

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

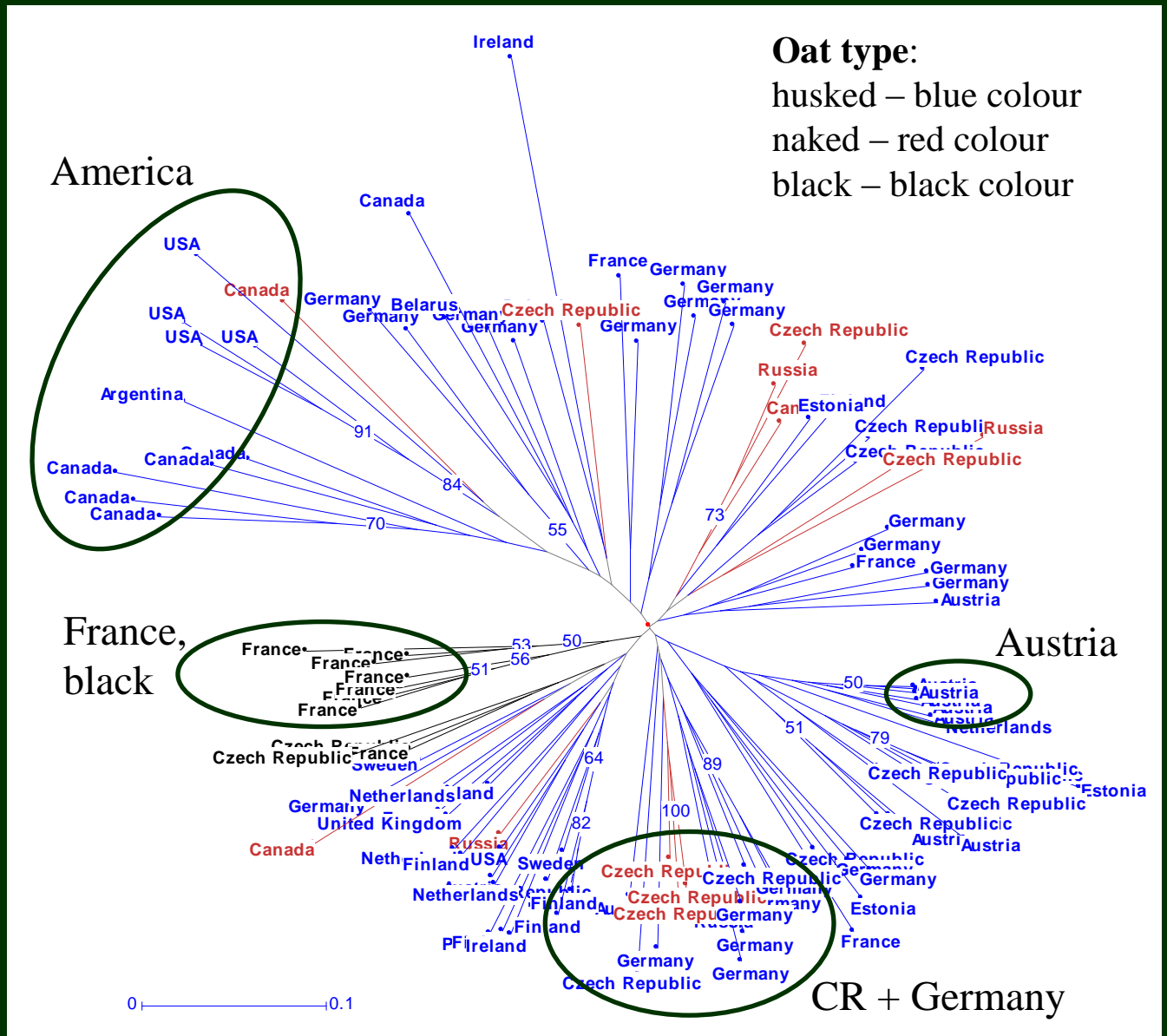
agronomic traits:
 HEAD - heading
 HGHT - plant height (cm)
 LO01 - lodging (9-1)
 DMAT - date of maturity
 (days after 20 June)
 TGWT - 1000 grain weight
 (g)
 HLWT - hectolitre weight
 (kg/hl)

