

Single-cell metal-phenolic nanocoatings protect strictly anaerobic methanogen for methane production under atmospheric oxygen level

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This supporting information contains 15 pages with 9 figures and 4 tables.

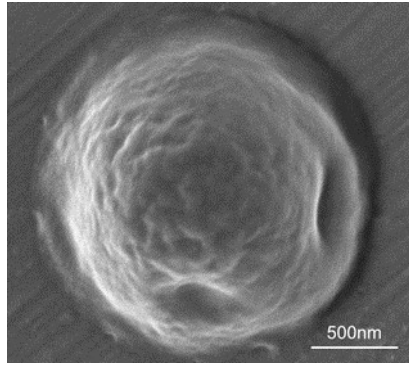


Figure S1. SEM images of *M. acetivorans* with 1.2 mM $\text{FeCl}_2 \cdot 4\text{H}_2\text{O}$, 0.12 mM TA under anaerobic environment.

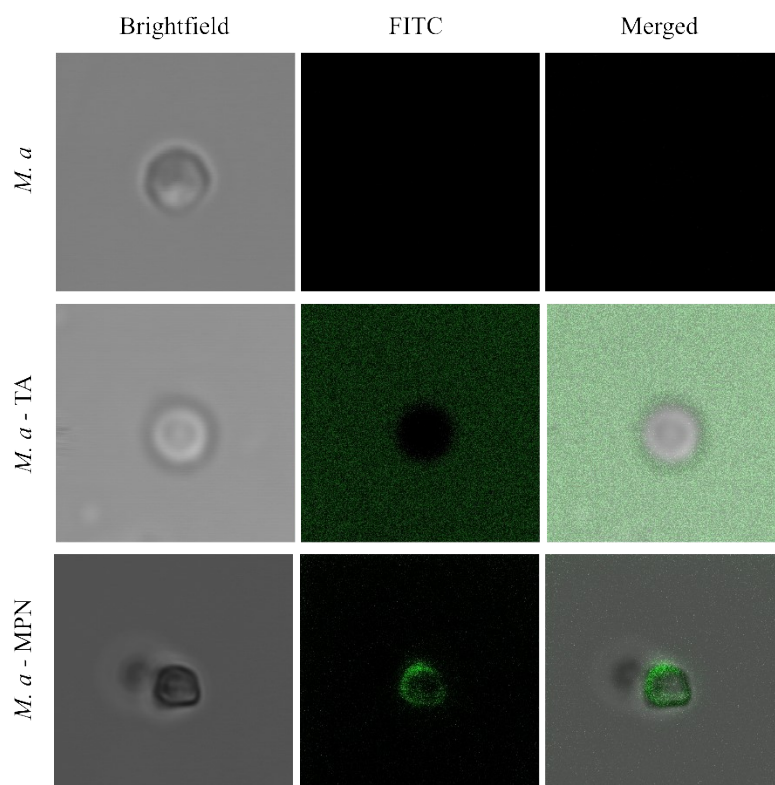


Figure S2. Confocal fluorescence microscopy bright-field and fluorescence images of native, FITC-labeled TA, FITC-labeled TA and Fe^{2+} (MPN) assembled *M. acetivorans* (abbreviated as *M. a.* in the figure). TA cannot adsorb on the surface of *M. acetivorans* without Fe^{2+} , indicating that MPN formation on *M. acetivorans* requires the presence of both Fe^{2+} and TA.

