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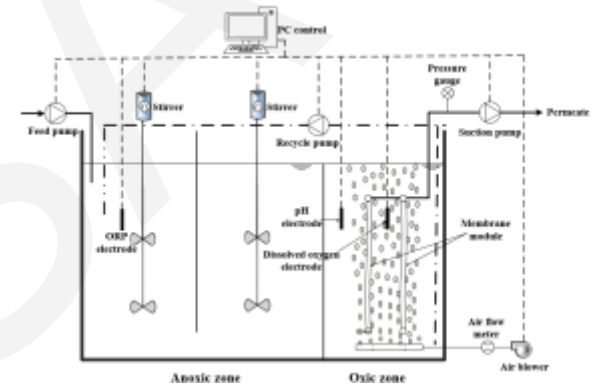
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Membrane fouling behavior and microbial community succession in a submerged membrane bioreactor treating harbor oily wastewater

Key words: Membrane bioreactor (MBR) fouling, Extracellular polymeric substances (EPS), Harbor oily wastewater, Microbial community

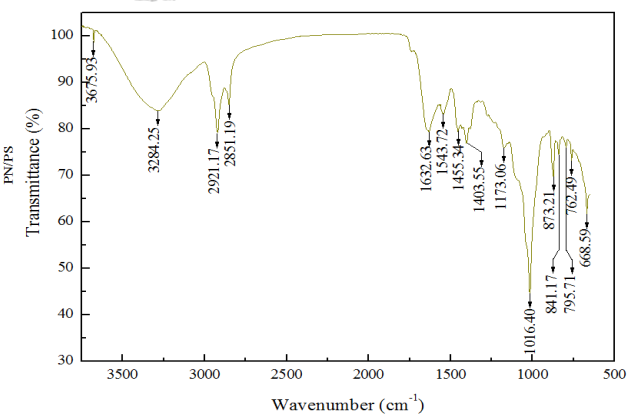
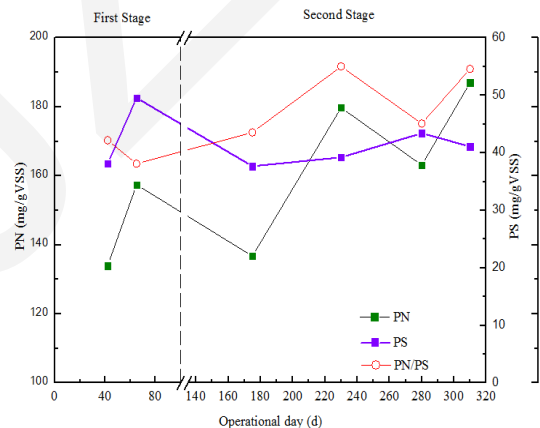
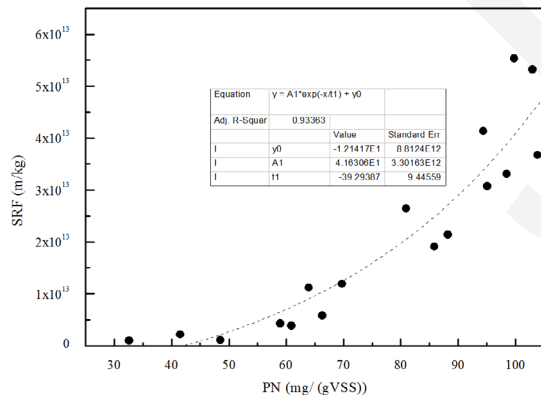
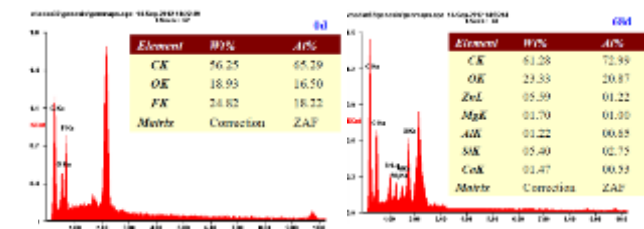
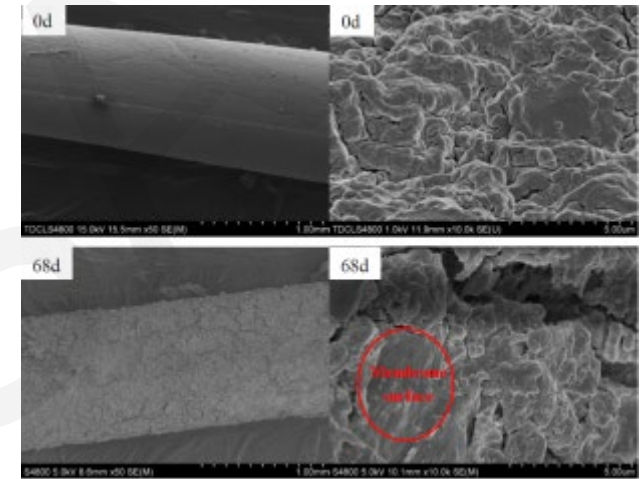
MEMBRANE FOULING BEHAVIOR

