

Allium genotyping

- 15 microsatellite (SSR) markers tested (which were also utilised to genotype Swedish *Allium* accessions)
- DNA markers: AMS04, AMS06, AMS07, AMS08, AMS10, AMS12, AMS13, AMS14, AMS16, AMS22, AMS23, AMS25, AMS26, AMS29, AMS30
- Genotyped to date: AMS06, AMS08, AMS10, AMS12, AMS13, AMS14, AMS16, AMS23, AMS30 (9 loci)

(Fischer and Bachman, Theor Appl Genet (2000) 101:153–164)

Allium samples

- A total of 282 DNA samples isolated and analysed
- DNA was extracted from 2 bulbs (bulked prior to extraction) (except for the 2 Estonian generatively propagated accessions)

Country	Name	number of samples for DNA analysis	Institute	DNA extracted
Croatia	Smiljana Goreta Ban	25	Institute of Agriculture and Tourism	25 samples
Czech Republic	Stavelikova	129	Crop Research Institute	129 samples
Estonia	Küllli Annamaa	4	Estonian Crop Research Institute (ECRI)	22 (2 vegetatively propagated samples, 2x10 generatively propagated samples)
Finland	Terhi Suojala-Ahlfors	28	Natural Resources Institute Finland (Luke), Horticulture,	24 samples
Latvia	Ms Liga Lepse	39	Pure Horticultural Research Centre Abavas iela 2, Pure, Tukuma nov. LV-3124 Latvia	38 samples
Lithuania	Danguolė Juškevičienė	12	Institute of Horticulture, LRCAF, Kaunas st. 30, Babtai LT54333, Lithuania	12 samples
Norway	Ingunn Molund Vågen	21	NIBIO – Norwegian Institute of Bioeconomy Research, NIBIO Landvik, Reddalsveien 215, N-4886 Grimstad	23 samples
Sweden	Matti Leino		Nordiska museet, Swedish Museum of Agriculture, SE-643 98 Julita, Sweden	9 samples

Identification of more than 2 alleles in one accession at a marker locus may indicate genetic diversity within accessions or triploid accessions.

accession	country	AMS 06		AMS 08		AMS 10		AMS 12		ASM 13		AMS 14			AMS 16		AMS 23		AMS 30					
3098	CzechR	138	154	190	214	158	160	270	274	154	156	164	164	166	172	256	264	142	170	340	340			
3100	CzechR	138	154	190	190	162	162	270	270	156	164	164	172	248	248	130	146	170	340	340				
3057	CzechR	146	150	205	208	214	158	158	268	270	154	160	162	164	166	256	262	142	170	342	346			
3055	CzechR	146	150	205	208	214	158	160	268	270	274	154	160	162	166	168	256	260	262	142	170	340	342	346
3018	CzechR	154	154	208	208	160	160	270	272	160	164	166	168	172	248	248	170	170	340	340				

Genetic diversity parameters of all analysed samples

	AMS06	AMS08	AMS10	AMS12	ASM13	AMS14	AMS16	AMS23	AMS30
No. of analysed individuals	260	274	273	274	258	269	275	275	274
No. of alleles	11	8	6	10	17	8	10	19	15
No. of effective alleles (with higher frequencies)	5.525	2.834	1.991	4.080	8.401	3.069	5.657	8.642	5.794
Observed heterozygosity	0.400	0.547	0.150	0.774	0.581	0.535	0.771	0.709	0.383
Expected heterozygosity	0.819	0.647	0.498	0.755	0.881	0.674	0.823	0.884	0.827
Fixation index	0.512	0.154	0.698	-0.025	0.340	0.206	0.064	0.198	0.537

