

Accepted Manuscript

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PII: S1385-8947(16)31299-2
DOI: <http://dx.doi.org/10.1016/j.cej.2016.09.063>
Reference: CEJ 15773

To appear in: *Chemical Engineering Journal*

Received Date: 18 May 2016
Revised Date: 10 September 2016
Accepted Date: 12 September 2016

Please cite this article as: C. Hong Neoh, P. Yi Yung, M. Hafizuddin Razak, A. Aris, M. Fadhil Md Din, Z. Ibrahim, Z. Zainon Noor, Correlation between Microbial Community Structure and Performances of Membrane Bioreactor for Treatment of Palm Oil Mill Effluent, *Chemical Engineering Journal* (2016), doi: <http://dx.doi.org/10.1016/j.cej.2016.09.063>

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Correlation between Microbial Community Structure and Performances of Membrane Bioreactor for Treatment of Palm Oil Mill Effluent

Chin Hong Neoh^a, Pui Yi Yung^b, Mohd Hafizuddin Razak^a, Azmi Aris^a, Mohd Fadhil Md Din^a, Zaharah Ibrahim^c, Zainura Zainon Noor^{a*}

^a*Centre for Environmental Sustainability & Water Security, Universiti Teknologi Malaysia, 81310 Skudai, Johor, Malaysia*

^b*Singapore Centre on Environmental Life Sciences Engineering (SCELSE), Nanyang Technological University, 60 Nanyang Drive, SBS-01N-27, Singapore 637551*

^c*Department of Biosciences and Health Sciences, Faculty of Biosciences and Medical Engineering, Universiti Teknologi Malaysia, 81310 Skudai, Johor, Malaysia*

*Corresponding author. Tel.: +6075535485; fax: +6075581463

Email address: zainurazn@utm.my

ABSTRACT

River pollution from the agriculture industry has become an important cause of unscheduled water disruptions in Malaysia. Thus, rigorous control and treatment of high strength wastewater prior to discharge into the river are needed. This study aims at evaluating the performance of a pilot membrane bioreactor (MBR) for the treatment of palm oil mill effluent (POME). POME was subjected to MBR operating in an aerobic environment for 40 days, followed by 10 days without aeration and water pumping to simulate failure event, and finally resumed to operational condition. Higher proportions of protein (-PN) compared to polysaccharides (-PS) were present in both the mixed liquor and biofilm, indicating that protein was the main constituent of extracellular polymeric substances (EPS). Biological samples from the mixed liquor and biofilm on the membrane surfaces were collected on day 25, 50 and 75 to investigate taxonomic distribution of microbial community. High throughput sequencing of the 16S rRNA gene was used to investigate the composition of microbial communities in the MBR. Microbial groups such as the phyla Proteobacteria (19-23%), OD1 (11-15%), Chloroflexi (11-13%)

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