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VALORIZATION OF EXTENSIVE BREEDING OF THE SPANISH MERINO SHEEP THROUGH THE QUALITY WOOL IMPROVEMENT: PRELIMINARY RESULTS OF GWAS OF FIBER DIAMETER FROM WHOLE GENOME SEQUENCES

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The autochthonous Spanish Merino is one of the most emblematic breeds in Spain, not only for its productive importance but also for the impact in our history since its origin. This breed was created and improved in the Iberian Peninsula centuries ago, becoming the sheep with the highest wool quality in the world, which is why it was the origin of the worldwide Merino and Merino-derived breeds. Currently its production system continues to have a high level of extensification, so the revaluation of its breeding has a high value in the maintenance of the pasture of mountain ecosystems where it is managed.

The wool market crisis in the last forty years forced the *National Association of Merino Sheep Breeders* to implement a breeding program aimed at improving meat production (but maintaining their rusticity, and wool characteristics). Currently, there is a worldwide trend of revaluation of natural fibers, among which wool stands out. This has led to an increase in the benefits associated with quality wool in our country, so many breeders are very interested in obtaining rams that improve the main quality traits of wool (fineness and fiber length).

For the present study, wool quality from a population of 6,200 purebred Spanish Merino (registered in the flock-book) were analyzed using the Australian OFDA 2000 to determine classical wool quality criteria such as average fiber diameter and its coefficient of variation, in addition to other very important criteria for the textile industry such the comfort factor, staple length, fibre curvature or spin Fineness. The evaluation of these animals determined that the Merino breed still has a high potential to produce fine quality wool but is currently highly heterogeneous. For this reason, in addition to the classical genetic evaluations for the selection of breeding animals, the aim is to search for molecular markers that improve the reliability of these evaluations and make possible an early selection of these breeding animals.

In this first approach, the most extreme animals in terms of fiber fineness were selected (44 animals with the highest fineness and 31 animals with the highest diameter). The Whole Genome Sequences of animals were obtained at an average coverage of 4.5x (Neogen, Ayr, Scotland), mapped against the Rambouillet 2.0 reference genome. Subsequently, and sequences with high quality levels were used for variant calling. The GWAS performed determined the presence of 17 regions associated with fiber diameter distributed in 8 chromosomes. After the ontological assay, 39 genes were detected. Of them, the 92 % were related with protein coding and the rest with the synthesis of different types of RNA. These preliminary results require further studies using a larger population to validate them.