

GENETIC PROFILES AND DIVERSITY OF BALTIC SPRING BARLEY MATERIAL

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The objectives of this study were to generate molecular passport data for identification and differentiation of Baltic spring barley accessions (cultivars, landraces and breeding lines) and to estimate the genetic variation within and among these accessions. Allelic profiles of 21 microsatellite and 8 isoenzyme loci were obtained and analysed for 64 Baltic spring barley accessions. The microsatellite data was successfully used to separate all of the accessions by individual allelic pattern and frequencies, whereas only 30 of the studied accessions could be distinguished by isozyme data. Variation was detected both among and within the accessions and was significant. The variation within accessions accounted for 20.6% and 14.3% of the total variation, based on microsatellite and isozyme data, respectively. The six-rowed and two-rowed material was well differentiated by both types of marker data: according to AMOVA this differentiation accounted for 16.9% of the microsatellite variation and 26.8% of isozyme variation. Differentiation of accessions based on the country of origin could be detected only by isozyme markers and accounted for 9% of the total isozyme variation. Both isozyme and microsatellite data showed that accessions of Latvian origin had the highest total diversity values, while material from Estonia was the least diverse.

Key words: barley, Baltic region, isoenzymes, microsatellites, molecular variation.

INTRODUCTION

Barley is one of the most important crops in the Baltic countries; the area planted annually is about 10% of the total crop area in Latvia and Lithuania, and 20% in Estonia (Anonymous, 2012). Professional breeding of this crop was initiated here about 90 years ago and significant improvements of agronomic performance of the crop have been achieved, e.g. yields of spring barley have more than doubled during the last century (<http://www.stat.ee>; <http://www.zm.gov.lv>; <http://wwwstd.lt>). Initially, the cultivars were selected from local and foreign landraces, and in the 1930s, this approach was replaced by combination breeding (Gaike, 1992). The pedigrees of modern cultivars have become complex, and introduction of exotic sources, e.g. sources of disease resistance genes, by number of back-crossing cycles, leads to more adapted materials. Therefore, it is presently difficult to classify material based on a genealogical approach only and molecular methods have become a useful tool to identify and classify breeding material and to estimate genetic variation. The objectives of this study

were to determine the genetic relationships and diversity of Estonian, Latvian and Lithuanian spring barley and to generate genetic profiles of the gene bank accessions and breeding material. The accessions discussed in this paper were also included in a larger study together with accessions from Sweden, Denmark, Finland and Norway to study genetic erosion in barley over the last century (Kolodinska Brantestam, 2005). The present paper, however, is focused on the Baltic material only, and assesses genetic diversity, its distribution and relatedness among Baltic spring barley.

MATERIALS AND METHODS

Materials. The material studied consisted of 64 accessions of spring barley from Estonia, Latvia and Lithuania and included landraces, cultivars and breeding lines (Table 1). Material was obtained from gene banks in the Baltic countries (Commission on Plant Genetic Resources for Food and Agriculture in Estonia; Genetic Resource Centre in Latvia and Plant Gene Bank in Lithuania) and plant breeding

Table 1

BARLEY ACCESSIONS, THEIR ORIGIN, TYPE AND YEAR OF RELEASE

Accession name	Gene bank number	Origin country	Year of release	Accession type	Pedigree	Spike type	Breeding Inst.
1	2	3	4	5	6	7	8
'Latvijas vietēje'	LVA00018	Latvia	-	landrace	-	two-rowed	-
'Vairogs'	LVA00017	Latvia	1930	cultivar	(S) local material from Priekuļi	six-rowed	Priekuļi Br. St.
'Kombainieris'	LVA00009	Latvia	1950	cultivar	'Maja' x Talsu local material	two-rowed	Stendes Br. St.
'Priekuļu 1'	LVA00011	Latvia	1959	cultivar	(S) Norwegian local	six-rowed	Priekuļi Br. St.
'Priekuļu 60'	LVA00012	Latvia	1972	cultivar	Talsu local material x 'Maja' x 'Tammi'	two-rowed	Priekuļi Br. St.
'Stendes'	LVA00016	Latvia	1972	cultivar	'Drost' x 'Maja'	two-rowed	Stendes Br. St.
'Abava'	LVA00001	Latvia	1978	cultivar	'Mari' x 'Elsa' x 'Domen'	two-rowed	Stendes Br. St.
'Ilga'	LVA00006	Latvia	1983	cultivar	'KM 1192' x 'Hadmersleben 70179/70'	two-rowed	Priekuļi Br. St.
'Agra'	LVA00002	Latvia	1984	cultivar	'Priekuļu 1' x 'Otra'	six-rowed	Stendes Br. St.
'Imula'	LVA00007	Latvia	1985	cultivar	'Abava' x 'Akka'	two-rowed	Stendes Br. St.
'Balga'	LVA00004	Latvia	1990	cultivar	'Gunilla' x 'KM 1192'	two-rowed	Priekuļi Br. St.
'Rasa'	LVA00013	Latvia	1991	cultivar	'France gold' x 'HE-R-54'	two-rowed	Stendes Br. St.
'Klinta'	LVA00008	Latvia	1992	cultivar	'Torkel' x 'CF-42'	two-rowed	Agricultural University of Latvia
'Rūja'	LVA00014	Latvia	1992	cultivar	('Kombainieris' x 'Triumph') x 'Abava'	two-rowed	Priekuļi Br. St.
'Sencis'	LVA00015	Latvia	1994	cultivar	'Rupal' x 'Ofir' x Torkel	two-rowed	Stendes Br. St.
'Ansis'	LVA00003	Latvia	1995	cultivar	'KM 246-3-78' x Taifun	two-rowed	Stendes Br. St.
'Gate'	LVA00005	Latvia	1995	cultivar	'H 497' x 'Hadmersleben x Nadja'*2 x 'Emir'	two-rowed	Priekuļi Br. St.
'Malva'	LVA00166	Latvia	1998	cultivar	'STN8142' x 'STN7542'	two-rowed	Agricultural University of Latvia
'L-1879'	LVA01393	Latvia	-	breeding line	unknown	two-rowed	Priekuļi Br. St.
'L-1883'	LVA01394	Latvia	-	breeding line	'Ida' x ('Mazurka' x 'KM 1192')	two-rowed	Priekuļi Br. St.
'L-1885'	LVA01396	Latvia	-	breeding line	unknown	two-rowed	Priekuļi Br. St.
'8154'	-	Latvia	-	breeding line	'Athos' x 'Ving'	two-rowed	Stendes Br. St.
'7978'	-	Latvia	-	breeding line	'Nadja' x 'Ofir'*2	two-rowed	Stendes Br. St.
'8993'	-	Latvia	-	breeding line	'7233' x 'Belfor'	two-rowed	Stendes Br. St.
'Jogeva'	EST17	Estonia	1931	cultivar	(S) 'Binder'	six-rowed	Jõgeva Pl. Br. Inst.
'Jogeva 1104'	EST18	Estonia	1953	cultivar	'Maja' x 'Rimpau Hanna'	two-rowed	Jõgeva Pl. Br. Inst.
'Toomas'	EST23	Estonia	1976	cultivar	(S) local population	six-rowed	Jõgeva Pl. Br. Inst.
'Liisa'	EST20	Estonia	1981	cultivar	'Hylkema' x 'Diamant'	two-rowed	Jõgeva Pl. Br. Inst.
'Miina'	EST21	Estonia	1981	cultivar	'Jogeva' x 'Hylkema'	two-rowed	Jõgeva Pl. Br. Inst.
'Esme'	EST16	Estonia	1982	cultivar	'Foma' x 'Hylkema'	two-rowed	Jõgeva Pl. Br. Inst.
'Elo'	EST15	Estonia	1989	cultivar	'Triumph' x 'Lofa'	two-rowed	Jõgeva Pl. Br. Inst.
'Teele'	EST22	Estonia	1991	cultivar	(M) 'Otra'	six-rowed	Jõgeva Pl. Br. Inst.
'Anni'	EST14	Estonia	1993	cultivar	'Lola' x 'Lisa'	two-rowed	Jõgeva Pl. Br. Inst.
'Leelo'	EST19	Estonia	1995	cultivar	'Ansgar' x 'Sv 2552' x 'Elo'	two-rowed	Jõgeva Pl. Br. Inst.
'Roosi'	EST240	Estonia	1999	cultivar	'Abava' x 'Nadja' x 'Piggi'	two-rowed	Jõgeva Pl. Br. Inst.
'2686.10.1.6'	EST575	Estonia	-	breeding line	'1338.3.4' x 'Moskva 2'	two-rowed	Jõgeva Pl. Br. Inst.
'2734.2.5.5'	EST576	Estonia	-	breeding line	'Sv 86298' x 'Digger'	two-rowed	Jõgeva Pl. Br. Inst.
'2867.14.3.3'	-	Estonia	-	breeding line	'546.11.27' x 'Ellinor'	two-rowed	Jõgeva Pl. Br. Inst.
'2878.1.6.4'	-	Estonia	-	breeding line	'546.11.27' x 'KM 1192'	two-rowed	Jõgeva Pl. Br. Inst.
'2928.10.9.9'	-	Estonia	-	breeding line	'Elo' x 'Ultra'	two-rowed	Jõgeva Pl. Br. Inst.
'2951.6.9.3'	-	Estonia	-	breeding line	'Roland' x 'Defra'	two-rowed	Jõgeva Pl. Br. Inst.
'2975.4.1.2'	-	Estonia	-	breeding line	'Corgi' x 'Ilka'	two-rowed	Jõgeva Pl. Br. Inst.
'2987.1.2.1'	-	Estonia	-	breeding line	'1338.3.4' x 'Corgi'	two-rowed	Jõgeva Pl. Br. Inst.
'3038.3.7.4'	-	Estonia	-	breeding line	'546.11.27' x 'Maresi'	two-rowed	Jõgeva Pl. Br. Inst.
'Auksinai'	AGB00255	Lithuania	1927	cultivar	(S) 'Gul'	two-rowed	Lithuanian Institute of Agriculture

