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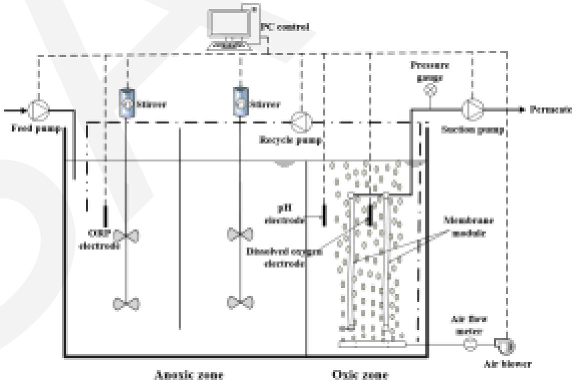
Membrane fouling behavior and microbial community succession in a submerged membrane bioreactor treating harbor oily wastewater

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

MEMBRANE FOULING BEHAVIOR

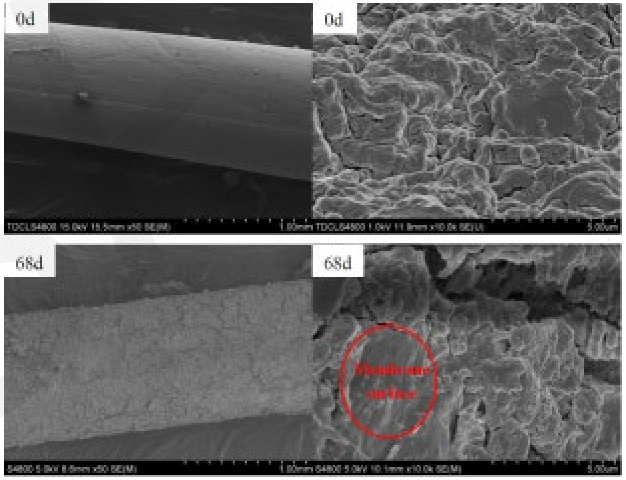
- The membrane bioreactor (MBR) has been widely applied in wastewater treatment and reuse. However, inevitable membrane fouling, consequently leading to a decline in membrane permeability and an increase in operational cost , is still the major obstacle that hampers further development of MBR technology..

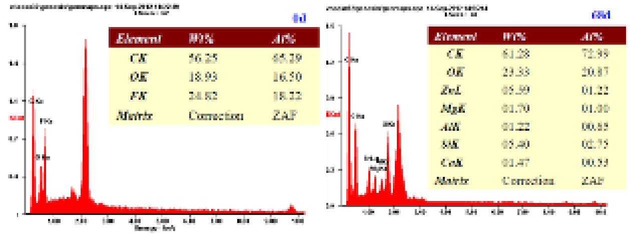
- Due to the complexity of MBR systems and various wastewaters to be treated, the complex relationship of those fouling factors is still not clear. A better elucidation, clarifying the key fouling factors, will help in defining the optimum approach to mitigate membrane fouling in an MBR system.



MEMBRANE FOULING BEHAVIOR

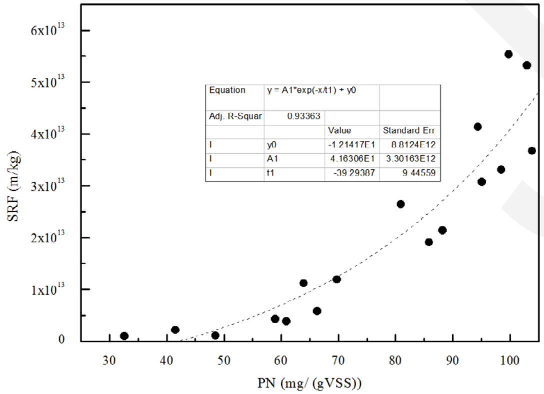
- It is reasonable to consider that the EPS content would be a probable index for membrane fouling by means of SEM images, EDX analysis and FTIR spectra.
- The qualitative analysis further verified that the EPS accumulated on the membrane surface, especially the proteins, were of great importance for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



