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Статьи

Bioinformatic Data Analysis from Metagenomic Whole Genome Sequencing of Endometrial Microorganisms in Cows with Normal and Pathological Conditions

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Аннотация

There remains no consensus on the microbiological causes of endometritis in cows. The aim of this study, therefore, was to analyze the endometrial microbiome using metagenomic whole genome sequencing (WGS) with subsequent bioinformatic data analysis using high-yielding cows kept on an organic farm (Group 1A) compared to animals kept on a large industrial complex as follows: clinically healthy (Group 2A), with subclinical (Group 2B), or purulent-catarrhal endometritis (Group 2C). Using Illumina MiSeq platform, WGS results revealed that the dominant bacterial phyla were Bacillota in Groups 2A, 2B and 2C, as well as Bacteroidota, Fusobacteriota and Bacillota in Group 1A. In industrial farm conditions, subclinical and clinical endometritis was associated with an increase in the amount of *Clostridium botulinum* in the uterus ($p < 0.05$). In contrast to Group 2A, the dominant bacterial species in the organic eco-farm Group 1A were *Bacteroides fragilis* (55.1 ± 3.92%) and *Fusobacterium* *necrophorum* (28.8 ± 2.63%). The use of bioinformatic techniques demonstrated that the endometrial microbiome of clinically healthy cows kept in eco-farm conditions (Group 1A) was enriched in bacteriocin genes compared to other studied animal Groups 2A, 2B and 2C. Thus, the standards of feeding and cattle husbandry adopted to eco-farm conditions imply a different composition and functionality of the cattle endometrial microbiome compared to the more common industrial approaches.

Bioinformatic Data Analysis from Metagenomic Whole Genome Sequencing of Endometrial Microorganisms in Cows with Normal and Pathological Conditions

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Keywords: Bioinformatics, metagenomic whole genome sequencing, endometrial microbiome, high-yielding cows, eco-farm

Abstract

There remains no consensus on the microbiological causes of endometritis in cows. The aim of this study, therefore, was to analyze the endometrial microbiome using metagenomic whole genome sequencing (WGS) with subsequent bioinformatic data analysis using high-yielding cows kept on an organic farm (Group 1A) compared to animals kept on a large industrial complex as follows: clinically healthy (Group 2A), with subclinical (Group 2B), or purulent-catarrhal endometritis (Group 2C). Using Illumina MiSeq platform, WGS results revealed that the dominant bacterial phyla were Bacillota in Groups 2A, 2B and 2C, as well as Bacteroidota, Fusobacteriota and Bacillota in Group 1A. In industrial farm conditions, subclinical and clinical endometritis was associated with an increase in the amount of *Clostridium botulinum* in the

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