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# Transgenerational epigenetics in quail : whole genome DNA methylation analysis

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## Abstract

Prenatal environment influence on adult phenotype 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 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 including reproduction and 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, we generated DNA methylation data from blood samples of the third generation using WGBS (Whole Genome Bisulfite Sequencing) and ONT (Oxford Nanopore Technologies). To analyse the DNA methylation states, we developed a bioinformatics pipeline in order to detect differentially methylated cytosines (DMCs) due to transgenerational phenomena. We detected thousands of DMCs between both groups (Table 1). In addition to these analyses, these data allowed us to perform a comparative analysis between the WGBS and ONT sequencing technologies (Fig. 1).

| | measured CpGs sites | epiline DMCs detected |
|---|---|---|
| WGBS | 5 881 815 | 12 872 |
| ONT | 7 537 007 | 22 325 |

Table 1. Number of measured CpGs sites and epiline DMCs detected from WGBS and ONT methylation data. A CpG site refers to a dinucleotide CG.

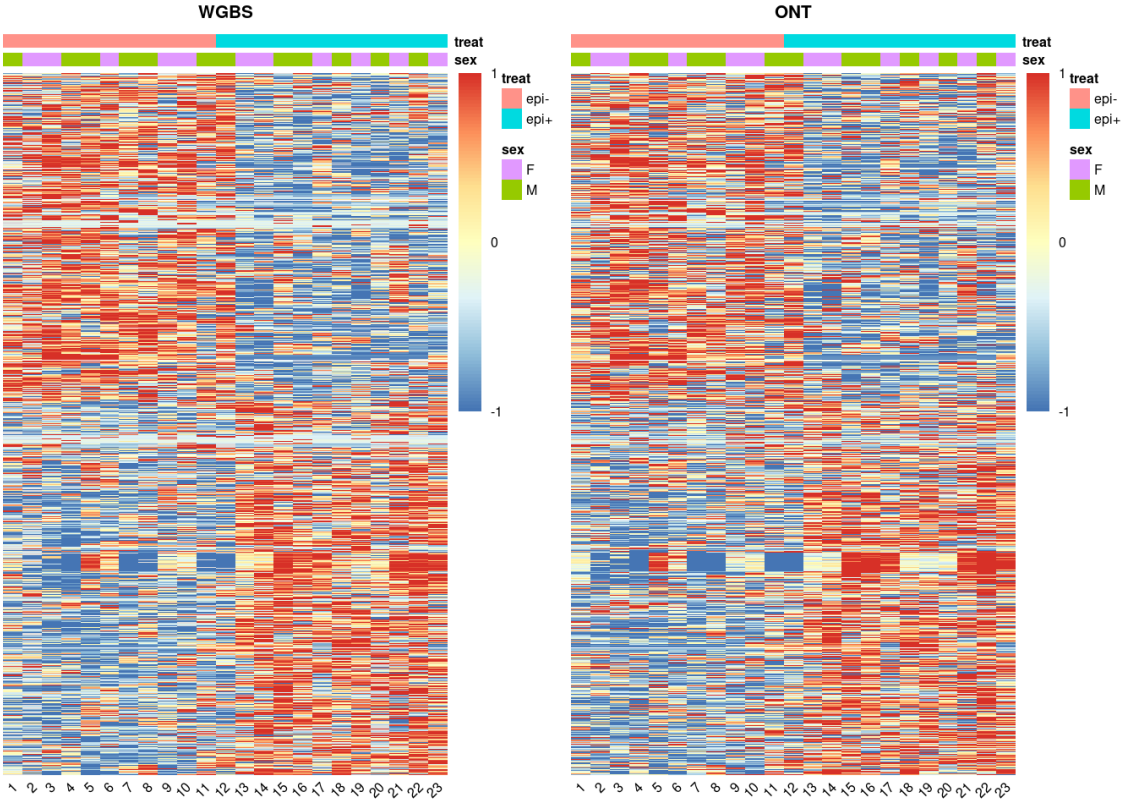


Figure 1. Heatmap of methylation rate of 10,000 common epilines DMCs detected from WGBS and ONT. The red and blue colors refer to the epi- and epi+ groups, respectively. The violet and green colors refer to the female (F) and male (M) quails, respectively. The diverging color gradient refers to a low (blue) or a high (red) methylation rate.

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