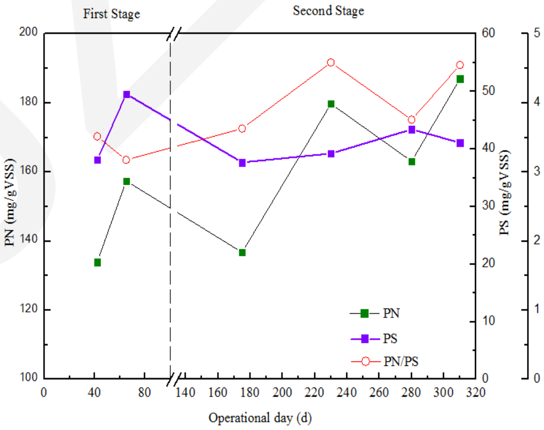


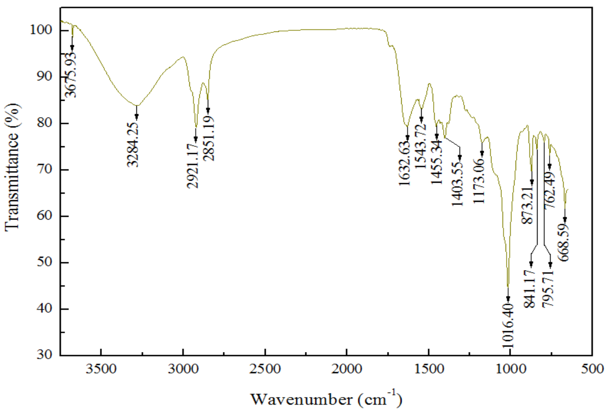
Element	Wt%	At%
CK	56.25	65.29
OK	18.93	16.50
FK	24.82	18.22
Matrix	Correction	ZAF

Element	Wt%	At%
CK	61.28	72.99
OK	23.33	20.87
ZnL	05.59	01.22
MgK	01.70	01.00
AlK	01.22	00.65
SiK	05.40	02.75
CaK	01.47	00.53
Matrix	Correction	ZAF



Equation	y = A1*exp(-x/t1) + y0		
Adj. R-Squar	0.93363		
		Value	Standard Err
I	y0	-1.21417E1	8.8124E12
I	A1	4.16306E1	3.30163E12
I	t1	-39.29387	9.44559





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.

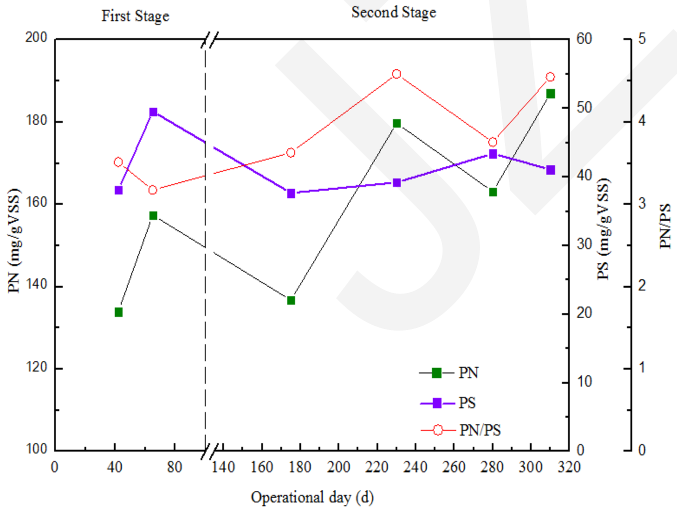
$$U_{Lr} = \left[\frac{2gh_D(\varepsilon_r - \varepsilon_d)}{\frac{K_T}{(1-\varepsilon_r)^2} + K_B\left(\frac{A_r}{A_d}\right)^2 \frac{1}{(1-\varepsilon_d)^2}} \right]^{0.5}$$

