



Characterization of Slovak dual-purpose cattle breed diversity based on genomic data

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The Aim

- detailed insight on genetic diversity of nucleus
 - Slovak Pinzgau Cattle
 - Slovak Spotted Cattle
- level of diversity using genome-wide data
 - ROH
 - LD
 - N_e
- population structure, fragmentation, admixture

Material and Methods:

- Pinzgau nucleus
 - bulls 19 active (18 gene bank)
 - COWS 35
- Slovak Spotted nucleus
 - bulls 36
 - COWS 50
- specific computation algorithm of unsupervised learning (STRUCTURE, BAPS)
 - identification and expansion of selection signatures
- principal components analysis
 - multivariate analysis to determine candidate genes

Slovak Pinzgau level of diversity:

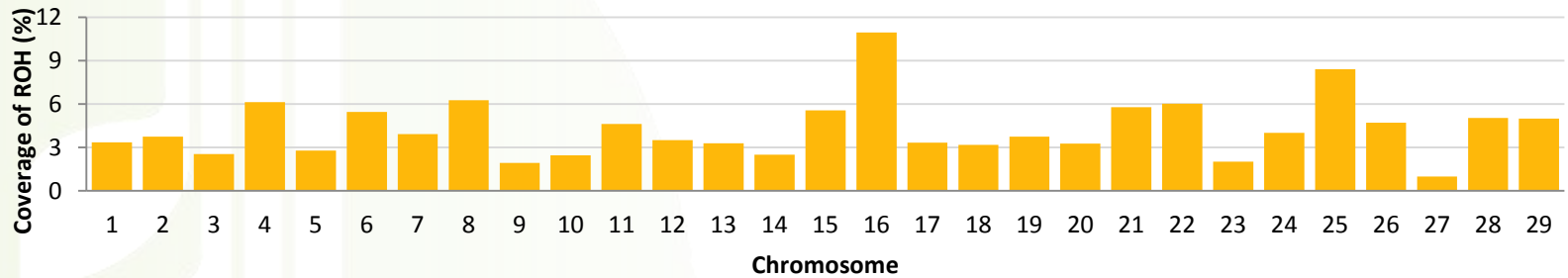
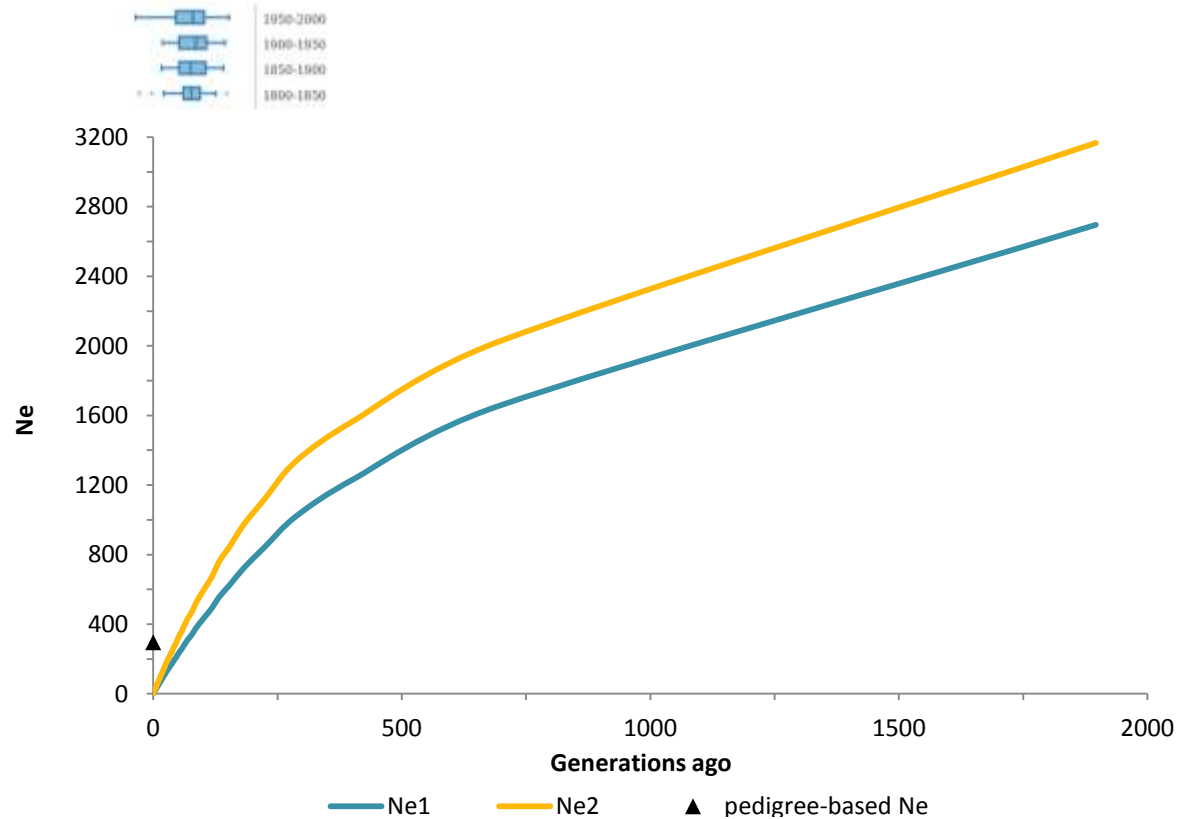


