

## Fatty acid synthase gene sequence from Alentejano pig, an autochthonous obese breed

André Albuquerque<sup>(1)</sup>, Maria do Rosário Félix<sup>(1,2)</sup>, Marta Laranjo<sup>(1,3)</sup>, José Neves<sup>(1,4)</sup>, José Manuel Martins<sup>(1,4)</sup>

(1) ICAAM, Universidade de Évora, Portugal.

(2) Departamento de Fitotecnia, Universidade de Évora, Portugal.

(3) IIFA, Universidade de Évora, Portugal.

(4) Departamento de Zootecnia, Universidade de Évora, Portugal.

Most of swine industry nowadays is about productive and profitable fast-growing lean breeds raised under intensive conditions leading to meat and fat rich in saturated fatty acids. Its consumption is generally associated with increased health risks such as the development of cardiovascular diseases.

The Alentejano (AL) pig is an autochthonous breed referred as genetically similar to the Iberian pig. Different from lean breeds, traditionally raised AL pigs produce carcasses with higher contents of oleic acid (C18:1) and consequently lower contents of saturated fatty acids. Their meat and fat are used for the manufacture of regional high quality meat products of worldwide recognition. This obese breed is characterized by slow growth rates and precociously high lipogenic activity. In fact, and contrary to industrial lean breeds, the AL breed features the thrifty genotype, responsible for a higher potential and ability for fat deposition.

*De novo* synthesis is an endogenous recycling process of fatty acid (FA) synthesis responsible for about 80% of all FA synthesis in swine adipose tissue, although independent intramuscular synthesis can also occur. The key enzyme in *de novo* synthesis pathway is fatty acid synthase (FAS), a multi-enzymatic complex composed of two identical and multifunctional monomers of about 270 kDa. The final FA obtained, palmitate (C16:0), is a precursor to longer and more complex fatty acids.

The aim of this study was to determine the gene sequence of the porcine FAS lipogenic enzyme of an obese AL pig in subcutaneous adipose tissue, the most relevant lipogenic tissue. Total RNA was extracted from tissue samples obtained in an industrial slaughterhouse. cDNA was generated by reverse transcription in order to perform subsequent specific polymerase chain reactions (PCR) using previously described primers along with newly designed ones. PCR products were cloned before sequencing.

To our knowledge this is the first published FAS gene sequence in AL purebred pigs. The obtained partial sequence (about 82% of the coding gene portion) was compared to previously reported gene sequences of other breeds and has been submitted to the GenBank database under the accession number KM658506. Six single missense polymorphisms on FAS specific domains were detected in relation to the Iberian pig sequence previously reported (AY954688.1). Future studies will be required in order to assess the effects of these polymorphisms on meat quality traits in the AL pig.