Exploring the link between blood transcriptome and plasma lipidome in pigs

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The present work is part of the METAPIGEN project, focused on exploring the relationship between porcine immunity and energy metabolism to identify biomarkers that improve immunocompetence without impairing production efficiency. A moderate genetic determinism of the porcine plasma lipidome has been stated in previous studies. The aim of the present study was to further investigate the genetic basis of porcine plasma lipidome by evaluating the genomic regions associated with the abundance of different lipid metabolites and their colocalization with regulatory regions of the blood transcriptome. Untargeted lipidome data from plasma samples of 300 commercial Duroc pigs was obtained through mass spectrometry, detecting a total of 982 metabolites. Genotypes of these animals were imputed at genome level from a commercial 70K GGP porcine array. A Genome-Wide Association Study (GWAS) was performed between the 8.5M filtered polymorphisms and the normalized lipid data using GCTA. Additionally, blood transcriptome RNA-seq data was obtained for 255 of these pigs and used to perform an expression GWAS analysis. A total of 124 genomic regions comprising 62,582 polymorphisms were associated to the abundance of 104 lipid metabolites. The genomic region with the strongest association was found on chromosome 8, associated with three different lipids. Several QTLs were associated to at least five lipid metabolites in porcine chromosomes 2, 8, 10, and 17. Further analyses allowed identifying 408 candidate genes within these regions, potentially involved in immunity, energy metabolism, or lipid metabolism. Colocalization analyses revealed the overlap between lipidome-associated genomic regions and blood transcriptome cis-eQTLs associated to the expression levels of 229 genes involved in metabolic or immunological functions, such as *ST3GAL1* or members of the *FADS* family. Our study found genomic *loci* and candidate genes linked to the porcine lipidome, highlighting the genetic interplay between lipids, metabolism and immunity.