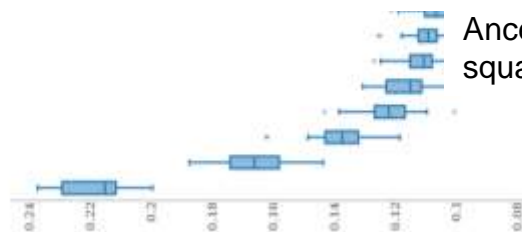
Table 1 Descriptive statistics of the molecular inbreeding coefficients calculated from runs of homozygosity (ROH) and pedigree inbreeding (F_{PED}) in 19 Pinzgau bulls.

Inbreeding coefficient	Mean	Range	Lower 95% CI	Upper 95% CI
$F_{ROH>1}$	0.0418 ± 0.0239	0.0130 - 0.1031	0.0303	0.0534
$F_{ROH>2}$	0.0276 ± 0.0224	0.0009 - 0.0880	0.0168	0.0384
$F_{ROH>4}$	0.0199 ± 0.0201	0.0000 - 0.0785	0.0103	0.0296
$F_{ROH>8}$	0.0139 ± 0.0163	0.0000 - 0.0625	0.0061	0.0218
$F_{ROH>16}$	0.0058 ± 0.0080	0.0000 - 0.0246	0.0019	0.0096
F_{PED}	0.0048 ± 0.0107	0.0000 - 0.0317	0.0003	0.0100

Slovak Pinzgau level of diversity:

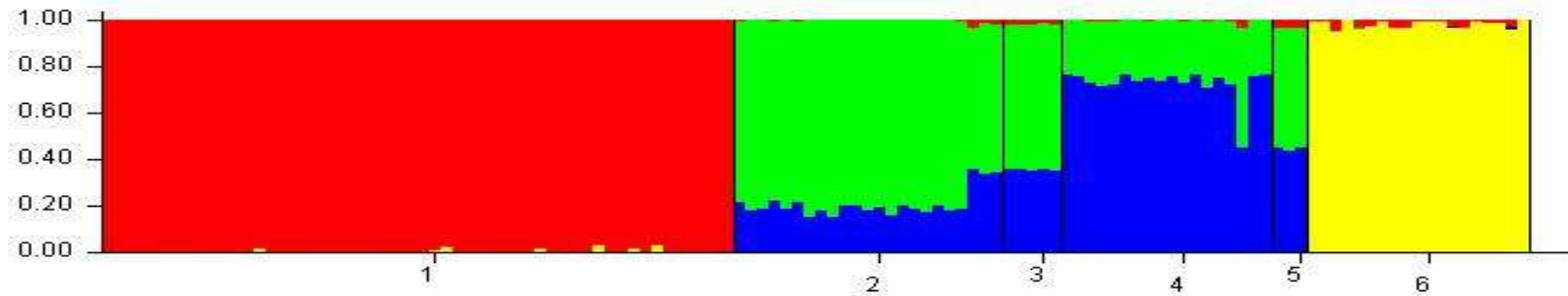


Ancestral and recent effective population size based on the squared correlation coefficient (r^2) between SNPs



