University of Ljubljana

LUDWIG-
MAXIMILIANS-
UNIVERSITÄT
MÜNCHEN

LMU

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

M. Simčič, I. Medugorac, D. Bojkovski, S. Horvat

Dubrovnik, Croatia, 27th - 31st August 2018

Introduction

Photo: V. Rezar

a)

Herd size:
50 100 150 200

- 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
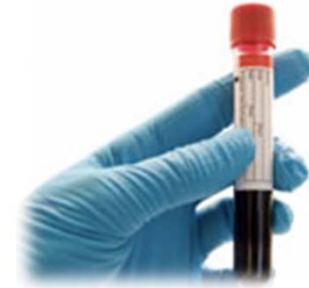
Photo: V. Rezar

Objectives

- to obtain:
    - unbiased estimates of the genetic diversity parameters
    - population structure
    - inbreeding level
    - possible admixture

- in the autochthonous Drežnica goat in Slovenia

Photo: V. Rezar

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)

N (breeds)	Abbreviation	Breed name	N (animals)	County of origin	Reason to include	Origin of data
01	**DRZ**	**Drežnica goat**	**96**	**Slovenia**	**Studied breed**	**DNA**
02	APP	Appenzell	21	Switzerland	Geographically close Introgression Similar type traits	DRYAD, Burren et al., 2016
03	GST	Grisons striped	26			
04	TGR	Tessin grey	27			
05	CHA	Chamois coloured	61			
06	VAG	Valais	24			
07	NVE	Nera Verzasca	29			
08	PEA	Peacock	22			
09	SAA	Saanen goat	34			
10	SGB	Booted	16			
11	TOG	Togenburg goat	24			
12	AR	Angora	30	Argentina	Outgroups	DRYAD, Visser et al., 2016
13	FR	Angora	26	France		
14	SA	Angora	48	South Africa		
Together			673			

Methods

- Genotypisation - Illumina Caprine SNP50 array
  - standard procedures (http://www.ilumina.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*
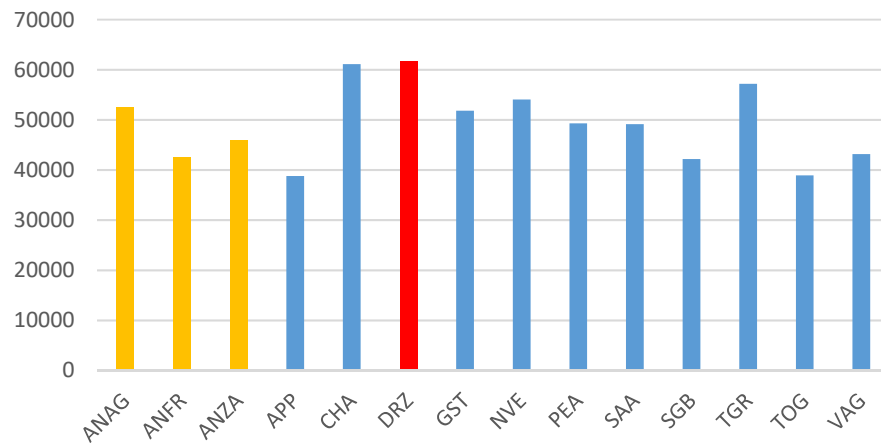 - the best *K* - the lowest cross-validation error

Results

- Drežnica goat:

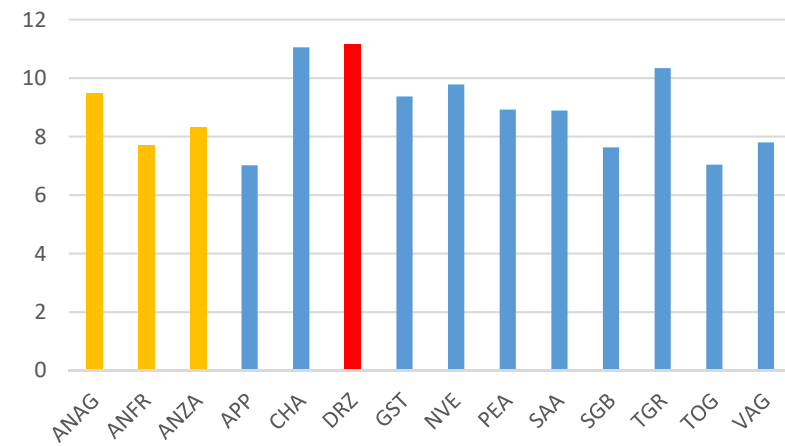 - IBD = 0.1676 ± 0.0963

  - F = 0.1144 ± 0.0800
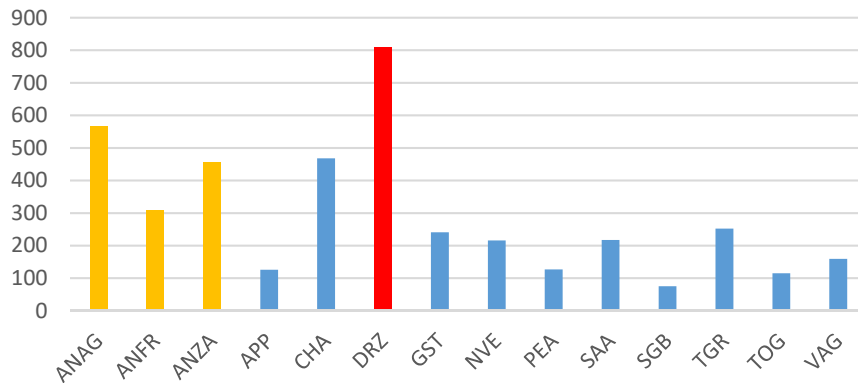   - Max F = 0.5365

