Genetic Diversity in Slovak Pinzgau Cattle Based on Microsatellites

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Outline

- Pinzgau cattle

- Information on diversity and population fragmentation

- Aim of the study

- Material and methods

- Results

- Further investigation
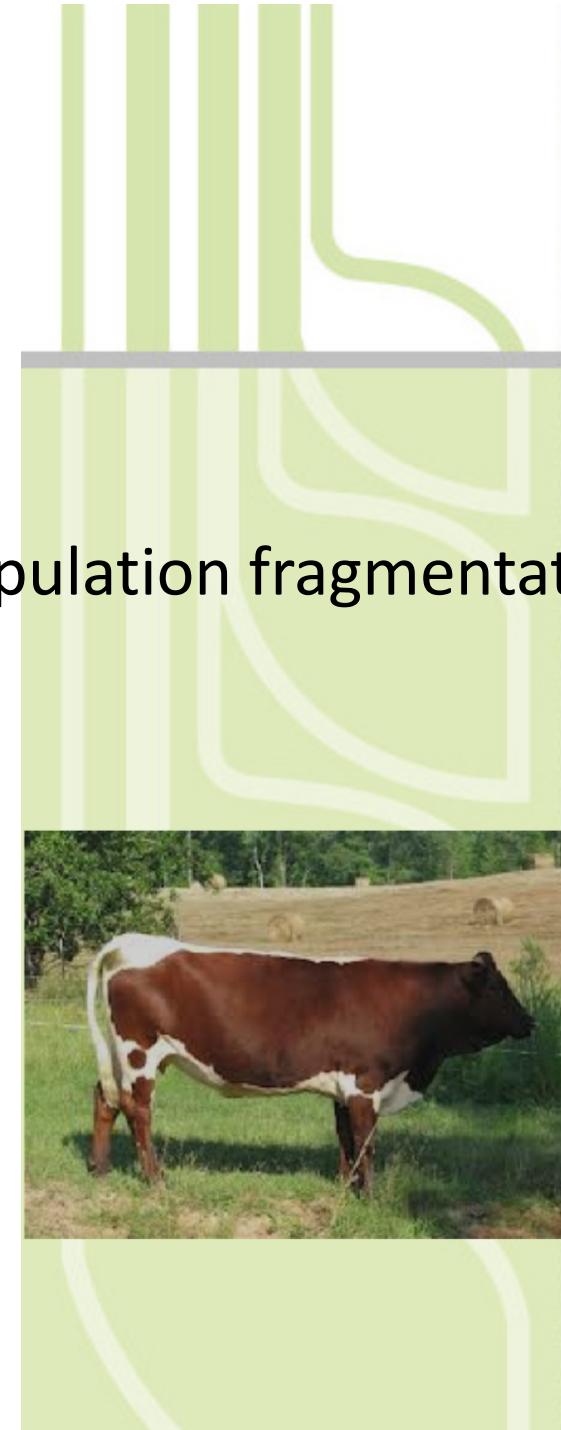
Pinzgau cattle

- Alpine breed

- Dual-purpose - average milk yield – 4,420 kg (3.93 % fat, 3.38 % protein)

