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The methylome of the hypothalamus of prepubertal and pubertal goats.

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Abstract

Puberty is the fulfillment of fertility, a process involving physiological and morphological development. It is well known that the increased hypothalamic secretion of the gonadotropin-releasing hormone (GnRH) is essential for the activation of this process, even if the elements coordinating the timing of puberty have not been fully identified^{1,2}. Recent studies provide proof that there is an epigenetic regulation of female puberty, and DNA methylation, the most studied epigenetic modification, plays a major role in it³. We analyzed DNA methylation patterns of 5 Alpine goats at their prepubertal stage and 5 that reached puberty in order to highlight differences in their methylome. Detection of methylated regions across the goat genome involved a Methyl Binding Domain (MBD) enrichment followed by deep sequencing (Hiseq2000 Illumina). The software ChIPseeqer4 permitted the identification of peaks corresponding to hyper-methylated regions. We have observed a higher methylation level in prepubertal goats. The distribution of the methylation peaks across the genome and within CpG islands per chromosome per group of animals has been analyzed. Furthermore, we have investigated differential methylation in genes associated with puberty. Specifically, Cbx7, coding for a core component of the Polycomb group silencing complex, and GnRHR, the gene coding for GnRH receptor, showed a higher number of peaks into two intragenic fragments within prepubertal goats. These results, accompanied by transcriptome analysis, provide a foundation for elucidating the role of DNA methylation in the complex mechanisms that drive puberty in goat species.

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