Table 1 (continued)

1	2	3	4	5	6	7	8
'Dotnuvos Keturėliai'	AGB00256	Lithuania	1930	cultivar	(S) local material	six-rowed	Lithuanian Institute of Agriculture
'Auksinai II'	AGB00258	Lithuania	1947	cultivar	Abed Kenia x Akerman Isaria	two-rowed	Lithuanian Institute of Agriculture
'Dziugiai'	AGB0257	Lithuania	1947	cultivar	(S) local material	two-rowed	Lithuanian Institute of Agriculture
'Gintarinai'	AGB00260	Lithuania	1973	cultivar	'KM 1081252' x 'Pallas'	two-rowed	Lithuanian Institute of Agriculture
'Dainiai'	AGB00261	Lithuania	1981	cultivar	'1561-12' x 'Abed 3371'	two-rowed	Lithuanian Institute of Agriculture
'Vilnieciai'	AGB002263	Lithuania	1982	cultivar	(M) 'Pallas'	two-rowed	Lithuanian Institute of Agriculture
'Gausiai'	AGB00255	Lithuania	1998	cultivar	'Auksinai II' x (MIX) 'Viner'+ 'Bingo'+ 'Abed' +Archer'	two-rowed	Lithuanian Institute of Agriculture
'Auksinai III'	AGB00262	Lithuania	1983	cultivar	'Carina' x 'Tarra 26'	two-rowed	Lithuanian Institute of Agriculture
'Aidas'	AGB00264	Lithuania	1990	cultivar	('KM 1192' x Ofir) x 'Effendi'	two-rowed	Lithuanian Institute of Agriculture
'Ūla'	AGB002265	Lithuania	1992	cultivar	'Roland' x 'Ca 33787'	two-rowed	Lithuanian Institute of Agriculture
'Alsa'	AGB002266	Lithuania	1993	cultivar	('Minera' x (M)'Gintarinai') x (Abava x Emir)	two-rowed	Lithuanian Institute of Agriculture
'Aura'	AGB00267	Lithuania	1996	cultivar	('Mirena' x (M)'Gintarinai) x 'Lina'	two-rowed	Lithuanian Institute of Agriculture
'LIA 6107-26'	AGB00541	Lithuania	-	breeding line	'Roland' x 'Ca 53102'	two-rowed	Lithuanian Institute of Agriculture
'LIA 6700-28'	AGB00544	Lithuania	-	breeding line	'Vega' x (Sv 73608 x WW 6405) x two-rowed 'HVS 929/77 x ('Chellas' x 'Mirena')		Lithuanian Institute of Agriculture
'LIA 6782-33'	AGB00546	Lithuania	-	breeding line	'Vega' x ('Ofir' x 'Berenice) x 'Liisa'	two-rowed	Lithuanian Institute of Agriculture
'Luokė'	AGB00268	Lithuania	2001	cultivar	'Vega' x ('Ofir' x 'Berenice) x 'Flare'	two-rowed	Lithuanian Institute of Agriculture
'LIA 6804-62'	AGB00545	Lithuania	-	breeding line	'Ūla' x 'Korru'	two-rowed	Lithuanian Institute of Agriculture
'LIA 6121-02'	AGB00543	Lithuania	-	breeding line	'Krinichnij' x ('KM 1192' x 'Ofir') two-rowed x'Deba' x 'KM 1192')		Lithuanian Institute of Agriculture
'LIA 6186-03-01'	AGB00542	Lithuania	-	breeding line	('KM 1192' x 'Ofir') x ('KM 1192' two-rowed x 'Mami') x ('KM 1192' x 'Ofir') x ('Maris Mink' x 'Nadia')		Lithuanian Institute of Agriculture

companies (Jõgeva Plant Breeding Institute, Priekuļi and Stende Plant Breeding Stations in Latvia and Lithuanian Institute of Agriculture in Lithuania). Both six-rowed (7 accessions) and two-rowed (57 accessions) types were included in this study.

Isozyme analysis. Fresh leaves of one-week-old plants were harvested for the isozyme analysis. Ten individual plants per accession were examined. The methods for isozyme electrophoresis, staining and nomenclature were used as in Kolodinska Brantestam *et al.* (2003). Three isozyme systems (aconitase, esterase and phosphogluconate) for detecting polymorphism were employed for genetic profiling of the spring barley material. Eight isozyme loci where characterised. The designation of alleles at the Aco-1 and Pgd-2 loci followed that of Nielsen and Johansen (1986), at Est-1; Est-2, Est-4 and Est-5 loci Hvid followed Nielsen (1977) and at Aco-2 locus — Liu *et al.* (1999).