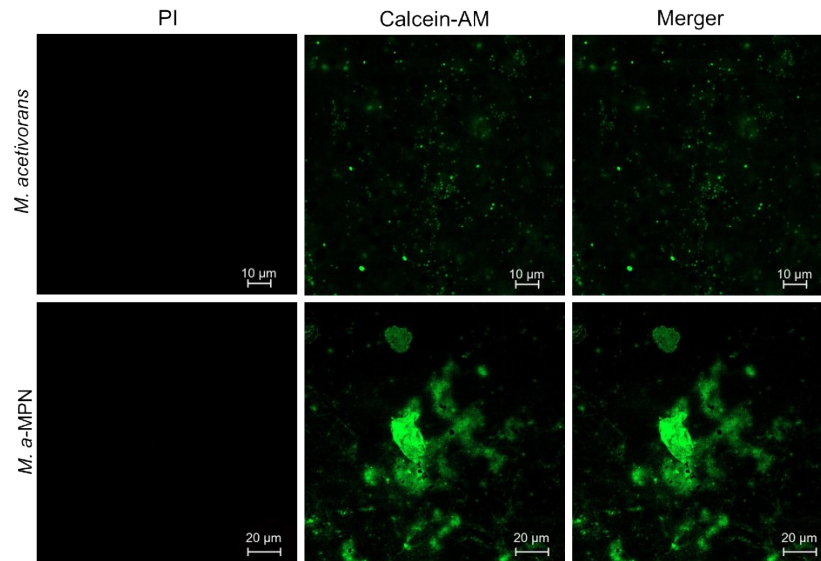


Figure S3. Confocal fluorescence microscopy images of *M. acetivorans* and MPN-coated *M. acetivorans* (*M. a-MPN*), depicting cell viability. Red fluorescence (PI dye) indicates dead cells, while green (Calcein-AM) signifies all cells.

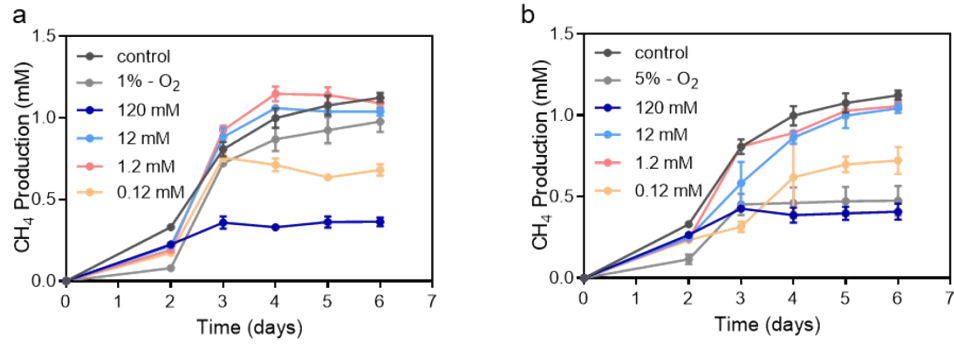


Figure S4. *M. acetivorans*-coated MPN optimization. Methane production profiles by MPN-coated *M. acetivorans*, with coatings prepared with Fe²⁺ (0.12, 1.2, 12 and 120 mM) and TA (0.012, 0.12, 1.2 and 12 mM) under (a) 1% and (b) 5% oxygen. The methanogenesis of the MPN-coated *M. acetivorans* (MPN coating: 0.12 mM TA, 1.2 mM FeCl₂·4H₂O) was not significantly different from that of the control group regardless of the oxygen concentration (1% or 5%). MPN coatings prepared at concentrations of 0.12 mM TA and 1.2 mM FeCl₂·4H₂O were used as the encapsulation material in subsequent experiments. Values are the mean of three biological replicates. Data are shown as the mean ± SD (*n* = 5).

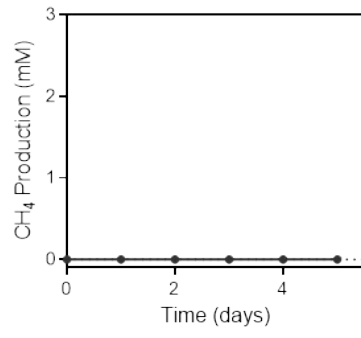


Figure S5. Methanogenic curve of MPN incubated in an anaerobic environment.

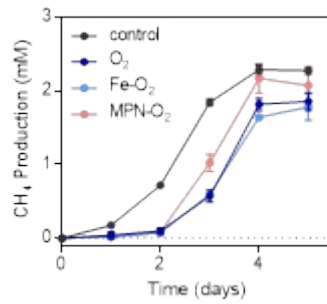


Figure S6. Methanogenic curves of *M. acetivorans* incubated in an anaerobic environment after 7 days of incubation under normal (anaerobic) (control), 21% oxygen (O₂), 1.2 mM FeCl₂ and 21% oxygen (Fe-O₂), and MPN (0.12 mM TA, 1.2 mM FeCl₂·4H₂O) and 21% oxygen (MPN-O₂) conditions. Values are the mean of three biological replicates. Data are shown as the mean ± SD ($n = 5$).

