



EAAP

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Genetic diversity measures of local European cattle breeds for conservation purposes



University of
Zagreb

University of Ljubljana



University of Natural Resources
and Life Sciences, Vienna

V. Kukučková^{1*}, N. Moravčíková¹, I. Curik²,
M. Simčič³, G. Mészáros⁴, R. Kasarda¹

OBJECTIVE

- ▶ to provide the detailed insight into genomic characterisation of the Pinzgau cattle (Slovak and Austrian Pinzgau, SP, AP) by utilizing high-throughput molecular information
- ▶ Bayesian clustering algorithms were used to detect gene flow among Pinzgau breeds (SP and AP), Cika and Piedmontese

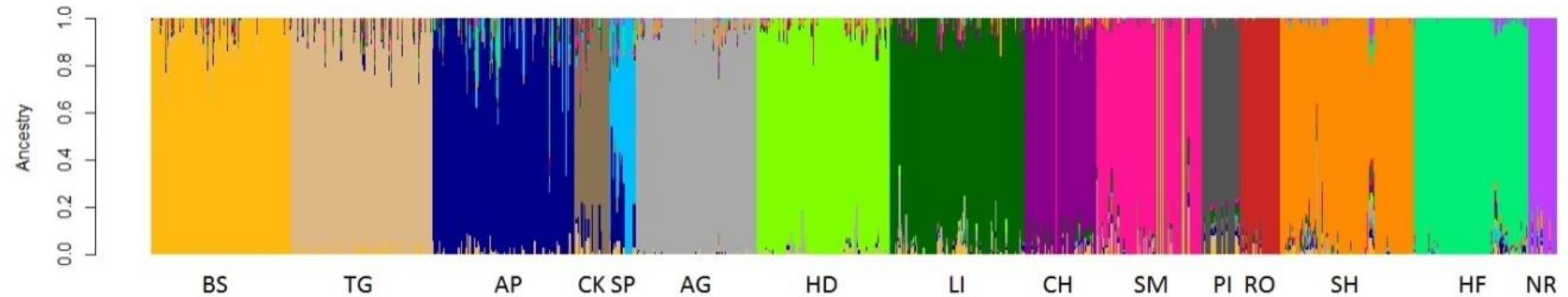
Material



Methodology

- ▶ 179 individuals
 - ▶ BovineSNP50 BeadChip - v1 and v2
- ▶ Standard QC
 - ▶ All individuals with >10% missing SNPs
 - ▶ SNPs missing in >10% of individuals were removed
 - ▶ MAF (0.05)
 - ▶ LD (0.05)
- ▶ 9,433 autosomal SNPs
 - ▶ Bayesian approach
 - ▶ gene flow network for the clusters estimated from admixture results was produced