Microsatellite analysis. Fresh leaves of two-week-old plants were harvested for microsatellite analysis. Depending on the breeding period each accession was represented by a different number of examined individuals: eight individuals were selected for landraces and cultivars released until 1950, and four individuals for the rest of material with the exception of breeding lines in which only two individuals were assessed. The methods of Kolodinska Brantestam *et al.* (2007) were used for DNA extraction, PCR reaction and fragment visualisation and 21 microsatellite primer pairs were used: Bmac0399, Bmac0032, WMC1E8, HVM36, Bmag0125, EBmac0415, HvLTPBB, Bmac0067, Bmac0067, Bmac0013, Bmac0384, EBmac0701, HVM67, EBmac0970, Bmac0223, AF043094, Bmag0173, EBmac0806, Bmac0040, Bmac0007, Bmac0273, Bmag0135. Twenty-two loci in total were characterised, as HvLPBB amplified fragments occurred at two sites.

Statistical analysis. Gene diversity at each locus was calculated using the gene diversity index of Nei (1973). Total genetic diversity for the groups of accessions (H_T) was estimated according to Hamrick and Godt (1997). Genetic distances (Rogers, 1972) between the accessions were calculated using the NTSYS-pc statistical package (Rolf, 1998). The analysis of molecular variance was performed using ARLEQUIN 3.1 software (Excoffier *et al.*, 2005).

RESULTS

Marker diversity. For the three isozyme systems a total number of eight loci were analysed. Of these loci two were monomorphic and in six loci polymorphism was detected.

In total 15 alleles were found (1 to 3 alleles per locus) and the average genetic diversity (H_T) was 0.244 (gene diversity h varied from 0 to 0.390 depending on the locus). Of the 22 microsatellite loci, all were polymorphic and in total 141 alleles (2 to 14 alleles per locus) were distinguished. The average genetic diversity based on microsatellite markers (H_T) was 0.561 (gene diversity h varied from 0.031 to 0.858 depending on the locus) (Table 2).

Genetic profile and within accession variation. Individual genetic profiles at each isozyme and microsatellite locus for each accession are available in the complementary material of this paper (Appendix 1 and Appendix 2). Isozyme data showed that 34 accessions did not have within accession variation, whereas SSR data detected variation at one or

Table 2

ISOZYME AND MICROSATELLITE MARKER DIVERSITY

Marker type	Loci	Alleles detected*	Number of alleles	Gene diversity (h)
Isozymes	Aco-1	Ge, Fn	2	0.34
	Aco-2	A, B	2	0.08
	Est-1	Al, Ca, Pr	3	0.39
	Est-2	Fr	1	0
	Est-4	At, Su	2	0.5
	Est-5	Pi, Te	2	0.17
	Pdg-1	Ak	1	0
	Pdg-2	Ps, Tn	2	0.47
Average values for isozyme loci				1.9
				0.24
Microsatellite	Bmac0399	123, 126, 134, 136, 138, 145, 147	7	0.79
	Bmac0032	212, 214, 216, 218, 220, 224, 240	7	0.69
	WMC1E8	190, 236	2	0.17
	HVM36	106, 108, 110, 114, 119	5	0.60
	Bmag0125	133, 135, 137, 139, 143, 145	6	0.69
	EBmac0415	224, 235, 241, 245, 250	5	0.56
	HvLTPBBA	218, 220	2	0.03
	HvLTPBBb	207, 211	2	0.13
	Bmac0067	167, 169, 171, 173, 175, 177, 179, 181, 183	9	0.56
	Bmac0013	150, 152, 154, 156, 158, 162, 165	7	0.64
	Bmac 0384	112, 114, 116, 118	4	0.43
	EBmac 0701	138, 140, 142, 144, 146, 148, 150, 152, 160	9	0.73
	HVM67	110, 114, 116, 120	4	0.50
	EBmac0970	188, 190, 192	3	0.33
	Bmac0223	157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 187	14	0.86
	AF043094 A	145, 146, 147	3	0.38
	Bmag0173	121, 123, 126, 130, 142, 144, 146, 148, 150, 152, 0**	11	0.83
	EBmac0806	162, 164, 170	3	0.54
	Bmac 0040	182, 198, 202, 204, 210, 216, 221, 225, 227, 229, 231, 233, 235, 239	14	0.80
	Bmac0007	186, 190, 192, 194, 196, 198, 200, 202, 204, 224	10	0.79
	Bmac0273	177, 179, 183, 185, 187, 189	6	0.68
	Bmag0135	120, 144, 146, 148, 150, 160, 162, 164	8	0.63
Average values for microsatellite loci				6.4
				0.56

* for isozymes allele names follow the references in which these alleles were designated (see methods), for microsatellites alleles are determined as fragment sizes in bp.