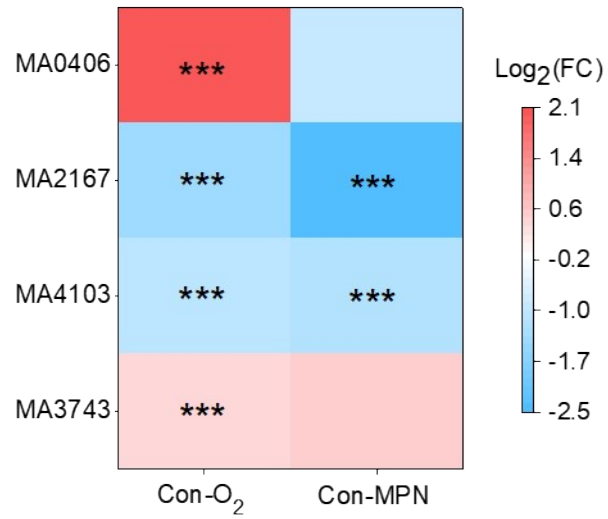


Figure S7. Transcript abundance analysis of methanogenic genes in *M. acetivorans* in 21% O₂ relative to anaerobic control (Con-O₂), and MPN-coated *M. acetivorans* in 21% O₂ relative to anaerobic control (Con-MPN), presented as log₂(fold change) values. **P* < 0.05, ***P* < 0.01, ****P* < 0.001 (negative binomial distribution).

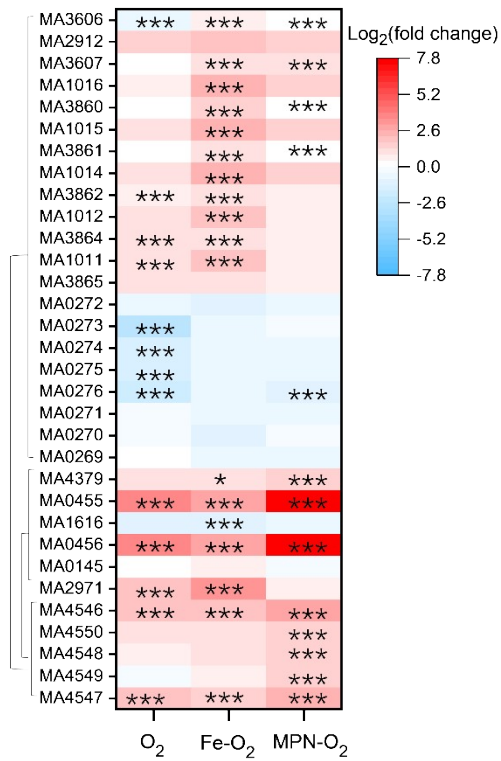


Figure S8. Transcript abundance analysis of methanogenic genes in *M. acetivorans* cultured for 3 days in 21% oxygen (O₂), 1.2 mM FeCl₂ and 21% oxygen (Fe-O₂), or MPN (0.12 mM TA, 1.2 mM FeCl₂·4H₂O) and 21% oxygen (MPN-O₂), presented as log₂(fold change) values. **P* < 0.05, ***P* < 0.01, ****P* < 0.001 (negative binomial distribution).

