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What potential of genome-wide integrative approaches to predict vaccine responses?

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The impact of host genetic variations in shaping innate and adaptive immune responses is an emerging lever to consider in new vaccination strategies. Merging genetic and genomic data to identify prospective biomarkers that could predict individual's immune capacity and response to vaccines is a challenging question addressed by the H2020-funded SAPHIR project, both in chickens and in pigs. Large White pigs (48 families) were vaccinated against *Mycoplasma hyopneumoniae* (*M. hyo, 182 piglets*) or Influenza A Virus (IAV, 98 piglets) at weaning (around 28 days of age) with a booster vaccination three weeks later. The humoral vaccine response was measured by following the dynamics of seric *M. hyo*- or IAV-specific IgG every week during five weeks post-vaccination, and before slaughtering at 21 weeks-of-age. For chickens, vaccine responses were measured on vaccinated commercial broilers (Cobb 500) and on a subset of animals challenged with *Eimeria maxima* (from 96 to 36 chickens). Animals' responses were evaluated by the measure of serum levels of IL-10 with an in-house developed ELISA system, body weight gain, lesion scores and parasite load. For each species design, blood was sampled prior vaccination on the vaccine day for high-density SNP genotyping and RNAseq analysis. We have identified significant associations between gene expression in blood prior vaccination and vaccine responses in pigs or body weight as a measure related to the vaccine follow-up in chickens. Thus, we provide a proof of concept that blood could be used as a relevant source of biomarkers predictive of vaccine responses. We will further discuss the potential of integrating multi-level genomic and phenotypic data to better understand individual vaccine responses and identify levers of action.