of cultivated ones. In addition to the classical objectives of genetic resources management, our main aim is to characterize the genetic diversity present in the cherry collections. A broad investigation of the variability of the French National Cherry collection (150 accessions) is being carried out based in more than 15 phenotypic traits; on the other hand the genetic diversity is assessed using SSR and SNP. These studies will generate representative samples, i.e. “core collections”, suitable for further association genetics and genome wide selection analyses, which will reinforce current marker-assisted selection strategies.

Haibo Xuan: **Identification of Sweet (*Prunus avium*) and Sour Cherry (*Prunus cerasus*) Cultivars using the SSRs as proposed by the ECPGR**

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Sweet (*Prunus avium* L.) and sour cherries (*Prunus cerasus* L.) are two economically important species in Europe. The capability to distinguish among cherry cultivars in breeding, cultivation and germplasm collection is extremely important for scientific as well as for economic reasons. There is a demand for a rapid and reliable method of cultivar identification for cultivar registration, protection, cultivation and management. Normally morphological traits are used to identify cultivars but these traits are often differently expressed in different environments and production practices.

DNA-based markers are useful for germplasm identification, diversity analysis and verification of rootstock identity. Microsatellites (Simple Sequence Repeats (SSRs)) have become the marker of choice for fingerprinting the majority of fruit crops. A need to harmonise fingerprinting protocols led the European Cooperative Programme for Plant Genetic Resources Fruit Network (ECPGR) to propose a standardised set of SSR markers and a common control genotype for apples, pears and several *Prunus* species including cherry.

Using the newly proposed international standards based on 16 SSRs, a set of more than thousand sweet- (> 1000) and sour cherry (> 300) cultivars from five preservation orchards in Germany have been fingerprinted using a CEQ 8000 Sequencer and then compared with eight control genotypes selected from the East Malling Research Station.

The polymorphism information content (PIC), frequencies of 15 SSR loci distributed on 73 cultivars are described and discussed.

Discussion and poster presentation

Posters: 1. Békefi Zs. - Papp M. - Simon G. - Timon B.: **SSR marker analysis of cultivated and wild sweet cherry genotypes originated from different geographical places**

[1] *NARIC National Agricultural Rsearch Center, Fruitculture Research Institute*
[2] *University of West Hungary,Faculty of Forestry, Department of Botany and Natural preservation*
[3] *Corvinus University of Budapest, Faculty of Horticulture Science, Fruit Science Department*

KEYWORDS: sweet cherry, wild cherry, genetic relationship, SSR analysis

Sweet cherry (*Prunus avium* L.) is a common fruit species native to the Carpathian Basin, their wild and cultivated forms often cross pollinate each other. Presumably Carpathian Basin is a meeting point of those Western European cultivated types that escaped the Ice Age and cultivars originating from Asia through Turkey.
In our work commercial sweet cherry cultivars as well as wild and cultivated individuals of different geographical origin were investigated in order to detect their potential genetic relationship. For our analysis selected SSR markers recommended by IPGRI were used, and a dendrogram was constructed.
According to the SSR results, all sweet cherry genotypes could be distinguished. Altogether 52 alleles were detected, ranging from 4 to 10 alleles per locus (Table 2). Average number of alleles per locus was 6.5. The allele PceGA34 was alone able to distinguish among accessions analysed, thus this SSR marker is highly recommended for cultivar identification work in cherry. Closer relationship was observed between 'Germersdorfi 3' and „Budakalászi", 'Szomolyai fekete' and „Felsőgeszeg", „BK-1" and „BK-2".
Our results may be used in research programs on sweet cherry domestication.

2. Anikó Veres, Erika Selyem, Ogboro Samson Edosa, Kitti Tóth-Lencsés, Erzsébet Kiss
Microsatellite fingerprinting of sweet and sour cherry varieties in Hungary.

