Genetic diversity measures of local European cattle breeds for conservation purposes

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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
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

- 1 - Austrian Pinzgau
- 2 - Cika
- 3 - Slovak Pinzgau
- 4 - Piedmontese
A network of clusters indicating gene flow by weighted arrows

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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