- Endangered - in 1990 – over 90,000 Pinzgau cows

  in 2013 – 3,101 Herd book cows (718 suckler cows)
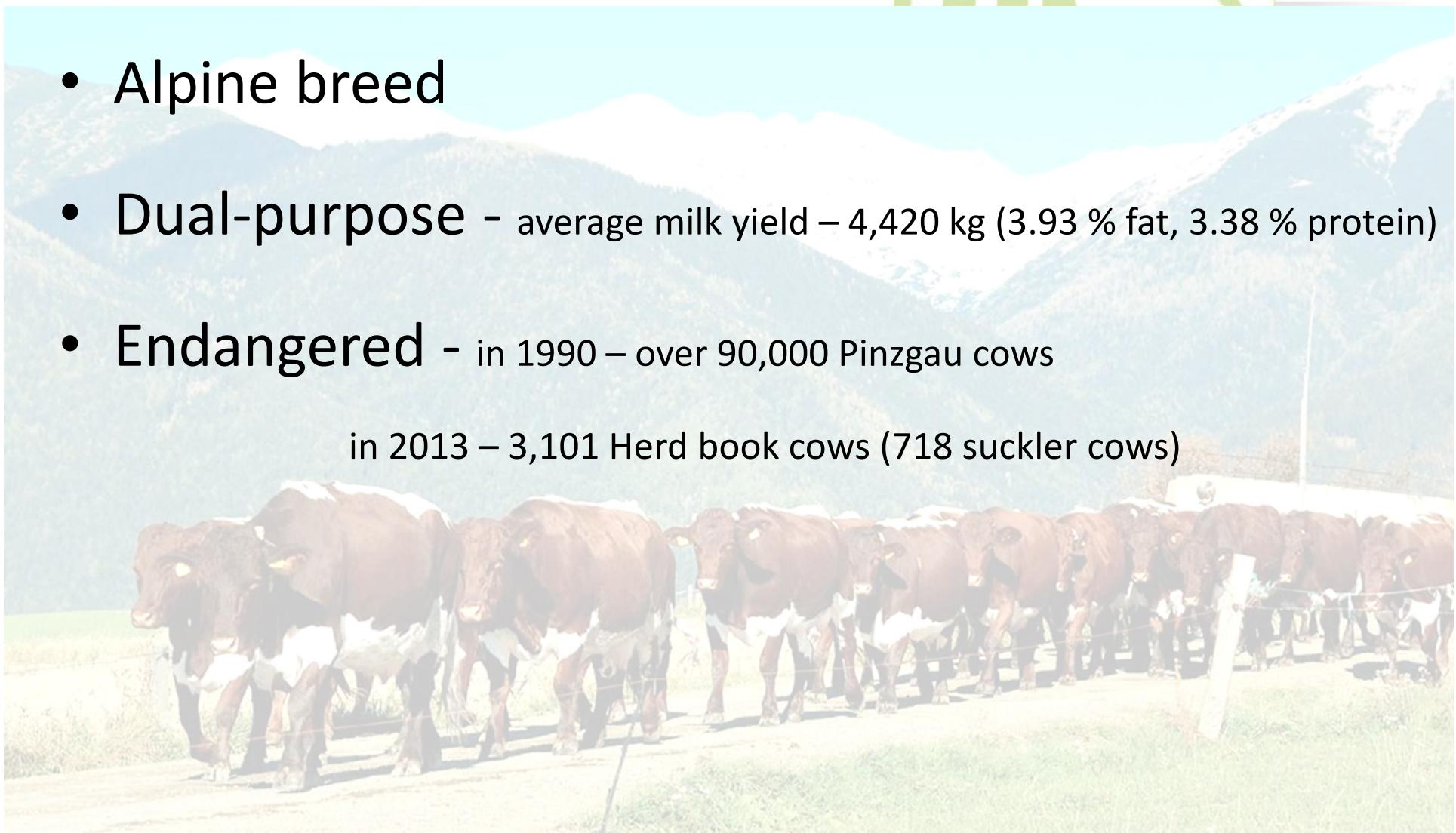
Information on diversity and population structure

- Loss of genetic diversity within breeds
  - Decrease of effective size of population
  - Increase of inbreeding
  - Increase of homozygosity

- Population fragmentation
  - Origin
  - Herd/ farm
  - Alleles

- Molecular DNA markers
  - Microsatellites

Aim of the study

- To evaluate the genetic diversity of Slovak Pinzgau cattle

- To analyze genetic structure of population without prior information

Material and methods

- ## DNA isolation

  – 302 Slovak Pinzgau

- ## PCR

  – 8 microsatellites recommended by FAO / ISAG

locus	label	primer sequence 5`- 3`	chromosome
CSRM60	NED	AAGATGTGATCCAAGAGAGAGGCA AGGACCAGATCGTGAAAGGCATAG	10
CSSM66	NED	ACACAAATCCTTTCTGCCAGCTGA AATTTAATGCACTGAGGAGCTTGG	14
TGLA227	6FAM	CGAATTCCAAATCTGTTAATTTGCT ACAGACAGAAACTCAATGAAAGCA	18
ETH3	VIC	GAACCTGCCTCTCCTGCATTGG ACTCTGCCTGTGGCCAAGTAGG	19
ILST006	NED	TGTCTGTATTTCTGCTGTGG ACACGGAAGCGATCTAAACG	7
TGLA122	PET	CCCTCCTCCAGGTAAATCAGC AATCACATGGCAAATAAGTACATAC	21
SPS115	6FAM	AAAGTGACACAACAGCTTCTCCAG AACGAGTGTCCTAGTTTGGCTGTG	15
BM1824	VIC	GAGCAAGGTGTTTTTCCAATC CATTCTCCAACTGCTTCCTTG	1

