FAANG-Europe

Functional Annotation of Sheep Milk Transcriptome

Why was this STSM important for you?

The use of massive parallel RNA sequencing technologies (RNA-Seq) has acquired a high importance in the last decade. In livestock species, RNA-Seq has been mainly used for the identification of differential expressed genes under different conditions, tissues and time-points related to production traits. The development of RNA-Seq has also allowed the discovery of thousands of previously unannotated functional elements which characterization is not usually the main objective in livestock transcriptome studies. FAANG, and particularly European-FAANG cost action, aims to promote the identification of functional elements, especially regulatory elements, in the major domesticated species genomes. In previous RNA-Seq analyses, performed during my PhD studies at the Animal Production department (University of León), we found a large percentage of unannotated intergenic transcripts (60%) in the mammary gland transcriptome of lactating dairy sheep. Thus, I found interesting to applied for the STSM COST Action CA15112-FAANG Europe grant to perform a short stay at the GenRoc and Genotoul labs (INRA-Tolouse) to develop the required pipelines for the identification and annotation of the long noncoding RNAs (lncRNAs) present in the lactating sheep mammary gland. The identification and characterization of lncRNAs has become a major challenge over the last years due to their putative role as regulators of gene expression. In addition, in the case of livestock species, the annotation of novel functional genome elements is especially interesting, as the identification of these elements can be of great help for the assessment of mutations in parts of the genome that do not encode for proteins and may be associated with productive traits of interest. On top of that, the exchange visit funded by the STSM COST Action has allowed me to increase my expertise on the analytical approaches implemented for the annotation of functional elements on RNA-Seq data.

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