

Supporting Information

Impact of Acclimation Methods on Microbial Communities and Performance of Anaerobic Fluidized Bed Membrane Bioreactors

Nicole LaBarge^a, Yaoli Ye^a, Kyoung-Yeol Kim^a, Yasemin Dilsad Yilmazel^a,

Pascal E. Saikaly^b, Pei-Ying Hong^b, and Bruce E. Logan^{a,*}

^a Department of Civil and Environmental Engineering, The Pennsylvania State University,
University Park, PA, 16802

^b Biological and Environmental Sciences and Engineering Division, Water Desalination and Reuse
Center, King Abdullah University of Science and Technology (KAUST), 4700 King Abdullah Boulevard,
Thuwal 23955-6900, Saudi Arabia

Reactor Setup

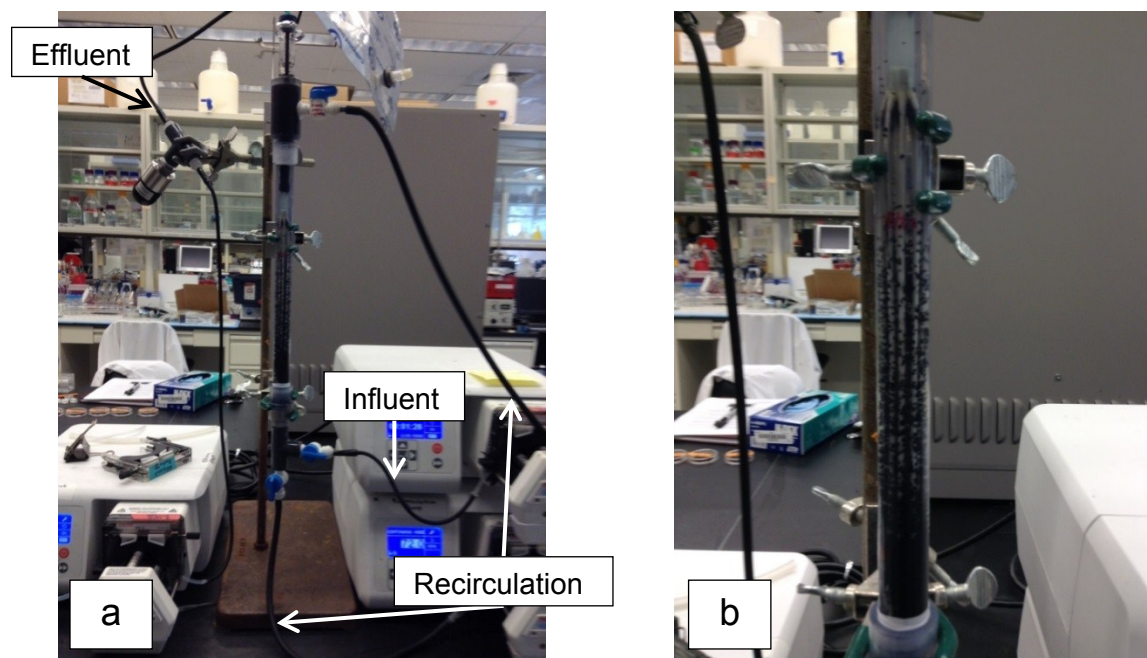


Fig. S1. AFMBR with settling chamber (Reactor D), showing (a) the experimental setup and (b) a close-up view of the fluidized GAC.

COD removal

Table S1. COD removal for AFMBRs M, W, D, A, M_A, and MFC.

	M	W	D	A	M _A	MFC
Influent tCOD (mg/L)	106 ± 25	112 ± 21	92 ± 14	153 ± 19	111 ± 20	114 ± 24
Influent sCOD (mg/L)	47 ± 11	48 ± 6	53 ± 11	87 ± 18	50 ± 7	72 ± 9
Effluent tCOD (mg/L)	42 ± 14	43 ± 8	33 ± 13	24 ± 10	33 ± 7	37 ± 5
COD removal (%)	62 ± 12%	63 ± 7%	64 ± 13%	84 ± 6%	70 ± 6%	67 ± 7%

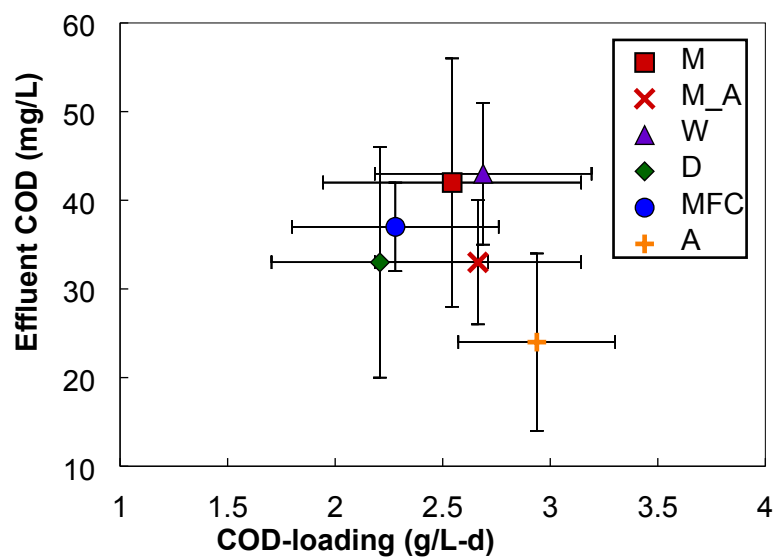


Fig. S2. Relationship between COD loading rate on effluent COD for AFMBRs M, M_A, W, D, MFC-fed, and A.

DNA extracted from samples

The mass of sample taken for DNA extraction, as well as the mass of extracted DNA in a 100 μ L volume, is shown in Table S3. DNA concentration should only be considered an accurate measure of order of magnitude, as precision of Nanodrop readings was low.

Table S2. DNA extracted from AFMBR samples, showing mass of the sample used for DNA extraction, concentration of extracted DNA, and calculated DNA yield per gram of sample for the 100 μ L of final fluid containing the extracted DNA.

AFMBR	Sample location	sample	ng DNA/ μ L	ng(DNA)/g(sample)
M_A	GAC	0.416 g	15.0	3,600
M_A	Reactor fluid	13 mL	7.7	59*
M_A	Influent	52 mL	5.7	11
W	GAC	0.419	14.4	3,400
W	Reactor fluid	13 mL	13.3	100
W	Influent	52 mL	5.7	11
D	GAC	0.275	10.2	3,700
D	Reactor fluid	13 mL	34.3	260
D	Influent	52 mL	19.8	38
A	GAC	0.322	11.0	3,400
A	Reactor fluid	13 mL	11.3	87
A	Influent	52 mL	38.0	73
MFC	GAC	0.194	4.5	2,300
MFC	Reactor fluid	13 mL	7.4	57
MFC	Influent	52 mL	46.5	89

*DNA yields for liquid samples are calculated assuming 1 mL sample = 1 g.

Similarity among DNA samples

Table. S3. Bray-Curtis similarity (%) among GAC and reactor fluid (RF) DNA samples, calculated from square-root transformed relative abundances. Darker shades correlate with more similar samples.

GAC	M_A	W	D	MFC	A
M_A		79	61	55	63
W	79		59	52	64
D	61	59		54	56
MFC	55	52	54		57
A	63	64	56	57	

RF	M_A	W	D	MFC	A
M_A		79	56	55	35
W	79		59	54	31
D	56	59		44	20
MFC	55	54	44		44
A	35	31	20	44	