DNA methylation pattern of hypothalamus and ovary in *Capra hircus*

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Introduction

One of the key determinants in the control of gene expression in mammals, and the most common covalent modification of DNA in eukaryotes, is methylation of cytosine residues. Although methylomes from several tissues have been investigated in a wide range of species, the methylome of goats is still unexplored.

Objectives

Aim of the work is to set up a pipeline for methylome analysis and to take the first steps to explore the potential epigenetic involvement in the biology of the goat.

Methods

We analysed the DNA methylation pattern at DNA level of hypothalamus and ovary from 3 adult Saanen goats, in order to evaluate differentially methylated regions. We used methylated DNA binding domain sequencing (MBD-seq) to methylated DNA fragments (Figure 1), and next generation sequencing (NGS - Hiseq 2000 Illumina). We produced at least 20 million reads per sample, covering an average of about 30% of the goat genome. Further analyses were performed to identify peaks corresponding to hyper-methylated regions using ChIPseeqer, an informatic tool for the ChIP-seq data.

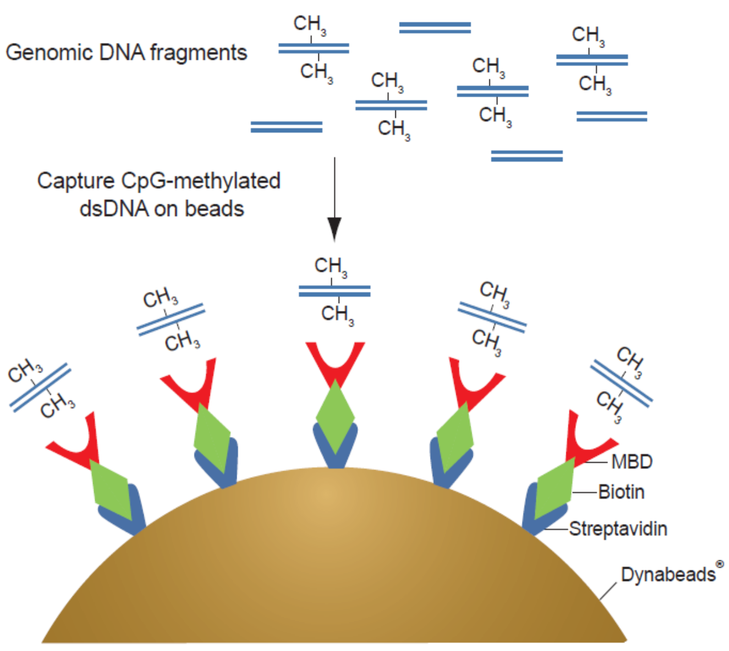

Figure 1. Workflow of the MethylMiner™ Methylated DNA Enrichment Kit (www.lifetechnologies.com)

Results and discussion

In our analysis we found 382 850 methylation peaks in hypothalamus and 413 010 in ovary.
Chromosomes X and 20 showed the lowest density of methylated fragments for both organs. Chromosomes 22 and 28 had the highest methylation frequency in hypothalamus, with 19 and 22 highest in ovary (Figure 2).