ABI PRISM 310 Genetic Analyser

- Fragmentation analysis

  – fluorescently-labelled primers

  – capillary fractionation
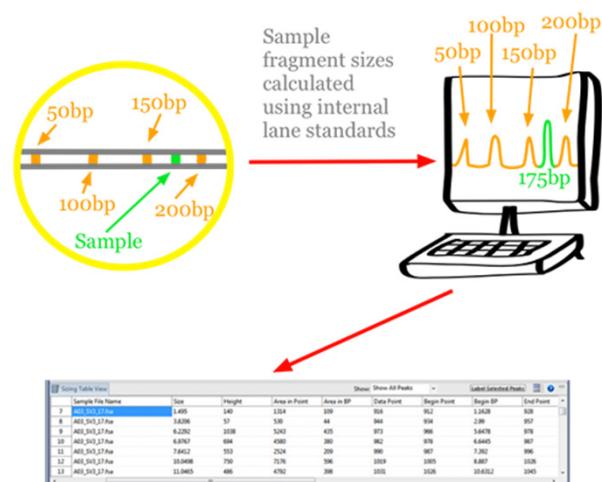
  – allele size

Tabular data output for further analysis
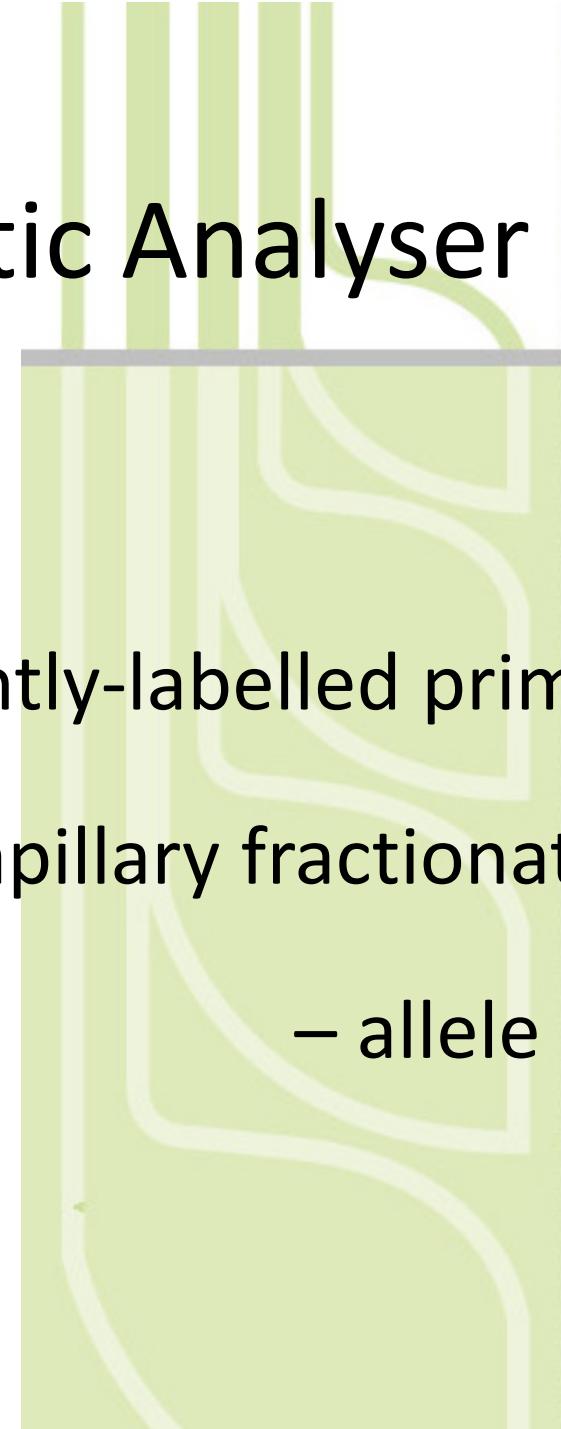
PowerMarker