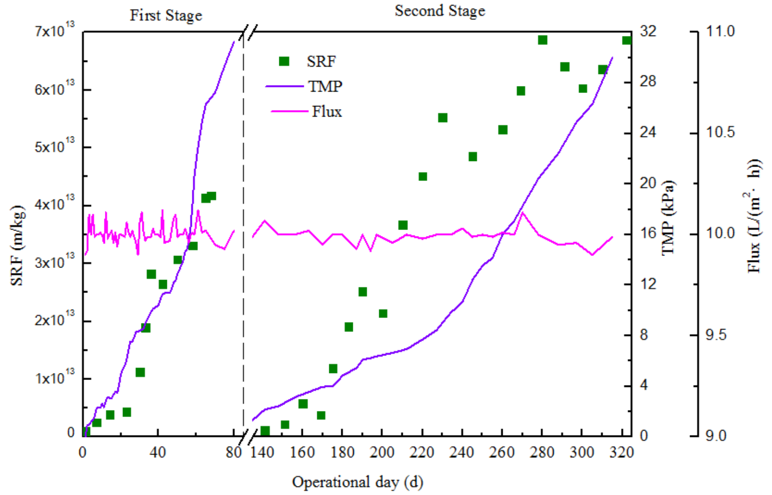
$$K_B = 11.402\left(\frac{A_d}{A_b}\right)^{0.789}$$

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

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

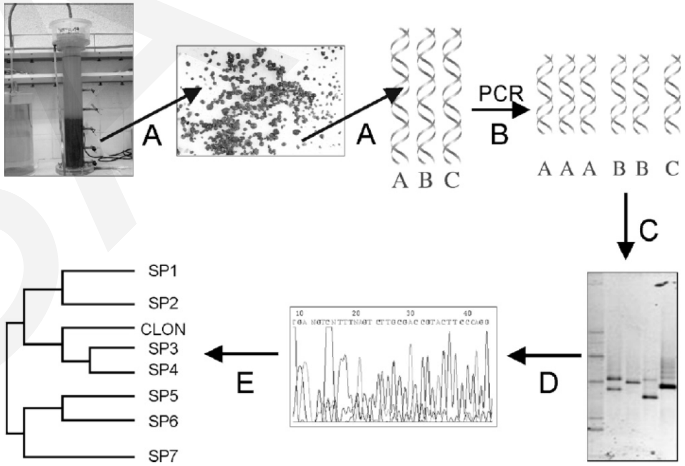
$$U_{Gr} = \frac{Q_g}{3600 \times A_r}$$





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.



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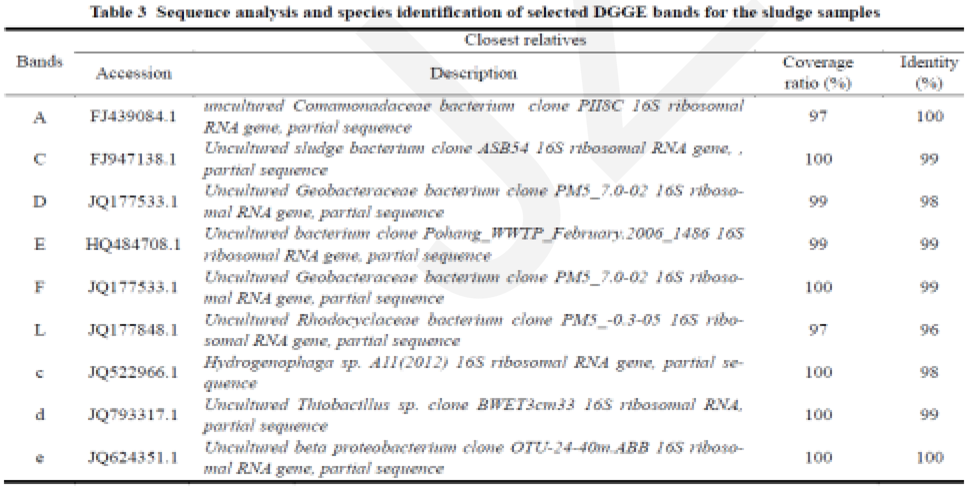

Table 3 Sequence analysis and species identification of selected DGGE bands for the sludge samples

Bands	Closest relatives			
	Accession	Description	Coverage ratio (%)	Identity (%)
A	FJ439084.1	*uncultured Comamonadaceae bacterium clone PII8C 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