



CHARACTERISATION OF LATVIA CHERRY GENETIC RESOURCES BY APPLICATION OF MOLECULAR MARKERS

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FRUIT CROP GENETIC RESOURCES

- A diversity of fruit crop varieties is maintained at the Latvia State Institute of Fruit-Growing genetic resources collection, which consists of landraces and selections of local breeding as well as germplasm that result from years of scientific exchange and co-operation.
- Presently germplasm collection comprises about **2500 accessions** of **17 fruit crops**
- **676 accessions** of fruit crops are designated as **national genetic resources**.
- **Main activities:**
 - acquisition
 - maintenance
 - characterization
 - utilization



FRUIT CROP GENETIC RESOURCES

Crop	Number of Accessions	Number of National GR Accessions	Number of Genotyped Accessions
Apple	1061	283	157
Pears	405	101	40
Plums: domestic	151	45	108
diploid	152	25	11
Cherries: sweet	170	40	170
sour	62	33	50
Black currants	144	38	118
Red and white currants	30	16	8
Gooseberries	109	23	26
Raspberries	71	11	43
Sea buckthorn	36	-	36
Strawberries	13	2	23*
Apricots	35	35	-
Peaches	2	2	-
Grapes	26	14	-
Japanese quince	40	6	-
Honeysuckle	2	2	-
Total:	2509	676	790

* Strawberry accessions from Püre HRC collection included in characterization

LATVIAN CHERRY COLLECTION

○ Main features:

- Adaptivity to northern climate
- Local developments – introduction was very difficult
- Diversity of local forms, landraces
- High presence of varieties developed in east and central Europe
- High phenotypical diversity



'Aleksandrs'



'Aija'



'Jānis'

MOLECULAR MARKERS IN PGR MANAGEMENT

- **Implementation of molecular markers:**
 - **2000–2004** – characterization of cherry GR collection in cooperation with Swedish University of Agricultural Sciences (SLU) and Michigan State University (MSU) – PMS marker set (Cantini et al., 2001), S-allele specific markers (Sonneveld et al., 2001; Wiersma et al., 2001)
 - **2006-2007** – National programm in PGR evaluation and characterization (collection-wide genotyping, additional UDP markers (Testolin et al., 2000)):
 - Identification of genotypes – detection of duplication in the collection
 - Evaluation of collection genetic diversity and structure
 - **2008-2012** – Research project on MAS methods in cherry breeding (implementation of ECPGR *Prunus* WG marker set, additional markers for S-allele (Vaughan et al., 2008), S4' allele markers (Ikeda et al., 2004; Zhu et al., 2004) implementation in breeding)

RESULTS – SWEET CHERRIES



- ✘ **262 sweet cherry accessions** have been genotyped by SSR markers:
 - ✘ 96 accessions – using all 23 SSR markers, including ECPGR Prunus WG recommended marker set and additional highly polymorphic markers
 - ✘ 142 accessions – using ECPGR recommended markers
 - ✘ 24 accessions – using combination 17 SSR markers
- ✘ **Markers:**

LSIFG marker set:		ECPGR marker set:	
1	PceGA59	1	BPPCT037
2	PMS2	2	CPPCT6
3	PMS40	3	CPPCT22
4	PMS67	4	EMPA002
5	PS08E08	5	EMPA003
6	PS12A02	6	EMPA017
7	UDP96-005	7	EMPA026
8	UDP97-402	8	EMPaS01
		9	EMPaS02
		10	EMPaS06
		11	EMPaS10
		12	EMPaS12
		13	EMPaS14
		14	PceGA34
		15	UDP98-412

RESULTS – SWEET CHERRIES

NONSPECIFIC MARKERS (1)



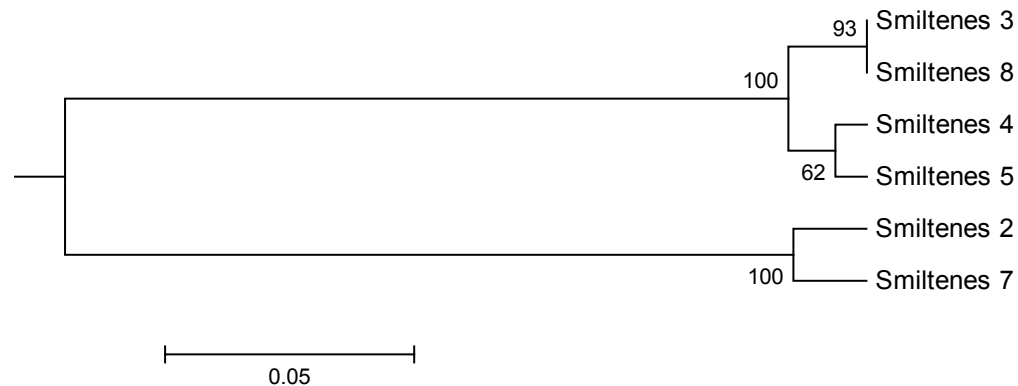
- **92 sweet cherry accessions:**
 - Breeding material – 30 accessions
 - Landraces, collected material – 25 accessions
 - Latvian advanced cultivars – 3 accessions
 - East European cultivars – 19 accessions
 - West (European and American) cultivars – 15 accessions
- **23 SSR molecular markers**
- **Evaluation of genetic diversity**

