Analysis of bacterial diversity in activated sludge from livestock wastewater treatment by next-generation sequencing technology [1]

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Abstract

The purpose of this study was to explore the bacterial diversity in activated and anaerobic sludge in livestock wastewater treatment facilities by next-generation sequencing, so as to understand the differences in bacterial community composition in different activated sludges, and to extend the utilization. Four sludge samples were collected, including 2 aerobic and 1 anaerobic samples collected in the hot season and 1 aerobic sample collected in the cool season. The microbial DNA in the four sludge samples was directly extracted by the method of ceramic bead shaking, and then the V3-V4 hypervariable regions of the 16S rRNA gene sequence was revealed by the next-generation sequencing method, and the bacterial diversity in the samples was analyzed by bioinformatics tools. The analysis results showed that the anaerobic sludge samples had the highest species abundance, with an average of 2,205 species, and the activated sludge samples ranged from 1,682 to 1,854 species. The bacteria in the activated sludge samples were *Bacteroidetes* and *Proteobacteria* with a higher proportion; the anaerobic sludge samples were *Bacteroidetes* and *Patescibacteria*. Based on the OTU analysis of 4 sludge samples, top 10 genera with higher frequency included *Denitratisoma*, *Ferruginibacter*, DMER64, Bacterium enrichment culture clone R4-41B, *Smithella*, *Limnobacter*, *Ignavibacterium*, *Nitrosomonas*, *Christensenellaceae* R7 group, and *Arcobacter*. Besides, the results of PCoA (principal component analysis), NMDS (non-metric multidimensional scaling), PLS-DA (partial least squares discriminant analysis), and t-SNE (t-distributed stochastic neighbor embedding) analyses showed that the 4 samples could be divided into 3 groups, namely 2 aerobic samples collected in the hot season as the same group, the other one group of anaerobic sample, and another group of an aerobic sample collected in the cool season. In summary, revealing the microbial composition of sludge samples collected from the hot and cool seasons by next-generation sequencing analysis is an important approach, and the important information of dominant bacteria obtained in this study can be a reference for further research or applications.

Key words: Activated sludge, Bacterial diversity, Wastewater treatment.