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Blood transcriptome as an emerging molecular phenotype to study immunocompetence in swine

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As disease resistance traits are difficult or impossible to measure directly in livestock, potential indirect immunocompetence criteria are measurements of immune traits (ITs). In this perspective, we are currently studying porcine ITs by combining genetics and functional genomics approaches, with no initial focus on resistance to a specific pathogen (Flori et al., BMC Proc, 2011). Blood was sampled from a population of 60 days old Large White pigs (N=443) three weeks after vaccination against *Mycoplasma hyopneumoniae*. The measured ITs were related to blood cell counts (hemogram, proportions of cell sub-populations by flow cytometry), inflammation (seric inflammatory proteins), innate immunity (phagocytosis, *in vitro* production of IL-1 β , IL-6, IL-8, IL-12, TNF), and adaptive immunity (specific and non specific antibodies, *in vitro* cell proliferation and production of IFNG, IL-2, IL-4, IL-10). Estimates of heritabilities and correlations revealed that numerous ITs show substantial genetic variation despite limited co-variation (Flori et al., PLoS ONE, 2011). For functional genomic studies, in-house developed microarray (SLA-RI/NRSP8-13K chip; Gao et al., BMC Genomics, 2010) were used in blood tissue. We compared groups of animals contrasted in levels of white blood cell count, CD4-CD8⁺ or TCR $\gamma\delta$ ⁺ lymphocyte counts, phagocytosis, *in vitro* production of IL-2, IL-10, TNF, IFNG, and specific antibodies. For each phenotype, the two analysed groups comprised 4 to 10 animals from the extreme tails of the trait distribution. Among the nine ITs studied, blood transcriptome analysis revealed differentially expressed genes for five traits. The expression of genes in blood was not significantly affected for animals traits contrasted in levels of TNF or IFNG production, specific IgGs, and TCR $\gamma\delta$ ⁺ cell count. Within the differentially expressed genes, we uncovered significantly enriched pathways related to immunity. An extensive analysis of the transcriptome data is ongoing to decipher the biological insights at the level of functional modules. In conclusion, we show that differences in some ITs' levels are associated with transcriptome modifications, meaning that blood transcriptome is a relevant molecular phenotype for these ITs. Thus, blood gene expression levels could be combined with genetic studies to identify candidate genes underlying heritable immunity traits.