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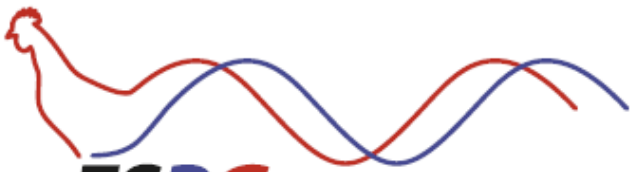

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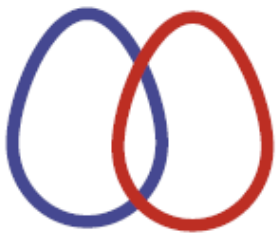

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Serum color as a biomarker for indirect selection of digestive efficiency

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With the diversification of feedstuffs used in poultry diets, the relative importance of digestive efficiency (DE) in feed efficiency is becoming more important. Technologies as near infrared spectroscopy facilitated the measure of DE on a large number of animals, but sample preparation is still time consuming and the total collection of feces is ethically questionable as animals have to be reared in cage. Serum color, which has previously been found to differ between two lines of chickens selected for high (D+) or low (D-) digestive efficiency, could be used as a biomarker of DE for selection.

Digestive efficiency assessed by AMEn and serum color at 3 weeks have thus been measured on 417 chickens from the D+/D- lines. Spectra of serum color have been compared between the two lines for wavelengths every 2 nm between 300 and 572 nm. Genetic parameters of all traits have been estimated to detect whether serum color was heritable and genetically correlated with DE.

Serum color was significantly yellower in D+ than in D- birds from 376 to 572 nm, the most significant differences were observed at 490-492 nm. Heritability of serum color was significantly different from 0 between 462 and 502 nm, with a maximum value of 0.31±0.09 at 492 nm. At this wavelength, genetic correlation with AMEn was high (0.84±0.28), thus indicating that serum color can be used as an indirect criterion of selection of DE. Further studies are now undertaken to confirm the interest of this criterion on other genotypes and diets.

Keywords: biomarker, digestive efficiency, genetic parameters, blood, colorimetry

How to predict that some animals respond better to vaccination than others: application to vaccination against Eimeria maxima in chickens

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In the same flock, not all birds, even vaccinated simultaneously and with the same dose, will respond equally to a vaccine. This genetic variability is an emerging lever, so far not considered by breeders in a view of integrated animal health management strategies.

The aim of the study was to focus on the host genetic variability of the response to *Eimeria maxima* vaccination of chickens and to search for blood biomarkers predictive of vaccine response intensities. Commercial broilers (90 Cobb 500 males) were vaccinated by inoculation with 100 *E. maxima* Weybridge strain oocysts at 16 days of age. Nine days later, a subset of 79 birds were challenged with 50,000 parasites of the homologous species/strain. Animals' responses were evaluated by measuring IL-10 serum levels, body weight gain, lesion scores and parasite load. RNAseq data from blood sampled before vaccination were produced for 63 chickens that were ranked according to their vaccine responses. For each response phenotype, high and low responders were selected (upper and lower quartiles) and sparse Partial Least Squares-Discriminant Analyses (sPLS-DA) were carried out to identify the best predictive blood biomarkers classifying animals into each group. We selected 108 candidate genes that were predictive with an accuracy higher than 97% for all vaccine responses.

In conclusion, we provide a proof of concept that blood before vaccination can be used as a relevant source of biomarkers predictive of vaccine responses. We designed a custom OpenArray for high-throughput RTqPCR assays to test our candidate biomarkers in validation populations.

Keywords: chicken, coccidiosis, vaccination, genetic variability, biomarkers