** ‘zero allele’, primer pairs did not amplify fragment at this loci

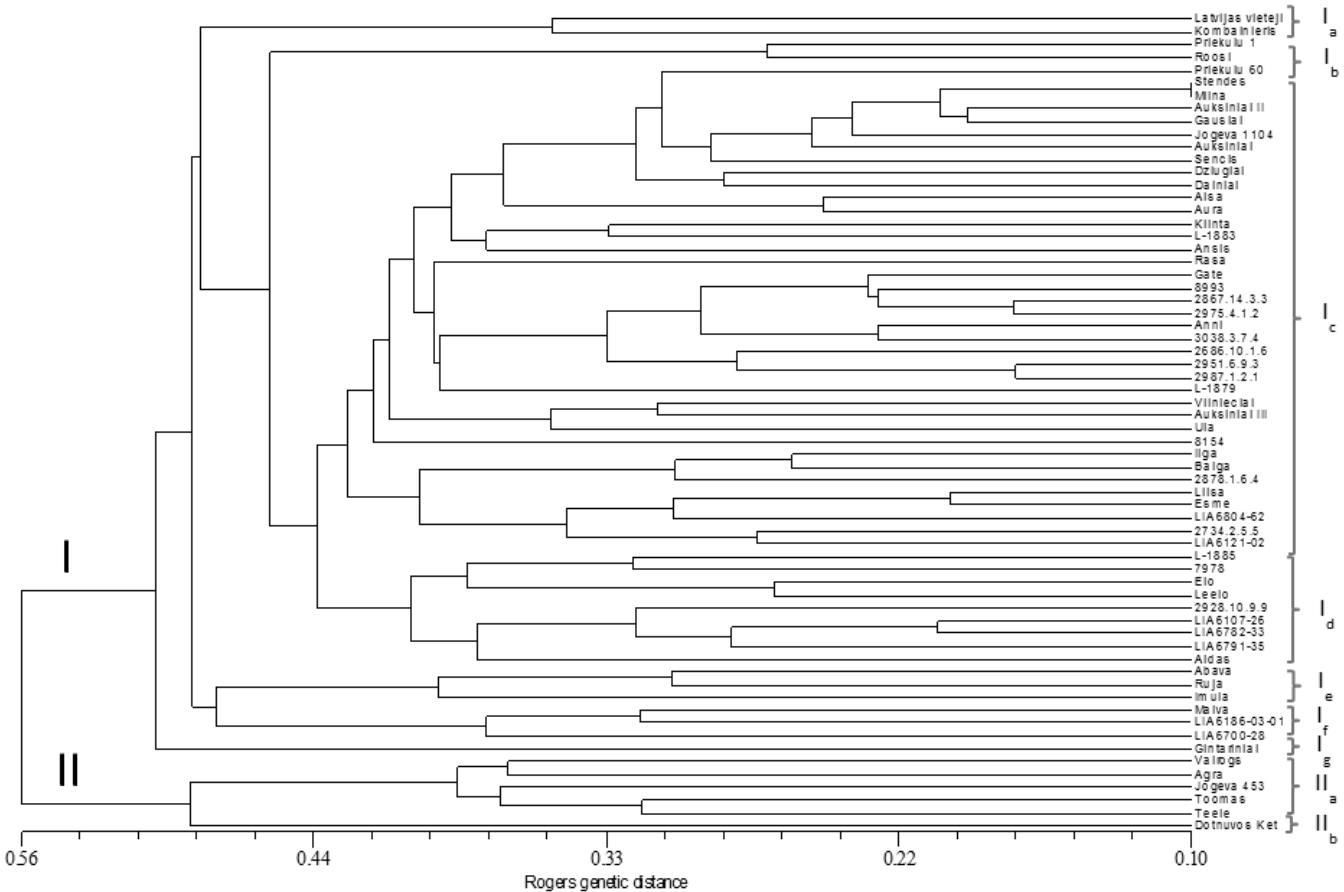


Fig. 1. Dendrogram based on pooled isozyme and microsatellite data demonstrating relationships between Baltic spring barley accessions.

more loci for all accessions analysed, with the exception of Estonian breeding line '2686.10.1.6' and Lithuanian cultivar 'Aura'. Based on isozyme data, 30 of the accessions could be distinguished by individual patterns of alleles and allele frequency distribution, whereas the remaining accessions formed groups from two to eight accessions which could not be separated. However, all of the accessions were distinguished by microsatellite data.

Genetic relationships. The dendrogram based on pooled isozyme and microsatellite data clearly separated material in two distant groups (I & II) of accessions (Fig. 1). One included exclusively only six rowed accessions (II), whereas the other contained all of the two rowed accessions, with the exception of the 'Priekuļu 1' cultivar that had a six-rowed spike (I). The group of six-rowed material was further divided into two sub groups (II_a & II_b), where 'Dotnuvos Keturleliai' (II_b) appeared to be distant from the other six-rowed accessions in II_a. The predominantly two-rowed group of accessions (I) was divided into seven subgroups: subgroup I_a containing landrace 'Latvijas vietējie' and cultivar 'Kombainieris', I_b included two-rowed cultivars 'Roosi' and 'Priekuļu 60'; I_d – Estonian and Lithuanian breeding lines 'L1885', '7978', '2928.10.9.9', 'LIA6107-26', 'LIA6782-33', 'LIA6791-35' and cultivars

released after 1989 'Elo', 'Leelo' and 'Aidas'; I_e – Latvian cultivars 'Abava', 'Rūja' and 'Imula'; I_f – Latvian cultivar 'Malva' and Lithuanian breeding lines 'LIA6186-03-01' and 'LIA670028'; I_c included the remaining two-rowed accessions with the exception of cultivar 'Gintariniai', which fell into the seventh group – I_g.

Genetic diversity. When material from each country was analysed separately, the highest values for number of alleles and average gene diversity for SSR data were found for accessions released in the period between 1981 and 2000 (Table 3). For isozyme data, a similar pattern was observed. In Lithuanian accessions the total number of alleles was 12 for all periods, not including cultivars released from 1951 to 1980 in which this value was 10, but the H_T value was highest in accessions released from 1981 to 2000, following the same trend as in Latvian and Estonian material (Table 3). When diversity was compared between accessions with different country of origin, the most diverse accessions according to isozyme data was material from Latvia ($H_T = 0.27$, $A = 15$), followed by material from Lithuania ($H_T = 0.24$, $A = 14$). The Estonian material had the least diversity ($H_T = 0.14$, $A = 14$). Microsatellite data showed also that Latvian accessions were most diverse ($H_T = 0.56$, $A = 114$), followed by material from Lithuania ($H_T = 0.53$, $A = 109$) and Estonia ($H_T = 0.52$, $A = 96$).

Table 3

DIVERSITY OF ACCESSIONS IN DIFFERENT TYPES OF MATERIAL AND COUNTRY OF ORIGIN

Country	Type of material	SSR		Isozyme	
		number of alleles	HT (average gene diversity)	number of alleles	HT (average gene diversity)
Latvia	Landraces and cultivars before 1950	49	0.41	13	0.28
	Cultivars 1951–1980	53	0.39	13	0.28
	Cultivars 1981–2000	92	0.53	15	0.28
	Cultivars after 2001 and breeding lines	61	0.45	11	0.15
Estonia	Landraces and cultivars before 1950	42	0.27	8	0
	Cultivars 1951–1980	55	0.42	12	0.24
	Cultivars 1981–2000	71	0.51	13	0.11
	Cultivars after 2001 and breeding lines	63	0.40	11	0.08
Lithuania	Landraces and cultivars before 1950	73	0.44	12	0.15
	Cultivars 1951–1980	27	0.08	10	0.06
	Cultivars 1981–2000	71	0.47	12	0.21
	Cultivars after 2001 and breeding lines	62	0.46	12	0.15
All Baltic	Landraces and cultivars before 1950	93	0.55	14	0.27
	Cultivars 1951–1980	82	0.50	13	0.29
	Cultivars 1981–2000	110	0.55	15	0.24
	Cultivars after 2001 and breeding lines	93	0.51	12	0.18

DISCUSSION

Genetic diversity. The distribution of molecular variation in Baltic spring barley demonstrated variation not only among but also within the accessions (Table 4a and 4b). The variation within accessions was significant when examined both by microsatellite and isozyme data and accounted for 20.6% or 14.3%, respectively, of the total variation. This is an important fact to consider not only when developing management strategies for conservation in gene banks, but also when characterizing/evaluating these accessions and utilising them in research and breeding.

Several studies have reported changes in diversity due to plant breeding. These have shown different conclusions de-

pending on the country of origin of material, and have detected either temporal flux without genetic erosion, or somewhat lower diversity in modern material (Russel *et al.*, 2000; Matus and Hayes, 2002; Koebner *et al.*, 2003; Reeves *et al.*, 2004; Kolodinska Brantestam *et al.*, 2007). A meta study of diversity trends in released crop varieties in the twentieth century for eight different field crops (Wouw *et al.*, 2010) concluded that significant decrease of diversity could not be detected. In our study groups of accessions from early breeding periods were unfortunately under-represented, since there was only a limited set available in the gene banks. Thus, even though the highest diversity values were detected in cultivars released from 1981 to 2000, it cannot be safely concluded that this material is more diverse than material grown in the Baltic States in the early 20th century. The few accessions representing landraces ‘Latvijas vietējie’ and early cultivars based on selection from local material, like ‘Vairogs’, ‘Toomas’, Dotnuvos Ketureililai’ and ‘Dziugiai’ also demonstrated rather large genetic distances among them and were distributed in different clusters and sub-clusters in the dendrogram, with the exception of ‘Vairogs’ and ‘Toomas’ in sub-cluster II_a (Fig. 1).

