Whole blood transcriptome analyses in pigs with extreme percentages of T-cell populations

Teodor Jové-Juncà[1], Maria Ballester[1], Olga González-Rodríguez[1], Raquel Quintanilla[1], Daniel Crespo-Piazuelo[1]*

[1]Animal Breeding and Genetics Program, IRTA, Torre Marimon, 08140 Caldes de Montbui, Spain.

[*]teodor.jove@irta.cat

Summary:

With the increasing concern in Europe about antimicrobial resistance the importance of limiting the use of antibiotics in animal production has become more evident. Finding alternatives to produce robust and resilient animals, without impairing production efficiency or altering the organoleptic properties of meat, will be one of the industries challenges in the forthcoming future. Our study aimed to identify candidate genes and genetic markers for immuno-related traits in domestic pig (*Sus scrofa*). Hence, we sequenced the blood transcriptome of 30 Duroc pigs from the IMMUPIGEN population, composed of 432 individuals. Two analyses were performed according to the phenotypic value of different T-cell populations. For the study 1 samples were classified into two groups of 15 individuals each with the highest and lowest values for both CD4+ (T-helper) and CD4+/CD8+ double positive (T-helper memory) T-cells percentages. For the other study (study 2) we selected two extreme groups of 11 individuals according to their γδ T-cell percentage. Differential gene expression analyses carried out with edgeR reported a total of 264 differentially expressed (DE) genes. For the study 1, a total of 18 DE genes were identified, where 8 genes have a prominent role in the immune system and the differentiation and maintenance of T-cell populations, such as *CAPG, CD4, DNTT, KLRD1* and *RAG1*. It is worth mentioning the co-localization of *CAPG*, *CD4* and *KLRD1* with regions significantly associated with T-helper memory and T-helper cell populations in a previous study. The study 2 reported 246 DE genes between individuals with divergent percentage of γδ T-cells. Further pathway analyses conducted with ClueGO, STRING and enrichR reported that 72 out of those 246 DE genes were involved in the differentiation and maintenance of T-cell populations, such as *SOX13*, a transcription factor directly responsible for normal γδ T-cell development. Our results identify candidate genes with a clear role in the genetic modulation of the composition of T-cells populations, which should be considered for the evaluation of adaptative immune responses and as potential markers to increase robustness and disease resistance in pigs.

Keywords: Pig, Adaptive immunity, RNA-seq, robustness, T-helper memory, T-helper, γδ T-cell, Blood