Type - husked, naked, black

Results

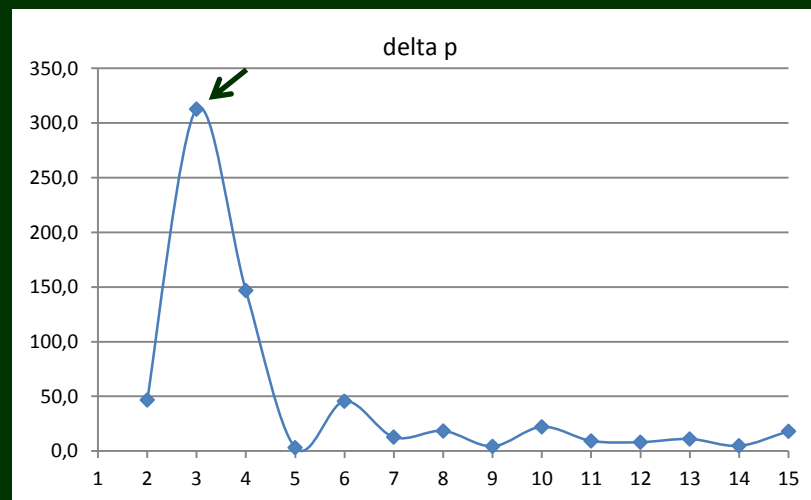
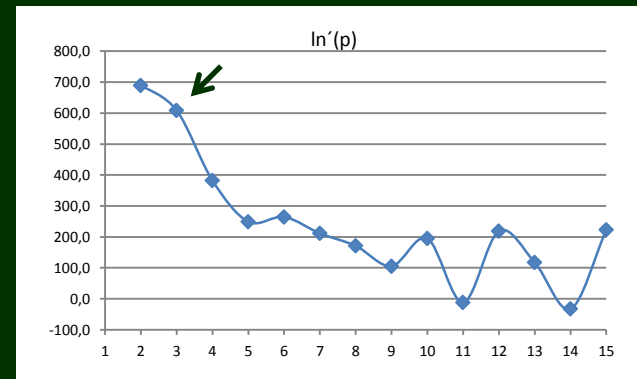
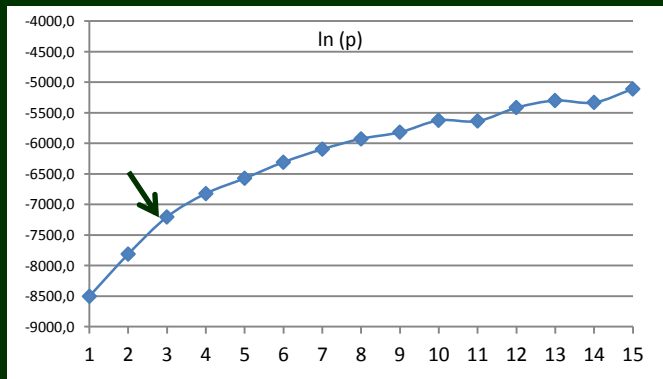
112 genotypes
56 loci
253 alleles
4.5 alleles per locus

