

Supporting Information

Deciphering the long-term performance and underlying mechanisms of an engineering-scale anaerobic-anoxic-oxic-anaerobic-vibrating MBR process

Shujuan Che^{a,#}, Weichen Lin^{b,c,#}, Haojie Ding^b, Congcong Zhang^b, Xiangyu Li^c, Kaichang

Yu^a, Huanhuan Guan^a, Jie Shi^a, Yun Yang^d, Xia Huang^{b,e*}

^a Beijing OriginWater Membrane Technology Co., Ltd., Beijing 101407, China

^b State Key Laboratory of Regional Environment and Sustainability, School of Environment,

Tsinghua University, Beijing 100084, China

^c School of Environment, Beijing Normal University, Beijing 100875, China

^d Taicang Water Group Co., Ltd., Taicang 215499, China

^e Research and Application Center for Membrane Technology, School of Environment,

Tsinghua University, Beijing 100084, China

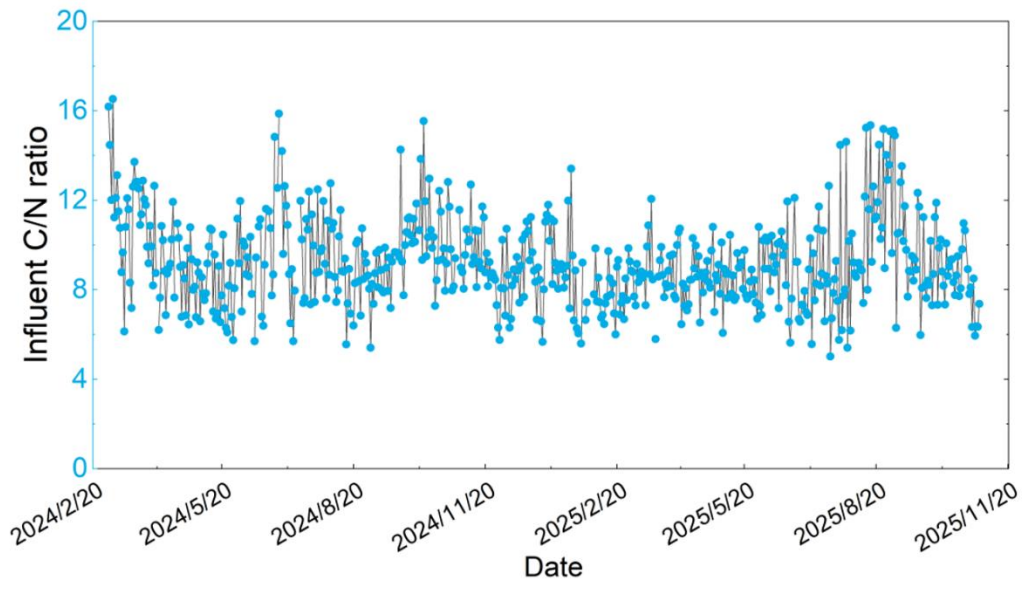


Fig. S1. The variation of C/N ratio of the treated influent with the time.

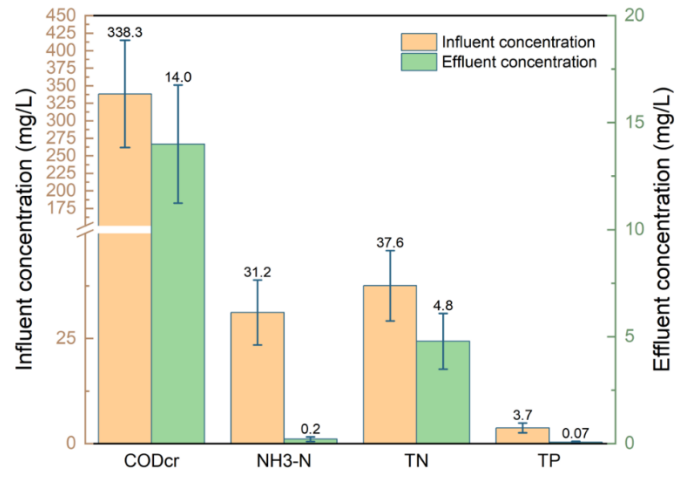


Fig. S2. The comparison of the water quality between the influent and the effluent treated by the AAOA-rMBR system.



Fig. S3. The on-site photo of the fouled membrane module showing the spatial heterogeneity of foulant deposition.

