SUPPORTING INFORMATION

Convergent development of anodic bacterial communities in microbial fuel cells

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Table S1. Multiplex identifiers for the nine libraries produced by pyrosequencing.

Sample	Barcode
P1	TATATATACA
P2	TCGCTGCGTA
P3	TCTGACGTCA
U1	TGTCGTCGCA
U2	ACATGACGAC
U3	ACGTCTCATC
B1	ACTCATCTAC
B2	AGAGCGTCAC
B3	AGTAGTGATC

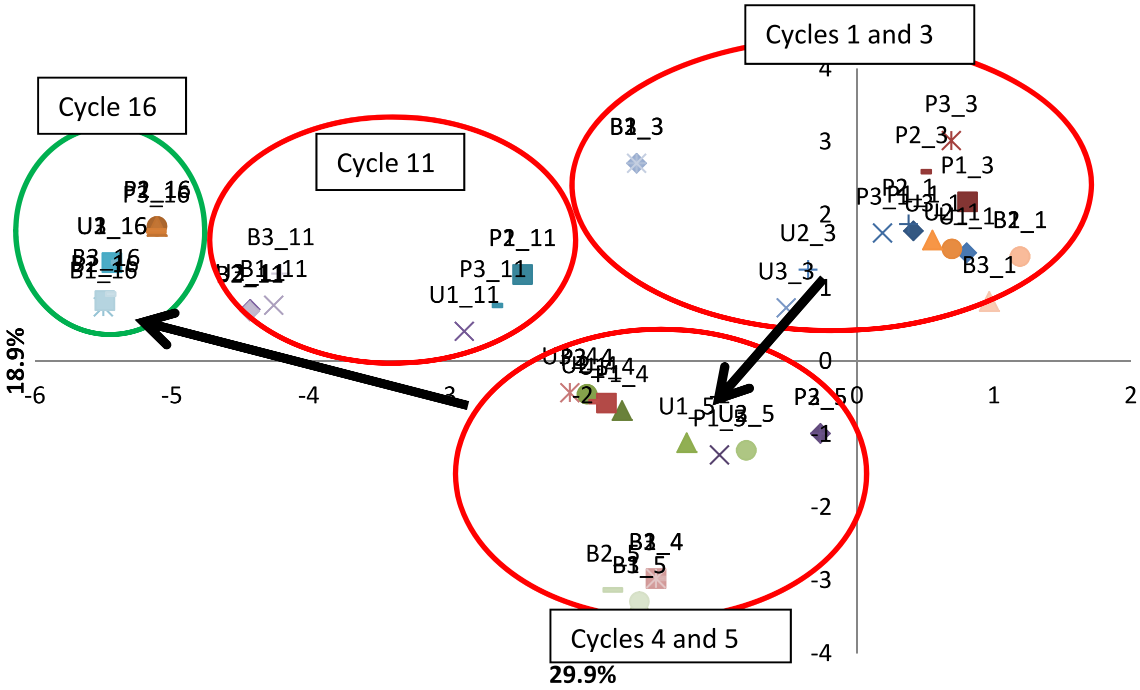

Figure S1. PCA plot of all reactors and all time points taken from DGGE gels. The general trend shows that all reactors initially start in the top right and move in a similar fashion as designated by the arrows until all reactors converge at the final time point. It can also be seen that the Bog reactors are clustered away from the wastewater reactors until cycle 11. It also shows that by cycle 16 all communities have converged regardless of inoculum.

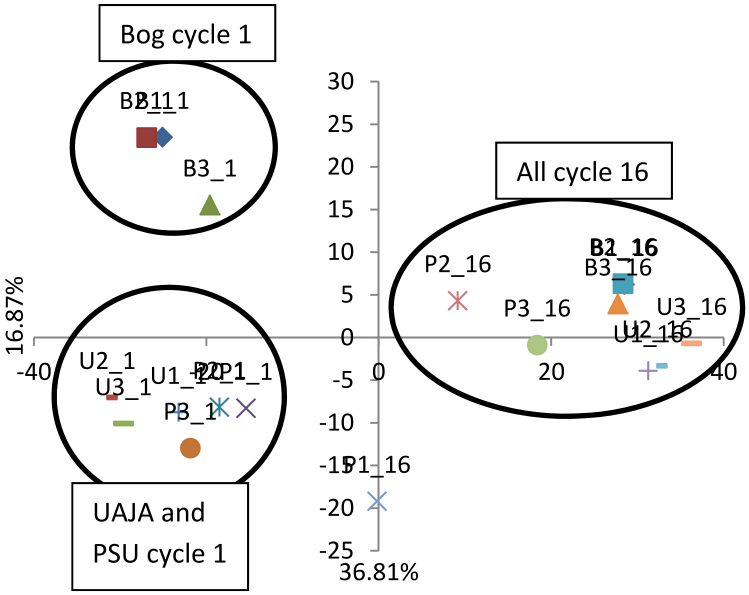

Figure S2. PCA graph of cycle 1 and 16 using the computer program GelCompar II. This graph also shows that the Bog and PSU reactors initially cluster in different quadrants, but finally converge to cluster in a similar position. This graph shows that the two methods of generating PCA plots to identify the bacterial community shift over time are comparable.