

DIVERSITY OF OAT GENETIC RESOURCES



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Introduction

Oat (*Avena sativa*) is cereal grown for grain for food and feed. It is autogamous allohexaploid characterized by large genome (1.4×10^{10} bp/1C). Haploid genome has 7 chromosomes $n = 3x = 21$.



Aim of the study

- To evaluate genetic variability of oat genetic resources selected by project partners
- To compare genetic structure based on genetic data and on some agronomical traits

Material and Methods

Country of origin	Number of genotypes
Argentina	1
Austria	11
Belarus	1
Canada	9
Czech Republic	23
Estonia	3
Finland	7
France	12
Germany	24
Ireland	2
Netherlands	4
Poland	2
Russia	4
Sweden	3
United Kingdom	1
United States	5
Total 16 countries	112

Genotype

analysis of microsatellites
40 primer combinations

Phenotype

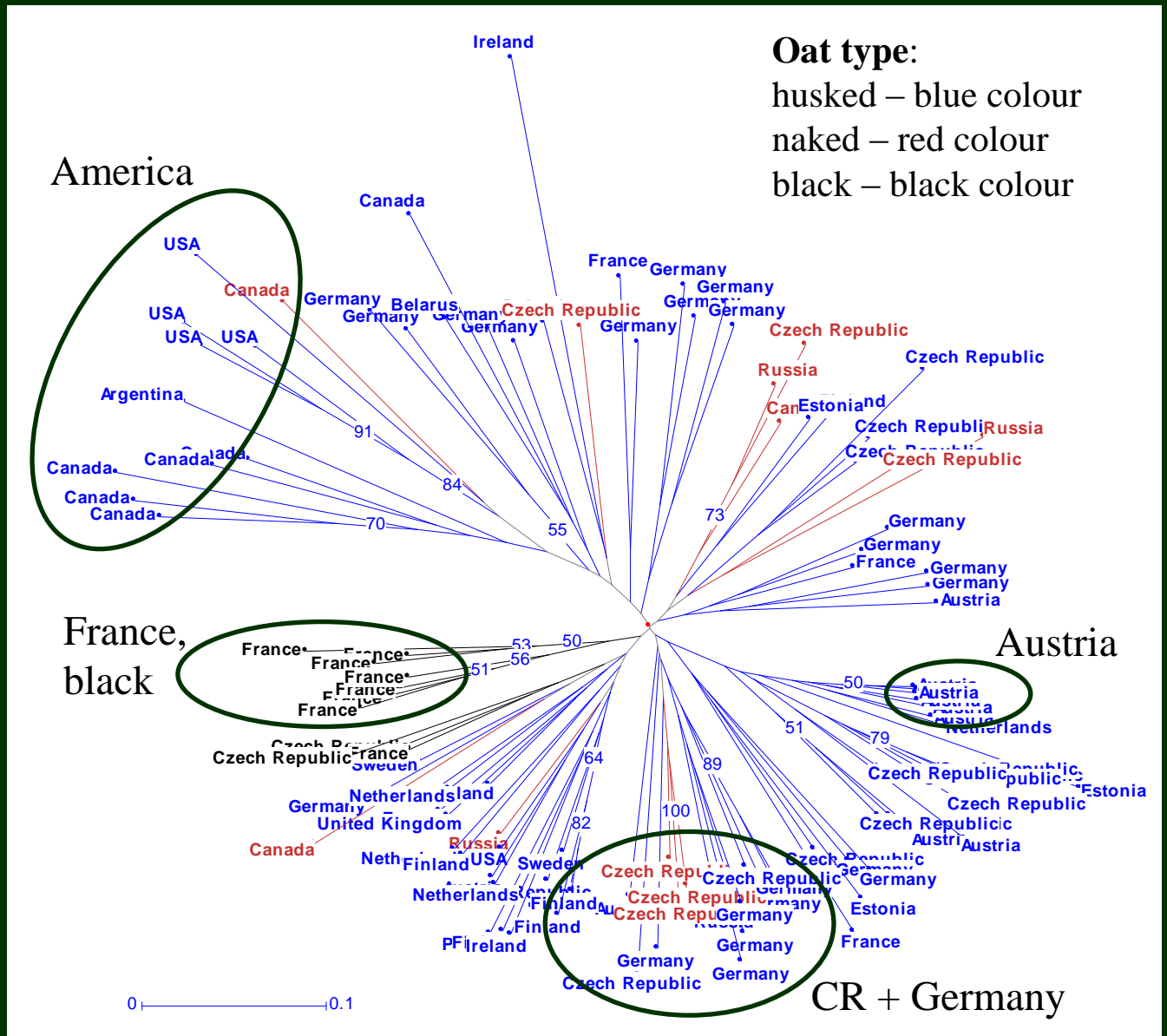
agronomic traits:
 HEAD - heading
 HGHT - plant height (cm)
 LO01 - lodging (9-1)
 DMAT - date of maturity
 (days after 20 June)
 TGWT - 1000 grain weight
 (g)
 HLWT - hectolitre weight
 (kg/hl)