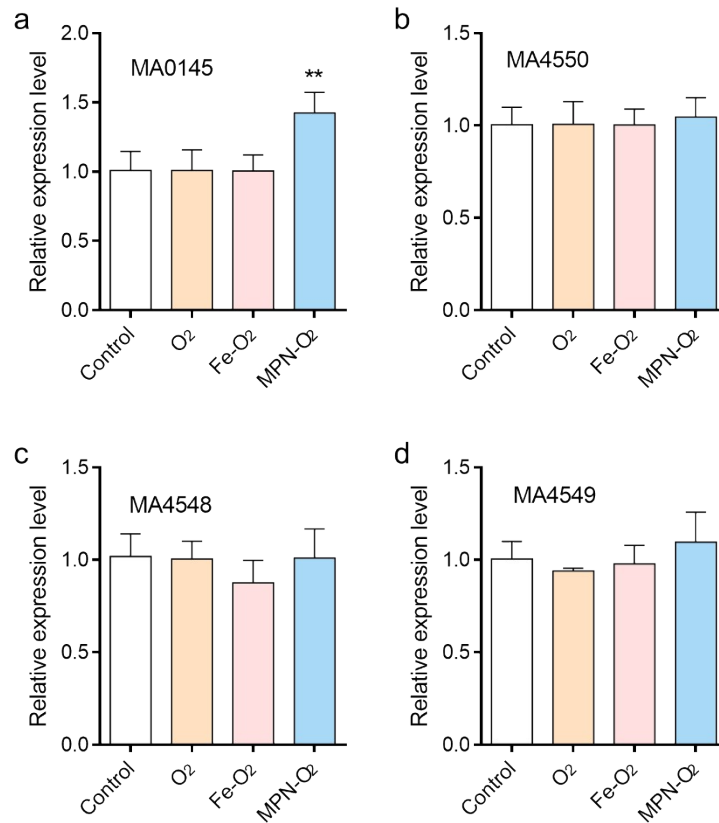


Figure S9. qPCR validation of methanogenesis metabolism-related genes (a) MA0145, (b) MA4550, (c) MA4548, and (d) MA4549 in *M. acetivorans* cultured for 2 days under normal (anaerobic) (Control), 21% oxygen (O₂), 1.2 mM FeCl₂ and 21% oxygen (Fe-O₂), or MPN (0.12 mM TA, 1.2 mM FeCl₂·4H₂O) and 21% oxygen (MPN-O₂) conditions. Values are the mean of three biological replicates. Data are shown as the mean ± SD ($n = 3$), * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$ (two-tailed t -test).

Table S1. Composition of the anaerobic medium used for *M. acetivorans* culture

Component	Concentration (g/L)
NaCl	23.400
NaHCO ₃	4.000
Yeast extract	1.000
MgSO ₄ ·7H ₂ O	9.450
Na ₂ HPO ₄ ·12H ₂ O	1.510
NH ₄ Cl	1.000
KCl	0.800
CaCl ₂	0.106
Nitrilotriacetic acid	1.500
MgSO ₄ ·7H ₂ O	3.000
MnSO ₄ ·H ₂ O	0.500
NaCl	1.000
FeSO ₄ ·7H ₂ O	0.100
CoSO ₄ ·7H ₂ O	0.100
CaCl ₂ ·2H ₂ O	0.100
ZnSO ₄ ·7H ₂ O	0.100
CuSO ₄ ·5H ₂ O	0.010
AlK(SO ₄) ₂	0.010
H ₃ BO ₃	0.010
Na ₂ MoO ₄ ·2H ₂ O	0.010

Table S2. Thickness of MPN films formed at different times for O₂ and methanol separation studies

Time (h)	O ₂ separation study				Methanol separation study			
	2	4	6	14	0.5	1	2	12
Thickness (nm)	25 ± 4	48 ± 2	57 ± 4	157 ± 7	15 ± 1	16 ± 2	26 ± 4	142 ± 19

Table S3. Transcript analysis for genes identified in methanogenic metabolic pathway