Mean genetic diversity parameters in samples from each country of origin

		AMS06	AMS08	AMS10	AMS12	ASM13	AMS14	AMS16	AMS23	AMS30
No. of analysed individuals	Mean	32.500	34.250	34.125	34.250	32.250	33.625	34.375	34.375	34.250
	SE	12.591	13.189	13.068	13.189	12.075	13.132	13.176	13.176	13.054
No. of alleles	Mean	6.000	4.500	3.750	5.250	9.000	5.250	6.000	8.625	7.500
	SE	0.926	0.463	0.313	0.491	1.225	0.526	0.732	1.085	1.180
No. of effective alleles (with higher frequencies)	Mean	3.512	2.446	2.120	3.412	5.623	2.745	4.413	5.291	4.529
	SE	0.501	0.156	0.274	0.240	0.911	0.382	0.467	0.691	0.695
Observed heterozygosity	Mean	0.421	0.566	0.189	0.800	0.627	0.540	0.767	0.757	0.381
	SE	0.100	0.080	0.051	0.044	0.103	0.069	0.040	0.055	0.093
Expected heterozygosity	Mean	0.654	0.579	0.476	0.696	0.767	0.585	0.747	0.786	0.702
	SE	0.068	0.028	0.062	0.022	0.053	0.057	0.036	0.029	0.080
Fixation index	Mean	0.361	0.028	0.612	-0.165	0.201	0.052	-0.043	0.010	0.524
	SE	0.163	0.133	0.078	0.089	0.120	0.096	0.074	0.112	0.116

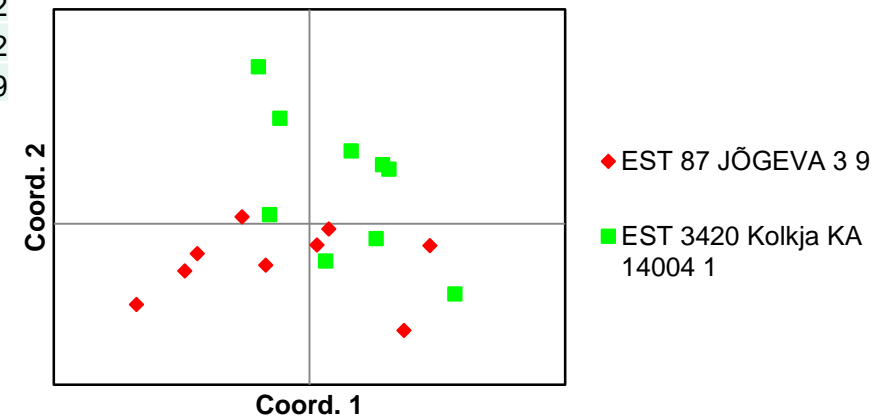
Seed propagated Estonian accessions



Genetic diversity parameters

Pop		AMS06	AMS08	AMS10	AMS12	ASM13	AMS14	AMS16	AMS23	AMS30
EST 87 JÕGEVA 3 9	No. of analysed individuals	8	9	9	9	9	9	9	9	9
	No. of alleles	5	3	4	5	7	5	6	7	9
	No. of effective alleles (with higher frequencies)	4.741	1.409	3.176	3.951	4.909	4.765	5.226	5.063	7.043
	Observed heterozygosity	0.625	0.333	0.444	0.778	0.889	0.889	0.667	0.444	0.556
	Expected heterozygosity	0.789	0.290	0.685	0.747	0.796	0.790	0.809	0.802	0.858
	Fixation index	0.208	-0.149	0.351	-0.041	-0.116	-0.125	0.176	0.446	0.353
	EST 3420 Kolkja KA 14004 1	No. of analysed individuals	9	9	9	9	9	9	9	9
No. of alleles		7	4	5	6	10	6	5	9	8
No. of effective alleles (with higher frequencies)		4.765	3.057	3.306	3.522	8.100	4.765	3.447	7.043	6.750
Observed heterozygosity		0.556	0.667	0.556	0.778	0.889	0.778	0.667	0.889	0.222
Expected heterozygosity		0.790	0.673	0.698	0.716	0.877	0.790	0.710	0.858	0.852
Fixation index		0.297	0.009	0.204	-0.086	-0.014	0.016	0.061	-0.036	0.739

Principal Coordinates (PCoA)



Genotyping



- 30 groups of accessions with identical multilocus genotypes (143 individuals)
- 132 unique genotypes

