

## Abstract

The avian immune system is a complex system of defence mechanisms that protect bird hosts against threats from ubiquitous pathogens. According to the co-evolutionary models, variability in immune traits of hosts is the key component providing ability to adapt and enhance their defence mechanisms in presence of constant selective pathogen pressure. Domestic chicken (*Gallus gallus* f. *domestica*) is used as a model organism in avian biology and also is one of the most important food-producing animals, not only for their meat but also for the egg production. Unfortunately, in research usually only inbred chicken lines are used and modern poultry husbandry is tight with unilateral breeding towards highly productive breeds. Those approaches decrease intra-population polymorphism in chickens. However, especially in case of farm animals, searching and extending the pool of immune variability and enhancing pathogen resistance is crucial for sustaining healthy and biologically secure populations and their products. Morphologically highly distinct traditional chicken breeds, which have evolved for hundreds years under different selective pressures, may represent this desirable immunological variability.

In my thesis I described variability in chosen immunological traits, haematological parameters and proteomic composition of defence proteins in an egg white, in five traditional chicken breeds: Araucana, Booted Bantam, Czech Golden Pencilled, Minorca and Rosecomb Bantam. At first, using Phytohaemagglutinin skin-swelling test my collaborators and I highlighted large effect of blood cellular composition on the course of pro-inflammatory response, showing importance of the haematological variance in birds. As a next step, by novel and modified method of flow cytometry with fluorescently labelled antibodies we showed immunologically relevant variability in a blood cellular composition between chicken breeds. We also described a complete chicken egg white proteome using a tandem mass spectrometry analysis and revealed differences in amounts of egg antimicrobial defence proteins, pointing towards variance in egg-protective capacity of the chosen breeds. Egg white properties could be largely influenced by maternal organism as it is formed in a part of hen oviduct called magnum. Utilizing next generation Illumina sequencing, we were the first to sequence whole magnum transcriptome and compare it with the complete egg white proteome. Although mean protein amount in egg white and mean mRNA expression are strongly correlated, in mRNA expression we did not find the same pattern of inter-breed variability as in proteome. We presuppose that the observed variation in egg white composition probably results from a post-transcriptional regulation creating a discrepancy between proteomic and transcriptomic data. Taken together, results of my thesis show great variability in immune-phenotype of chicken breeds with potential effect on their parasite resistance and biosecurity of their eggs.