Box-plots of average *LD* for all 29 autosomes plotted against physical distance bins in kb

Slovak Pinzgau level of diversity:

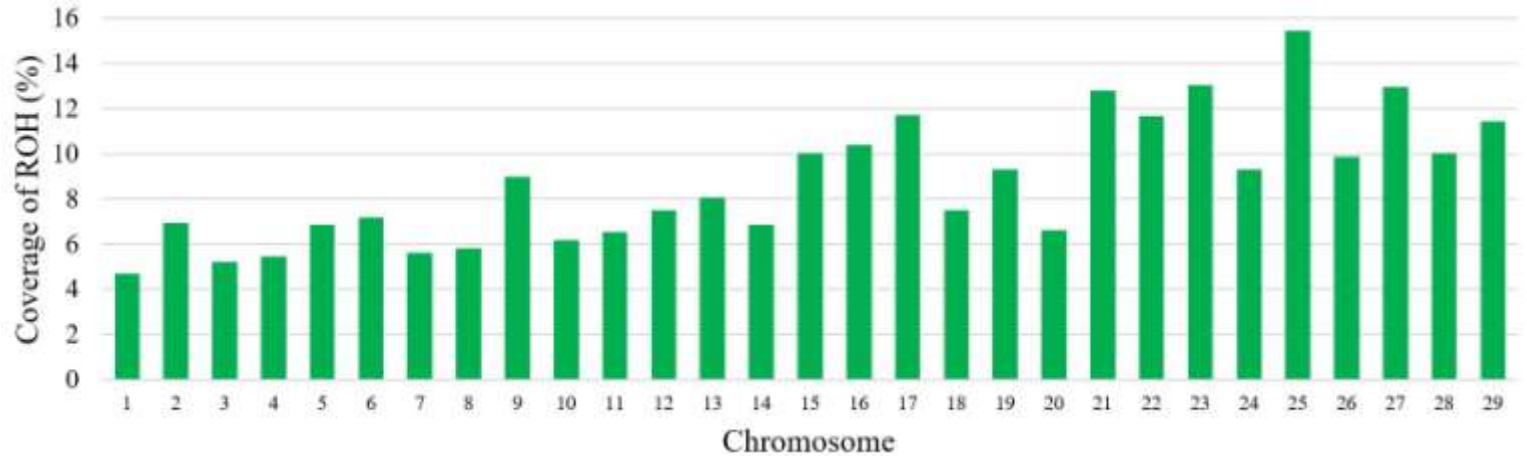


Unsupervised hierarchical clustering of an inferred number of clusters K varying from 2 to 6 (i.e. the number of breeds)

