

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).