How to predict that some animals respond better to vaccination than others: application to vaccination against Mycoplasma hyopneumoniae in pigs?

Fany Blanc, Jordi Estellé, Gaëan Lemonnier, Jean-Jacques Leplat, Yvon Billon, Olivier Bouchez, Marie-Noelle Rossignol, Jean Pierre Bidanel, Claire Rogel Gaillard

How to predict that some animals respond better to vaccination than others: application to vaccination against *Mycoplasma hyopneumoniae* in pigs.

Blanc Fany[1], Estellé Jordi[1], Lemonnier Gaëtan[1], Leplat Jean-Jacques[1], Billon Yvon[2], Bouchez Olivier[3], Rossignol Marie-Noëlle[1], Bidanel Jean-Pierre[1,] Pinard-van der Laan Marie-Hélène[1] and Rogel-Gaillard Claire[1]

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

2 GenESI, INRA, 17700 Surgères, France

3 GeT-PlaGe, INRA, 31326 Castanet-Tolosan, France

Our aim was to study whether host genetic variability can influence vaccine responses and be considered to improve vaccine strategies. We focused on the vaccine response to *Mycoplasma hyopneumoniae* (*M. hyo*) in pigs and searched for genetic markers and blood biomarkers predictive of vaccine response intensities. Large White pigs (48 families, 186 animals) were vaccinated at weaning (around 28 days of age) with a booster vaccination three weeks later (commercial inactivated vaccine). Seric *M. hyo*-specific IgGs were measured at three time points corresponding to early response (just before booster, 21 days post-vaccine (dpv)), maximum response intensity after the booster vaccination (28 or 35 dpv), or long-term IgG persistence (118 dpv). Genome-wide association studies with a 658K SNP chip revealed a candidate genomic region on SSC4 associated with early vaccine responses at 21 dpv. In parallel, RNAseq data from blood sampled before vaccination were produced for a subset of 92 piglets that were ranked according to the *M. hyo*-specific IgG levels. At each time point, high and low responders were selected and sparse Partial Least Squares-Discriminant Analyses (sPLS-DA) were carried out to identify the best predictive blood biomarkers that classify animals into each group. We detected 94 candidate genes that were predictive with an accuracy higher than 99% for the three time points.

In conclusion, we show that specific IgG production after vaccination against *M. hyo* is under genetic control and provide proofs of principle that blood biomarkers measured prior vaccination can predict individual vaccine response levels. We designed a custom OpenArray for high-throughput RTqPCR assays to test our list candidate biomarkers in validation populations.