SNPs significantly associated with milk production

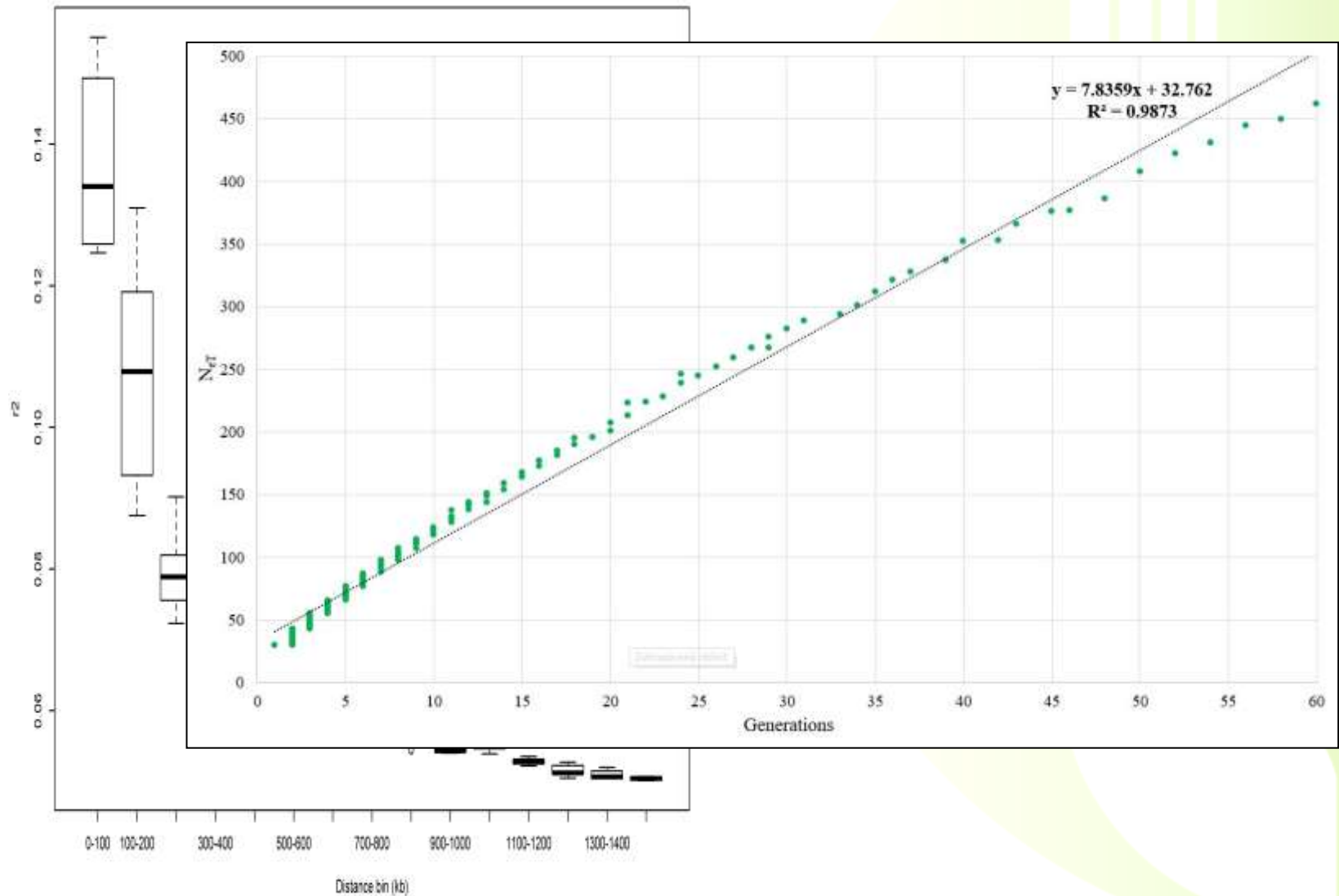
CHR	Illumina ID	Position	P value	QTL traits
1	ARS-BFGL-NGS-18066	111357945	4.77e-06	Milk Yield, Dressing percentage
7	BTB-00955523	105621232	4.74e-06	Milk Yield, Protein Yield, SCS score
8	Hapmap48090-BTA-81304	60269047	4.47e-06	
9	Hapmap60949-rs29020404	52283151	7.68e-06	Marbling Score, Milk, Protein and Fat yield
15	ARS-BFGL-NGS-12339	20018872	1.05e-06	
	ARS-BFGL-NGS-118767	24021537	2.93e-06	
16	BTA-38204-no-rs	3075859	2.52e-06	
18	ARS-BFGL-NGS-15438	53224638	5.18e-06	

Slovak Spotted level of diversity:

