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Published in:
Proceedings of 5th Annual Danish Bioinformatics Conference

Publication date:
2019

Document Version
Publisher’s PDF, also known as Version of record

Link back to DTU Orbit

Citation (APA):

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DNA methylation analysis on gene bodies of reference sequence genes for boar taint in Danish pigs

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Boar taint (BT) is an offensive flavor in non-castrated male pigs. However, studies of genome-wide DNA methylation profiles on gene bodies of reference sequence genes (RefSeqGenes) to reveal epigenetic information associated with BT was scarce. Reduced representation bisulfite sequencing (RRBS) is an efficient technology to identify candidate epigenetic biomarkers associated with BT. Three different BT levels were analyzed using RRBS data to calculate differentially methylated genes (DMGs), promoters (DMPs), exons (DMEs) and introns (DMIs). The DMGs, DMPs, DMEs and DMIs were defined using R package GeneDMRs (https://github.com/xiaowangCN/GeneDMRs) after the comparisons against methylation levels on RefSeqGenes and their gene bodies. Additionally, the GO and pathway terms were analyzed in hypo-methylated and hyper-methylated categories of Sus scrofa organism. In this study, a total of 4,473 RefSeqGenes with 4,412 promoters, 36,286 exons and 31,912 introns along the genome were investigated. We found that cytosines in the cytosine and guanine dinucleotide (CpG) sites were only involved in 3029 RefSeqGenes with 2,295 promoters, 2,725 exons and 4,349 introns based on RRBS data. According to filtration standard criterion of Q-value < 0.05 after multiple hypothesis testing of false discovery rate (FDR), 536 DMGs with 123 DMPs, 194 DMEs and 402 DMIs were finally retained. If only considering the 123 DMP related genes, they were mainly located on chromosome 2, 6, 7 and 14. Meanwhile, the most significant DMP related gene (Q-value = 3.43e-16) was POU2AF1 on the chromosome 9 in the hypo-methylated category. However, the most significant GO term (Q-value = 0.0062) and pathway (Q-value = 0.06) were alpha-amino acid metabolic process (GO: 1901605) and toll-like receptor signaling pathway (ssc04620)/insulin resistance (ssc04931), respectively, both in the hyper-methylated DMPs’ categories. Actually, 81 genes of them were hypo-methylated and only 42 genes were in the hyper-methylated category that were mostly enriched in the significant GO terms and pathways. These results could contribute to the understanding of methylation levels on reference sequence genes and the related gene bodies in pigs and the usage of epigenetic biomarkers for the genomic selection in the breeding programs, especially for the hyper-methylated DMP related genes.