Genetic architecture of adaptive immunity traits in pigs

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Summary

Animal Health in the pig industry is a major contributor to productivity, profitability and welfare. In the midst of strong investment for designing alternatives to antimicrobials in veterinary medicine, breeding programs should also promote resilience and wellbeing for a more competitive and sustainable swine production. The IMMUPIGEN project focused on the genetic arquitecture of global immunocompetence in pigs, with the final aim of incorporating genetic markers of immunity in selection programs to produce more robust and disease resistant pigs. The objective of the present work was to study the genetic determinism of adaptive immunity traits in pigs, as well as to identify genomic regions associated with them. For this purpose, we stained peripheral blood mononuclear cells (PBMCs) to measure the proportions of seven lymphocyte populations (T-cells, Cytotoxic T-cells, T-helper cells, T-helper memory cells, naïve T-cells, Natural Killer cells and B-cells) from 391 healthy male and female piglets aged 8 weeks belonging to a Duroc commercial line. All animals were genotyped for 68,516 SNPs with the GGP Porcine HD Array (Illumina, San Diego, CA). Medium to high heritabilities were obtained for most traits ranging between 0.36 and 0.84. PBMCs proportions of T-cells (h^2=0.77) and T-helper memory cells (h^2=0.84) were among the most heritable traits. Positive genetic correlations were obtained between T-cells and Cytotoxic T-cells, T-helper memory cells and naïve T-cells whereas T-cells correlated negatively with B-cells and different plasma immunoglobulins (IgA, IgG and IgM). A genome-wide association study pointed out 32 significantly associated SNPs (FDR<0.1) located in four chromosomal regions on *Sus scrofa* chromosome (SSC) 3, SSC5, SSC8, and SSCX for T-helper cells, T-helper memory cells and naïve T-cells. Several genes mapped in the associated regions have been proposed as candidate genes to explain the variation of adaptive immunity traits, also in humans, such as *CD69*, *CD8A*, *CD8B*, *CHMP3*, *CLEC4D*, *CLEC4E*, *KLRD1*, *KLRK1* and *RMND5A*, among others. Our results enhance the knowledge about the genetic control of traits related with adaptive immunity which could be considered to optimize the induction of cellular responses to vaccines against pathogens. Furthermore, they support the possibility of applying effective selection programs for improving immunocompetence in pigs.

Keywords: Adaptive immunity, genome-wide association, pig, robustness, lymphocytes