

Metagenomics Profile during the Bioremediation of Fischer-Tropsch Derived Short-Chain Alcohols and Volatile Fatty Acids Using a Moving Bed Biofilm Reactor

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Abstract : A moving bed biofilm reactor (MBBR) was used for the bioremediation of high strength chemical oxygen demand (COD) Fisher-Tropsch (FT) wastewater. The aerobic MBBR system was operated over 60 days. For metagenomics profile assessment of the targeted 16S sequence of bacteria involved in the bioremediation of the chemical compounds, sludge samples were collected every second day of operation. Parameters such as pH and COD were measured daily to compare the system efficiency as the changed in microbial diversity progressed. The study revealed that pH was a contributing factor to microbial diversity, which further affected the efficiency of the MBBR system. The highest COD removal rate of 86.4% was achieved at pH 8.3. It was observed that when there was more, A higher bacterial diversity led to an improvement in the reduction of COD. Furthermore, an OTU of 4530 was obtained, which were divided into 12 phyla, 27 classes, 44 orders, 74 families, and 138 genera across all sludge samples from the MBBR. A determination of the relative abundance of microorganisms at phyla level indicates that the most abundant phylum on day it was Firmicutes (50%); thereafter, the most abundant phylum changed to Proteobacteria.

Keywords : biodegradation, fischer-tropsch wastewater, metagenomics, moving bed biofilm reactor

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