RESULTS – SWEET CHERRIES NONSPECIFIC MARKERS (2)

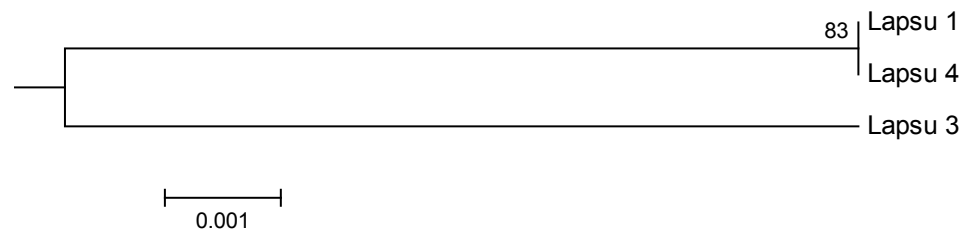


○ Evaluation of identity, collected plant material:

• Example 1



• Example 2



RESULTS – SWEET CHERRIES

SPECIFIC MARKERS (1)



- **Self-incompatibility gene (*Sf*) genotyping:**
 - Research on *Sf* gene allele distribution, their inheritance
 - Additional identification tool
 - Basis for MAS (Marker Assisted Selection) – application in the self-compatible sweet cherry cultivar breeding
- **Self-incompatibility in sweet cherries:**
 - **228 sweet cherry accessions** genotyped by S-allele specific markers:
 - Breeding material - 78 accessions
 - Landraces, collected material – 49 accessions
 - Latvian advanced cultivars – 14 accessions
 - East European cultivars – 55 accessions
 - West (European and American) cultivars – 32 accessions

RESULTS – SWEET CHERRIES SPECIFIC MARKERS (2)



- **Markers of self-compatibility allele S_4' implemented in MAS**
 - From crosses of winterhardy cultivar 'Iputj' with self-fertile 'Lapins' in 3 hybrids S_4' allele was found
 - In total 5 hybrids with identified S_4' allele have been selected for further evaluation

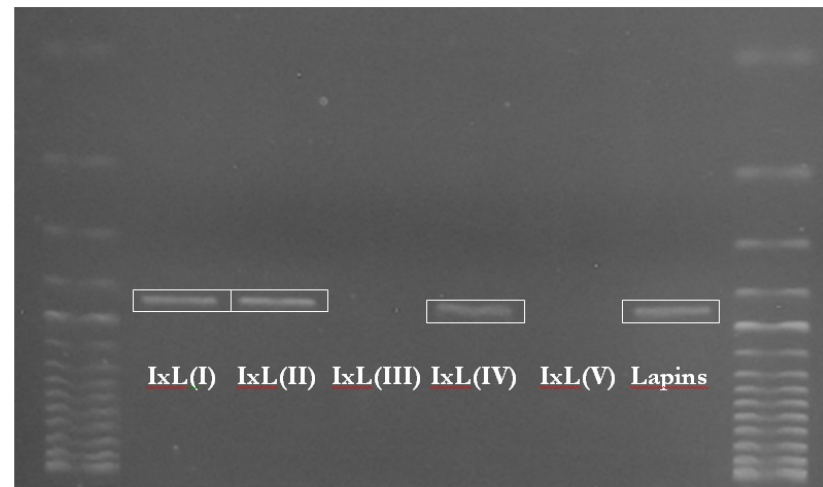


Figure 1 Self-compatibility allele (S_4') detection at the LIFG

RESULTS – SOUR CHERRIES NONSPECIFIC MARKERS (1)



- **50 sweet cherry accessions** have been genotyped
- **25 SSR markers:**

LSIFG marker set:		ECPGR marker set:			
1	PceGA59	1	BPPCT037	11	EMPaS10
2	PMS2	2	CPPCT6	12	EMPaS12
3	PMS3	3	CPPCT22	13	EMPaS14
4	PMS40	4	EMPA002	14	PceGA34
5	PMS49	5	EMPA003	15	UDP98-412
6	PMS67	6	EMPA017		
7	PS08E08	7	EMPA026		
8	Ps12A02	8	EMPaS01		
9	UDP96-005	9	EMPaS02		
10	UDP97-402	10	EMPaS06		

- The ECPGR marker set showed good applicability on new *Prunus* species – tetraploid *Prunus cerasus*.