Locus tag	Gene name	Log ₂ (fold change)			P-value		
		O ₂	Fe-O ₂	MPN-O ₂	O ₂	Fe-O ₂	MPN-O ₂
MA3606	AckA	-0.563471555	0.722207389	0.099228931	0.000222645	0.000488025	0.574970085
MA2912	AcsM3	1.540896511	2.089510428	1.613786086	9E-17	6.95E-15	1.44E-13
MA1016	CdhA1	0.822552025	2.450884118	1.465549063	7.96E-08	3.14E-25	2.28E-12
MA3860	CdhA2	0.104182662	1.330185667	0.408697394	0.569065996	3.43E-09	0.026174295
MA1015	CdhB1	1.071049515	2.364207674	1.65772676	0.000000042	3.83E-25	2.53E-13
MA3861	CdhB2	0.18842842	1.053562086	0.431857651	0.251005127	0.000000948	0.024607331
MA1014	CdhC1	0.938302858	2.401984094	1.550963431	1.61E-08	8.42E-23	2.55E-13
MA3862	CdhC2	0.610378654	1.039316878	0.516442156	0.000124931	0.0000034	0.00434895
MA1012	CdhD1	1.209248571	2.006765403	0.664670792	9.15E-15	1.86E-19	0.000975137
MA3864	CdhD2	0.890785447	1.03886697	0.571213354	9.81E-09	0.00000201	0.001429694
MA1011	CdhE1	1.22818701	1.942232696	0.552241895	7.95E-13	2.51E-18	0.006280797
MA3865	CdhE1	1.023396596	1.076517769	0.484849788	2.22E-10	0.00000103	0.00877315
MA0272	MtrA	-0.757144872	-0.959753575	-0.597236581	0.00000061	0.000815034	0.001311405
MA0273	MtrB	-2.632324963	-0.637810907	-0.432808801	5.27E-44	0.110732609	0.068961098
MA0274	MtrC	-1.624733411	-0.75099505	-0.433382665	3.29E-25	0.016464814	0.02511098
MA0275	MtrD	-1.419614577	-0.772684655	-0.600011352	9.35E-20	0.013158603	0.00138382
MA0276	MtrE	-1.923246723	-0.659882041	-1.255293456	5.13E-34	0.036341447	1.21E-10
MA0271	MtrF	-0.10296484	-0.853116023	-0.725350205	0.577338976	0.028291374	0.004760933
MA0270	MtrG	-0.368165079	-0.919824395	-0.426445834	0.13827599	0.010924336	0.072081631
MA0269	MtrH	0.113023908	-0.831108748	-0.462087641	0.482500549	0.001009268	0.007408783
MA4379	MtaA	0.996532505	1.1097553	1.424043752	5.16E-10	0.000000366	5.29E-14
MA0455	MtaB	3.49457005	2.741394376	7.758330485	2E-86	2.79E-16	3.43E-220
MA1616	MtaB1	-0.971260754	-1.112445169	-0.861890699	0.00000139	0.000158874	0.000121517
MA0456	MtaC	3.703494974	2.715281367	7.786107409	1.48E-91	6.17E-17	1.1E-213
MA0145	MtmC1	0.100513737	0.698552752	-0.160808743	0.588218066	0.005048935	0.526145703
MA2971	MtmC	1.868896431	3.270518716	0.808425902	2.66E-16	3.99E-14	0.02705676
MA4546	McrA	1.89587011	1.752963405	2.74845581	7.67E-26	2.97E-10	1.3E-35
MA4550	McrB	0.968565084	0.878715954	1.389506794	7.17E-09	0.001852266	2.63E-12

MA4548	Mcrc	0.668057164	0.878810454	1.647918392	0.0000379	0.000642359	1.62E-19
MA4549	McrcD	-0.270360511	0.794411823	1.338704035	0.091856609	0.002964413	7.22E-13
MA4547	McrcG	1.750885758	1.315501124	2.413948104	1.18E-21	0.0000115	1.56E-26
MA2167	Isf	-1.363878	-0.756775	-2.504374	1.48829E-11	0.00044	2.8016E-21
MA0406	Isf	2.125658	1.374984	-0.886991	1.3758E-07	0.00277	0.211682
MA3743	FprA	0.400687	0.823335	0.480182	0.000958	6.94182E-05	0.062069
MA4103	\	-0.995635	-1.11847	-1.153404	2.17531E-08	1.704E-07	4.48234E-07

Table S4. Primers used in this study^a

Primer name	Sequence (5'→3')
Arc349f	GYGCASCAGKCGMGAAW
Arc806r	GGACTACVSGGGTATCTAAT
ma1616-qpcrf	TACGACTGTGCTCTGATGAATG
ma1616-qpcrr	CTATCGCCTCTCCTACTCTGTAA
ma4379-qpcrf	CACACCAACCCTGAACTGAT
ma4379-qpcrr	GACAAGGACAGTAAGGCAGTAG
ma0145-qpcrf	GAAGCTGCTGAGGTCTTTCTAC
ma0145-qpcrr	GGTTCCTTCCTCTCCTTCTACT
ma4550-qpcrf	AACGAAGGTCTTGGCTTCTC
ma4550-qpcrr	GATACCGGACTGCTCATAGATTG
ma4548-qpcrf	GTGAGTGTGCTTGTACTCTACTC
ma4548-qpcrr	CATTTCAATCTGTGCGACTTCTAC
ma4549-qpcrf	TTCAGATCGGAGATCAGGTTATTG
ma4549-qpcrr	GGAGCATCTTGTTCGCATACT

^a “f” indicates forward primer and “r” indicates reverse primer. A one-letter code for degenerate bases is used according to the International Union of Biochemistry (IUB), where Y stands for C, T; K for G, T; S for C+G; W for A, T; and M for A, C.