

Additional File -1

Comparative metabolic state of microflora on the surface of the anode electrode in a microbial fuel cell operated at different pH conditions

AMB Express

Daisuke Sasaki¹, Kengo Sasaki¹, Yota Tsuge², and Akihiko Kondo^{1,3,4}

¹ Graduate School of Science, Technology and Innovation, Kobe University, 1-1 Rokkodaicho, Nada-ku, Kobe, Hyogo 657-8501, Japan

² Institute for Frontier Science Initiative, Kanazawa University, Kakuma-machi, Kanazawa, Ishikawa 920-1192, Japan

³ Graduate School of Engineering, Kobe University, 1-1 Rokkodai-cho, Nada-ku, Kobe, Hyogo 657-8501, Japan

⁴ RIKEN Center for Sustainable Resource Science, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Corresponding author: Prof. Akihiko Kondo (E-mail: akondo@kobe-u.ac.jp)

Table S1.

Phylogenetic affiliations and number of bacterial clones obtained from retained and suspended fractions in MFC operated for 30 days at pH 4.0.

OTU ^a	No. of clones ^b		Phylogenetic group	The closest isolated strain (accession no., similarity)	The closest environmental clone (accession no., similarity)	Isolated source of environmental clones
	Retained	Suspended				
1	1		<i>Proteobacteria; Deltaproteobacteria</i>	<i>Desulfovibrio desulfuricans</i> (NR_104990, 99.6%)	uncultured <i>Desulfovibrio</i> sp. (FJ393090, 99.7%)	MFC using glucose and lactate
2	3		<i>Proteobacteria; Gammaproteobacteria</i>	<i>Frateuria</i> sp. EC-K130 (AB264175, 100%)	uncultured bacterium (EF201736, 99.4%)	lake sediment core
3		6	<i>Proteobacteria; Gammaproteobacteria</i>	<i>Enterobacter asburiae</i> (JF772078, 99.7%)	uncultured <i>Citrobacter</i> sp. (GQ416219, 99.9%)	biological degreasing systems
4	6		<i>Proteobacteria; Betaproteobacteria</i>	<i>Pandoraea sputorum</i> (JQ839144, 100%)	<i>Pandoraea</i> sp. G5084 (AF247693, 100%)	blood cultures
5	6		<i>Proteobacteria; Betaproteobacteria</i>	<i>Burkholderia pseudomultivorans</i> (NR_117661, 98.6%)	<i>Burkholderia</i> sp. MAC25 (HM587748, 98.6%)	forest soil
6	18	20	<i>Bacteroidetes; Bacteroidia</i>	<i>Bacteroides stercoris</i> (NR_112943, 86.8%)	uncultured bacterium (EF515298, 99.4%)	upflow MFC anode
7		10	<i>Bacteroidetes; Bacteroidia</i>	<i>Prevotella paludivivens</i> (AB081578, 97.5%)	uncultured bacterium (JN245858, 99.9%)	wastewater treatment plant
8	3		<i>Firmicutes; Negativicutes</i>	<i>Pectinatus frisingensis</i> (NR_117702, 99.9%)	<i>Pectinatus</i> sp. H1 (FJ668028, 99.9%)	UASB hydrogen-producing bioreactor
9		1	<i>Firmicutes; Negativicutes</i>	<i>Selenomonas bovis</i> (JN613164, 90.7%)	uncultured bacterium (EU828397, 92.0%)	Hydrogen-producing bioreactor
10	2		<i>Firmicutes; Clostridia</i>	<i>Clostridium swelofunium</i> (NR_126179, 98.4%)	uncultured bacterium (HQ266807, 98.8%)	rice field soil
Sum	39	38				

^a Sequences with more than 97.0% homology were considered as being the same as the operational taxonomic unit (OTU).

^b Suspended: the suspended fraction obtained from fermentation broth, Retained: the retained fraction obtained from anode graphite felts.

Figure S1.

Comparison of intracellular metabolite concentrations related to central metabolism in microbial cells growing on the MFC anode (pH 7.0: black bars, pH 5.5: gray bars, and pH 4.0: white bars). The metabolite concentrations ($\mu\text{mol g-cell}^{-1}$) were measured after 30 days' operation. Error bars indicate \pm standard deviation.

Abbreviations: 1,3 BPG, 1,3-bisphosphoglycerate; 2PG, 2-phosphoglycerate; 3PG, 3-phosphoglycerate; 6PGA, 6-phosphogluconate; 6PGL, 6-phosphogluconolactone; AMP, adenosine-monophosphate; DHAP, dihydroxyacetone phosphate; E4P, erythrose-4-phosphate; F6P, fructose-6-phosphate; FBP, fructose-1,6-bisphosphate; G6P, glucose-6-phosphate; GAP, glyceraldehyde-3-phosphate; PEP, phosphoenolpyruvate; PYR, pyruvate; Pi, phosphoric acid; PPi, pyrophosphoric acid; R5P, ribose-5-phosphate; Ru5P, ribulose-5-phosphate; S7P, sedoheptulose-7-phosphate; X5P, xylulose-5-phosphate.