RESULTS – SOUR CHERRIES NONSPECIFIC MARKERS (2)



- **Collection contain a high level of genetic diversity and represent valuable material for breeding and research.**

SSR locus	No of alleles	No of genotypes	Heterozygosity	Gene diversity	Discrimination power
Average (ECPGR primer set)	9.1	14.1	0.850	0.700	0.697
Average (LIFG primer set)	9.4	14.6	0.988	0.761	0.697
Total average	9.3	14.4	0.919	0.731	0.697

RESULTS – SOUR CHERRIES NONSPECIFIC MARKERS (3)

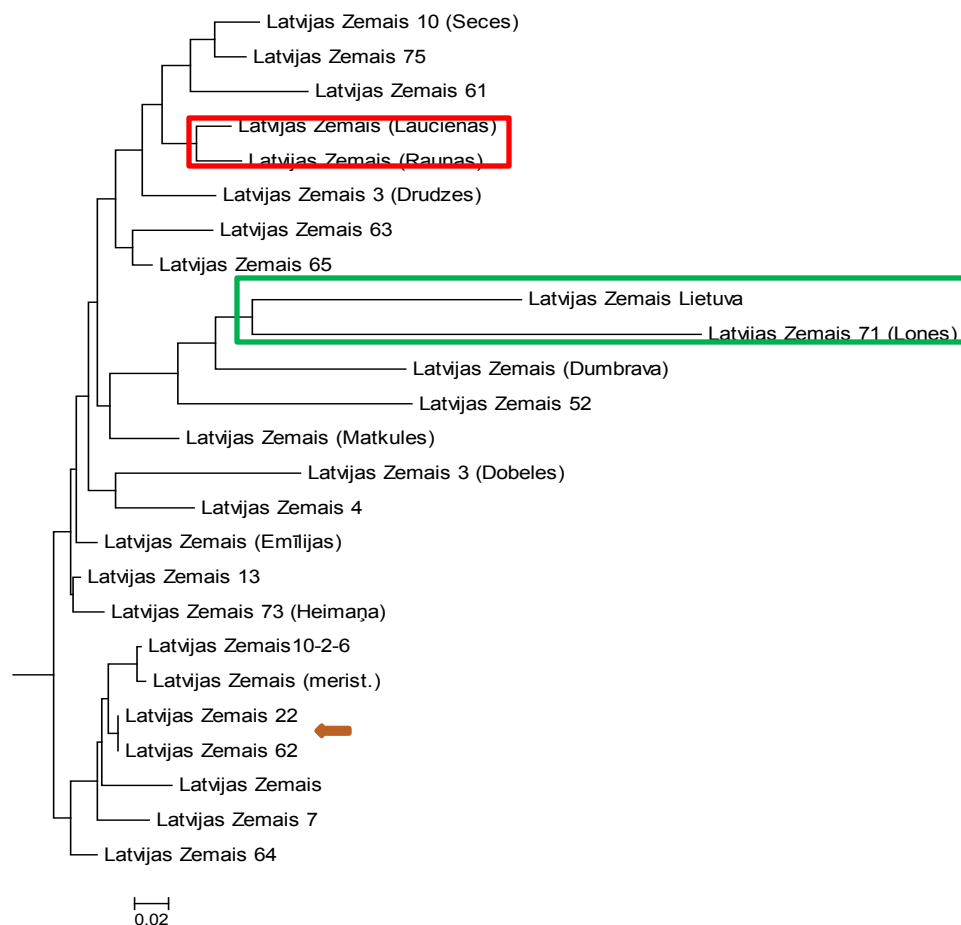


○ Discrimination of closely related clones of local landraces

- Example – landrace 'Latvijas Zemais' (syn. 'Leišu Ķirsis', 'Lietuvas Zemais', 'Žagares Ķirsis', 'Griotte d'Ostheim', 'Litovka' (RU), 'Lāti madalkirss' (EST), 'Žagarvyšnė' (LT))



cv. 'Latvijas Zemais'



PUBLICATIONS

○ Sweet cherry:

- Lacis, G., Kaufmane, E., Rashal, I., Trajkovski, V., Iezzoni, A.F. (2008). Identification of self-incompatibility (S) alleles in Latvian and Swedish sweet cherry genetic resources collections by PCR based typing. *Euphytica* 160, 155–163.
- Lācis G., Ruisa S., Kota I. 2008. Molecular marker application in breeding of self- and cross-compatible sweet cherry (*P. avium* L.) varieties. Proceedings of International scientific conference „Sustainable Fruit Growing: From Plant to Product”, pp. 158-164.
- Lacis, G., Rashal, I., Ruisa, S., Trajkovski, V., Iezzoni, A.F. (2009). Assessment of genetic diversity of Latvian and Swedish sweet cherry (*Prunus avium* L.) genetic resources collections by using SSR (microsatellite) markers. *Scientia Horticulturae* 121(4), 451-457.

○ Sour cherry:

- Lācis G., Rashal I., Trajkovski V., 2011. Implementation of a limited set of SSR markers for screening of genetic variability in Latvian and Swedish sour cherry (*Prunus cerasus* L.) genetic resources collections. Proceedings of the Latvian Academy of Sciences. Section B: Natural, Exact and Applied Sciences, 65(1/2), 21–28.
- Lācis G. and Kota I., 2013. SSR marker-based fingerprinting for sour cherry (*Prunus cerasus*) genetic resources identification and management. *Acta Horticulturae*, 976, 251-256.

**Thank you for
attention!**

