IV Annual Congress for Young Researchers
Barcelona, October 09-10

Animal Breeding and Genetics Program, IRTA

Genetic determinism of porcine plasma lipidome.

Hernández-Banqué Carles[1], Junhui Liu[2], Jové-Juncà Teodor[1], Folch Josep Maria[2,3], González-Rodríguez Olga[1], Portero Otin Manuel[4], Pascual Mariam[1], Quintanilla Raquel[1], Ballester Maria[1]

[1]Animal Breeding and Genetics Program, IRTA, Torre Marimon, Caldes de Montbui, Spain.
[2]Plant and Animal Genomics, CRAG, Consorcio CSIC-IRTA-UAB-UB, Campus UAB, 08193, Bellaterra.
[3]Departamento de Ciencia Animal y de los Alimentos, Facultad de Veterinaria, UAB, 08193 Bellaterra.
[4] Department of Experimental Medicine, University of Lleida-Biomedical Research Institute of Lleida, 25196, Lleida, Spain
*carles.hernandez@irta.cat

The present work is part of the METAPIGEN project which aims to study the relation between the energetic metabolism and the immunity of pigs to identify biomarkers that improve the immune response without negatively affecting production and quality traits. In this work, we aimed to study the genetic determinism of plasma lipid metabolites in pigs by estimating their genetic parameters and identifying associated genomic regions. For this purpose, plasma samples of 300 pigs were collected from a commercial Duroc population. Untargeted lipidomics data was obtained by mass spectrometry followed by quality control adjustments, normalization and filtering for retention time >3; a total of 982 metabolites remained for further analysis. Genotypes of the individuals were obtained by using the commercial GGPSNP70 array and subsequently were imputed against a multiple-breed reference population of 1,602 WGS data with Beagle software. A total of 9,739,308 SNPs were kept after filtering out those with more than 10% missing genotype data and minor allele frequency below 5%. GWAS was conducted between the filtered polymorphisms and the normalized untargeted lipidomic data using the fastGWA tool from GCTA/1.93.2. After Benjamini-Hochberg correction, a total of 141,123 significant associations were found between 72,327 polymorphisms and 140 metabolites, establishing a total of 197 associated genomic regions. Further analysis of these regions revealed a total of 278 genes that play a role in lipid metabolism or immune capacity. The most associated polymorphisms were rs338500538, rs701893123 and rs338500538 located in chromosome 8, and were found to be the most significant variants associated to three different metabolites. Within the genomic regions for these variants we detected relevant metabolic genes such as *ELOVL6* and *PLA2G12A*, along with several immunity modulators like *IL2* and *IL21.* Further studies are being conducted to identify candidate genes involved in modulating the levels of lipid metabolites in pig serum.

Acknowledgments: Project funding by grant PID2020-112677RBC21 awarded by MCIN/AEI/10.13039/501100011033 and by the FPI grant PRE2021-097825 granted by the Spanish Ministry of Science and Innovation.