Szent István University, Institute of Genetics and Biotechnology, Páter K. u. 1. H-2100 Gödöllő, Hungary

Cherry cultivation in the Carpathian basin area have been started more than 100.000 years ago. Adapting to the basin specific ecological conditions, high degree of genetic variability can be observed among the cherry cultivars. The SSR (Simple Sequence Repeat) markers allow the discrimination of the cultivars, and to determine its specific DNA fingerprints. Due to the high degree of polymorphism of SSR markers it's enough only six SSR markers to apply for differentiating the varieties. Microsatellite markers are used not only for cultivar identification but also for the discrimination of clones and for the verification of synonyms and homonyms. Due to their locus specificity and Mendelian codominant inheritance, they can be used for the pedigree identification of cultivars. The parent-progeny relationships may be clearly identified even if the actual or assumed crossing partners are heterozygous in the given microsatellite locus, because the diploid progeny will receive one allele from one parent and the other allele from the other parent.
Consequently for pedigree analysis the local, autochthonous varieties should be taken into consideration. Microsatellite or SSR (Simple Sequence Repeats) fingerprints have become efficient tools for characterizing the cherry cultivars.
In our present study varieties autochthonous and bred sweet and sour cherry cultivars in Hungary began to be characterized at 3-4 microsatellite loci. The obtained allele size data can help to determine the genetic distances between the cultivars; preparing pedigrees of the varieties; discovery of primary and secondary relationships between cultivars.

04. 03. 2014. 14:00

Goran Barać: **Genotypic and phenotypic diversity in cherry species collected in Serbia**

G. Barac[1], V. Ognjanov[1], D. Obreht[2], M. Ljubojevic[1], D. Bosnjakovic[1], K. Gasic[3]

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Department of Fruit Science, Faculty of Agriculture, Novi Sad is leading a project “Selection of sweet and sour cherry dwarfing rootstock and development of intensive cultivation technology based on the sustainable agriculture principles” supported and funded by the Ministry of Science and Technological Development of Serbia. Genetic diversity of cherry species collected in Serbia were investigated using 26 simple sequence repeat (SSR) markers developed in *Prunus*. Analyzed material included 77 cherry accessions representing 5 species, *P. cerasus*, *P. avium*, *P. fruticosa*, *P. mahaleb* and *P. serrulata*. A total of 98 alleles were detected, with an average of 3.7 putative alleles per primer combination. The average number of alleles ranged from 1.61 to 1.98 in *P. serrulata* and *P. cerasus*, respectively. Mean effective number of alleles (A_e) ranged from 1.55 for *P. serrulata* to 1.98 for *P. cerasus*, while the mean observed heterozygosity (H_e) for each locus ranged from 0.34 for *P. avium* to 0.43 for *P. cerasus*. The clustering analysis classified accessions into four groups according to their taxonomy, where *P. avium* and *P. cerasus* were grouped together, supporting *P. avium* as one of the progenitors of sour cherry. Future work on biodiversity assessment will be focused, mainly, on European ground cherry (*P. fruticosa*) and “Oblacinska” Sour cherry together with other *P. cerasus* landraces, from our and surrounding countries.

Mirela Kajkut: **Using molecular markers for germplasm identification in Bosnia and Herzegovina**

Mirela Kajkut[1], Gordana Đurić[1,2]

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The territory of Bosnia and Herzegovina (B&H) has been historically exposed to the influences of different civilizations. In B&H, through spontaneous or planned hybridization and selection, introduced germplasm participated in the creation of new autochthonous varieties (Đurić et al., 2009, Đurić et al., 2013). Identification and molecular characterization of the Bosnian germplasm is very important for conservation and sustainable use.

In the last few years, a few diversity studies with molecular markers were done on B&H germplasm. The studies were performed on *Malus* germplasm (Gaši et al., 2010) and *Pyrus* germplasm (Gaši et al., 2013) using SSR (Simple sequence repeats) markers. A total of 39 accessions of apple, 24 traditional B&H cultivars and 15 modern international cultivars were investigated using 10 SSR (simple sequence repeats) markers and 23 morphologic characteristics. This study showed that traditional apple cultivars from B&H, have a high number of unique alleles, and that there is no correlation between the molecular and morphologic set (Gaši et al., 2010). Using 13 microsatellite markers 64 pear accessions were analyzed, 27 traditional B&H cultivars and 9 international reference cultivars. Traditional B&H pear accessions differentiated genetically from the international pear cultivars and genetic structure revealed that most international cultivars grouped in a single reconstructed panmictic population (Gaši et al., 2013).

