

Supporting Information

Efficient Removal of Butachlor and Change in Microbial Community Structure in Single-Chamber Microbial Fuel Cells

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Table S1. The Alpha-diversity indices of controls. The CK and CK-NaAC were the control for BUT and BUT-NaAC, respectively. The value was mean $\pm$ SE with two duplicates.

Controls	Observed Species	SE	Chao1	SE	ACE	SE	Shannon	SE	Simpson	SE
CK.A	736	347	816.2635	406.6385	840.496	426.817	4.876	0.382	0.9045	0.0035
CK.A-NaAC	720	267	820.0465	327.5175	845.4995	347.0835	5.612	0.087	0.938	0.002
CK.C	706.5	319.5	779.831	370.307	807.6485	397.9135	5.1765	0.3695	0.921	0.004
CK.C-NaAC	765	311	868.974	383.367	872.647	381.519	5.3305	0.1425	0.9145	5.00×10^{-4}

Table S2. The abundance changes of BUT treatment–Control. The CK and CK-NaAC were the controls of BUT and BUT-NaAC, respectively. The value was mean $\pm$ SE with two duplicates.

Taxonomy	CK.A	CK.C	CK.A-NaAC	CK.C-NaAC	BUT.A	SE	BUT.A-NaAC	SE	BUT.C	SE	BUT.C-NaAC	SE
<i>γ-Proteobacteria</i>	25.5	44.7	37.0	52.4	1.2	2.3	15.1	4.9	-22.9	4.2	-8.1	4.2
<i>α-Proteobacteria</i>	28.6	34.4	12.5	26.8	-4.3	5.6	0.8	0.8	21.8	7.3	-2.9	4.9
<i>δ-Proteobacteria</i>	10.3	2.4	14.8	2.8	7.2	2.8	-0.6	0.6	0.0	0.4	-0.1	0.5
<i>Bacteroidia</i>	27.8	11.2	23.5	7.8	-2.6	5.1	-10.3	3.0	0.3	4.7	2.2	5.8
<i>Verrucomicrobiae</i>	0.2	2.0	0.2	1.4	0.1	0.0	0.0	0.0	-1.5	0.1	6.0	1.2
<i>unidentified_Bacteria</i>	0.2	0.1	3.0	0.2	-0.1	0.0	-1.7	0.5	0.0	0.0	0.0	0.0
<i>Spirochaetia</i>	0.4	0.3	0.7	0.9	-0.1	0.0	-0.1	0.0	0.1	0.0	1.6	0.3
<i>Clostridia</i>	1.5	1.2	1.4	2.6	-0.2	0.0	-0.3	0.1	0.2	0.0	-0.4	2.0
<i>Bacilli</i>	0.7	0.7	1.0	0.9	0.4	0.4	0.9	0.0	1.5	0.3	0.6	0.1
<i>Synergistia</i>	1.9	0.3	1.4	0.3	-0.6	0.5	-0.8	1.4	-0.1	1.1	0.0	0.1
<i>Actinobacteria</i>	0.3	0.5	0.4	0.5	0.8	0.0	-0.1	0.0	0.8	0.2	0.0	0.0

Table S3. The microbial abundance of controls at the genus level. The CK and CK-NaAC were the controls of BUT and BUT-NaAC, respectively.

Taxonomy	CK.A	CK.C	CK.A.Na	CK.C.Na
<i>Thauera</i>	0.08	0.14	0.09	0.22
<i>Geobacter</i>	0.070923	0.008567	0.117681	0.013447
<i>Pannonibacter</i>	0.016669	0.078306	0.014998	0.074921
<i>Dokdonella</i>	0.007883	0.161963	0.007658	0.043021
<i>Paracoccus</i>	0.002144	0.005317	0.004449	0.006057
<i>Azospirillum</i>	0.08229	0.009844	0.009216	0.003857
<i>Comamonas</i>	0.039474	0.00421	0.081627	0.007214
<i>Aquamicrobium</i>	0.051637	0.050636	0.025998	0.032599
<i>Stappia</i>	0.027571	0.030709	0.006036	0.058682
<i>Dechlorobacter</i>	0.048253	0.001742	0.021091	0.002454
<i>Pseudomonas</i>	0.002299	0.002658	0.015069	0.027606
<i>Proteiniphilum</i>	0.007531	0.019088	0.01093	0.01057
<i>Stenotrophomonas</i>	0.000994	0.006078	0.008257	0.011162
<i>Pseudofulvimonas</i>	0.004739	0.019829	0.007869	0.023636
<i>Arcobacter</i>	0.001869	0.000606	0.027472	0.001417
<i>Petrimonas</i>	0.001699	0.006212	0.001262	0.001128
<i>Chryseobacterium</i>	0.003307	0.001163	0.01057	0.00294
<i>unidentified_Rhizobiaceae</i>	0.004055	0.009759	0.005465	0.012946
<i>Desulfovibrio</i>	0.017762	0.005817	0.007348	0.006783
<i>Acinetobacter</i>	0.000141	0.000148	0.011451	0.004943
<i>Chelativorans</i>	0.000212	0.00098	0.000261	0.000677
<i>Taibaiella</i>	0.001396	0.005345	0.002447	0.011804
<i>Yersinia</i>	0	0	0.003011	0.005733
<i>Psychrobacter</i>	0	0	0.000134	0.000035
<i>Hydrogenophaga</i>	0.000381	0.010471	0.000275	0.000282
<i>Nitrosomonas</i>	0.002172	0.002066	0.009682	0.002313
<i>Janthinobacterium</i>	0.000028	0.000402	0.002531	0.002644
<i>Halomonas</i>	0.000134	0.000303	0.00019	0.000346
<i>unidentified_Rikenellaceae</i>	0.001389	0.002066	0.010979	0.001319
<i>Acetoanaerobium</i>	0.000423	0.000642	0.001587	0.008765
<i>Carnobacterium</i>	0	0	0.000536	0.001135
<i>Brochothrix</i>	0	0	0.000106	0.000085
<i>Leuconostoc</i>	0	0	0.000028	0.000042