v3.25

- **Genetic diversity parameters**

  → number of alleles

  → number of genotypes per locus

  → expected heterozygosity

  → observed heterozygosity

  → PIC

  → F_{IS}

- **1000 bootstrap replicates**

Basic observations

| Marker	N_G	N_A	H_e	H_O	PIC	F_{IS}
TGLA122	47	14	0.7747	0.745	0.7447	0.0399
TGLA227	45	12	0.8394	0.8675	0.8207	-0.0318
CSSM66	47	12	0.8598	0.8874	0.8438	-0.0304
CSRM60	32	10	0.8019	0.8344	0.7767	-0.039
ILST006	27	10	0.7732	0.7781	0.7396	-0.0048
SPS115	24	9	0.714	0.7053	0.6836	0.0139
ETH3	31	9	0.8257	0.8543	0.8022	-0.033
BM1824	20	8	0.7474	0.7086	0.7108	0.0535
Average ± sd	34.241 ± 3.6445	10.46 ± 0.6609	0.7914 ± 0.016	0.7984 ± 0.0234	0.7653 ± 0.0182	-0.0039 ± 0.0122

What are we looking for?

– **structure of population**

   – Bayesian approach

      – without any a priori information

• BAPS – simple algorithm

   – overestimation of no. of clusters (17)

      (more sensitive to low no. of microsatellites)

STRUCTURE – longer computation time
– more accurate results
– subjective interpretation
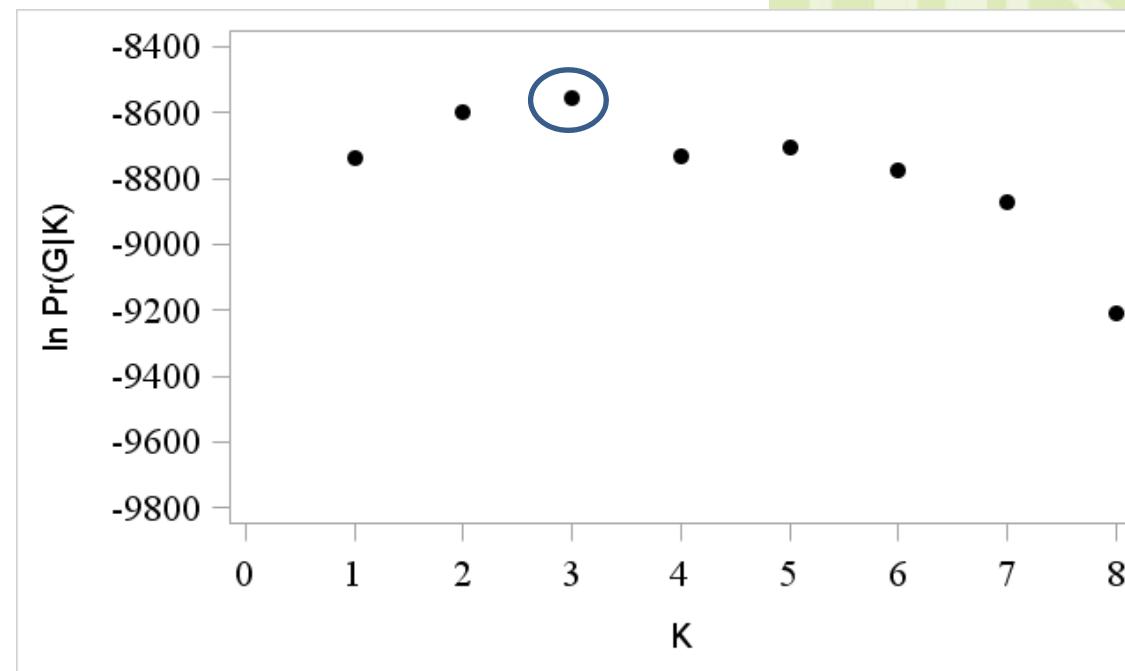
- Ln Pr(G|K) values presented as a function of the number of clusters

