Analysis of bacterial community structure and function as a tool in assessing the pollution due to palm oil mill effluent

ABSTRACT

Malaysia is ranked as the second largest producer of palm oil in the world. The major problem in this industry is the production of a highly polluting wastewater known as palm oil mill effluent (POME). POME is considered as the most harmful waste generated from palm oil processing industry if the waste was not properly treated. In Malaysia, 85% of palm oil mill used the ponding system as their preferable treatment method for POME, which later will be discharged into the nearby river. Numerous studies have shown that bacterial population are highly dynamic and can differ strongly in their response to resource availability such as organic carbon, nitrogen and phosphorus. Hence, the loss or changes of microbial diversity is considered a major threat because of its important for ecosystem functions. To date, little is known about microbial communities involved in the polluted river due to POME, either their structural and functional diversity or their response to environmental constraints. Therefore, this study aims to identify and compare the bacterial community structure and function present in the effluent-receiving river located near palm oil mill. The PCR-DGGE and Illumina Miseq have been used in analysing the microbial community structures, whereas the nucleic acid double staining (NADS) assay based on flow cytometry has been used in assessing the microbial community function. The findings demonstrated a significant difference of microbial community present in the upstream and downstream part of the effluent-receiving river water, in relation with the changes of the physicochemical properties. Hence, it is believed that the microbial community that play a key role in biogeochemical processes caused by POME final discharge has the potential to be used as indicator microorganism capable of indicating contamination caused by POME.