Previous admixture analysis of 15 European cattle breeds



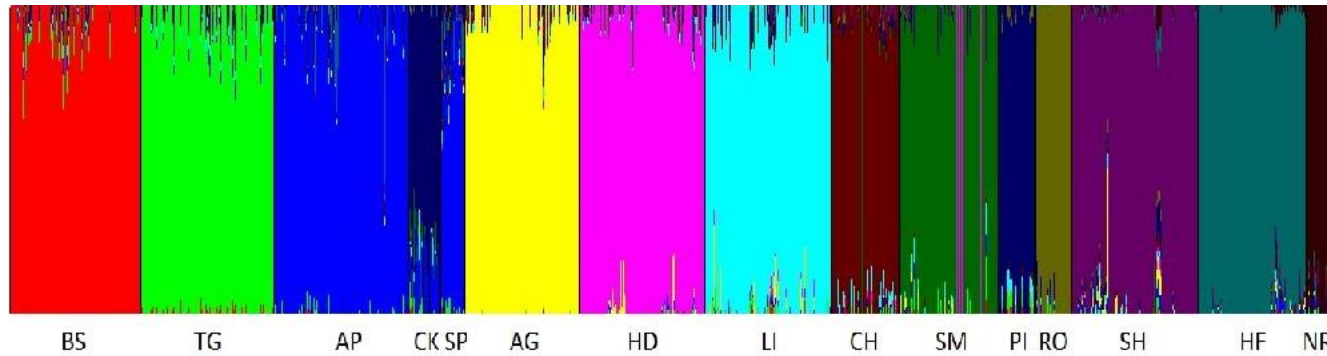
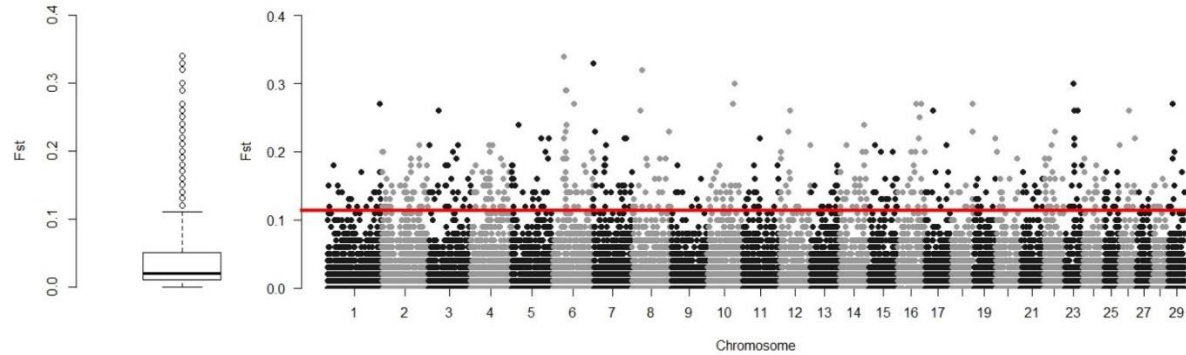
BS - Brown Swiss, TG - Tyrol Grey, **AP - Austrian Pinzgau**, CK - Cika, **SP - Slovak Pinzgau**, AG - Angus, HD - Hereford, LI - Limousine, CH - Charolais, SM - Simmental, PI - Piedmontese, RO - Romagnola, SH - Shorthorn, HF - Holstein, NR - Norwegian Red

Similarity

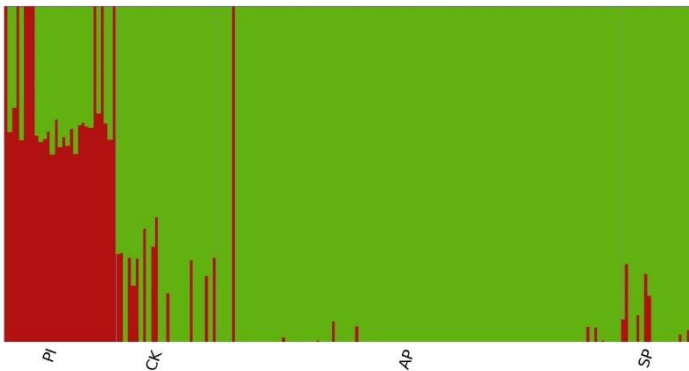
Low differentiation

- AP is a common donor of DNA to SP breed
- common historical origin and high gene flow

- several analyses showed genetically similar breeds
 - SP and AP, as well as CK and PI
- deeper analysis is essential