Table 4

DISTRIBUTION OF VARIATION AMONG AND WITHIN ACCESSIONS

a

AMOVA based on isozyme data

Source of variation	d.f.	Sum of squares	Variance components	Percentage of variation
Among accessions	63	988.974	0.8669*	85.68
Within accessions	1086	157.343	0.1449*	14.32
Total	1149	1146.317	1.0118	

b

AMOVA based on microsatellite data

Source of variation	d.f.	Sum of squares	Variance components	Percentage of variation
Among accessions	63	1802.138	4.1709*	79.37
Within accessions	360	390.312	1.084*	20.63
Total	423	2192.450	5.2551	

* P < 0.000001

The higher diversity values in Latvian barley material compared to the other Baltic countries might be due to the history of breeding. Since the early 20th century, two breeding companies have been actively working with cereal breeding. Some cereal breeding has also been performed at the Agricultural University of Latvia. The existence of several entities involved in breeding might have contributed to the diversity of the existing cultivars in Latvia, since different breeding strategies may have been employed and different material was used in crosses.

Differentiation of accessions. The differentiation between two-and six rowed accessions based on molecular markers has been reported both in cultivars and landraces of barley from different countries of origin (Lasa and Igartua, 2001; Chaabane *et al.*, 2009; Chen *et al.*, 2009). The differentiation of two-rowed and six-rowed accessions was apparent also in Baltic barley material (Fig. 1) Also the AMOVA showed a significant share of variation that was explained by differentiation of two-rowed and six-rowed accessions (microsatellite data 16.95%, $P < 0.001$, isozyme data 26.84% $P < 0.001$). There were some differences in grouping of six-rowed versus two rowed accessions based on isozyme and microsatellite data. When only microsatellite data were used the two-rowed Latvian cultivar 'Imula' grouped together with the six-rowed accessions (data not shown). On the other hand, when data of microsatellite and isozyme were pooled, 'Imula' grouped together with the other two-rowed accessions (Fig. 1). This inconsistency might be because the accession has six-rowed Finnish and Norwegian material in the pedigree and thus depending on the DNA regions analysed, either similarity to two-rowed or six-rowed accessions can be detected.

Closer genetic relations between the accessions can be explained by common material used in the pedigrees. For example, the cultivar 'Abava' is found both in the pedigree of cultivar 'Imula' and 'Rūja' and these three cultivars are found in the same cluster I_e. However, 'Abava' is also present in the pedigree of Estonian cultivar 'Roosi' and Lithuanian cultivar 'Alsa', which are genetically rather distant and were found in different clusters I_b and I_c, respectively.

There was no clear grouping of accessions according to the country of origin (Fig. 1). AMOVA analysis based on microsatellite data showed that the variation explaining differentiation among countries was not significant. The isozyme data, however, showed some variation (9%, $P = 0.001$) that explained differences between countries. The weak differentiation of accessions by country of origin can

be explained by common ancestors that were used in the breeding programmes in the Baltic countries. For example, on the basis of ancestral trees of Baltic barley, often common foreign material can be found, like 'Gull' from Sweden, 'Binder' and 'Hanna' from Moravia and 'Ackerman's Bavaria' from Bavaria. A more recent example is line 'KM 1192', which has been used by breeders in all three countries, and thereby can explain the location of Estonian breeding line '28781.6.4' and Latvian cultivars 'Ilga' and 'Balga' in the same sub cluster of I_c (Fig. 1). Line 'KM 1192' predominantly was used as a powdery mildew resistance source (Tueryapijna *et al.*, 1996) and other accessions (breeding line 'L1183', 'LIA612102', 'Aidas' and 'LIA6186-03-01') containing this line were not clustered together with 'Ilga', 'Balga' and '28781.6.4', which might be due to backcrossing with other material. It should also be noted that 'Ilga' and 'Balga' have the 'ulu2' gene from 'KM 1192', which it is not present in Lithuanian cultivar 'Aidas' (Tueryapijna *et al.*, 1996).

The isozyme variation represents variation of the coding region of the barley genome, whereas SSR in cereals predominantly represents the non-coding sequences (Kalia *et al.*, 2011). This can explain why a limited set of isozymes explained greater variation due to the country of origin than was explained by microsatellite genetic variation. Even though many Baltic cultivars contain common material in their pedigree and are interrelated, there has been selection for traits separating Estonian, Latvian and Lithuanian material, in order to reach better agronomical performance for the target country.

ACKNOWLEDGEMENTS

We thank the Baltic breeding companies and gene banks for providing accessions included in this study. This study was part of the project "Genetic diversity in Nordic-Baltic crops — a model study of genetic erosion in barley" supported by the Royal Swedish Academy of Agriculture and Forestry.

Appendix 1

ALLELIC PROFILES OF ISOZYME LOCI FOR BALTIC BARLEY ACCESSIONS

Accession	Aco-1	Aco-2	Est-1	Est-2	Est-4	Est-5	Pgd-1	Pgd-2
1	2	3	4	5	6	7	8	9
'Latvijas vietējie'	Ge	B	Ca/Pr	Fr	At	Pi	Ak	Tn
'Vairogs'	Ge	B	Pr	Fr	Su	Pi	Ak	Tn
'Kombainieris'	Fn	B	Ca/Pr	Fr	At	Te	Ak	Ps
'Priekuļu 1'	Fn	B	Pr	Fr	Su	Te	Ak	Tn
'Priekuļu 60'	Ge	B	Ca	Fr	At	Pi	Ak	Ps
'Stendes'	Ge	B	Ca	Fr	At	Pi	Ak	Ps/Tn
'Abava'	Ge	B	Pr	Fr	Su	Pi	Ak	Ps
'Ilga'	Ge	B	Al/Ca	Fr	At	Te	Ak	Ps/Tn
'Agra'	Ge	A/B	Ca/Pr	Fr	Su	Pi	Ak	Ps/Tn
'Imula'	Fn	B	Pr	Fr	Su	Pi	Ak	Ps/Tn
'Balga'	Ge	B	Ca	Fr	At	Pi	Ak	Tn
'Rasa'	Fn/Ge	B	Pr	Fr	Su	Pi	Ak	Ps
'Klinta'	Ge	B	Ca/Pr	Fr	At/Su	Pi	Ak	Ps
'Rūja'	Fn/Ge	B	Pr	Fr	Su	Te	Ak	Ps

Appendix 1 (continued)