3009 CzechR	26
3019 CzechR	
3021 CzechR	
3026 CzechR	
3025 CzechR	
3024 CzechR	
3023 CzechR	
3002 CzechR	
3043 CzechR	
3036 CzechR	
3034 CzechR	
3037 CzechR	
SWE 484 Sweden	
SWE 191 Sweden	
SWE 319 Killeberg Sweden	
SWE 320 Karin Sweden	
SWE 99 Hanjre Sweden	
24 VIHTALAHTI Finland	
10276 NGB 17766 Norway	
10265 NGB 17765 Norway	
10199 NGB 17763 Norway	
10432 NGB 17775 Norway	
10310 NGB 17773 Norway	
10603 NGB 17778 Norway	
NGB 17765-2 Norway	
10281 NGB 17769 Norway	

3006 CzechR	14
3020 CzechR	
3022 CzechR	
3004 CzechR	
3003 CzechR	
3052 CzechR	
3069 CzechR	
3126 CzechR	
3137 CzechR	
3140 CzechR	
3033 CzechR	
8 ÄRMÄTTI 2 Finland	
10278 NGB 17767 Norway	
NGB 17762-2 Norway	

3086 CzechR	8
3085 CzechR	
3076 CzechR	
3074 CzechR	
3073 CzechR	
3072 CzechR	
3070 CzechR	
3062 CzechR	

IPT 238	Croatia	13
IPT 236	Croatia	
IPT 235	Croatia	
IPT 234	Croatia	
IPT 231	Croatia	
IPT 225	Croatia	
IPT 237	Croatia	
IPT 232	Croatia	
IPT 218	Croatia	
IPT 226	Croatia	
IPT 229	Croatia	
IPT 228	Croatia	
IPT 233	Croatia	

3028 CzechR	7
3030 CzechR	
3042 CzechR	
3040 CzechR	
3031 CzechR	
KVERVE Norway	
SØRFOLD Norway	

3124 CzechR	9	
256 Latvia		
39 Latvia		
256 Latvia		
975 Latvia		
35 Latvia		
977 Latvia		
980 Latvia		
973 Latvia		
IPT 021	Croatia	5
IPT 211	Croatia	
IPT 214	Croatia	
IPT 212	Croatia	
IPT 213	Croatia	

3090 CzechR	5
3093 CzechR	
3113 CzechR	
3131 CzechR	
3130 CzechR	

3084 CzechR	2
3060 CzechR	
2 Latvia	2
18 Latvia	
25 Latvia	2
6 Latvia	
3071 CzechR	3
3045 CzechR	
16 PTU 14 Finland	
3089 CzechR	3
3128 CzechR	
3125 CzechR	
3119 CzechR	4
3121 CzechR	
3138 CzechR	
3139 CzechR	

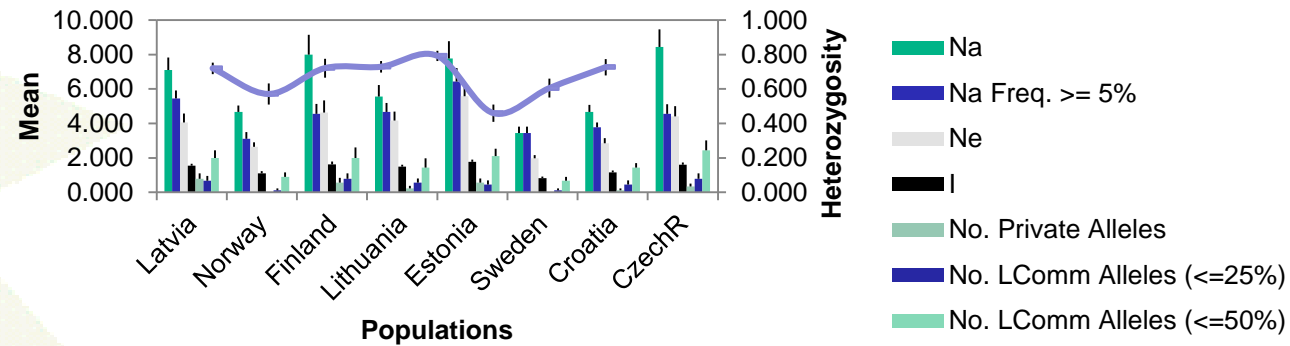
11 KANGASNIEMI Finland	2
LUNTEVIKA NGB 17975 Norway	
969 Latvia	3
3 Latvia	
649 Latvia	
49 Latvia	2
659 Latvia	
3075 CzechR	2
3051 CzechR	
3015 CzechR	2
3095 CzechR	
4 Latvia	2
11 Latvia	
V 11 Lithuania	2
V 6 Lithuania	
V 14 Lithuania	2
V 2 Lithuania	