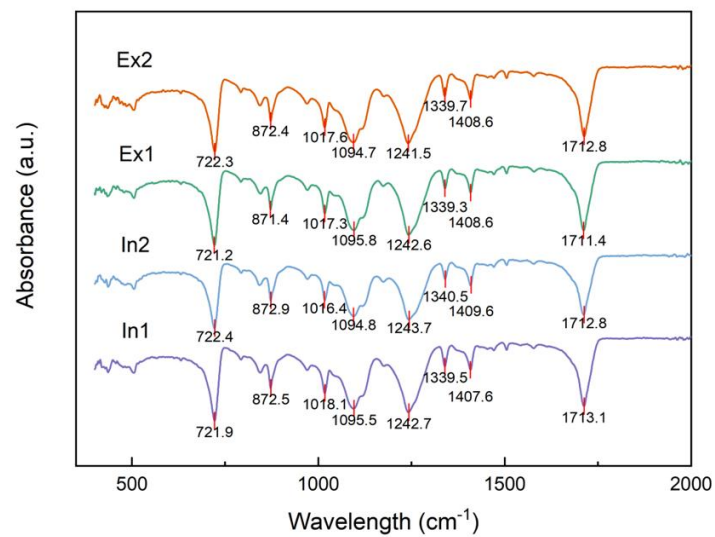


Fig. S4. The FTIR spectroscopy of the fouling layers of the external (Ex1, Ex2) and internal (In1, In2) membrane fibers.

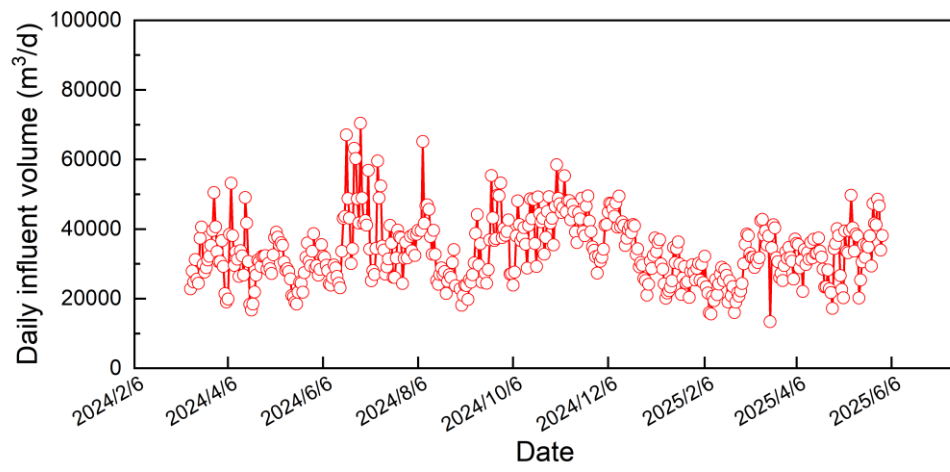


Fig. S5. The variation curve of daily influent volume during the monitoring period.

Table S1. Top functional genera involving in P and N removal with samples taken from the anaerobic, anoxic, aerobic, post anoxic, and membrane unit.

Functional genera	Genus	Anaerobic (%)	Anoxic (%)	Aerobic (%)	Post anoxic (%)	Membrane (%)
PAO (DPAO)	<i>f__Saprospiraceae_Unclassified</i>	2.99	2.85	3.06	3.23	2.95
	<i>f__Comamonadaceae_Unclassified</i>	2.75	3.02	3.05	2.64	2.99
	<i>f__Steroidobacteraceae_Unclassified</i>	1.98	2.23	2.15	2.16	2.17
	<i>Denitratisoma</i>	1.38	1.51	1.46	1.45	1.39
	<i>Dechloromonas</i>	1.01	1.49	1.37	1.33	1.53
	<i>OLB12</i>	0.52	0.53	0.52	0.63	0.53
	<i>f__Rhodocyclaceae_Unclassified</i>	0.51	0.53	0.55	0.52	0.54
	<i>Thauera</i>	0.28	0.30	0.22	0.19	0.22
	<i>Ca._Accumulibacter</i>	0.07	0.06	0.06	0.06	0.08
Total		11.50	12.53	12.45	12.12	12.39
GAO	<i>Ca._Competibacter</i>	5.70	4.94	5.01	4.54	5.12
	<i>Defluviicoccus</i>	1.47	1.42	1.19	1.63	1.43
Total		7.17	6.36	6.20	6.17	6.55
AOB	<i>Ellin6067</i>	4.81	5.60	5.47	4.88	5.65
NOB	<i>Nitrospira</i>	1.90	1.85	1.90	1.21	1.66
DNB	<i>Terrimonas</i>	1.95	1.85	1.98	1.92	1.79