# Systems immunology approaches to decipher individual variability of immune capacity: application to the pig species

Claire Rogel Gaillard, Tatiana Maroilley, Fany Blanc, Jordi Estellé

# Systems immunology approaches to decipher individual variability of immune capacity: application to the pig species

Claire Rogel-Gaillard[1], Tatiana Maroilley[1], Fany Blanc[1] and Jordi Estellé[1]

[1] GABI, INRA, AgroParisTech, Université Paris-Saclay, 78350, Jouy-en-Josas, France

The capacity to produce multi-omics data together with large panels of immunological parameters on big populations renews the studies that cross genetics with health. We report results from two studies that aimed at identifying markers predictive of immunity traits in Large White pigs vaccinated against *Mycoplasma hyopneumoniae* (*M. hyo*). In a first study, 186 pigs were vaccinated at weaning with a booster vaccination three weeks later and *M. hyo*-specific IgGs were measured 21 days post-vaccine (dpv), after the booster and at 118 dpv. Genome-wide association studies revealed a candidate genomic region on pig chromosome 4 associated with early vaccine response. RNAseq data from blood sampled before vaccination and sparse Partial Least Squares-Discriminant Analyses (sPLS-DA) allowed us to identify predictive biomarkers that classify animals into groups of high and low responders. In a second study, 550 60-day-old pigs vaccinated at 35 days of age with a booster one week later were monitored for immunity traits measured either directly from blood (cell counts, seric anti *M hyo* IgG and haptoblobin) or after *in vitro* stimulation of total blood (phagocytosis, production of IL-1β, IL-8, IL-10, IL-17, TNFα, IFNγ). We explored covariations between gene expression profiles in blood and immunity trait levels, and could draw lists of candidate blood biomarkers that are potentially predictive of immune trait variations. Thus, our findings confirm individual variability of numerous immune traits including vaccine response, and open the way for a better understanding of the underlying biology and the identification of markers predictive of these variabilities in pig.