Cluster analysis
SM
UNJ
bootstraps 2000



Structure analysis

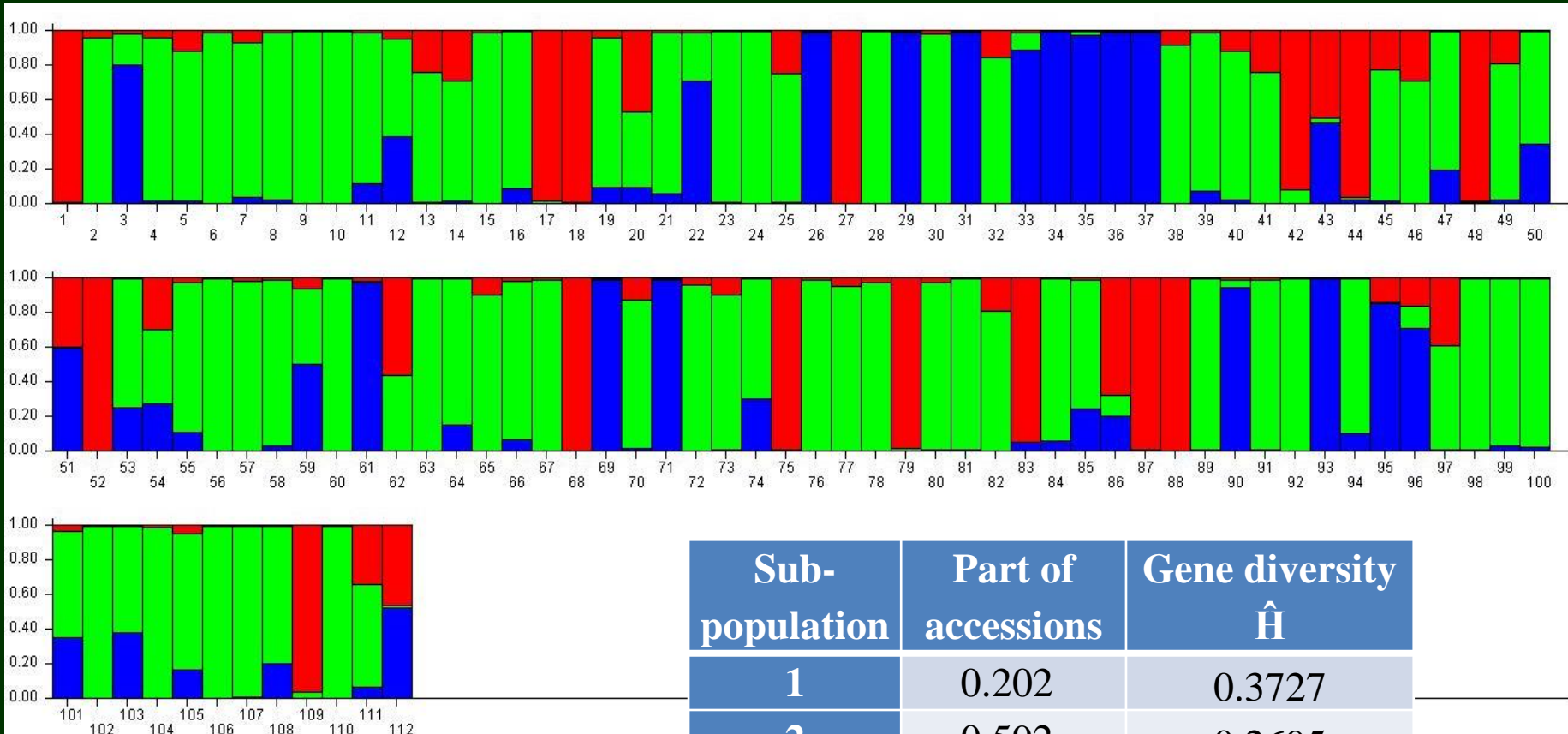
$K = 1 - 15$, 10 repetitions, MCMC 20000