- The membrane bioreactor (MBR) has been widely applied in wastewater treatment and reuse. However, inevitable membrane fouling, consequently leading to a decline in membrane permeability and an increase in operational cost, is still the major obstacle that hampers further development of MBR technology..
- Due to the complexity of MBR systems and various wastewaters to be treated, the complex relationship of those fouling factors is still not clear. A better elucidation, clarifying the key fouling factors, will help in defining the optimum approach to mitigate membrane fouling in an MBR system.



MEMBRANE FOULING BEHAVIOR

- It is reasonable to consider that the EPS content would be a probable index for membrane fouling by means of SEM images, EDX analysis and FTIR spectra.
- The qualitative analysis further verified that the EPS accumulated on the membrane surface, especially the proteins, were of great importance for the TMP increment and membrane fouling.



OPTIMIZATION OF THE MBR SYSTEM

- In order to achieve a longer membrane life, the MBR was optimized according to a model proposed by Chisti and Moo-Young (1993) and Li *et al.* (2000)
- As a result, the TMP of the MBR system still increased, but slowly, indicating that the optimization could significantly mitigate membrane fouling.
- The content of protein accumulated on the membrane surface also increased slowly, implying that the optimization played a crucial role in slowing down the increasing rate of EPS content (mainly the proteins content) of the fouling layer.

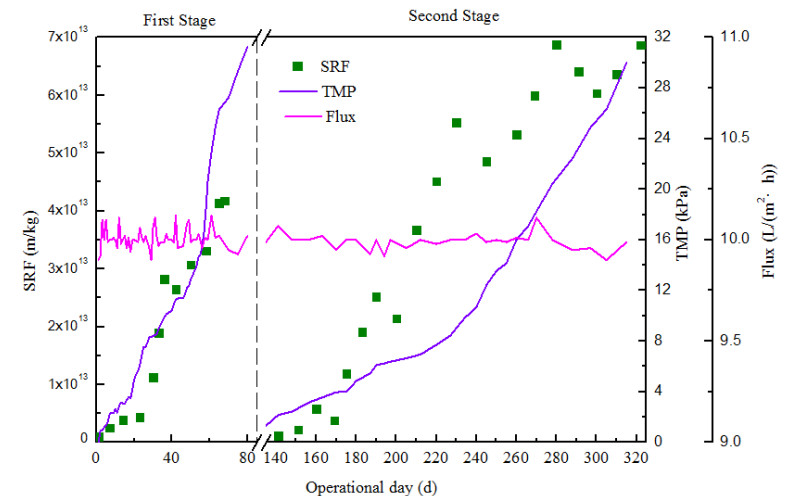
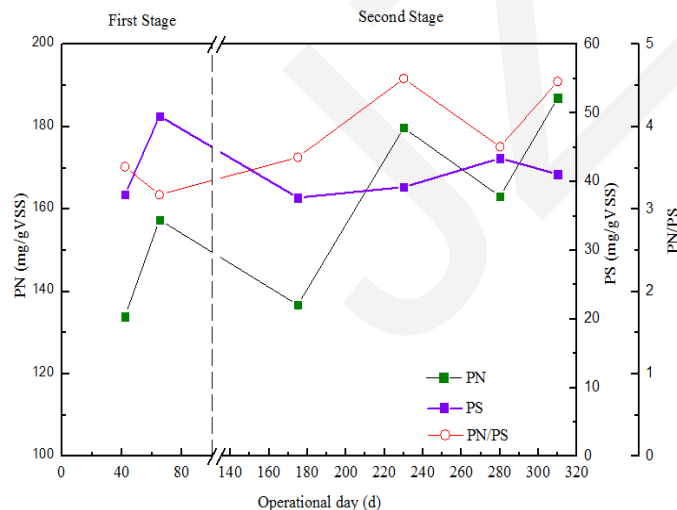
$$U_{Lr} = \left[\frac{2gh_D(\varepsilon_r - \varepsilon_d)}{\frac{K_f}{(1-\varepsilon_r)^2} + K_b \left(\frac{A_r}{A_d}\right)^2 \frac{1}{(1-\varepsilon_d)^2}} \right]^{0.5}$$