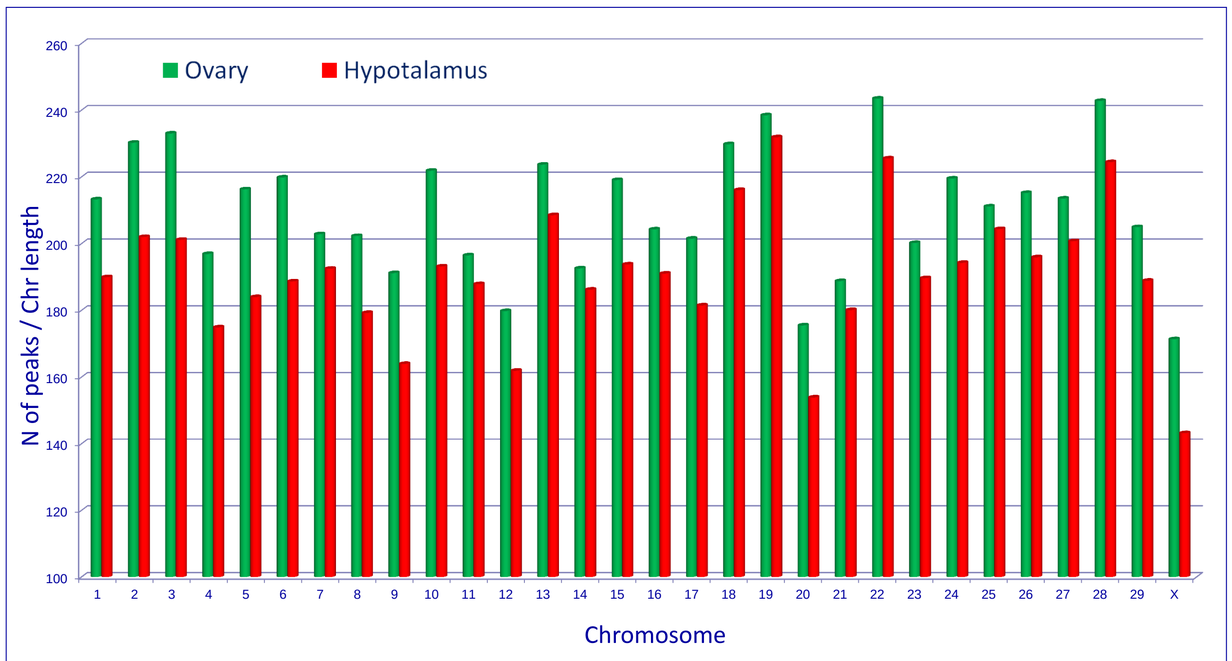

Figure 2. Number of methylation peaks per chromosome corrected for chromosome length in the 2 organs studied

We also investigated methylation distribution in promoter, intron, exon, downstream, distal and intergenic regions of genes. Introns showed the highest methylation frequency for both hypothalamus (35% of the region detected) and ovary (37.2%) (Figure 3). Matching the methylation pattern of hypothalamus versus ovaries of the 3 goats, the genes that showed methylation peaks in only one organ were identified. 166 genes had methylation peaks only in hypothalamus, 699 genes showed peaks only in ovary. The ongoing transcriptome analysis of these two tissues will allow a deeper comprehension of the methylation effect on expression and the molecular and physiological pathways.

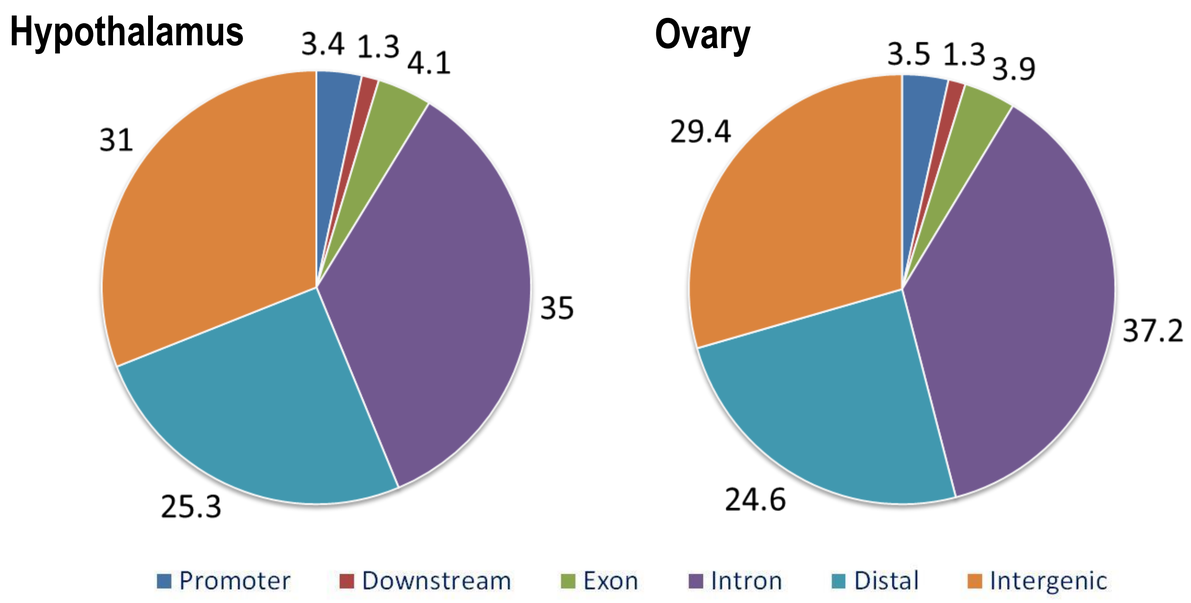

Figure 3. Percentage of methylation peaks in 6 different genomic regions in hypothalamus and ovary

Conclusions

This work presents a global methylation pattern for hypothalamus and ovary in *Capra hircus*. These results, associated with transcriptome analysis, could be helpful for a deeper comprehension of the complex epigenetic machinery in this species.

Acknowledges

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