SWE 94 Anna Sweden	4
VEGA Norway	
10279 NGB 17768 Norway	
10309 NGB 17772 Norway	
3038 CzechR	3
10575 NGB 17776 Norway	
10195 NGB 17762 Norway	
3041 CzechR	2
3133 CzechR	
3087 CzechR	2
3081 CzechR	
3087 CzechR	2
3081 CzechR	
V 5 Lithuania	4
41 Latvia	
982 Latvia	
27 Latvia	

3146 CzechR	2
3145 CzechR	
3013 CzechR	4
3012 CzechR	
3014 CzechR	
3027 CzechR	

These groups will be checked and analysed with additional markers

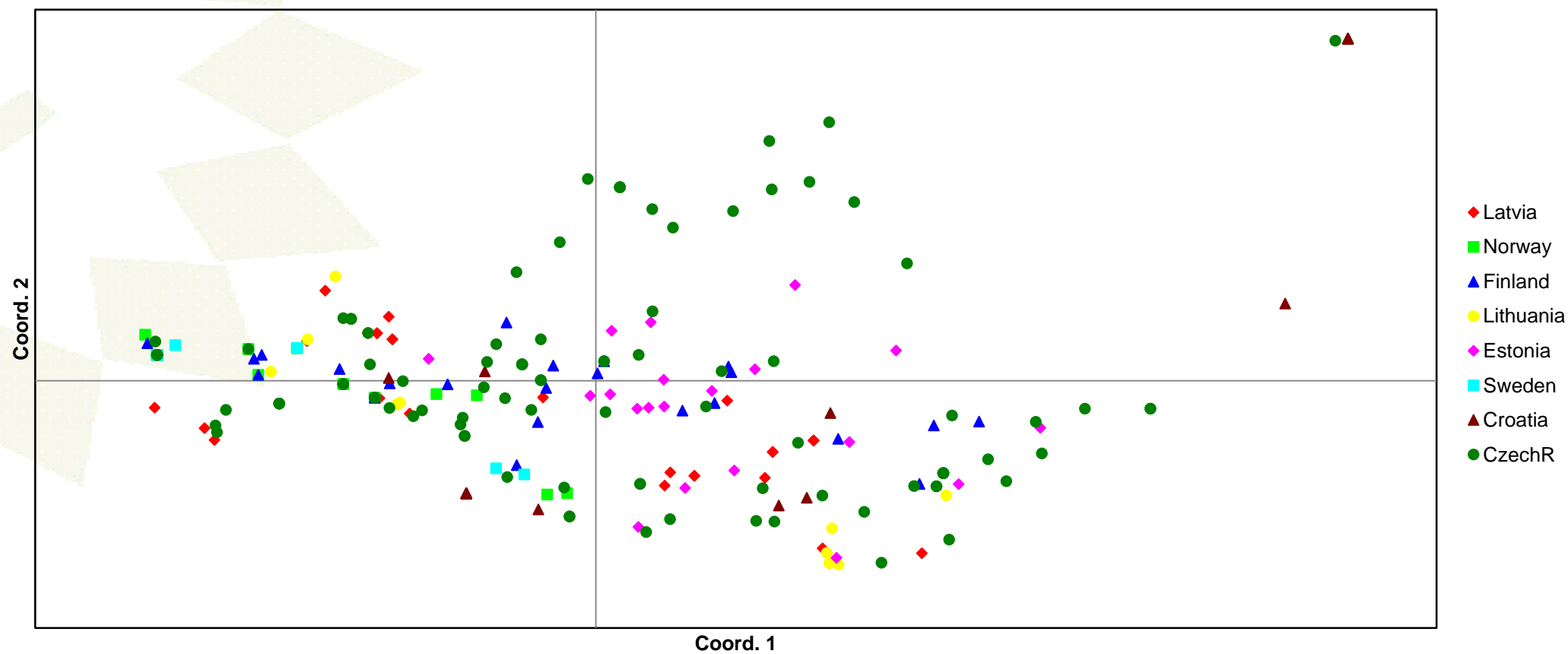
Allelic Patterns across Populations



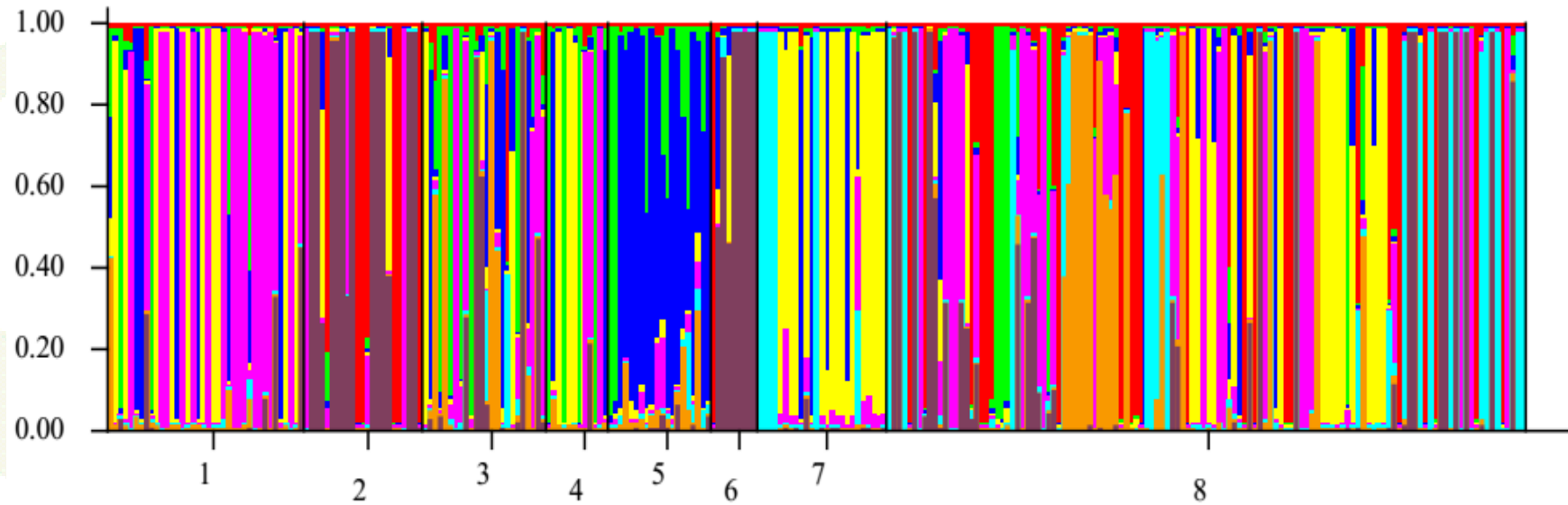
Mean values								
Population	Latvia	Norway	Finland	Lithuania	Estonia	Sweden	Croatia	CzechR
No. of individuals	38	23	24	12	20	9	25	124
No. of alleles	7.111	4.667	8.000	5.556	7.778	3.444	4.667	8.444
No. of alleles (Freq. >= 5%)	5.444	3.111	4.556	4.667	6.444	3.444	3.778	4.556
No. of unique alleles	0.778	0.000	0.556	0.222	0.556	0.000	0.111	0.333
No. of locally common alleles (found in less than <=25% of collections)	0.667	0.111	0.778	0.556	0.444	0.111	0.444	0.778
No. of locally common alleles (found in less than <=50% of collections)	2.000	0.889	2.000	1.444	2.111	0.667	1.444	2.444
Expected heterozygosity	0.720	0.571	0.721	0.729	0.792	0.460	0.605	0.726

PCoA based on pairwise genetic distances between all analysed individuals

Principal Coordinates (PCoA)



Structure software analysis (number of populations set to 8 – the number of collections)



1. Latvia
2. Norway
3. Finland
4. Lithuania
5. Estonia
6. Sweden
7. Croatia
8. Czech Republic

