

Supplementary Materials: Biofouling Formation and Bacterial Community Structure in Hybrid Moving Bed Biofilm Reactor-Membrane Bioreactors: Influence of Salinity Concentration

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Table S1. Ecological coverage of massive parallel sequencing analyses.

	Coverage (%)	Actual Effort (Mbp)	Required Effort (Mbp)
CFB1	92.61	12.5	3.915
CFB2	92.6	73.21	11.93
CML1	92.83	11.1	3.884
CML2	89.69	4.738	3.964
VFB1	96.59	12.42	1.328
VFB2	96	31.69	2.43
VML1	95.44	10.72	1.835
VML2	97.74	15.64	1.21

CFB: Constant salinity Fixed Biofilm; CML: Constant salinity Mixed Liquor; VFB: Variable salinity Fixed Biofilm; VML: Variable salinity Mixed Liquor.

Table S2. α -diversity of massive parallel sequencing samples.

Index	CFB1	CFB2	CML1	CML2	VFB1	VFB2	VML1	VML2
Species richness	506	734	452	431	333	470	311	326
Chao-1	595.2	836.3	557.7	594.3	424.3	614.1	381.7	482
Shannon-Wiener	4.728	5.052	4.141	4.652	3.342	3.691	3.261	3.146
Simpson	0.9805	0.9871	0.954	0.9806	0.8818	0.9299	0.8737	0.8497
Pielou's evenness	0.7594	0.7656	0.6773	0.767	0.5753	0.6	0.5681	0.5437
Berger-Parker	0.05792	0.0521	0.1527	0.06778	0.3154	0.2159	0.329	0.3674

CFB: Constant salinity Fixed Biofilm; CML: Constant salinity Mixed Liquor; VFB: Variable salinity Fixed Biofilm; VML: Variable salinity Mixed Liquor.

Table S3. Best hits against the NCBI database for the 16S rRNA genes of isolated strains with high biomineralization capacity.

Strain	Accession	Identity (%)	Length Query (bp)	Query Cover (%)	e-value	Max Score	Species
C_MC1	AB548826.1	99.794	1456	100	0	2676	<i>Citrobacter freundii</i>
C_MC1	AB548577.1	99.725	1456	100	0	2671	<i>Citrobacter freundii</i>
C_ME1	MF574004.1	99.863	1460	100	0	2689	<i>Bacillus licheniformis</i>
C_ME1	MF470191.1	99.863	1460	100	0	2689	<i>Bacillus licheniformis</i>

C_ME2	JX188071.1	100	1460	100	0	2697	<i>Bacillus pumilus</i>
C_ME2	KY754576.1	100	1459	100	0	2695	<i>Bacillus pumilus</i>
C_ME3	AF025365.1	99.725	1454	100	0	2667	<i>Citrobacter freundii</i>
C_ME3	DQ294289.1	99.725	1454	100	0	2665	<i>Citrobacter freundii</i>
C_ME4	KM515969.1	99.589	1459	100	0	2663	<i>Citrobacter freundii</i>
C_ME4	AB548826.1	99.589	1459	100	0	2663	<i>Citrobacter freundii</i>
C_ME5	KM494494.1	99.931	1454	100	0	2680	<i>Citrobacter freundii</i>
C_ME5	CP016762.1	99.862	1454	100	0	2675	<i>Citrobacter freundii</i>
V_MC1	CP014869.1	99.605	1520	100	0	2771	<i>Brevibacterium linens</i>
V_MC1	KX369590.1	99.474	1520	100	0	2763	<i>Brevibacterium linens</i>
V_ME1	EU718490.1	99.87	1541	100	0	2837	<i>Bacillus licheniformis</i>
V_ME1	AY052767.1	99.741	1542	100	0	2826	<i>Bacillus licheniformis</i>

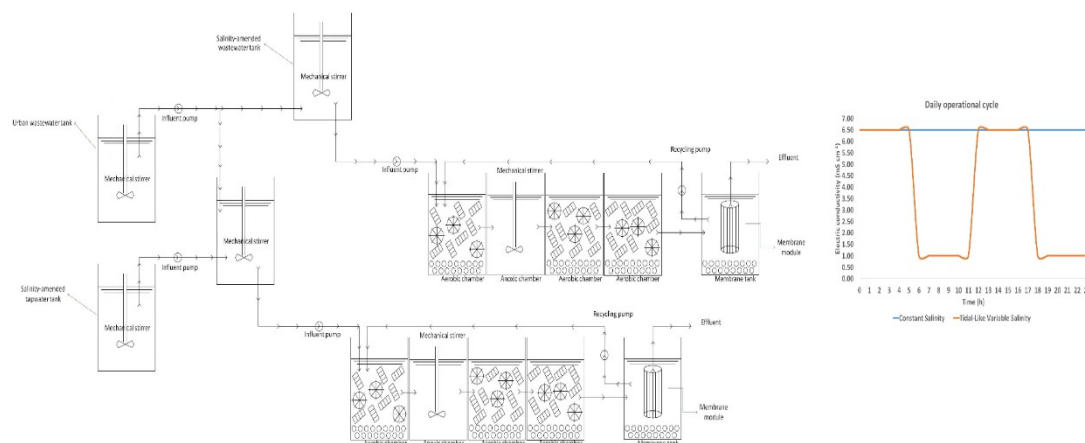


Figure S1. Schematic representation of the hybrid MBBR-MBR systems.

Domain	Phylum	Order	Class	Family	Genus	Constant (%)	Variable (%)
Bacteria	Actinobacteria	Actinobacteria	Corynebacteriales	Corynebacteriaceae	Corynebacterium		
Bacteria	Actinobacteria	Actinobacteria	Corynebacteriales	Mycobacteriaceae	Mycobacterium		
Bacteria	Actinobacteria	Actinobacteria	Frankiales	Nakamurellaceae	Nakamurella		
Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	Cryocola		
Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	Microbacterium		
Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	Mycetocola		
Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Arenibacter		
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Ferruginibacter		
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	uncultured		
Bacteria	FBP	FBP_cl	FBP_fa	FBP_ge	FBP_ge		
Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Paraclostridium		
Bacteria	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	uncultured		
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Nitrobacter		
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	MNG7	MNG7_ge		
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	Phyllobacteriaceae_ge		
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Acidisphaera		
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Acidovorax		
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Comamonas		
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Ottowia		
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	uncultured		
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas		
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Dokdonella		
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Dyella		
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Mizugakiibacter		
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Rhodanobacter		
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Rudaea		
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Thermomonas		
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	uncultured		

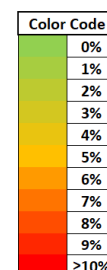


Figure S2. Heat map showing the results of the SIMPER analyses differentiating the phylotypes that contributed to >1% dissimilarity between the fixed biofilm and mixed liquor samples for the constant and variable salinity scenarios.