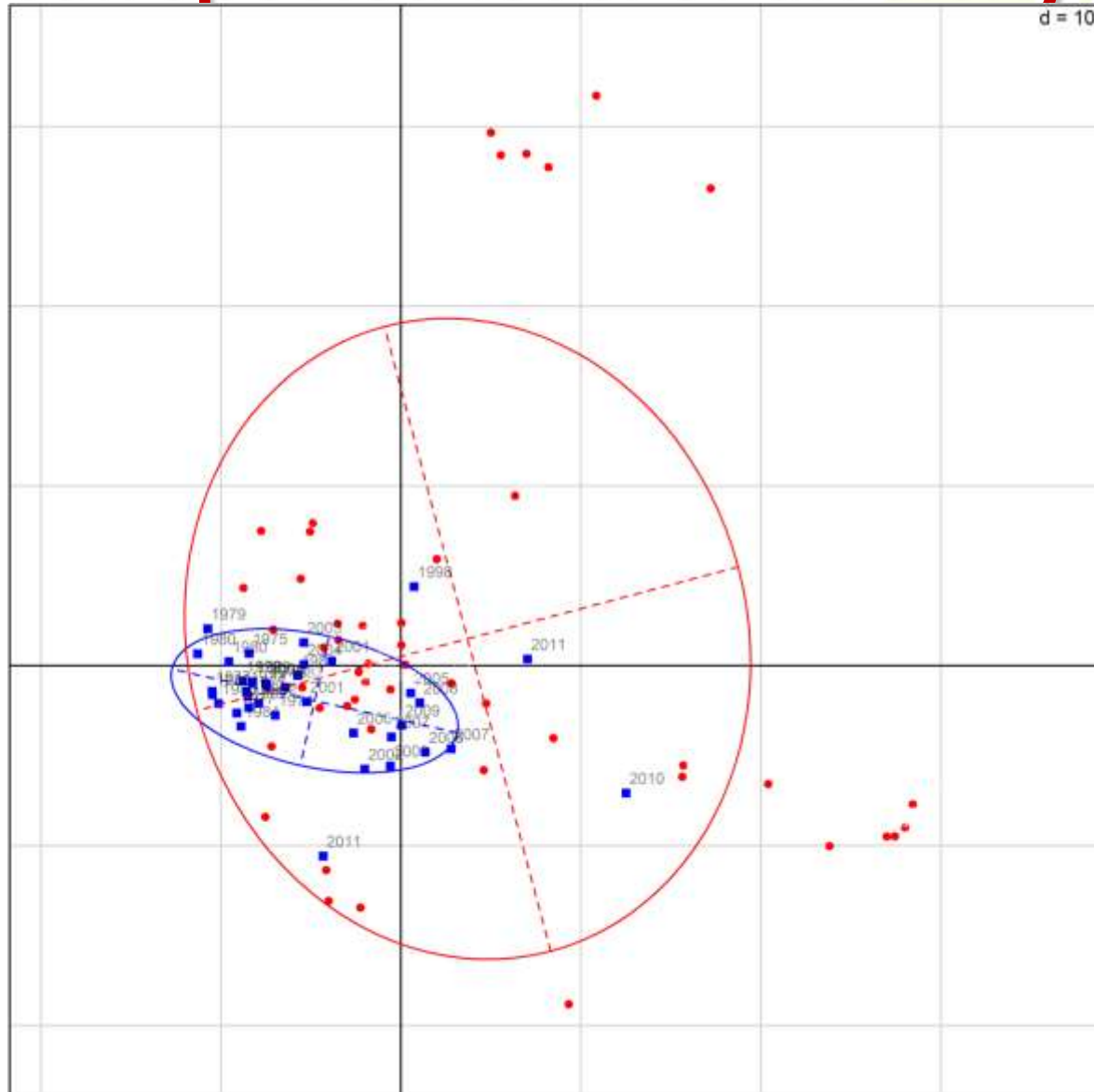


Inbreeding coefficient	Mean \pm SD	Range	Lower 95% CI	Upper 95% CI
$F_{ROH>1}$	0.0215 \pm 0.0162	0.0000 - 0.1154	0.0180	0.0249
$F_{ROH>2}$	0.0214 \pm 0.0161	0.0000 - 0.1153	0.0179	0.0249
$F_{ROH>4}$	0.0177 \pm 0.0147	0.0000 - 0.1144	0.0145	0.0208
$F_{ROH>8}$	0.0086 \pm 0.0119	0.0000 - 0.0920	0.0060	0.0112
$F_{ROH>16}$	0.0043 \pm 0.0110	0.0000 - 0.0885	0.0019	0.0067
F_{PED}	0.0036			

