Methylation analysis in monocytes at postpartum period in dairy cattle

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Epigenetic modifications such as DNA methylation play a role in regulating gene expression and consequently in biological processes, such as those involved in health and disease. In dairy cows, profound changes occur during the post calving period, leading to immunosuppression and increased susceptibility to diseases. In order to monitor the postpartum health status of cows, one challenge is to describe the methylome of a purified subpopulation of immune cells, such as monocytes, and to determine its alterations/modifications in response to environmental or physiological changes. In this study, genome-wide DNA methylation profiles were obtained from purified monocytes (n=11), Peripheral Blood Mononuclear Cells (PBMC; n=4) sampled at D15 after calving and fibroblasts (n=2) using Reduced Representation Bisulfite Sequencing (RRBS). After sequencing and mapping to the reference genome (UMD3.1 assembly), 34.6% to 40.2% of uniquely mapped reads were obtained. Only CpGs covered between 10X and 500X ($CpG_{10\text{-}500}$), were analyzed, which represented 55 ± 9.8 % of total CpGs with no significant differences between libraries. The chromosomic distribution of $CpG_{10\text{-}500}$ was independent of the chromosome length (pvalue=0.48) but significantly associated with the coding gene content (pvalue=0.0001076). The global $CpG_{10\text{-}500}$ methylation scores varied between cell types (fibroblasts: 47% ± 0.1, monocytes: 54.5% ± 2.9 and PBMC: 54.1% ± 1.8), and 19417 monocyte-specific Differentially Methylated Cytosines (DMCs) corresponding to 1572 DMRs were identified. This study therefore highlights CpGs and regions displaying a specific methylation pattern in monocytes, which could be targeted by epigenetic changes induced by environmental conditions (husbandry, nutrition, infection challenges…).

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