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Genetic determinism of porcine plasma lipidome and its relationship to immunity

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Abstract

The modulation, activation and differentiation of several immune cells is highly dependent on lipid metabolism. The objective of this study was to analyse the genetic determinism of the porcine plasma lipidome and its association to animals' immune capacity. For this purpose, we quantified the plasma levels of 982 lipid molecules from a population of 300 healthy Duroc pigs. We estimated the heritability of the lipidome and their phenotypic and genetic correlations with 41 health-related traits. Additionally, genome wide associations studies (GWAS) were performed between the lipidome and 9,739,308 imputed single nucleotide polymorphisms.

Mean heritability estimates for the lipid species ranged from 0.04 to 0.91, with 186 of them obtaining mean estimates over 0.4. A total of 903 lipid species were found to be genetically associated with at least one of the health-related traits. GWAS analyses revealed 157.989 significant associations (adjusted p < 0.05) between 72,327 polymorphisms and 139 metabolites, identifying a total of 172 associated genomic regions. The strongest associations were found on chromosome 8 for the polymorphisms rs338500538, rs701893123 and rs338500538, which were associated with three lipid molecules. By overlapping the genomic regions associated to lipids with previously defined QTL for immunity traits, we revealed 22 regions associated to eight immunological traits. Within these genomic regions, relevant immunity modulators such as *ST3GAL1, SLA* and *IL2* genes were identified.

In conclusion, our results confirmed the genetic determinism of the blood lipidomic profile in pigs and highlight the relationship of lipid species with immunity and health-related phenotypes.

Keywords

Pig, Lipidome, Immunocompetence