Transgenerational epigenetics in quail: whole genome DNA methylation analysis

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Abstract:

The influence of the prenatal environment on the adult phenotype development is partially mediated by epigenetics phenomena. One study highlighted significant effects of the *in-ovo* injection of endocrine disruptors or DNA methyltransferase inhibitor on quail development, significantly reducing their weight [1]. Recently, an increasing number of studies highlighted the transmission of epigenetics marks between generations following an environmental exposure. However, there is much debate about their acquired transmission beyond the exposed individuals. Recent studies revealed that non-genetics inheritance was probably present in avian species. In one of them [2], fertilized eggs were divided into two groups: one group injected with an endocrine disruptor, Genistein, and a non-injected control group. After three generations without any other injection, several traits were impacted by the ancestor treatment such as the reproduction and the behavior. This pilot study highlighted the potential existence of transgenerational transmission of environmental effects in quails. To better understand the transgenerational transmission of these environmental effects, DNA methylation data are available from blood samples from the third generation (WGBS and ONT). To analyse the DNA methylation state, we developed a bioinformatics pipeline in order to detect differential methylated cytosines (DMCs) affected by these transgenerational phenomena. We detected thousands of DMCs between both groups. In addition to these analyses, these data allowed us to perform a comparative analysis between the WGBS and ONT sequencing technologies.

References:

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2. Leroux, S., et al., Genet Sel Evol, 2017. 49(1). 14.