Grapevine cultivars were also analyzed with AFLP (Amplified fragment length polymorphism) and SSR markers. Because unknown origin, cultivar "Žilavka" was analyzed with SSR markers in order to obtain a standard "Žilavka" genotype. Also, AFLP markers were used to

investigate the genetic basis of variability within the cultivar (Tomić et al., 2010). A set of B&H grapevine cultivars was analyzed by SSR markers in order to assess true cultivar identity, genetic relationships and to detect the level of genetic diversity. Fifty-one collected grapevine cultivars of Bosnia and Herzegovina were analyzed by 22 microsatellite markers. Twenty-five unique fingerprints representing 23 cultivars and 2 unnamed genotypes were found. The results of the study will be used for establishing a non-redundant grapevine germplasm collection (Tomić et al., 2012).
RAPD (Randomly amplified polymorphic markers) was applied for initial molecular analysis of ray (*Secale cereale* L.) and pear (*Pyrus communis* L.) accessions in the Gene Bank of Republic of Srpska. Comparasion of five ray accessions showed that in the Gene Bank exist duplicate ray accession (Kajkut et al., 2012). Eleven pear accessions were also analyzed, and obtained results showed that five accessions are duplicates (Kajkut, 2013).

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Elisabeth Schüller: **Comparing results of phenotypic characterization and genetic fingerprints for traditional sweet cherry varieties**
Elisabeth Schüller, Felicidad Fernandez, Verena Pilz, Andreas Spornberger

Traditional Austrian sweet cherry (*Prunus avium*) varieties were characterized and partly identified based on phenotypic and morphologic markers. In order to support this characterization and identification process genetic fingerprints were acquired using 12 SSR markers in a multiplex PCR approach. In addition to the acquisition of characteristic fingerprints for traditional varieties, we also found some possible synonyms. Those cultivars show the same genetic fingerprint, but were identified as distinct cultivars. By analyzing and comparing the phenotypic and genotypic data using selected statistical methods these findings should be further proved

Discussion

15.30 Coffee break

Aleš Vokurka: **Case studies about authenticity of planting material in nurseries**

Molecular identification of suspected synonyms among local varieties, and investigation of biodiversity depends on the availability of 'true-to-type' genotypes as a referent starting point for research. It is usually expected that nursery mother-block trees are reliable, as a result of official controls and certification procedures they undergo. However, the situation may be quite opposite.

I will present two cases where the reliability of 'true-to-type' planting material was under question. The first case is early-stage identification of 'Lovranska' sweet cherry (local variety) and its comparison with putative synonyms using RAPD markers. One of the candidate for synonyms was 'Lambert', also grown in the same orchard. The samples for DNA analyses were obtained from two different nurseries, in addition to those from the investigated orchard. The analysis clearly revealed two different DNA profiles.

The second case is the situation in several nurseries where at least nine well-known varieties are not 'true-to-type' within all investigated nurseries. Clearly different profiles were detected by SSR methods and they are different in at least six SSR loci. The situation existing in nurseries is a ringing alarm for the implementation of systematic analysis of mother-block-trees in the nurseries.

Henryk Flachowsky: **Genotyping of the "German National Fruit Genebank"**

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The preservation of fruit genetic resources has a long tradition in Germany, because it is a pre-requisite for ensuring a sustainable fruit production for future generations. First activities on preservation of fruit genetic resources reach back to the Middle Age, when cultivar collections were grown in abbeys, royal houses, and other manor houses. Later on fruits were cultivated by farmers in meadows for their own food supply. In the early decades of the 20th century national collections were established as a basis for the increasing breeding activities. Since that time, cultivar and wild species collection consisting of a multitude of genotypes are held by public, but also in private gene repositories. Unfortunately, a general overview of all the ongoing activities is currently missing. The loss of individual genotypes, which are only preserved in one or a few collections, can therefore not be excluded. On this account the German National Fruit Genebank has been established in 2009 to minimize the risk of losing fruit genetic resources. The German National Fruit Genebank is a decentral network, which is aimed on the coordination of different germplasm collections including species specific sub-networks for strawberry, cherry, apple, plum, *Rubus*-species and pear. All genotypes will be investigated for trueness-to-type. In the cherry network, which consists of seven different collections, 97 sour cherry cultivars and 289 sweet cherry cultivars are preserved. Each cultivar will be maintained in at least two collections with a minimum of two trees per collection. These selected cultivars represent primarily German cultivars and cultivars which have been bred in Germany, cultivars with regional, historical or sociocultural importance, and cultivars containing important traits for breeders. All selected cherry cultivars were evaluated by pomologists using morphological characters and by DNA fingerprinting. Fingerprinting was performed using a set of SSR markers suggested by ECPGR. Individual collections, like the Fruit Genebank of the Julius Kühn-Institut in Dresden, are further characterized using markers for self-incompatibility, fruit size and resistance to selected fungal diseases.