Type - husked, naked, black

Results

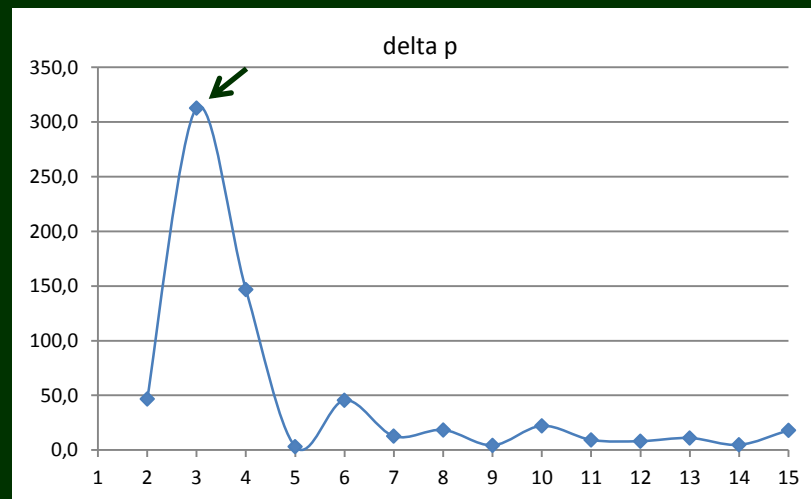
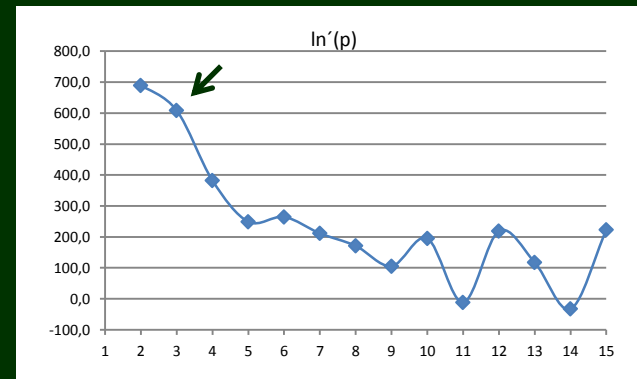
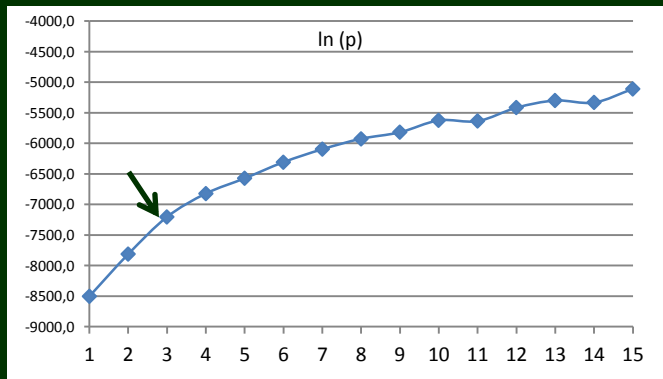
112 genotypes
56 loci
253 alleles
4.5 alleles per locus