1	2	3	4	5	6	7	8	9
'Sencis'	Ge	B	Ca/Pr	Fr	At	Pi	Ak	Ps/Tn
'Ansīs'	Ge	B	Ca	Fr	Su	Pi	Ak	Ps
'Gate'	Ge	B	Ca	Fr	Su	Pi	Ak	Tn
'Malva'	Fn	B	Pr	Fr	Su	Te	Ak	Ps
'L-1879'	Ge	B	Ca	Fr	At	Pi	Ak	Tn
'L-1883'	Ge/Fn	B	Ca	Fr	At	Pi	Ak	Tn
'L-1885'	Ge/Fn	B	Ca	Fr	At	Pi	Ak	Tn
'8154'	Ge	B	Ca	Fr	Su	Pi	Ak	Ps
'7978'	Ge	B	Ca	Fr	At	Pi	Ak	Tn
'8993'	Ge	B	Ca	Fr	Su	Pi	Ak	Ps
'Jogeva 453'	Ge	A	Ca	Fr	Su	Pi	Ak	Tn
'Jogeva 1104'	Ge	B	Ca	Fr	At	Pi	Ak	Ps/Tn
'Toomas'	Fn	B	Pr	Fr	Su	Pi	Ak	Tn
'Liisa'	Ge	B	Ca	Fr	At	Pi	Ak	Tn
'Miina'	Ge	B	Ca/Pr	Fr	At	Pi	Ak	Ps/Tn
'Esmē'	Ge	B	Ca	Fr	At	Pi	Ak	Tn
'Elo'	Ge	B	Ca	Fr	At	Pi	Ak	Tn
'Teele'	Fn/Ge	B	Pr	Fr	Su	Pi	Ak	Tn
'Anni'	Ge	B	Ca	Fr	Su	Pi	Ak	Tn
'Leelo'	Ge	B	Al/Ca	Fr	At/Su	Pi	Ak	Tn
'Roosi'	Ge	B	Ca	Fr	Su	Pi	Ak	Tn
'2686.10.1.6'	Ge	B	Ca	Fr	Su	Pi	Ak	Tn
'2734.2.5.5'	Ge	B	Ca	Fr	At	Pi	Ak	Tn
'2867.14.3.3'	Ge	B	Ca	Fr	Su	Pi	Ak	Tn
'2878.1.6.4'	Ge	B	Ca	Fr	Su	Pi	Ak	Tn
'2928.10.9.9'	Ge	B	Ca	Fr	At	Pi	Ak	Ps/Tn
'2951.6.9.3'	Ge	B	Ca	Fr	Su	Pi	Ak	Tn
'2975.41.2'	Ge	B	Pr	Fr	Su	Pi	Ak	Tn
'2987.1.2.1'	Ge	B	Ca	Fr	At/Su	Pi	Ak	Tn
'3038.37.4'	Ge	B	Ca	Fr	Su	Pi	Ak	Tn
'Auksinai'	Ge	B	Ca/Pr	Fr	At	Pi	Ak	Ps/Tn
'Dotnuvos Ketureilai'	Ge	A/B	Ca/Pr	Fr	At	Pi	Ak	Ps/Tn
'Auksinai II'	Ge	B	Ca/Pr	Fr	At/Su	Pi	Ak	Ps
'Dziugiai'	Ge	B	Ca	Fr	At/Su	Pi	Ak	Ps
'Gintariniai'	Ge	B	Ca/Pr	Fr	At	Te	Ak	Ps/Tn
'Daina'	Ge	B	Ca/Pr	Fr	At	Pi	Ak	Ps/Tn
'Vilnieciai'	Ge	B	Pr	Fr	Su	Pi	Ak	Ps
'Gausai'	Ge	B	Ca	Fr	At	Pi	Ak	Ps
'Auksinai 3'	Ge	B	Pr	Fr	Su	Pi	Ak	Ps/Tn
'Aidas'	Fn	B	Ca	Fr	At	Pi	Ak	Tn
'Ula'	Ge	B	Ca/Pr	Fr	Su	Pi	Ak	Tn
'Alsa'	Fn/Ge	B	Ca	Fr	At	Pi	Ak	Ps/Tn
'Aura'	Ge	B	Ca	Fr	At	Pi	Ak	Tn
'6107-26'	Fn	B	Ca	Fr	At	Pi	Ak	Tn
'6700-28'	Fn	B	Ca/Pr	Fr	At/Su	Pi	Ak	Ps/Tn
'6782-33'	Fn	B	Ca	Fr	At	Pi	Ak	Ps/Tn
'6791-35'	Fn/Ge	B	Ca	Fr	At	Pi	Ak	Tn
'6804-62'	Fn	B	Ca	Fr	At	Pi	Ak	Tn
'6121-02'	Fn	B	Ca	Fr	At	Pi	Ak	Tn
'6186-03-01'	Fn	B	Ca/Pr	Fr	At/Su	Pi	Ak	Ps/Tn

ALLELIC PROFILES OF MICROSATELLITE LOCI FOR BALTIC BARLEY ACCESSIONS

Accession name	Bmac039	Bmac003	WMC1E	HVM36	Bmag012	EBmac06	HvLTPB	Bmac006	Bmac01	Bmac	HVM67	EBmac09	Bmac022	AF04309	Bmag017	EBmac08	Bmac	Bmac000	Bmac027	Bmac013			
1	9	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
'Latvijas viežēj'	123	216	236	119	143	224	218	207	171	156	114	142	114	190	169	146	130	170	231	202/204	185	160	
'Vairogs'	147	212	190	108	133	241	218	207	177	156	112	150	114	190	165	147	130	170	198	198/200/	179	120/146/	
'Kombainieris'	145	220	236	106	143	224/245	218	207	177	158	114	142	116	190	171	146	130	170	231	202/204	185	148/160	
'Priekuļu 1'	136	216	236	106	135/137	224	218	207	177	156	114	146	116	192	167/169	146	152	162	225	196	185	164	
'Priekuļu 60'	145	216	236	106	139	245	218	207	177	158	116	148	116	190	171/173/	146	142	170	233	198	189	150	
'Stendes'	136/145	212/216/	236	106	137/139	245	218	207	177	158	114/116	148	110/116	190	167/173/	146	142/144/	162	233	196/200	183/189	148	
'Abava'	134/136/	212	236	108	139	245/250	218	207	177	156/158	114	146	116	190	173/175	145/146	152	162/170	233	198	187	146	
'Iīga'	145	224	236	106	137	245	218	207	177	158	114	138	110	190	165/167	145/146	126	164	233	194	189	148	
'Agra'	138/147	212/240	190/236	110	133/137	245	218	207	169	156	112	148/150/	114	190	165/173/	146/147	130	170	198/202	200	179	120	
'Imula'	145	212	236	119	137	245	218	207	177	158	112/114	150	114	190	175/177	147	130	170	204/231	194	187	146	
'Balga'	145	216	236	106	139	224	218	207	177	156	114	138	110	190	165/167	146	no ampl.*	164	233	194	187	148	
'Rasa'	123	218	236	108	143	245	218	207	179	156	114	146	116	188	167/169/	146	130	162	221	196	185	162	
'Kinta'	138	218	236	106	137	224/245	218	207	177	165	114	138	116	190	173/175/	146	144	162	182	198/200	185	162	
'Rūja'	145	212	236	108	139	245	218	207	177	158	114	144/146	116	190	169/171/	146	130/152	170	231	202/204	183	150	
'Senčis'	136	236	108	137/139	224	218	207	177	158	114	148	116	190	159/175	145/146	144	162	233	194/198	187	148/160		
'Ansīs'	145	216	236	108	137	235	218	207	177	154/158	114	146	116	190	165/167	145	144	162	202	194	183	148	
'Gāle'	138	216	236	108	135	245	218	207	175	156	114	146	116	192	171/173	146	144	162	221	192/194	189	146	
'Malva'	145	216/218	236	106	137/139	245	218	207	177	154	114	150	116	190	167/169	146	144	170	221	192/194	189	148	
'L-1879'	123	218	236	114	139	245	218	207	179	156	114	148	116	190	161/163	146	146	170	221	196/198	183	144	
'L-1883'	123	218	236	108	137	245	218	207	177	154	114	146	116	190	161/	146	144	162	233	194	185	144	
'L-1885'	123	216	236	108	137	224	218	207	177	154/156/	112	148	114/116	190	175/177	147	142	170	239	192/194	185	146	
'8154'	123/126	216	236	106	137	245	218	207	175	154	114	148	114	190	159/169	145	146	162/170	210	192	189	148	
'7978'	126	216	236	108	137	224	218	207	179	154/156	114	148	116	190	167/169	145	142	162	221	192/194	185	148	
'8993'	138	218	236	108	137	224	218	207	177	156	114	150	116	192	179/181	146	144	162	221	192/194	189	148	
'Jogeva 453'	138/145	214	190	108	135/139	241/245	218	207	175/177	150/152	112	144/146/	114	190/192	169/171/	146/147	130	170	202/204	192/194/	177/189	146/148	
'Jogeva 1104'	126/136/	216/218	236	106/108	137/139	245	218	207	175/177	156	114	148	114/116	190	167/169/	146	no ampl.*/	173/175	152	170	198/200	185/189	148/160
'Toomas'	147	214	236	108	139	224	218	207	171/173	150	112	148	114	190	173/175	146/147	130	170	198	198/200	185	120/146/	
'Liisa'	123/136	216/218	236	106	135/139	224	218	207	175/177	156	114	146/148	114	190	167/169	145/146	150	162	233	196/202	189	148	
'Mīna'	145	216	236	106	137	245	218	207	177	158	114/116	148	116	190	173/175	146	150/152	162	231/233	196	189	148	

