

Table S1. Microbial genomes analyzed in this study.

Organism name	Genome size (Mb) (Accession no.)	Taxon*	Niche**	Description
<i>Pth Pelotomaculum thermopropionicum</i>	3.0 (AP009389)	F	SB	Thermophile
<i>Chy Carboxydotherrmus hydrogenoformans</i>	2.4 (CP000141)	F		Thermophile
<i>Moth Moorella thermoacetica</i>	2.6 (CP000232)	F	HA***	Thermophile
<i>Tte Thermoanaerobacter tengcongensis</i>	2.7 (AE008691)	F	FB	Thermophile
<i>Swol Syntrophomonas wolfei</i>	2.9 (CP000252)	F	SB	
<i>Cth Clostridium thermocellum</i>	3.8 (CP000568)	F	FB	Thermophile
<i>Cac Clostridium acetobutylicum</i>	4.1 (AE001437)	F	FB	
<i>Lla Lactococcus lactis</i>	2.5 (AE005176)	F		
<i>Lpl Lactobacillus plantarum</i>	3.3 (AL935263)	F		
<i>Efa Enterococcus faecalis</i>	3.4 (AE016830)	F		
<i>Bsu Bacillus subtilis</i>	4.2 (AL009126)	F		
<i>Wsu Wolinella succinogenes</i>	2.1 (BX571656)	EP		
<i>Sac Syntrophus aciditrophicus</i>	3.2 (CP000252)	DP	SB	
<i>Sfu Syntrophobacter fumaroxidans</i>	5.0 (CP000478)	DP	SB	
<i>Dde Desulfovibrio desulfuricans</i>	3.7 (CP000112)	DP	SRB	
<i>Gsu Geobacter sulfurreducens</i>	3.8 (AE017180)	DP		
<i>Zmo Zymomonas mobilis</i>	2.1 (AE008692)	AP		
<i>Pae Pseudomonas aeruginosa</i>	6.3 (AE004091)	GP		
<i>Tde Treponema denticola</i>	2.8 (AE017226)	S	FB	
<i>Pac Propionibacterium acnes</i>	2.6 (AE017283)	A	FB	
<i>Bfr Bacteroides fragilis</i>	5.2 (CR626927)	B	FB	
<i>Tma Thermotoga maritima</i>	1.9 (AE000512)	T		Hyperthermophile
<i>Msth Methanosaeta thermophila</i>	1.9 (CP000477)	EA	MA	Thermophile
<i>Mtth Methanothermobacter thermautotrophicus</i>	1.8 (AE000666)	EA	MA	Thermophile
<i>Mhu Methanospirillum hungatei</i>	3.5 (CP000254)	EA	MA	
<i>Mma Methanococcus maripaludis</i>	1.7 (BX950229)	EA	MA	Marine organism
<i>Mac Methanosarcina acetivorans</i>	5.8 (AE010299)	EA	MA	

*F, Firmicutes; EB, Epsilonproteobacteria; DP, Deltaproteobacteria; AP, Alphaproteobacteria; GP, Gammaproteobacteria; S, Spirochaeta; A, Actinobacteria; T, Thermotoga; EA, Euryarchaeota.

**SB, syntrophic bacteria; HA, homoacetogen; FB, fermentative bacteria; SRB, sulfate-reducing bacteria; MA, methanogenic archaea. Niches were indicated for organisms whose close relatives have been detected in anaerobic biodegradation processes (e.g., references 1-3).

****Moth* is a homoacetogen converting CO₂ plus H₂ to acetate and vice versa (4), and closely related organisms have been detected in methanogenic digesters (3). Production of CO₂ plus H₂ suggests that this organism is capable of forming syntrophic interaction with methanogens.

References

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