Cluster analysis
SM
UNJ
bootstraps 2000



Structure analysis

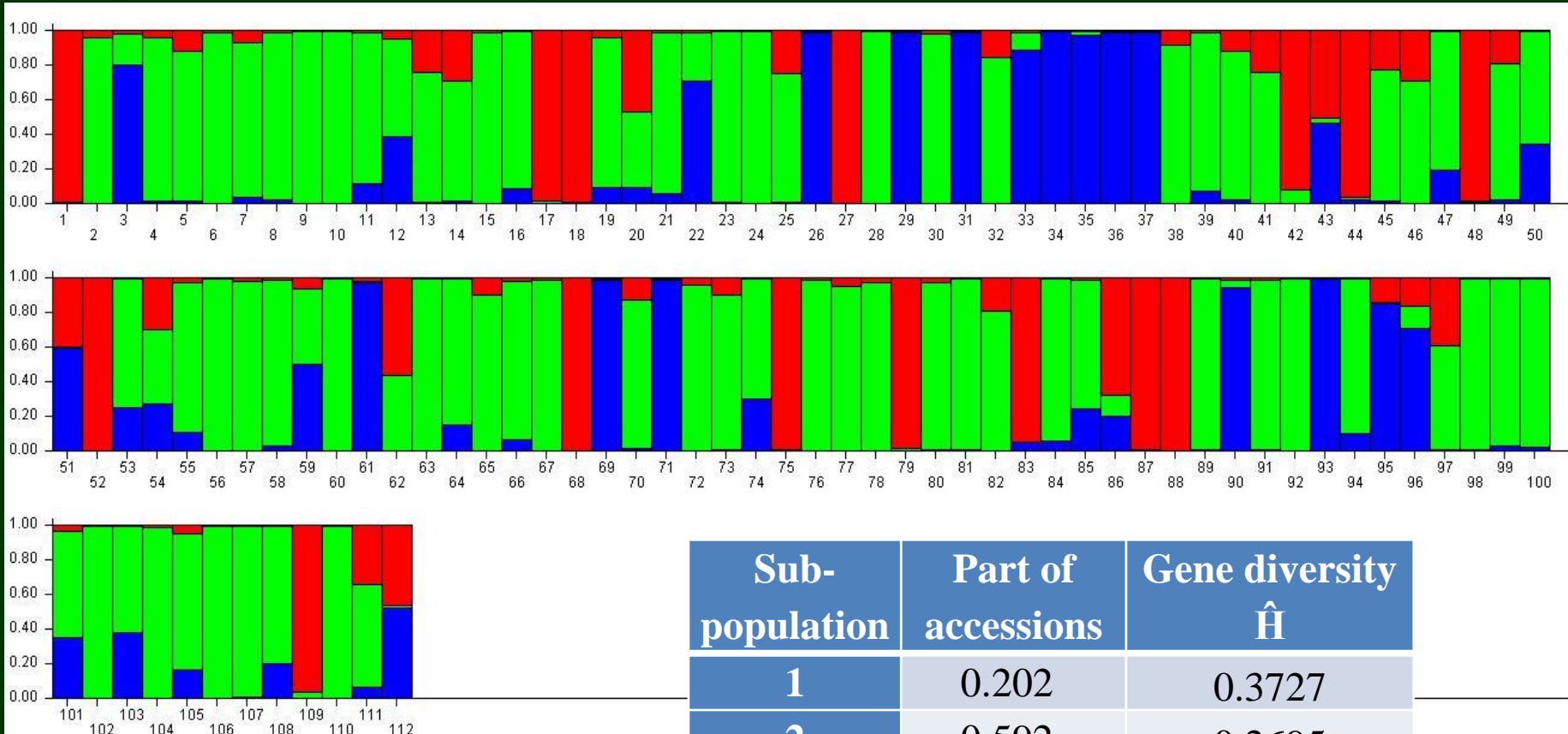
$K = 1 - 15$, 10 repetitions, MCMC 20000



