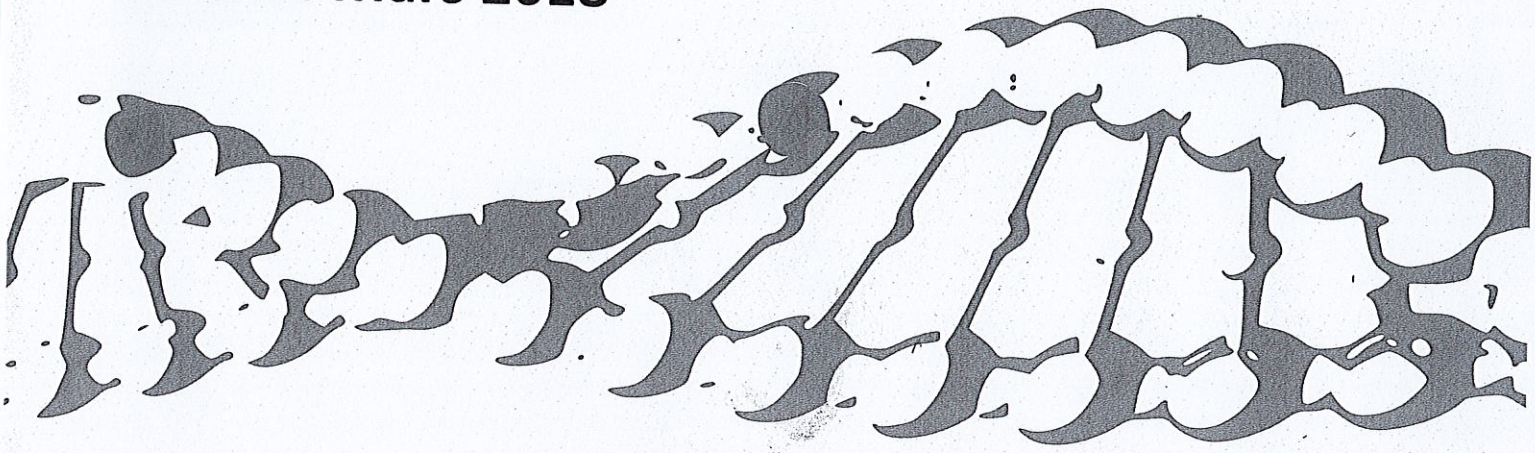
Methylation analysis in monocytes at postpartum period in dairy cattle: potential biomarkers of health

Hélène Kiefer, Maxime Gasselin, Jean-Philippe Perrier, Luc Jouneau, François Piumi, Audrey Prézelin, Marion Boutinaud, Christine Leroux, José Pires, E. Mariani, et al.

adebiotech

13 & 14 Mars 2018



EPIGEN

L'épigénétique dans la réponse du vivant aux facteurs environnementaux

Biocitech Romainville-Grand Paris

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incluant l'analyse de différentes altérations épigénétiques.

Perspectives

La stratégie développée pourrait permettre le criblage d'un grand nombre de conditions d'exposition, qu'il s'agisse de composés seuls ou en combinaison (effets « cocktail »). De plus, ce projet pourrait permettre d'identifier de nouvelles voies moléculaires de toxicité des PCE dans le cerveau immature et, par la suite, dans d'autres organes-cibles d'importance cruciale au cours du développement tels que le placenta, contribuant ainsi à améliorer l'évaluation globale de leur toxicité développementale.

POSTER #7 - SESSION 2

Methylation analysis in monocytes at postpartum period in dairy cattle: potential biomarkers of health

Hélène KIEFER - INRA

Kiefer H[1], Gasselin M[1], Perrier JP[1], Jouneau L[1], Piumi F[1], Prezelin A[1], Boutinaud M[2], Leroux C[3], Pires J[3], Mariani E[4], Zawadzki J[5], Jammes H[1]*

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, the post calving period is characterized by profound changes associated with an immunosuppression increasing the susceptibility to diseases. One challenge is to identify the monocyte methylome at postpartum period (D15 after calving) and to determine alterations /modifications in response to environmental changes. In this study, a genome-scale DNA methylation profiles were determined by Reduced Representation Bisulfite Sequencing (RRBS) of monocytes (n=11), Peripheral Blood Mononuclear Cells (PBMC; n=4) and fibroblasts (n=2) libraries. After sequencing, 87% ± 2.4 of the reads mapped to the reference genome (Bos Taurus UMD 3.1 assembly) with a low percentage of the uniquely mapped reads (range: 34.6% to 40.2%). For methylation analysis only the CpG covered between 10X and 500X (CpG10-500), were selected. A mean of 1.837.765 ± 327.615 of CpG10-500 was identified without significant difference between libraries and representing a range of 55% of total CpGs. The global CpG10-500 methylation scores varied between cell types and ranged from 47% ± 0.1 in fibroblasts to 54.5% ± 2.9 in monocytes and 54.1% ± 1.8 in PBMC. The chromosomic distribution of CpG10-500 was independent of the chromosomic length (p value=0.48) but significantly associated with the coding gene number (p value=0.0001076). Differential analysis described 19417 Differentially Methylated Cytosines and 1572 DMRs, highlighting a specific methylation pattern in monocytes with CpG/regions for a targeting by epigenetic changes induced by environmental conditions (husbandry, nutrition, infection challenges...).