Population structure and genetic diversity of Drežnica goat from Slovenia – preliminary results

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Introduction

• The only autochthonous goat breed in Slovenia
• Widespread in western Alps - adapted on mountain grazing
• A small area with a radius of less than 30 km
Drežnica goat in Slovenia

• At high risk of extinction – critically endangered
  • Population size = 629 animals
  • Small area

• Breeding program since 2005

• Two types (subpopulations?)
  • Dairy type – cheese production
  • Meat type – weaned kids production

• Milk production
  • 350 kg of milk in 200 days of lactation
  • 4.3% fat, 3.4% proteins
Large variability of coat colours

Photo: V. Rezar
Objectives

• to obtain:
  • unbiased estimates of the genetic diversity parameters
  • population structure
  • inbreeding level
  • possible admixture
• in the autochthonous Drežnica goat in Slovenia
Material

• **Blood samples**
  • Drežnica goat (n = 96)
  • 4 - 5 animals from each of 20 flocks (unrelated)

• 13 reference breeds – genotypes (n = 577)
  • **DRAYAD database**
    • Goat breeds from Switzerland (Burren et al., 2016)
    • Angora breeds (Visser et al., 2016)
Drežnica goat (n = 96)

- **Origin** – 20 flocks

- **Type (subpopulations?)**
  - Meat (n = 66)
  - Dairy (n = 30)

- **Gender**
  - ♂ (n = 17)
  - ♀ (n = 79)

- **Coat colour**
  - Black, black-brown (n = 48)
  - Spotted (n = 24)
  - Yellow, orange (n = 16)
  - Grey (n = 4)

- **Relationship coefficient**
  - < 0,25
  - CPZ database - pedigree
14 breeds (13 reference breeds)

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<th>Abbreviation</th>
<th>Breed name</th>
<th>N (animals)</th>
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Methods

• Genotypisation - Illumina Caprine SNP50 array
  • standard procedures (http://www.illumina.com)
  • Van Haeringen laboratory
• Quality control procedures excluded SNPs with:
  • genotyping errors
  • unknown chromosomal position
  • call rate < 95%
  • minor allele frequency < 0.025
  • the departure from Hardy-Weinberg equilibrium
• Missing genotypes imputed - Beagle
Methods

• Genome divided into blocks of 4 SNPs (5,530 block alleles)
• Genome-wide relationships - method of Powell et al. (2010)
• Genetic diversity parameters ($H_O$, $H_E$, ...)
• Genetic relationships between breeds
  • Nei genetic distances
• Neighbour network
  • constructed and plotted - SplitsTree4
• Unsupervised clustering
  • Admixture
  • the best $K$ - the lowest cross-validation error
Results

• Drežnica goat:

  • IBD = 0.1676 ± 0.0963
  • F = 0.1144 ± 0.0800
    • Max F = 0.5365
Genetic distances - Neighbour-Net

Independent origin of the breed!
Population structure
– Unsupervised clustering

Admixture (667 animals, $K = 14$)

The Drežnica goat is not divided into two subpopulations
Conclusion

- Phylogenetic analyses demonstrated unique genetic identity of Drežnica goat preserved in the Alps.

- Genetic distance matrix and unsupervised clustering showed independent origin of the breed.

- The population is not genetically divided into two types.

- The most purebred animals represent an important genetic nucleus for the conservation.
Thank you for your attention!