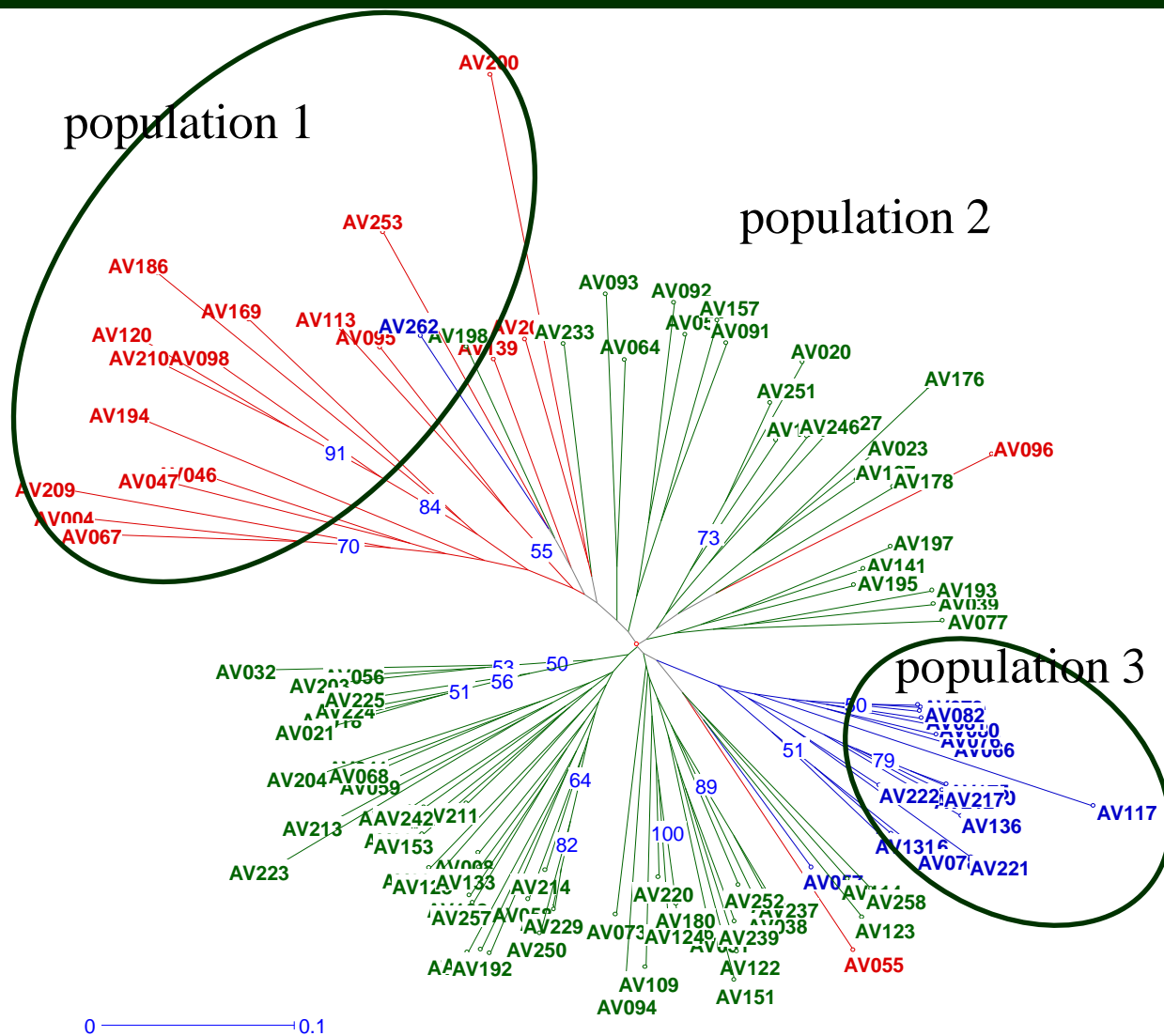
$K = 3$
three genetic
populations
in 112 oat
accessions
analysed

Structure analysis

K = 3, MCM 100.000



Sub-population	Part of accessions	Gene diversity \hat{H}
1	0.202	0.3727
2	0.592	0.2695
3	0.205	0.1772



