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Genome-wide methylation analysis of heat-acclimated chicken

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In both animals and Human, there is a memory of the embryonic environment that may be explained in part by changes in the epigenetic state of genes transmitted during cell division that influences the expression of genes involved in various physiological and metabolic processes. Understanding the molecular impact of early environmental influences, including maternal nutrition and husbandry practices for livestock, provides new opportunity to improve animal health and welfare.

The chicken, by its embryonic development in the egg, is an agronomic species of choice to directly manipulate the early environment and study its impact on the developing animal. In that context, it is possible to improve the heat tolerance of chicken in later-life by cyclically elevating the egg incubation temperature during embryogenesis. We showed that this treatment named embryonic thermal manipulation (TM) is associated with changes in gene expression that persist during the development of animals, potentially induced by epigenetic reprogramming at particular loci.

In the present study we analysed the impact of TM on DNA methylation across the genome. Two genome-wide methylation study approaches were used, whole genome bisulfite sequencing (WGBS) and reduced representation bisulfite sequencing (RRBS). Results of these analyses will be presented, along with insights into the advantages and technical issues of both technologies when applied on a livestock model of agricultural importance.