Supplementary Material

Efficiency of carbon-based electrodes on a microbial electrolysis system for the treatment of bilge water

**Georgia Gatidou1\*, Marios Constantinou2, Loukas Koutsokeras2, Georgios Constantinides2, Ioannis Vyrides1\***

1Laboratory of Environmental Engineering, Department of Chemical Engineering, Cyprus University of Technology, Anexartisias 57 Str., Lemesos, 3603, Cyprus

2Nano/Micro Mechanics of Materials Laboratory and Research Unit for Nanostructured Materials Systems, Department of Mechanical Engineering and Materials Science and Engineering, Cyprus University of Technology, P. O. Box 50329, Limassol, 3603, Cyprus

**Analytical Methods**

### Next-Generation Sequencing

The extracted DNAs were evaluated and analysed using 16S rRNA gene amplicon sequencing targeting the bacterial variable region V1-3 and the archaeal variable regions V3-5. 16S V1-3 rRNA gene sequencing libraries were prepared by a custom protocol based on Caporaso et al. (2012) for Bacteria and an Illumina protocol (Illumina, 2015) for Archaea. The adaptors contain 16S V1-3 specific primers for Bacteria: [27F] AGAGTTTGATCCTGGCTCAG and [534R] ATTACCGCGGCTGCTGG (Ward et al., 2012). As for Archaea, the forward and reverse tailed primers were designed according to Illumina (2015) and contain primers targeting the Archaea 16S rRNA gene region V3-5: [Arch340F] CCCTAHGGGGYGCASCA and [Arch-915R] GWGCYCCCCCGYCAATTC (Pinto and Raskin, 2012). The resulting amplicon libraries were purified using the standard protocol for Agencourt Ampure XP Beads (Beckman Coulter, USA) with a bead to sample ratio of 4:5. DNA concentration was measured using Qubit dsDNA HS Assay kit (Thermo Fisher Scientific, USA). Gel electrophoresis using Tapestation 2200 and D1000/High sensitivity D1000 screentapes (Agilent, USA) was used to validate the product size and purity of a subset of sequencing libraries. The samples were paired-end sequenced (2×300 bp for bacteria and 1x300 bp for Archaea) on a MiSeq (Illumina, USA) using a MiSeq Reagent kit v3 (Illumina, USA) and bioinformatics processing was performed by DNASense Company (Denmark).

**Supplementary Tables**

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| --- | --- | --- | --- | --- | --- | --- |
| **Reactor** | **Cycle A** | | **Cycle B** | | **Cycle C** | |
| *t=0* | *t=13* | *t=0* | *t=19* | *t=0* | *t=21* |
| R0-C | 1305 | 485 | 1656 | 885 | 1284 | 959 |
| R1-CF | 1205 | 409 | 2256 | 700 | 1144 | 779 |
| R2-CC | 1395 | 424 | 1464 | 760 | 1156 | 744 |
| R3-3DG | 1155 | 399 | 1086 | 760 | 1104 | 739 |

**Table S1.** Initial anf final COD values (mg/L) in MEC-AGS systems during each experimental cycle.

**Supplementary Figures**



**Figure S1.** COD (mg L-1) reduction over time during cycle A.



**Figure S2.** COD (mg L-1) reduction over time during cycle B.



**Figure S3.** COD (mg L-1) reduction over time during cycle C.



**Figure S4.** Variation of propionic acid concentration (mg L-1) over time both in the control and MEC reactors.

**References**

Caporaso, J.G., Lauber, C.L., Walters, W. a, Berg‐Lyons, D., Huntley, J., Fierer, N., Sarah, M.O., Betley, J., Louise Fraser, L. and Bauer, M. 2012. Ultra‐high‐throughput microbial community analysis on the Illumina HiSeq and MiSeq platforms. *The ISME journal* **6**: 1621–4.

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Ward, D.V., Gevers, D., Giannoukos, G., Earl, A.M., Methé, B.A., Sodergren, E., et al. 2012. Evaluation of 16s rDNA‐based community profiling for human microbiome research. *PLoS ONE* **7**: e39315.