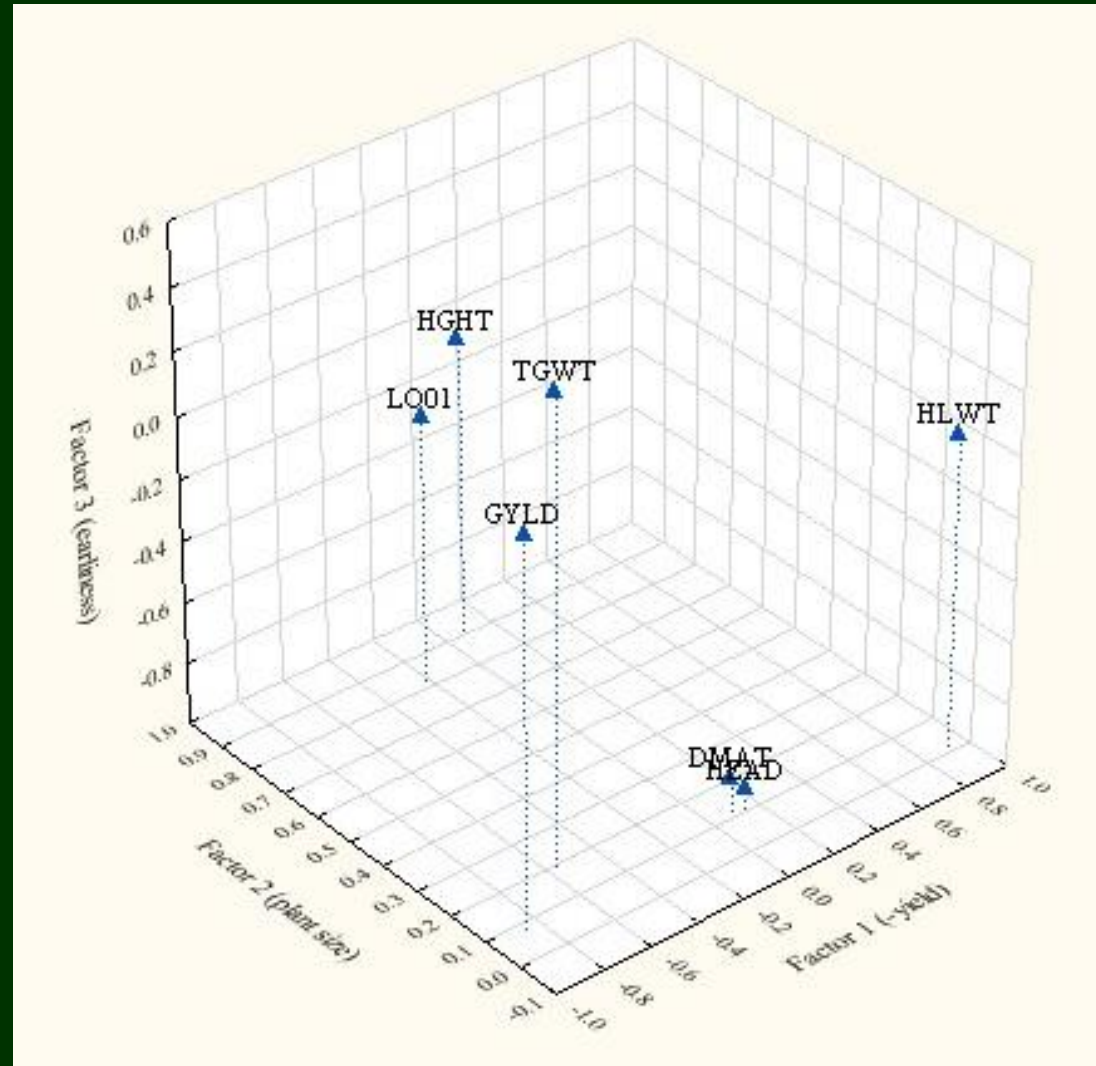
Phenotype

Factor analysis
Statistica

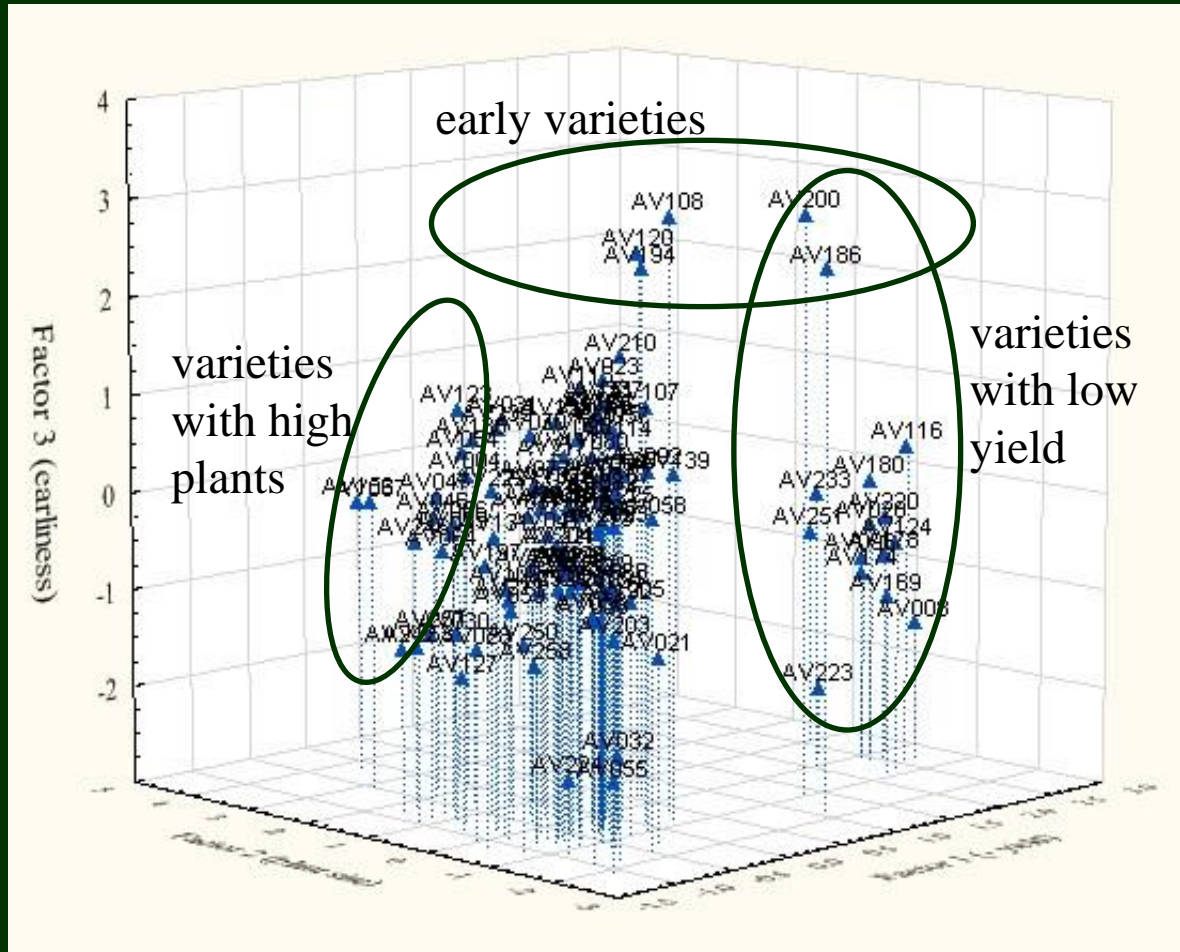
Factor 1 - -yield

Factor 2 - plant height

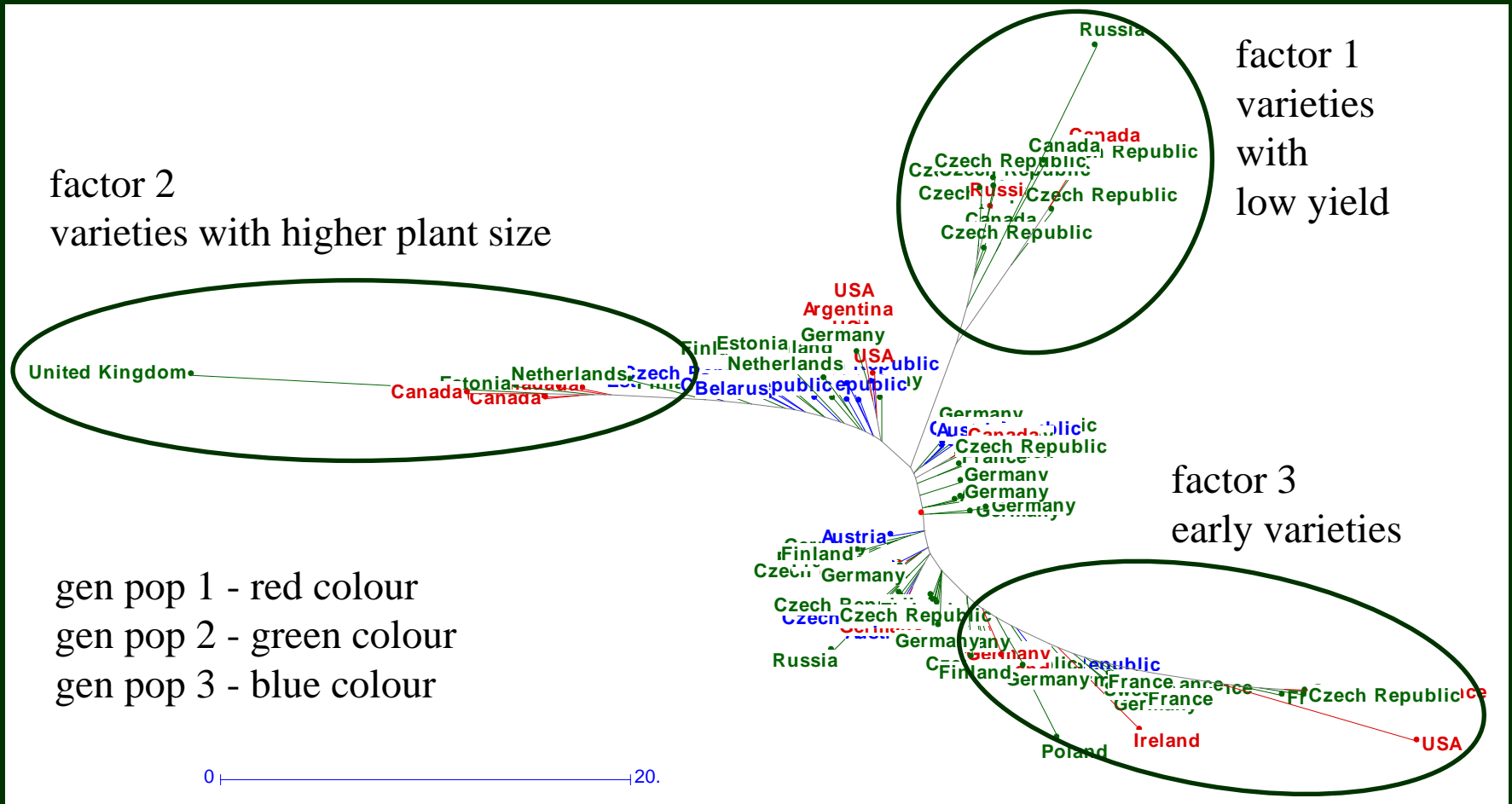
Factor 3 - earliness



Factor analysis - graph of component scores



Cluster analysis based on Euclidean distances computed from agronomical traits



Conclusions

- there is low level of genetic variability within the file of selected oat accessions
- oat genotypes analysed do not show a very pronounced genetic structure
- three different genetic populations can be identified
- crosses had occurred between the populations
- accessions classified to the genetic populations 1 and 2 are of higher genetic diversity and their agronomic traits are more influenced by environment conditions
- accessions involved in genetic population 3 are genetically more uniform and their agronomical traits are on intermediate level not much influenced by environment conditions



Foto Leona Svobodová

Acknowledgements

Marie and Vlastimil Chourovi
for agronomical data
and excellent collaboration

Hana Udavská for technical
assistance

Project EU FP7-KBBE-2013-
613609 for funding

Thank you for your attention!



Foto Jiří Svoboda