

# Genetic structure of Slovak Pinzgau cattle and related breeds



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## Aim

- to characterize the patterns of genetic structure in Slovak Pinzgau bulls population using genotyping array
- to determine the corresponding fraction of an individual's genome derived from an ancestry

## Introduction

- Slovak Pinzgau cattle - traditional breed of mountainous areas of Slovakia
  - dual-purpose + beef character
    - unique traits – longevity, fertility, health, grazing ability
  - crossbreeding » endangered breed



## Methods

- 19 breeding bulls of Slovak Pinzgau population
- Illumina BovineSNP50 v2 BeadChip (54 609 SNPs)
- 5 domesticated bovine breeds (103 animals)
  - the Bayesian clustering algorithm

## Conclusions

- historically, investigated populations were used in formation of Slovak Pinzgau breed, particularly in order to improve its performance

- In  $\ln Pr(G|K)$  increased from  $K=1$  to  $K=3$  and balanced
- 2 separate populations based on production type »  $K = 2$  «

- Slovak Pinzgau - closer to Holstein (milk production) than to Simmental (dual-purpose)
- systematic selection due to increasing of milk production is evident

## Conclusions

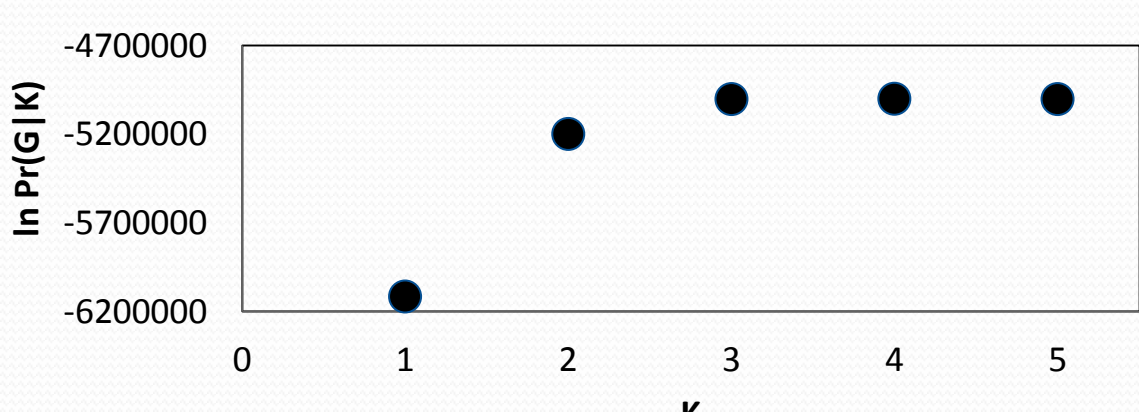
### Results

- studied breeds built Holstein and Simmental group

**Table 1** Proportion of membership of each pre-defined population in one of the 2 clusters

Given populations	Inferred clusters (%)		Number of individuals
	1	2	
1 Holstein	0.1	99.9	54
2 Simmental	99.7	0.3	23
3 Austrian Pinzgau	97.9	2.1	5
4 Ayrshire	99.7	0.3	18
5 MRI	96.3	3.7	3
6 Slovak Pinzgau	28.4	71.6	19

**Figure1**  $\ln Pr(G|K)$  values presented as a function of the number of clusters



**Figure2** Graphical presentation of the population structure analyses for a sample of 6 cattle breeds

