A genetic and functional analysis of innate and adaptive immunity in pigs

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Improving the robustness and the resistance of animals to pathogens is a high priority in most livestock species, particularly in pigs. A better understanding of the genetic determinism of the different components of immune response is a prerequisite to include health traits in pig selection schemes. Our laboratory has launched a program aiming at studying innate and adaptive immunity traits in French Large White pigs without focussing on a particular pathogen. A population of 443 castrated Large White males recorded for production traits was included in our study. Blood was sampled three weeks after vaccination against *Mycoplasma hyopneumoniae* and 54 non redundant parameters were scored. Blood cell subpopulations were counted by hemograms and flow cytometry was performed to detect cell subsets including IgM+ (B lymphocytes), γδTCR+ (γδ T lymphocytes), CD4+ and/or CD8+ (αβ T lymphocytes), CD16+/CD2+ (NK cells) and CD16+/CD172a+/MHCII+ (monocytes) cells. Innate immunity parameters included phagocytosis tests, *in vitro* production of IL1B, IL6, IL8, TNFA and IL12 from stimulated blood cells, IFNA release after blood stimulation by a viral antigen, measurement of C-reactive protein and haploglobin in the serum. For adaptive immunity, parameters included antigen-specific and non-specific cell proliferation, *in vitro* production of IL2, IL4, IL10 and IFNG from stimulated blood cells and quantification of total antibodies (IgA, IgM and IgG) and specific IgG levels in the serum. Genetic analyses revealed that 44 parameters show moderate to high heritabilities with an average of 0.4 +/- 0.2. The transcriptome of leukocytes from animals with contrasted immune response parameters was studied using a porcine generic array enriched in immunity-related genes. Our results show that this molecular phenotype is informative for part of the immune traits. Our overall results confirm that many immunity parameters are under genetic control and that including molecular phenotypes such as transcriptomic data is relevant to refine immunity phenotypes.