- The largest ln Pr(G|K) values within each K (among 10 runs) presented

STRUCTURE *k = 3*
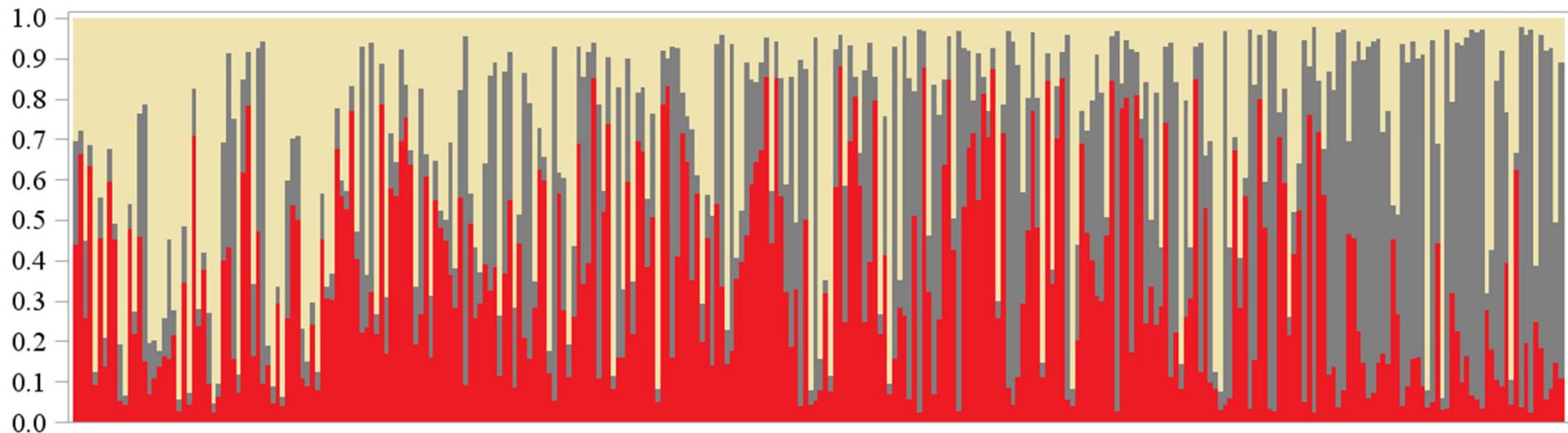
- population structure – without a priori information about subpopulations
- each cow is represented by a single vertical line broken into *k* color segments, with lengths proportional to the estimated membership of the inferred cluster.

Further investigation

- ## What is the population structure based on?
  - genealogical information – paternal lines???
- ## ROH – run of homozygosity
  - molecular inbreeding coefficients
  - total length (in Mb) and number of ROH
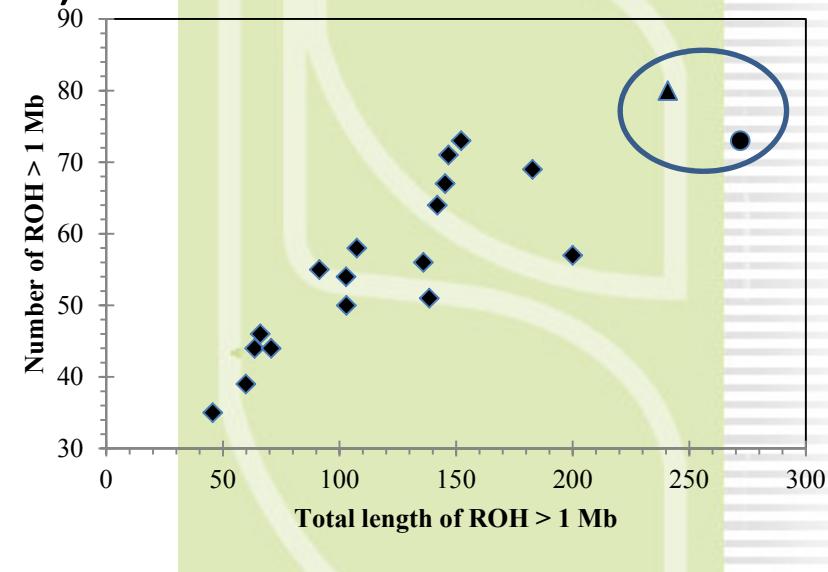
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Modern education for the knowledge society / Project is co-financed by the European Union

Development of International Cooperation for the Purpose of the Transfer and Implementation of Research and Development in Educational Programs

ITMS: 26110230085

demand-oriented project

Acknowledgement

- INSEMAS
- Slovak biological services
- Slovak association of Pinzgau breeders

Thank you for your attention!