Appendix 2 (continued)

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
'Esme'	136	216	236	106	135	224	218	207	177	158	114	148	114	190/192	167/169	146	152	162	233	196	185	148	
'Elo'	138	216	236	108	139	245	218	207	175	156	116	146/148	116	188	165/167/	146	142	170	235	194	185	146	
'Teie'	138	214	190/236	119	137/139	224/245	218	207	175	150	112	148/150	114	190	175/179	146/147	130	170	202/204	200	189	146/148/	
'Ann'	136/138	216	236	108	135	245	218	207	175	156	114	146	114	190	167/169	145/146	146	162	221	196	185	162	
'Lee'	136/138	212	236	108	137	245	218	207	175	156	116	148	116	190	173/175	146	142	170	198/233	192/194	183	146	
'Roosi'	136	216	236	106	135	224	218	207	177	156	114	146	116	192	167/169	145	150	162	225	196	185	162	
'2686.10.1.6'	136	212	236	108	139	245	218	207	177	156	114	138	110	190	173/175	146	no ampl.*	162	202	200	189	148	
'2734.2.5.5'	138	218	236	119	139	224	218	211	177	156	114	150	114	190	167/169	146	130	162	221	194	185	148	
'2867.14.3.3'	138	216	236	108	137	245	218	207	177	156	114	148	116	192	167/169	146	146	162	221	186	189	148	
'2878.1.6.4'	138	218	236	108	135	245	218	207	177	156	114	138	110	190	167/169	146	126	164	221/233	194	185	148	
'2928.10.9.9'	123	216	236	108	139	235	218	207	177	156	114	146	116	190	171/173	145/146	146	170	233/235	194/196	185	162	
'2951.6.9.3'	136	216	236	108	139	245	218	207	177	156	114	146	116	190	161/163	146	144	170	231/233	196	183	148	
'2975.4.1.2'	138	216	236	108	137	245	218	207	179	156	114	146	116	190	167/169	146	146	162	221	194	189	148	
'2987.1.2.1'	136	216	236	108	139	245	218	207	179	156	114	146	116	190	171/173	146	152	170	221/235	196/198	189	148	
'3038.3.7.4'	138	216	236	108	135	245	218	207	179	154/156	114	148	114	190	171/173	146	146	162	221	194/196	183	148	
'Aukšinai'	126/145	216/218	236	106/108	139	224	218	207	177/183	154/156/	114	148	116	190	159/165/	145/146	no	162/170	204/233	192/194/	185/189	144/148	
'Dotnuvos Keturėliai'	145/147	212/218	190/236	119	145	245	218	207	167/175/	152	112/114	148	114/116	190	171/173	146/147	121/123	170	202/233	190/192/	183	146/148	
'Aukšinai II'	138/145	218	236	106	137/139	245	218	207	177	152/154/	114	148	116	190	171/173	146	150	170	231/233	196/198	189	148	
'Daugiai'	138/145	220	236	108	139	245	218	207	175	154/158	114	140/142	116	188/190	171/173/	146	142/152	162/170	216/231/	196/198	189	148	
'Gintariniai'	136	218	190	106	139	235/245	218	207	179/181	154	114	148	116/120	190	169/171	146	146	162	182	202/204	185	148	
'Dainiai'	138	216/218	190/236	108	135/137/	245	218	207	173/175/	156	114	146	116	190	169/171	146	144	162/170	202/225	192/194	189	148	
'Vilniusciai'	145	218	190	106	137	224	218	207	175/177	154	114	146	114	190	167/169	146	130	162	221	196	189	148	
'Gausiai'	136/145	218	236	106/108	137	245	218	207	177	158/162	114	148	116	190	173/175/	145/146	121/150/	162/170	233	194/196/	187/189	148/162	
'Aukšinai III'	138/145	218	190/236	108	137/139	224	218	207	175/177	152/156	114/116	148	114	194/192	167/169/	146	144	162	221	196	189	148/162	
'Aidai'	126/134	216	236	106	139	224/235	218	211	177	158	114	148/150	116	188/192	161/167/	145/146	no	170	182/221	198/200/	189	162	
'Ula'	145	216	236	108	137	224	218	207	175/177	158	114	148/150	114/116	190	167/169	146	150	170	233	194/196	189	148	
'Alsa'	126	216	236	108	135	224	218	207/211	177	154/156	116	148/160	116	188	173/175	146	144	162	221	198	189	148	
'Aura'	126	216	236	106	135	245	218	211	175	154	116	148	116	190	171/173	146	144	162	221	196	189	148	
'LJA 6107-26'	136	216	236	108	139	224	218	207	177	156	116	150	116	190	167/169	147	144	170	225/227	196/198	185	148	
'LJA 6700-28'	145	218	190	119	135	224	218	207/211	175	156	116	150	116	192	167/169	146	144	170	221	194	189	148	
'LJA 6782-33'	123	216	236	108	139	224	218	207	175/177	156	118	146/150	116	190	167/169	146	144	170	227/233	196/198	185	162	
'LJA 6791-35'	123/138	216	236	106	139	224	218	207	177	158	118	150	116	190	167/169	146	144	170	233	194/196	183	146	
'LJA 6804-62'	138/145	216/218	236	106	139	224	220	211	177	156/158	114	148	114	190/192	165/167/	146	144	170	233	196	189	148	
'LJA 6121-02'	138/145	218	236	106/119	139	245	218	207	175/177	156	114	144/150	114	190	165/167/	146	150	162	202/229	194/200	185	146/148	
'LJA 6186-03-01'	126/136	218	236	108	135/139	224	218	207	177	154/156	114	150	116	190/192	167/169	145	144	170	233	194	185	148	

