

Hill-based dissimilarity indices and null models for analysis of microbial community assembly

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ADDITIONAL FILE 3 – EXPERIMENTAL DETAILS

Text S3.1. PCR protocol.

Duplicate PCR reactions were conducted in a 20 μ L volumes using 17 μ L of AccuPrime Pfx SuperMix (Life Technologies), 1 μ L of genomic DNA (20 ng template), and 1 μ L each of the forward and reverse primers (10 μ M). The PCR reactions were carried out in a BioRad T100 thermocycler using the following protocol: 5 min initial denaturation at 95°C; 30 cycles of denaturation (95°C, 20 s), annealing (50°C, 15 s) and elongation (68°C, 60 s); and finally 10 min elongation at 68°C. Purification of PCR products was done with the MagJET NGS Cleanup and Size Selection Kit (Thermo Scientific). The DNA concentrations were measured using a Qubit 3.0 (Invitrogen) and the dsDNA HS assay kit (Invitrogen). The PCR products were pooled and sequencing was carried out on an Illumina MiSeq using reagent kit v3.

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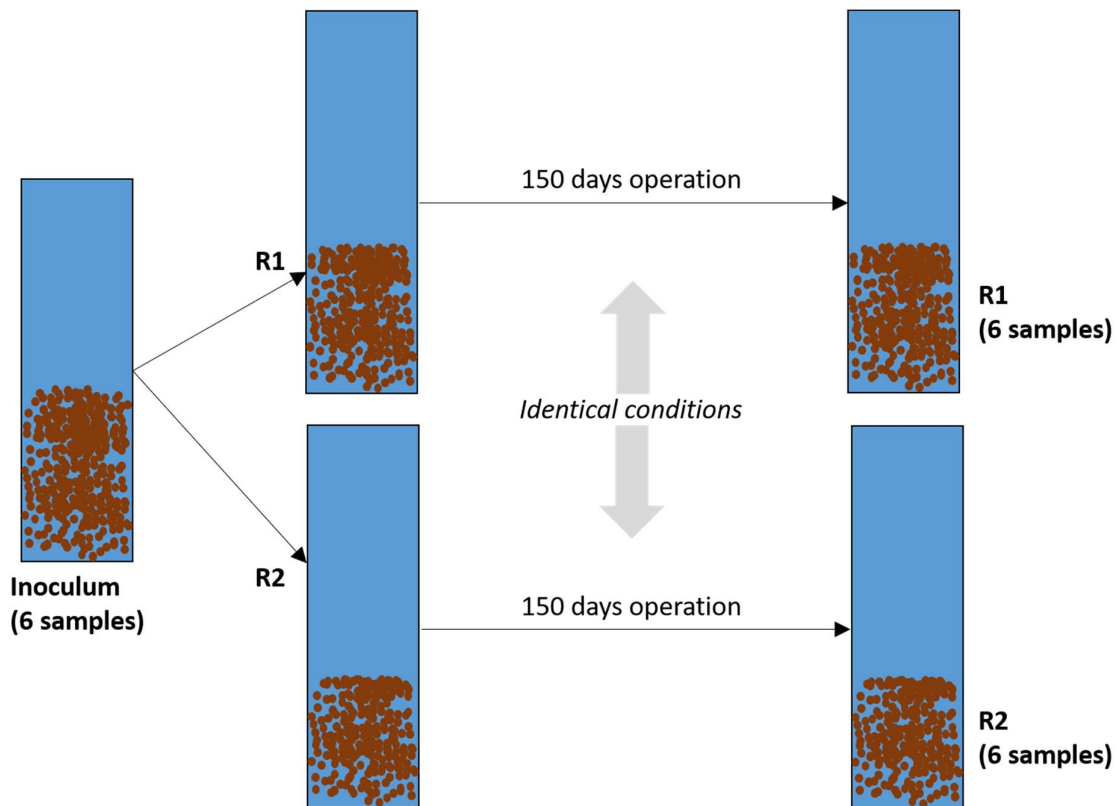


Figure S3.1. Schematic of the aerobic granular sludge (AGS) experiment. The sludge in a sequencing batch reactor was used to inoculate two parallel reactors (R1 and R2), which were operated under identical conditions. Six samples were collected from the inoculum and from R1 and R2 after 150 days.

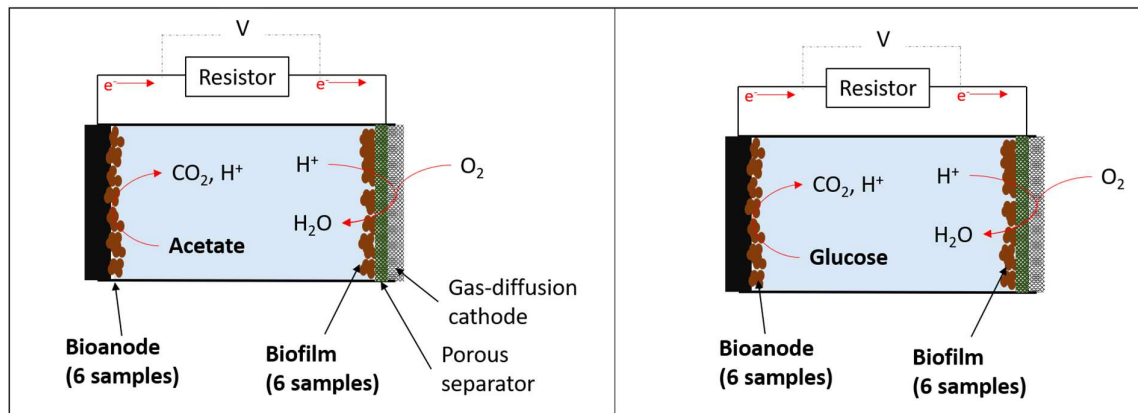


Figure S3.2. Schematic of the microbial fuel cell (MFC) setup. Samples were collected from the bioanode and the biofilm covering the porous separator near the gas-diffusion cathode. Samples were collected from both an MFC fed with acetate and one fed with glucose.