

Animal Breeding and Genetics Program, IRTA

## Exploring the link between blood transcriptomics and plasma untargeted lipidomics in pigs

**Hernández-Banqué Carles<sup>1</sup>, Jové-Juncà Teodor<sup>1</sup>, Folch Josep Maria<sup>2,3</sup>, González-Rodríguez Olga<sup>1</sup>, Portero-Otin Manuel<sup>4</sup>, Quintanilla Raquel<sup>1</sup>, Ballester Maria<sup>1</sup>**

<sup>1</sup>Animal breeding and genetics, IRTA, Torre Marimon, Caldes de Montbui, 08140, Spain.

<sup>2</sup>Plant and animal genomics, CRAG, Consorcio CSIC-IRTA-UAB-UB, Campus UAB, 08193, Bellaterra.

<sup>3</sup>Departament de Ciència Animal i dels Aliments, Facultat de Veterinària, UAB, 08193 Bellaterra.

<sup>4</sup> Department of experimental medicine, University of Lleida-Biomedical Research Institute of Lleida, 25196, Lleida, Spain

[\\*carles.hernandez@irta.cat](mailto:carles.hernandez@irta.cat)

The present work is part of the METAPIGEN project, which aims to investigate the interplay between energy metabolism and immunological responses in swine. Previous studies revealed certain genetic determinism of the porcine plasma lipidome, and the existence of genetic interactions with several immunity phenotypes. The aim of this work is deepening in the genomic regions associated with the abundance of the different components of the plasma lipidome, as well as studying their colocalization with regulatory regions of the blood transcriptome. For this purpose, plasma samples of 300 pigs were collected from a commercial Duroc population. Untargeted lipidomic data for 982 metabolites was obtained by mass spectrometry and underwent quality control adjustments and normalization. Genotypes of the individuals were obtained by using the commercial Illumina 70K GGP porcine array and subsequently were imputed at genome level. Genome-Wide Association Studies (GWAS) between the 8.5M filtered polymorphisms and the normalized untargeted lipidomic data were conducted using GCTA/1.93.2. Additionally, blood transcriptomic data from 255 pigs was obtained by RNA-seq, and expression GWAS were also performed. After Bonferroni correction (adjusted  $p < 0.05$ ), a total of 145,301 significant associations were found between 62,582 polymorphisms and 104 lipid metabolites, establishing a total of 124 associated genomic regions. The strongest association was found on chromosome 8. Pig chromosomes 2, 8, 10, and 17 contained regions associated to at least five different metabolites. Further analysis identified 408 candidate genes located within these regions, potentially involved in energy metabolism, lipid metabolism and/or immune function such as *ELOVL6*, *ST3GAL1* or members of the *FADS* family. By overlapping the lipid-associated genomic regions with the porcine transcriptome eQTLs, 229 blood-expressed genes regulated by cis-eQTLs were found to overlap with lipidomic genomic regions. Our study found genomic *loci* and candidate genes linked to the porcine lipidome, highlighting the genetic interplay between lipids, metabolism and immunity.

Acknowledgments: Project funding by grant PID2020-112677RB-C21 and PID2023-148961OB-C21 awarded by MCIN/AEI/10.13039/501100011033 and by the FPI grant PRE2021-097825 granted by the Spanish Ministry of Science and Innovation. We thank the company Selecció Batallé and the Lipidomics Service of the UdL for their collaboration.