$K = 3$
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

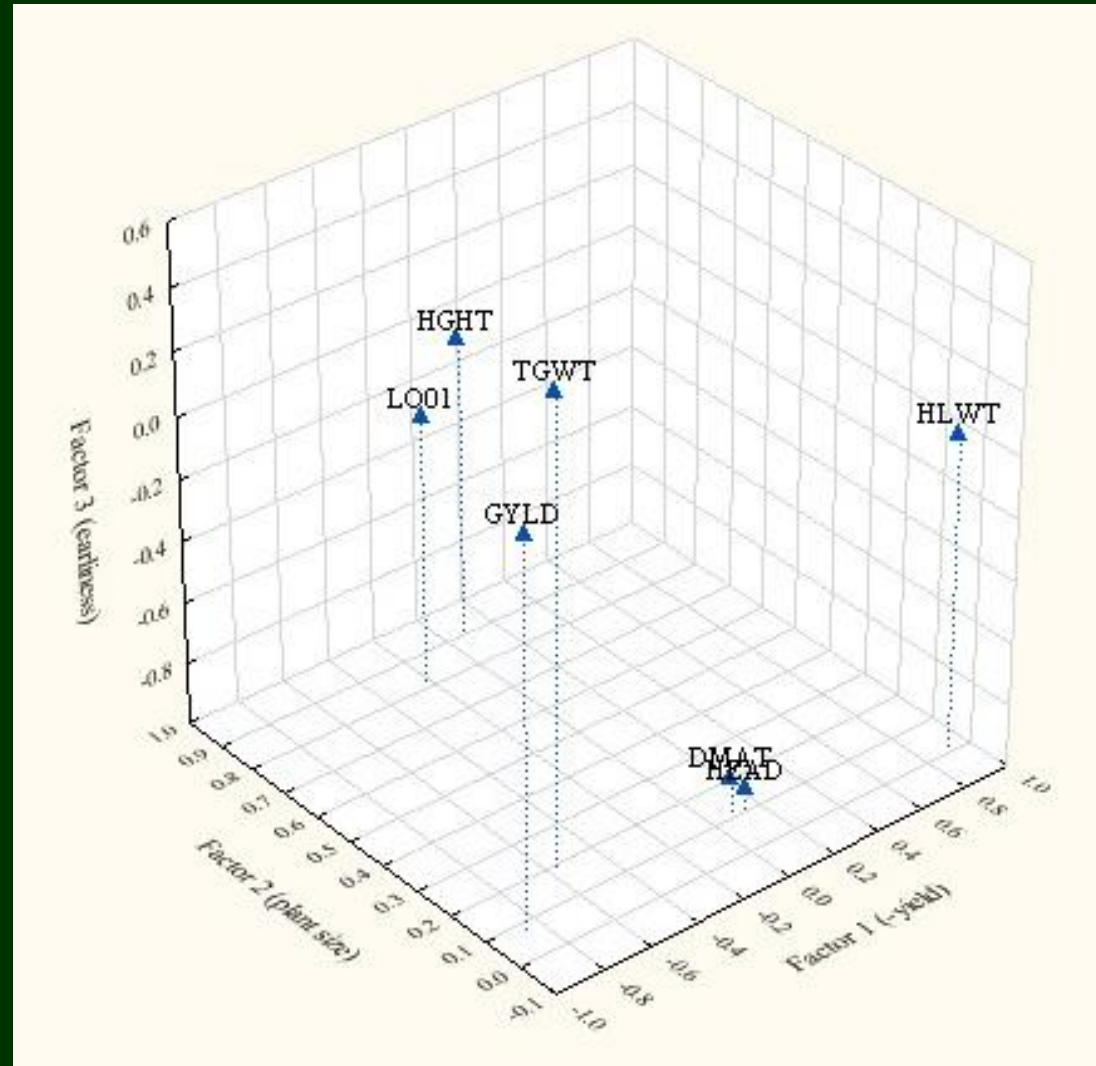
Phenotype

Factor analysis
Statistica

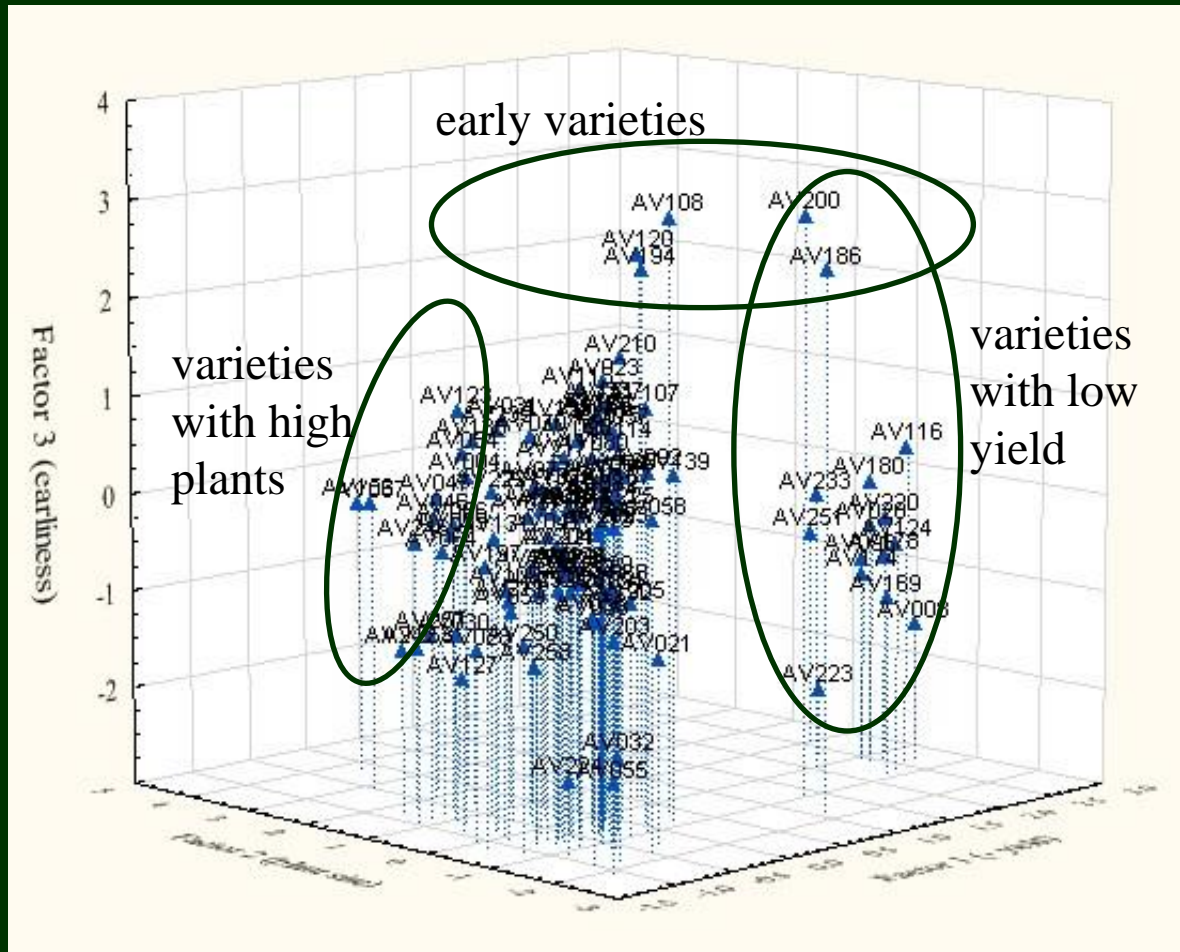
Factor 1 - -yield

Factor 2 - plant height

