brought to you by TCORE

Proceeding of Veterinary and Animal Science Days 2016, 8th- 10th June, Milan, Italy



Keywords

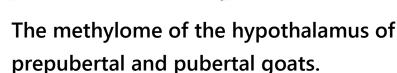
Goat, methylation, puberty

CORRESPONDING AUTHOR

Stefano Frattini stefano.frattini@unimi.it

JOURNAL HOME PAGE riviste.unimi.it/index.php/haf

Abstract



UNIVERSITÀ DEGLI STUDI DI MILANO DIPARTIMENTO DI SCIENZE VETERINARIE PER LA SALUTE, LA PRODUZIONE ANIMALE E LA SICUREZZA ALIMENTARE

S. Frattini^a, E. Capra^b, B. Lazzari^b, B. Coizet^a, D. Groppetti^a, P. Riccaboni^a, A. Pecile^a, S. Arrighi^c, S. Chessa^b, B. Castiglioni^b, A. Giordano^a, A. Talenti^a, J. L. Williams^d, S. D. McKay^e, P. Crepaldi^a, A. Stella^b, G. Pagnacco^a

^aDepartment of Veterinary Medicine, University of Milan, Milan, Italy. ^bInstitute of Agricultural Biology and Biotechnology, National Research Council UOS of Lodi, Lodi, Italy. ^cDepartment of Health, Animal Science and FoodSafety, University of Milan, Milan, Italy ^dSchool of Animal and Veterinary Sciences, University of Adelaide, Roseworthy, Australia

^eDepartment of Animal and Veterinary Science, University of Vermont, USA

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 identified1,2. 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. The research was funded by GenHome project.

References

Lomniczi, A. et al.; 2013. Epigenetic control of female puberty. Nat. Neurosci. 16, 281–289

Mayer, C. et al.; 2010. Timing and completion of puberty in female mice depend on estrogen receptor-signaling in kisspeptin neurons. Proc. Natl. Acad. Sci. 107, 22693–22698.

Lomniczi, A. et al.; 2015. Epigenetic regulation of puberty via Zinc finger protein-mediated transcriptional repression. Nat. Commun. 6, 10195. Giannopoulou, E. G. & Elemento, O.; 2011. An integrated ChIP-seq analysis platform with customizable workflows. BMC Bioinformatics 12,

HAF © 2013 Vol. III, No. 1s