Slovak Spotted level of diversity:

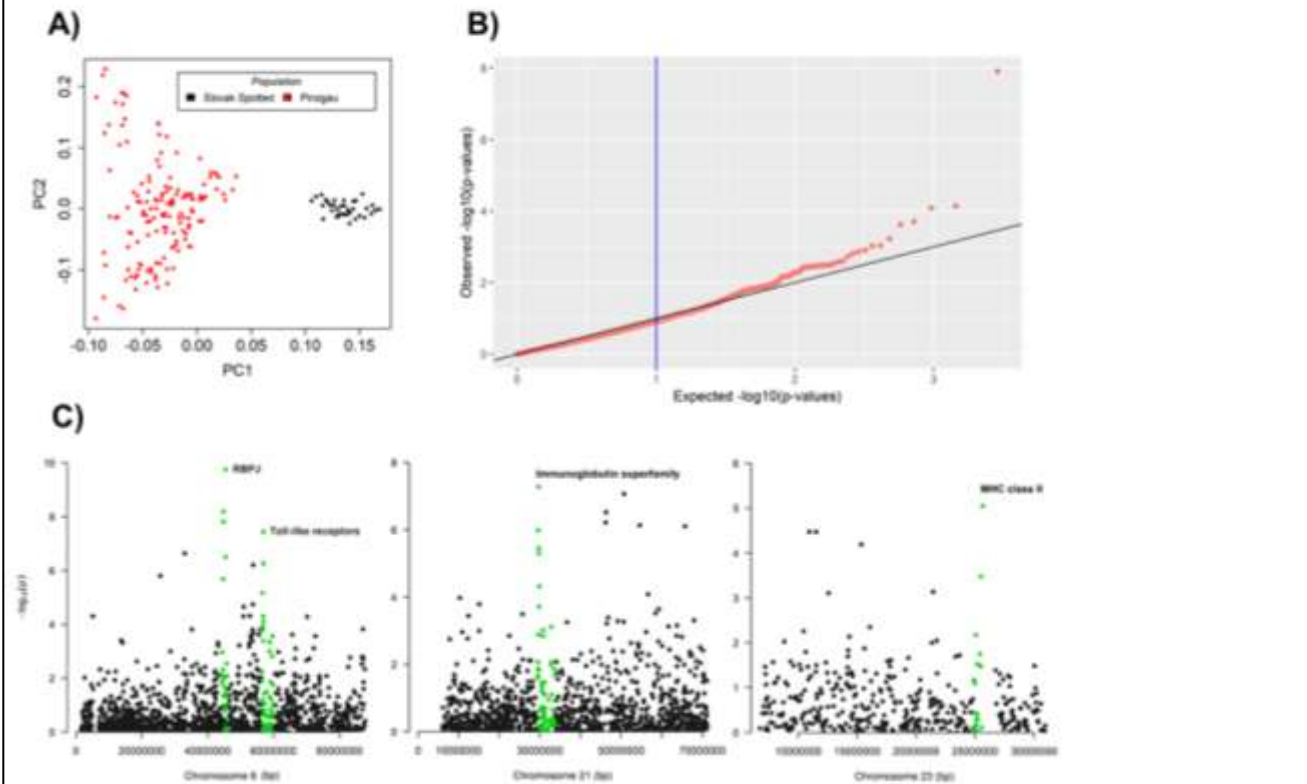


Slovak Spotted level of diversity:



Differences in important traits between breeds

The scatter-plot representing the population structure based on the first two principal components (A), distribution of p-values based on the Q-Q plot (B) and the Manhattan plots of $-\log_{10}$ (p-values) for BTA6, BTA21, and BTA23. The outlier loci characterizing the strongest signals of selection are coloured in green.



Conclusions

- is possible to design appropriate mating plans
 - derived from observing the fine-scale structure of the population according breeding goal
- signals of selection in genomic regions responsible for adaptive and innate immune response
 - result from the correlated selection response in way to maintain their fitness
- as in previous studies, farmers profit can be expected by use of the results
 - breed animals more suitable to respond environmental (production) conditions
 - faster compared to traditional methods

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