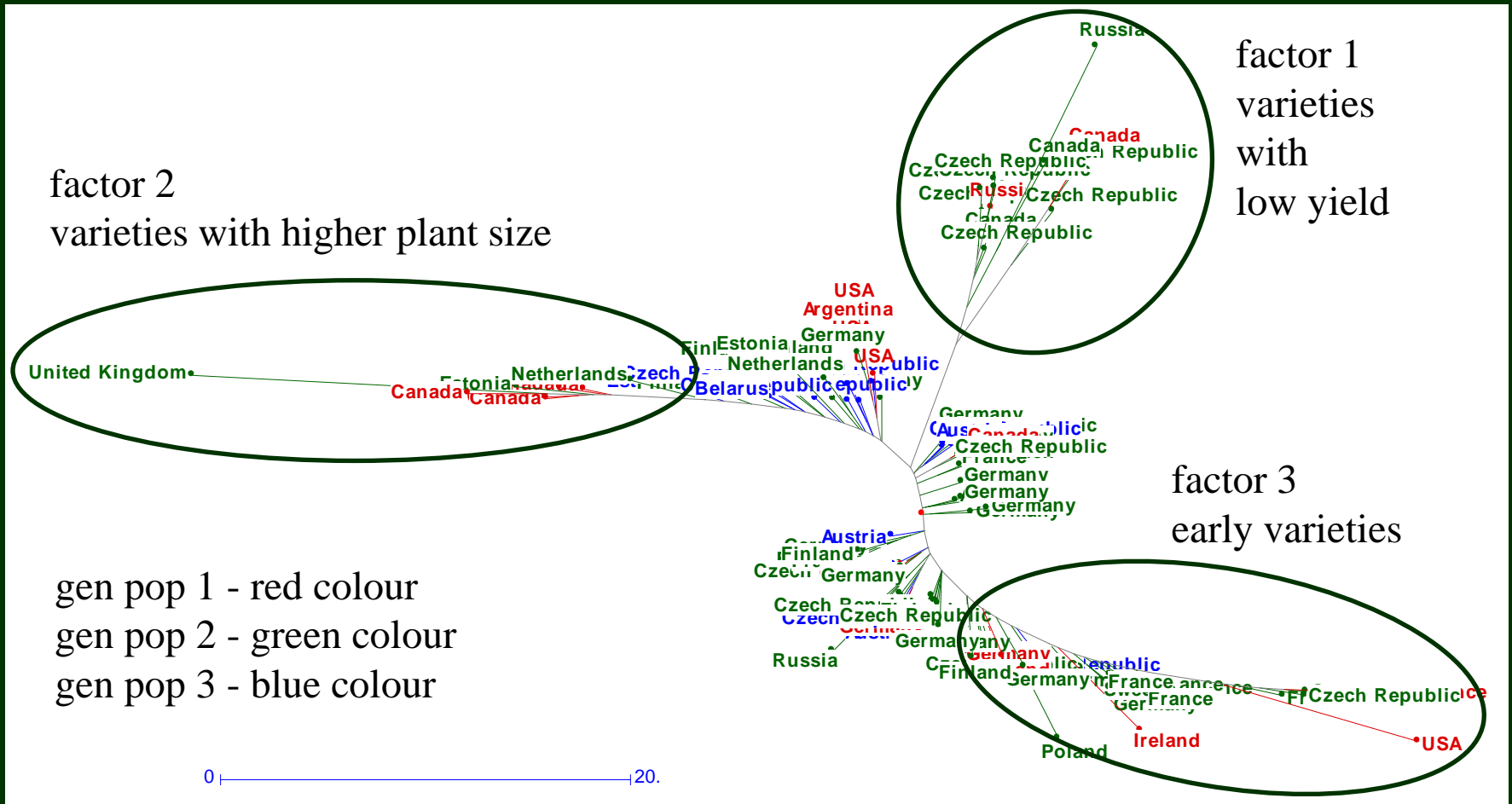
Factor 3 - earliness



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

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Thank you for your attention!



Foto Jiří Svoboda