K4



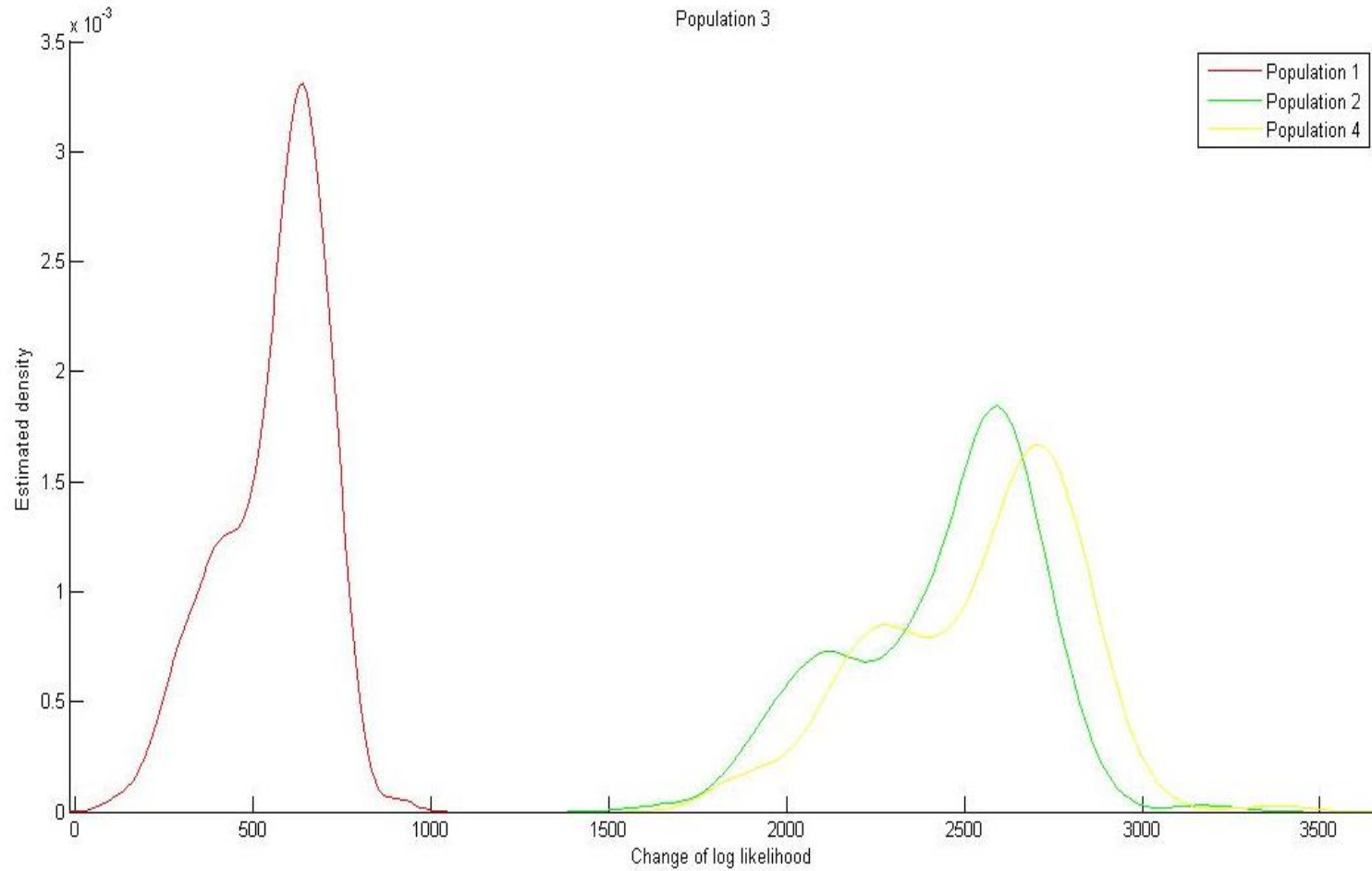
Gene flow

- ▶ Reduction of genetic variability between 2 groups or important source of genetic variability
- ▶ Includes lots of different kinds of events
 - ▶ human activities
 - ▶ movements from country to country
 - ▶ exchange of semen doses

Gene flow network

- ▶ genetic mixture model for unlinked markers
 - ▶ the changes in the log marginal likelihood close to zero indicate that the mixture model judges both assignments (source cluster and target cluster) to be statistically reasonable for an individual
 - ▶ network of clusters where gene flow is indicated by **weighted arrows**, such that the weights equal relative average amounts of ancestry in the source cluster among the individuals assigned to the target cluster