Daniela Giovannini: **Prioritise the characterisation of the most promising genetic resources for breeders: progress of the task**

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The access and the use of genetic resources (GRs) rich of diverse and high-impact traits, are not only the pre-requisite for a true varietal innovation but a powerful tool of breeding to respond adequately and promptly to the challenges of biotic and abiotic threats in changing agro-climatic conditions. Within the framework of the COST FA1104 project, an initiative (task 2) has been undertaken aimed at identifying a representative set of EU cherry accessions chosen according to criteria of richness in traits promising for breeding. The cherry subset will be described according to standardized descriptors and characterized through molecular markers. Task 2 is also aimed to encourage the broader use of the EU cherry GRs in present and future breeding activities.
The presentation will focus on the progress, the practicality and the potential bottlenecks of the action.

Discussion

05. 03. 2014. 9:00

Visit to the Faculty of Horticulture of the Corvinus University of Budapest

Welcome speech of the dean, Prof. Károly Hrotkó

Short presentations on the sweet and sour cherry research activities of the Faculty

Visiting departments

Presentation:

László Abrankó: **Genistein isoflavone glycoconjugates in sour cherry cultivars (*Prunus cerasus* L.)**

László Abrankó*[a], Ádám Nagy[a], Blanka Szilvássy[a], Éva Stefanovits-Bányai[a], Attila Hegedűs[b]

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Although the isoflavone genistein has well-established health-beneficial effects, it is not a major component of Western diet, since soy consumption, the main dietary source of genistein, is low in these populations. Genistein compounds were studied in twelve commercial sour cherry (*Prunus cerasus* L.) cultivars grown in Hungary. High performance liquid chromatography coupled to quadrupole/time-of-flight mass spectrometry, equipped with electrospray ion source (HPLC-ESI-qTOFMS) was used for screening and confirmatory analyses. Genistin and genistein were found in some Hungarian native sour cherry cultivars including ‘Pipacs1’, ‘Kántorjánosi’, ‘Debreceni bőtermő’ and ‘Éva’. Genistein content in fruits of

the latter three cultivars ranged between 0.4 to 0.6 mg, while in ‘Pipacs1’ a total of 4.4 mg genistein compounds (expressed as aglycone equivalents per 100 g of fresh fruit) was determined. These cultivars may play an important role as complementary genistein sources in the Western diet. Especially ‘Pipacs 1’, may be best utilized in functional food products.
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Gitta Ficzek: **The role of sour cherry fruits on the bacterial flora of human saliva**

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Hungarian cultivars bred by Pál Maliga, play important role in sour cherry production, as they are present in several sour cherry growing countries all over the world. Scientific research proves that the Hungarian bred sour cherry varieties have higher anthocyanin content compared to Western European and American sour cherry varieties. Our varieties are suitable not only for industrial processing, but also for fresh consumption because of their pleasant flavour.
We examined beneficial effect of sour cherry fruits on bacterial flora of human saliva. Biological activity of sour cherry juices prepared from fruits ‚Érdi jubileum’, ‚Érdi bőtermő’, ‚Maliga emléke’ and ‚Kántorjánosi 3’ harvested at different maturity stages was investigated on bacteria present in human saliva. The influence of sour cherry on a mixed bacterial flora of human saliva of 10 volunteers was determined by different experimental approaches. Bactericidal effects were evaluated by minimum inhibitory concentration (MIC) using agar diffusion methods and by minimum bactericidal dilution (MBD) assays counting the number of surviving bacterial cells in the diluted juices. Time-dependent antibacterial effects were also determined by monitoring the decrease in bacterial cell numbers after the treatment with undiluted juices. The investigated sour cherry juices displayed an impressive bactericidal effect against human saliva bacteria (10–100× reduction of cell numbers) within a short time frame (10–40 min). Érdi jubileum was more effective (100 000×reduction of cell number after 270 min) than the other studied cultivars. Bactericidal effect was influenced by the ripening of fruits of Érdi jubileum obtained at different harvesting dates. Biologically active components were effective against a large spectrum of opportunistic bacterial pathogens such as *Pseudomonas, Klebsiella, Pantoea* spp. and *Escherichia coli*, including the antibiotic-resistant *Pseudomonas aeruginosa* but they were ineffective against beneficial probiotic *Lactobacillus* spp. Results confirmed the antibacterial potential of all the investigated sour cherry fruits, therefore the consumption of the fruit or its juice for positive influence on oral hygiene is highly recommended.