

Exploiting genomic data of autochthonous pig breeds: conservation genetics comes of age

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Animal genetic resources are important reservoirs of genetic diversity derived by distinct selection pressures or as result of adaptation to production conditions. The TREASURE project has investigated genetic variability in 20 European autochthonous pig breeds with the aim to describe their singularity, evaluate their adaptation, develop new methodologies for their management and identify DNA markers for breed allocation and meat authentication. Genomic data have been obtained by genotyping candidate gene markers and high density single nucleotide polymorphism arrays in ~48 animals from each breed and by whole genome resequencing. Description of genetic diversity has been obtained using several parameters. Runs of homozygosity and genomic inbreeding measures have been correlated with pedigree inbreeding coefficients. A few breed specific markers have been identified and applied. Genome wide association studies have identified genomic regions affecting unique phenotypes. This project represents one of the few examples of exploitation of genomic information that not only benefits the investigated animal genetic resources but also can provide useful information that could impact commercial populations. Funded by European Union's H2020 RIA program (grant agreement no. 634476).

Structural differences among pig genomes illustrate genetic uniqueness of breeds

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The availability of high-throughput whole-genome sequencing (WGS) data illustrating differences among different pig breed genomes opened a new area of genomic research focused on variation caused by single nucleotide polymorphisms (SNP), small scale variation and structural variants which may all contribute to phenotypic variation among pig breeds. In our study (performed within TREASURE project) we re-analysed WGS-based data sets from more than 20 breeds, including commercial and local breeds as well as some wild boar genomes, deposited in publicly available databases. This bioinformatics tool enables discovery of new SNPs, estimation of allele frequencies (genotyping by sequencing) at candidate loci and identification of structural variation in a wide range of pig breeds. The analysis underlined the relevance of structural differences at KIT and MC1R locus involved in colour pattern formation, as well as LEPR locus associated with fatness, fatty acid metabolism and intramuscular fat composition. This approach allows discovery of important genomic differences between commercial breeds and local breeds which are analysed in the frame of the TREASURE project. Extensive mining of publicly available genomic data can together with the newly generated genomic information from local breeds, significantly contribute to the detailed characterisation of animal genetic resources present in local pig breeds. Funded by European Union's H2020 RIA program (grant agreement No. 634476).