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A first glance on the epigenome of *Capra hircus*

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ABSTRACT

DNA methylation and microRNAs (miRNA) are two important forms of epigenetic modifications that play an important role in gene regulation in animals. Methylation at the carbon 5 position of cytosine residues is a fundamental layer of cellular differentiation through the control of transcriptional potential. MiRNA are small noncoding RNA molecules that regulate gene expression. Complete DNA methylomes for several organisms are now available; at the present, methylome of the domestic goat is unexplored. There is also still limited knowledge about miRNAs expression profiles in small ruminant species. Therefore, to contribute information on epigenetic modification in *Capra hircus*, we analysed the methylome and the miRNA population of three tissues (hypothalamus, pituitary and ovary) from 3 adult Saanen goats. We used Methylated DNA binding domain sequencing with enrichment of methylated DNA fragments and next generation sequencing. We produced least 23 million reads per sample, which were aligned to the goat reference genome. Further analyses were performed to identify peaks corresponding to hyper-methylated regions. We sequenced miRNAs expressed in the three tissues with Illumina high-throughput sequencing. Reads were mapped on the *Capra hircus* reference genome and both known and novel miRNAs, and miRNA target sites were identified using information collected in miRBase and using specific bioinformatic tools. This study produced a comprehensive miRNA profile related to the biology of goat. Furthermore, this is the first work dealing with methylome in *Capra hircus*: our preliminary results could provide new information for a deeper comprehension of epigenetic mechanisms of this species.

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