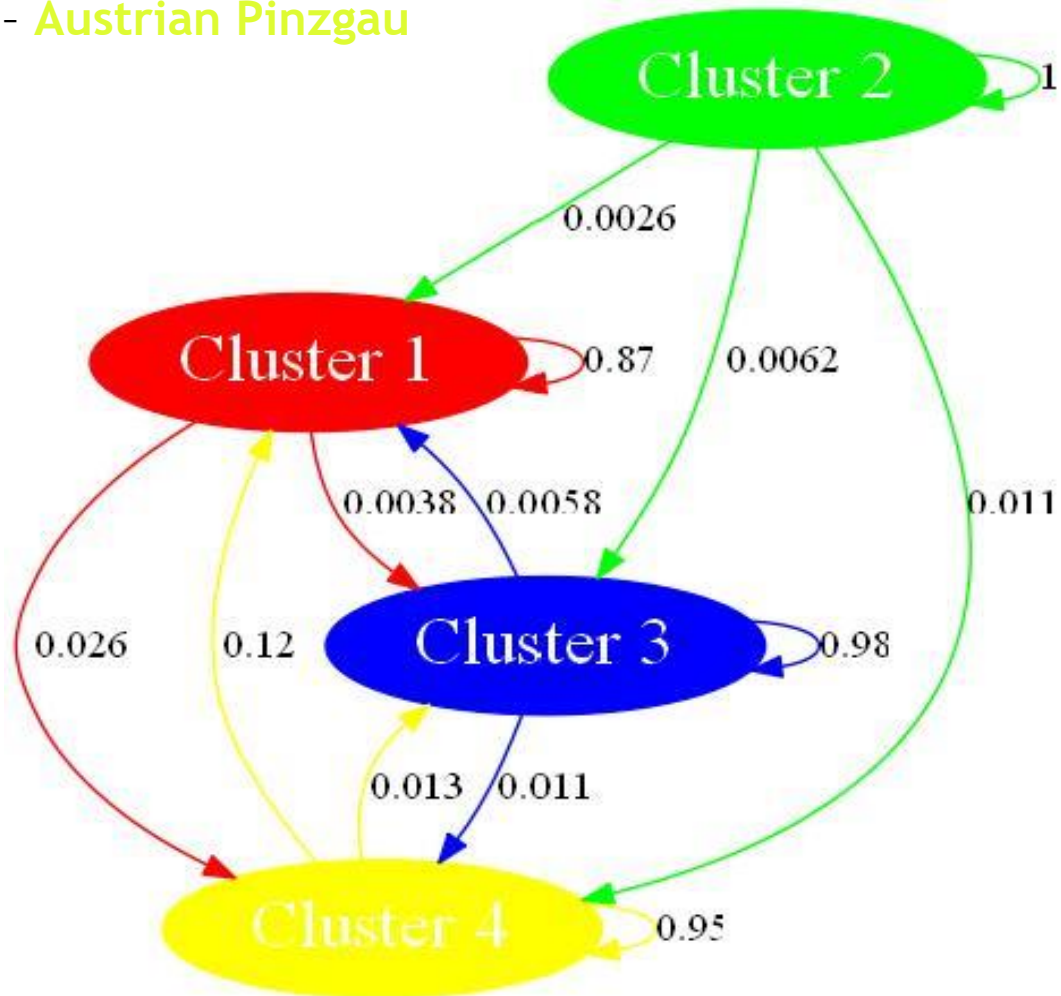
The changes in the log marginal likelihood



- Population 1 ▶ 1 - **Austrian Pinzgau**
- Population 2 ▶ 2 - **Cika**
- Population 3 ▶ 3 - Slovak Pinzgau
- Population 4 ▶ 4 - **Piedmontese**

A network of clusters indicating gene flow by weighted arrows

- 1 - Slovak Pinzgau
- 2 - Piedmontese
- 3 - Cika
- 4 - Austrian Pinzgau



All population except Piedmontese showed two ways of gene flow among populations which means:

- Piedmontese was involved in formation of analysed breeds while these breeds were not involved in creation of Piedmontese
- The same genetic segments from common ancestor

Conclusions

- ▶ power of high-throughput molecular information in clustering cattle breeds despite of weak differentiation
- ▶ changes in the log marginal likelihood also indicated AP as the most similar breed to SP
- ▶ Piedmontese contributed somehow to each of analysed populations creation

OR

- ▶ genetic segments of common ancestor are distributed into evaluated populations in unequal measure

Thank you for your attention!



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