REFERENCES

- Anonymous (2012). FAO. <http://www.fao.org>
- Chaabane, R., Felah, M. E., Salah, H.B., Nauceur, M.B.B., Abdelly, C., Ramala, D., Nada, A., Saker, M. (2009). Molecular characterization of Tunisian barley (*Hordeum vulgare* L.) genotypes using microsatellites (SSRs) markers. *Eur. J. Sci. Res.*, **36**, 6–15.
- Chen, F., Chen, D., Brau V., Pilar, M., Gao, Z., Chen, X. (2009). Analysis of diversity in Chinese cultivated barley with simple sequence repeats: Differences between eco-geographic populations. *Biochem. Gen.*, **48**, 44–56.
- Excoffier, L., Laval, G., Schneider, S. (2005). Arlequin ver. 3.0: An integrated software package for population genetics data analysis. *Evolutionary Bioinformatics Online*, **1**, 47–50.
- Hamrick, J.L., Godt, M.J.W. (1997). Allozyme diversity in cultivated crops. *Crop Sci.*, **37**, 26–30.
- Hvid, S., Nielsen, G. (1977). Esterase isoenzyme variants in barley. *Hereditas*, **87**, 155–162.
- Kalia, R.K., Manoj, K.-R., Kalia, S., Singh, R., Dhawan, A.K. (2011). Microsatellite markers: An overview of the recent progress in plants. *Euphitica*, **177**, 309–334.
- Koebner, R.M.D., Donini, P., Reeves, J.C., Cooke, R.J., Law, J.R. (2003). Temporal flux in the morphological and molecular diversity of UK barley. *Theor. Appl. Gen.*, **106**, 550–558.
- Kolodinska Brantestam, A. (2005). A century of Breeding — is genetic erosion a reality? Temporal diversity changes in Nordic and Baltic barley. Doctoral thesis No. 2005:30. Swedish University of Agricultural Sciences.
- Kolodinska Brantestam, A., von Bothmer R., Rashal, I., Weibull, J. (2003). Changes in the genetic diversity of barley of Nordic and Baltic origin, studied by isozyme electrophoresis. *Plant Gen. Res.: Characterization and Utilization*, **1**, 143–149.
- Kolodinska Brantestam A., von Bothmer R., Dayteg C., Rashal I., Tuvesson S., Weibull, J. (2007). Genetic diversity changes and relationships in spring barley (*Hordeum vulgare* L.) germplasm of Nordic and Baltic areas as shown by SSR markers. *Gen. Res. Crop Evol.*, **54**, 749–758.
- Lasa, J., Igartua, E. (2001). Morphological and agronomical diversity patterns in the Spanish barley core collection. *Hereditas*, **135**, 217–225.
- Liu F., von Bothmer R., Salomon, B. (1999). Genetic diversity among East Asian accessions of the barley core collection as revealed by six isozyme loci. *Theor. Appl. Gen.*, **98**, 1226–1233.
- Matus, I.A., Hayes, P.M. (2002). Genetic diversity in three groups of barley germplasm assessed by simple sequence repeats. *Genome*, **45**, 1095–1106.
- Nei, M. (1973). Analysis of gene diversity insubdivided populations. *Proc. Nat. Acad. Sci. USA*, **70**, 3321–3323.
- Nielsen G., Johansen, H. (1986). Proposal for identification of barley varieties based on the genotypes for 2 hordein and 39 isoenzyme loci of 47 reference varieties. *Euphitica*, **35**, 717–728.
- Reeves, J.C., Chiapparino, E., Donini, P., Ganal, M., Guiard, J., Hamrit, S., Heckenberger, M., Huang, X.-Q., van Kaauwen, M., Kochieva, E., Koebner, R., Law, J.R., Lea, V., Le Clerc, V., van der Lee, T., Leigh, F., van der Linden, G., Malysheva, L., Melchinger, A.E., Orford, S., Reif, J.C., Röder, M., Schulman A., Vosman, B., van der Wiel, C., Wolf, M., Zhang, D. (2004). Changes over time in the genetic diversity of four major European crops from the Gediflux Framework 5 project. In: *Proceedings of 17th EUCARPIA General Congress: Genetic variation for plant breeding* (pp. 3–7). Vollmann, J., Grausgruber, H., Ruckenbauer, P. (eds.). Vienna: University of Natural Resources and Applied Life Sciences.
- Rogers, J.S. (1972). Measures of genetic similarity and genetic distance. In: *Studies in Genetics. Vol. VII* (pp. 145–153). Publ. 7213. Austin: University of Texas.
- Rolf, M. (1998). *NTSYS-pc: Numerical taxonomy and multivariate analysis system. Version 2.1. Department of Ecology and Evolution*. New York: State University of New York.
- Russel, J., Ellis, R., Thomas, B., Waugh, R., Provan, J., Booth, A., Fuller, J., Lawrence, P., Young, G., Powell, W. (2000). A retrospective analysis of spring barley germplasm development from ‘foundation’ genotypes’ to currently successful cultivars. *Mol. Breed.*, **6**, 553–568.
- Tueryapina, R., Jensen, H.P., Rashal, I. (1996). Powdery mildew resistance genes in Baltic spring barley varieties and breeding lines. *Barley Gen. Newslett.*, **27**, 18–21.
- van de Wouw, M., van Hintum, T., Kik, C., van Treuren, R., Visser, B. (2010). Genetic diversity trends in twentieth century crop cultivars: A meta analysis. *Theor. Appl. Gen.*, **120**, 1241–1252.

Received 25 January 2012

BALTIJAS VALSTU VASARAS MIEŽU GENĒTISKIE PROFILI UN DAUDZVEIDĪBA

Šī darba mērķis bija iegūt datus molekulārai pasportizācijai, ko var izmantot dažādu Baltijas izcelsmes vasaras miežu paraugu identifikācijai, kā arī novērtēt to ģenētisko daudzveidību. Alēļu profili 21 mikrosateliitu un astoņos izoenzīmu lokusos tika noteikti 64 Baltijas vasaras miežu paraugiem. Pamatojoties uz mikrosateliitu alēļu sastāvu un frekvencēm, varēja izšķirt visus analizētos paraugus. Attiecīgie izoenzīmu dati, turpreti, ļāva izšķirt tikai 30 no analizētajiem paraugiem. Ģenētiskā mainība starp individuāliem paraugu robežā veidoja 20,6% no kopējās mainības, balstoties uz mikrosateliitu datiem, un 14,3% no kopējās mainības — pēc izoenzīmu datiem. Divkāsu un seškāsu miežus varēja skaidri izšķirt, gan izmantojot mikrosateliitu, gan izoenzīmu markieru datus. Saskaņā ar AMOVA analīzi ģenētiskās mainības daļa, kas noteica atšķirību starp divkāsu un seškāsu materiālu, veidoja 16,9% no kopējās mainības, pamatojoties uz mikrosateliitu datiem, un 26,8% — pamatojoties uz izoenzīmu datiem. Būtiska paraugu diferenciācija atkarībā no izcelsmes valsts tika konstatēta tikai attiecībā uz izoenzīmu datiem un veidoja 9% no kopējās mainības. Gan izoenzīmu, gan mikrosateliitu dati parādīja, ka Latvijas izcelsmes paraugi ir ģenētiski daudzveidīgākie, bet Igaunijas paraugi — vienveidīgākie Baltijas vasaras miežu paraugu vidū.