

First partial sequencing of an Iberian pig

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Researchers of the Faculty of Veterinary Medicine at Universitat Autònoma de Barcelona (UAB) and of the Centre for Research in Agricultural Genomics (CRAG), the Centre for Genomic Regulation (CRG) in Barcelona, the National Institute for Agrarian Technology and Research in Madrid and Wageningen Research Center (WUR, the Netherlands) have published the first partial genome sequencing of an Iberian pig. Using next-generation sequencing techniques, researchers have been able to sequence and analyse 1% of the genome. This is the first time an individual pig genome-sequence is published. The project, coordinated by ICREA researcher Miguel Pérez-Enciso, has been published in the online edition of the journal *Heredity*.

The sequenced animal is an Iberian sow from the *Guadyerbas* strain, a highly particular line which has been kept isolated on an experimental farm belonging to the government of Castilla-La Mancha and located in Oropesa, near Toledo, since 1945, thanks to years of work by INIA researchers. The *Guadyerbas* line thus represents one of the first original strains of the Iberian pig in Spain. These animals have a good appetite, are slow-growing, obese, hairless and black coloured. UAB and INIA teams have used these animals in several experiments aimed at identifying the genetic basis of the highly reputed meat quality of Iberian pigs. Researchers expect therefore that a complete sequencing could offer clues on these and other characteristics.

The sequenced animal is highly inbred, since the herd has been isolated for over 50 years. Researchers have taken this into account with the intention of using a particularly 'homogeneous' species presenting little

variability. Nevertheless, data from the sequencing offer surprising results, such as a higher than expected level of variability. Despite being highly inbred, a diversity which represents approximately half of all European populations can be observed. This aspect is important when seen from a conservation viewpoint, since it demonstrates that the Iberian pig is greatly representative of European populations.

Other genome regions present more uniformity and do not have this variability. The sexual chromosome (X) for example is a more uniform than theoretically expected. Comparison between regions of high and low variability offers clues on which genes are more relevant from a selective point of view in the Iberian pig. Among the regions with highest variability there are genes related to the olfactory and immune systems; those presenting less variability are genes related to the metabolism of carbohydrates.

The study of regions that differ most between international lean breeds and Iberian pigs will provide researchers and breeders with information on why Iberian pigs have specific characteristics which make the species unique in terms of their genetics. Before carrying out this detailed analysis, however, the full sequencing and annotation of the pig reference genome must be finished, which will be done by an international consortium. The analysis is foreseen to be completed by the end of the year.

Provided by Universitat Autònoma de Barcelona

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