Photo: V. Rezar

Genetic diversity parameters

Genetic distances - Neighbour-Net

Booted

Togenburg goat

Grisons striped

Appenzell

Tessin grey

Nera Verzasca

Peacock

Angora AG

Valais

Saanen goat

Chamois coloured

Drežnica goat

Angora FR

Angora SA

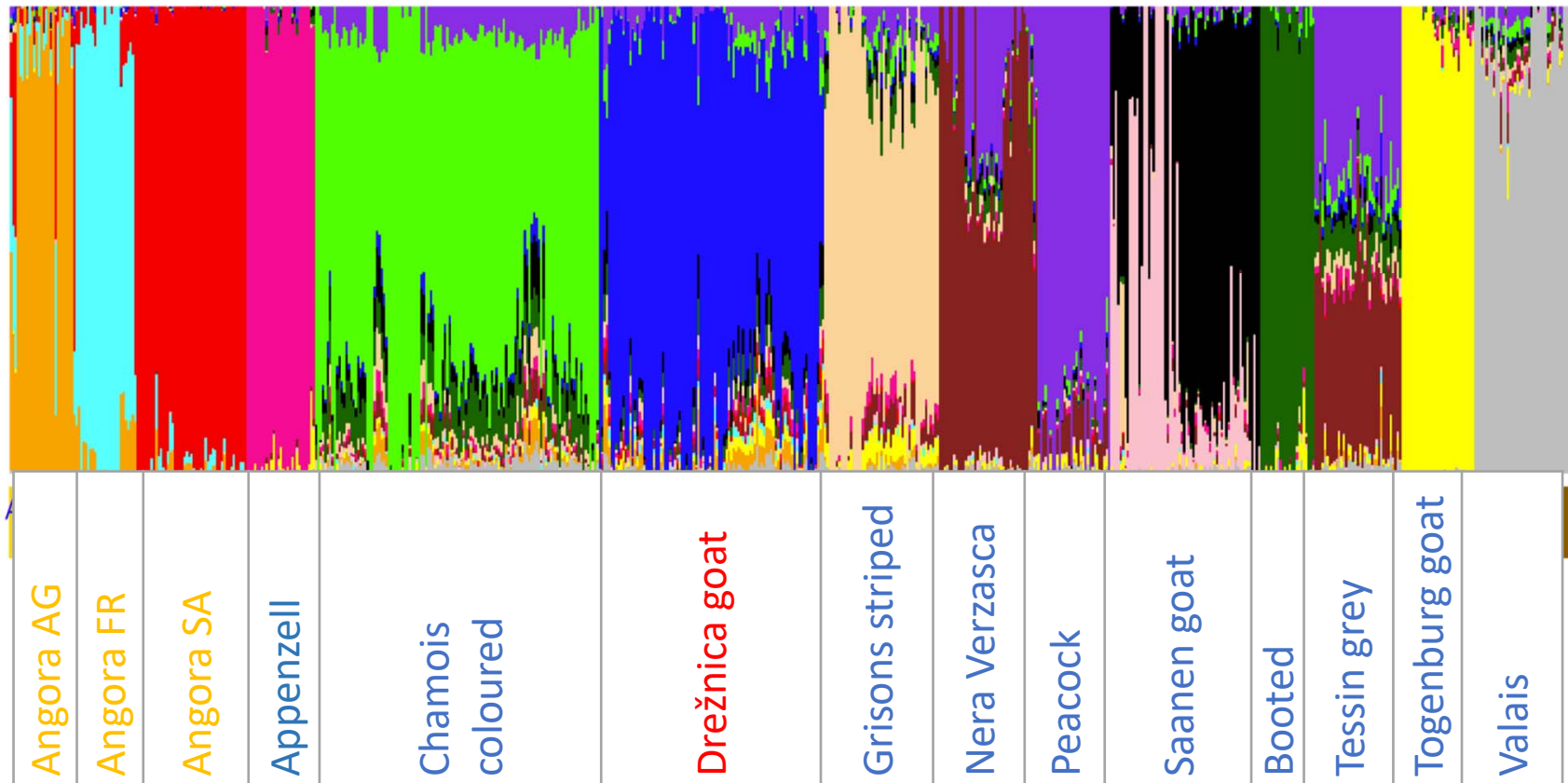*Independent origin of the breed!*

Population structure – Unsupervised clustering

Admixture (667 animals, *K = 14*)

Angora AG | Angora FR | Angora SA | Appenzell | Chamois coloured | Drežnica goat | Grisons striped | Nera Verzasca | Peacock | Saanen goat | Booted | Tessin grey | Togenburg goat | Valais

The Drežnica goat is not divided into two subpopulations

Conclusion

- Phylogenetic analyses demonstrated <u>unique genetic identity</u> of Drežnica goat preserved in the Alps

- Genetic distance matrix and unsupervised clustering showed <u>independent origin of the breed</u>

- 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!

Photo: V. Rezar