$$K_b = 11.402 \left(\frac{A_d}{A_b}\right)^{0.789}$$

$$h_D = \frac{h_L}{1-\varepsilon} \quad \varepsilon = \frac{\varepsilon_r A_r + \varepsilon_d A_d}{A_r + A_d}$$

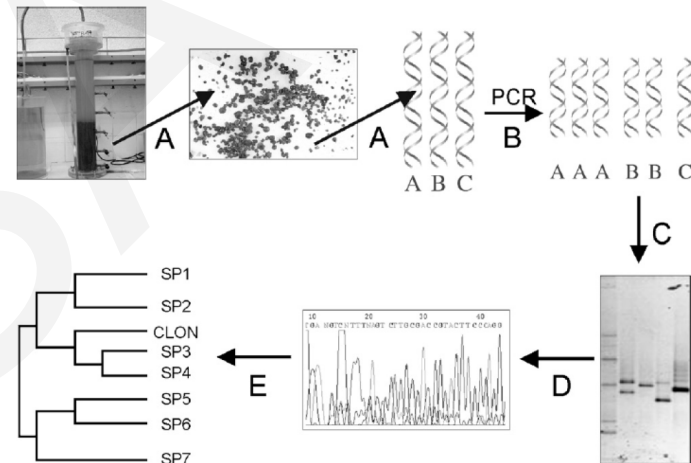
$$\varepsilon_r = \frac{U_{Gr}}{0.24 + 1.35(U_{Gr} + U_{Lr})^{0.93}}$$

$$U_{Gr} = \frac{Q_g}{3600 \times A_r}$$



MICROBIAL POPULATION DYNAMICS IN THE MBR SYSTEM

Microbial community evolution was monitored and analyzed. Results revealed that low community shift occurred during the whole operational period. *Geobacter* sp. and *Rhodocyclales* sp., which has also been identified by other authors in a petroleum refinery wastewater membrane bioreactor or an infiltration basin receiving highway runoff, dominated in the MBR system throughout. *Comamonas* sp. was thought to accommodate the low aeration rate in this study, while *Rhodocyclales* sp. preferred the higher aeration rate.



Cite: Sanz J L, Kochling T. Molecular biology techniques used in wastewater treatment: An overview [J]. *Process Biochemistry*, 2007, 42 (2):119-133.

Table 3 Sequence analysis and species identification of selected DGGE bands for the sludge samples

Bands	Closest relatives			
	Accession	Description	Coverage ratio (%)	Identity (%)
A	FJ439084.1	uncultured Comamonadaceae bacterium clone PIISC 16S ribosomal RNA gene, partial sequence	97	100
C	FJ947138.1	Uncultured sludge bacterium clone ASB54 16S ribosomal RNA gene, partial sequence	100	99
D	JQ177533.1	Uncultured Geobacteraceae bacterium clone PM5_7.0-02 16S ribosomal RNA gene, partial sequence	99	98
E	HQ484708.1	Uncultured bacterium clone Pohang_WWTP_February.2006_1486 16S ribosomal RNA gene, partial sequence	99	99
F	JQ177533.1	Uncultured Geobacteraceae bacterium clone PM5_7.0-02 16S ribosomal RNA gene, partial sequence	100	99
L	JQ177848.1	Uncultured Rhodocyclaceae bacterium clone PM5_-0.3-05 16S ribosomal RNA gene, partial sequence	97	96
c	JQ522966.1	Hydrogenophaga sp. A11(2012) 16S ribosomal RNA gene, partial sequence	100	98
d	JQ793317.1	Uncultured Thiobacillus sp. clone BWET3cm33 16S ribosomal RNA, partial sequence	100	99
e	JQ624351.1	Uncultured beta proteobacterium clone OTU-24-40m.ABB 16S ribosomal RNA gene, partial sequence	100	100

