

### Genomic regions associated with phenotypic differentiation in European local pig breeds

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Many local pig breeds have been raised in extensive systems and have adapted to the specific environment causing rich phenotypic and genetic diversity. The present study aimed to detect genomic regions associated with phenotypic differentiation on stature, fatness, growth and reproductive performance in 20 European local pig breeds using a newly developed approach to search selection signatures linked to phenotype at the breed level. The analysis revealed 16 significant genomic regions associated with stature, 24 with fatness, 2 with growth and 192 with reproduction. Among them, several regions contained candidate genes with possible link to biological effect on phenotype. In the stature group, for example, genes *ANTXR1* (interacts with actin cytoskeleton) and *ANXA4* (involved in membrane-related pathways) were identified, in the fatness group genes *POMC* (energy balance via the leptin/melanocortin pathway) and *DNMT3A* (CpG methylation; adipose tissue development), and in the reproduction group gene *HSD17B7* (biosynthesis of sex steroids and cholesterol). To conclude, the genome scan for selection revealed several strong candidate genes with potential implication in adaptation of European local pig breeds to different production systems, which will be helpful for future conservation approaches. Financing of Slovenian Agency of Research (grants P4-0133, J4-3094, PhD scholarship for KP), and project TREASURE (EU H2020 GA no. 634476) is acknowledged.

## Session 04

## Theatre 3

### Inbreeding evaluation in Latvian local breeds

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In this study, inbreeding and effective population size of the Latvian cattle, sheep and goat local breeds were analysed. Two cattle breeds, Latvian Brown old type (LB) and Latvian Blue (LZ), which has been selected in Latvia for more than 100 years, were included in the analysis. During the last decade, the inbreeding level in cattle populations increased and reached 2.61% for LB and 5.20% for LZ at the time of data selection. Effective population size during the last five years decreased and for LZ was 79 and 112 for LB. At the beginning of the 19th century, coarse-wooled short-tailed sheep were bred in Latvia. The Latvian Darkhead (LT) breed was mentioned for the first time after 1945. Pedigree data for LT started from 1976 with a total of 2296 records. The reference population included 47 males and 502 females that were alive at the time of data selection and defined as GR. In 2019 the effective population size was 122 animals and the inbreeding of animals was 3%. Latvian native goat (LVK) was kept in Latvia since the end of the 19th and the beginning of the 20th century. Pedigree data for LVK started from 1983; the total number of records in pedigree was 3547. The criteria for data selection for the reference population was an LVK abbreviation in pedigree, and the animal was alive at that moment. Over the years, the inbreeding level has increased from 0.36 to 2.3% for LVK offsprings. In the LVK population, there are animals with an inbreeding level higher than 20 %. According to the results in all local Latvian breeds, the level of inbreeding was increased and the number and rate of males and females should be controlled in the local populations. Research was supported by the Ministry of Agriculture of the Republic of Latvia.