Integrating blood transcriptome and immunity traits to identify markers of immune capacity in pigs

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Understanding individual variability of immune capacity in livestock has become a priority to improve sustainability, with the aim to increase disease resistance and resilience in breeding programs. In this study, 550 60-day-old French Large White pigs vaccinated against *Mycoplasma hyopneumoniae* (*M hyo*) were monitored for 55 immunity traits (ITs) measured from blood samples (SUS_FLORA ANR funded project). The ITs included two types of parameters. First, parameters directly measured from blood: complete blood counts, counts of various cell subsets by flow cytometry, serum dosage of anti *M hyo* IgG and haptoblobin. Second, parameters measured after *in vitro* stimulation of total blood: phagocytosis, production of cytokines (IL-1β, IL-8, IL-10, IL-17, TNFα, IFNγ) after stimulation by LPS or mitogenic agents. All animals were genotyped with 60K Illumina SNP chips. A subset of 243 piglets was chosen for blood transcriptome analysis using Agilent microarrays. We explored covariations between blood expression profiles and IT levels, and could draw lists of the most correlated genes with each IT. Each list represented candidate blood biomarkers potentially predictive of IT variations. As an example, we found 134 genes associated with phagocytosis capacity and we identified a subset of genes that could significantly predict levels of eight ITs related to phagocytosis by a sPLS approach. This gene subset included *CXCR1*, *CCR1* and *TLR2*. Few candidate biomarkers were previously shown to be genetically controlled for their transcription in blood by eGWAS. Thus, our results provide new data to decipher the genetic architecture of IT variations. A next step will be to understand how IT variations could reflect individual robustness while facing pathogens, and how blood biomarkers could be used as predictors of immune capacity.