Supplementary Material

Comparative analysis of Type IV pilin in *Desulfuromonadales*

Chuanjun Shu ***[1]*, *Ke Xiao*** ***[1]*, *Qin Yan*** ***[1]*, *and Xiao Sun*** ***[1*]***

[1]State Key Laboratory of Bioelectronics, School of Biological Science and Medical Engineering, Southeast University, Nanjing, China

*** Correspondence:** *Xiao Sun, Email:* *xsun@seu.edu.cn*.

Supplementary Figures and Tables

Table S1. The detail information of complete genome sequence of eleven bacteria

	GC	Gene	Protein	Submit	Update
G． metallireducens GS-15	59.48%	3608	3520	2005/10/27	2015/2/4
G． sulfurreducens PCA	60.90%	3711	3430	2002/2/14	2014/12/22
G． uraniireducens Rf4	54.20%	4506	4417	2007/5/11	2015/2/4
G． lovleyi SZ	54.77%	3685	3614	2008/6/5	2015/2/4
G． bemidjiensis Bem	60.30%	4055	3942	2008/8/19	2015/2/4
G． sp. M21	60.50%	4143	4047	2009/7/7	2015/2/24
G． daltonii FRC-32	53.50%	3828	3750	2009/1/27	2015/2/4
G． sp. M18	61.20%	4522	4415	2011/1/27	2015/2/4
G． sulfurreducens KN400	61.00%	3610	3289	2010/6/17	2014/12/17
P. carbinolicus DSM 2380	55.10%	3386	3167	2012/9/13	2015/2/4
P. propionicus DSM 2379	59.00%	3598	3481	2006/10/31	2015/2/4

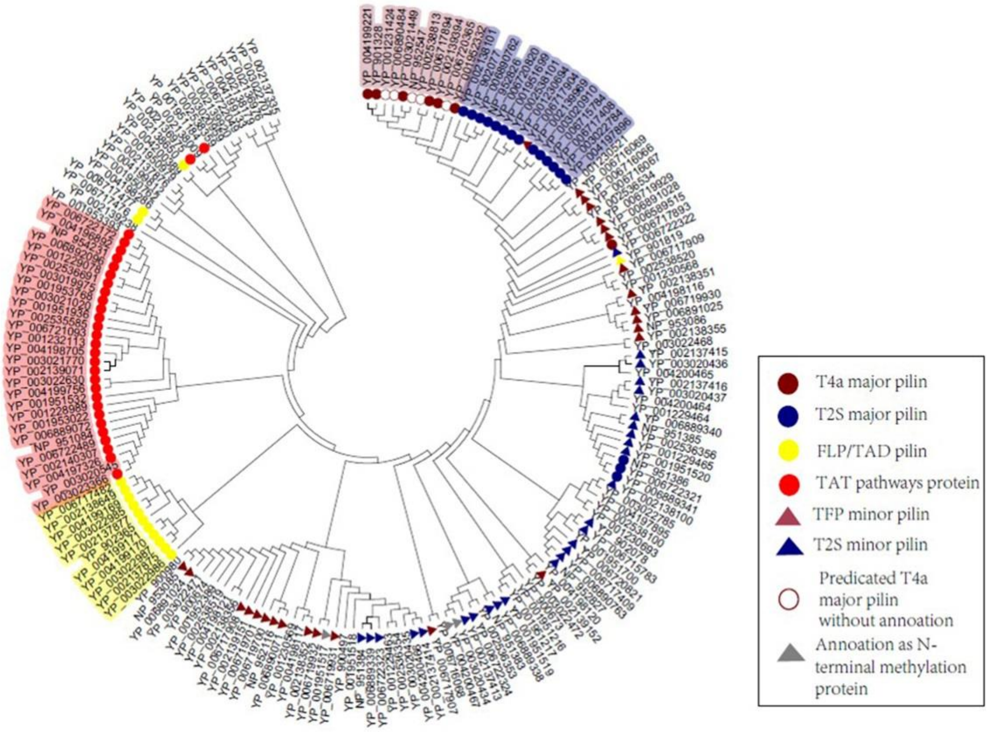


Figure S1. The cluster diagram of 183 predicted pilins

In this picture, there is a sign before pilin's names means that it have corresponding annotation. Otherwise, the pilin may be have no annotation or is a false positive protein. The brown and blue shad areas cluster in one type. The brown shade area is T4a major pilins, blue shad area is T2S major pilins. The solid round in above shad areas means this pilin have annotation, however the hollow circle means no annotation. The yellow and red shade areas corresponding to non-TFP/T2S pilin.

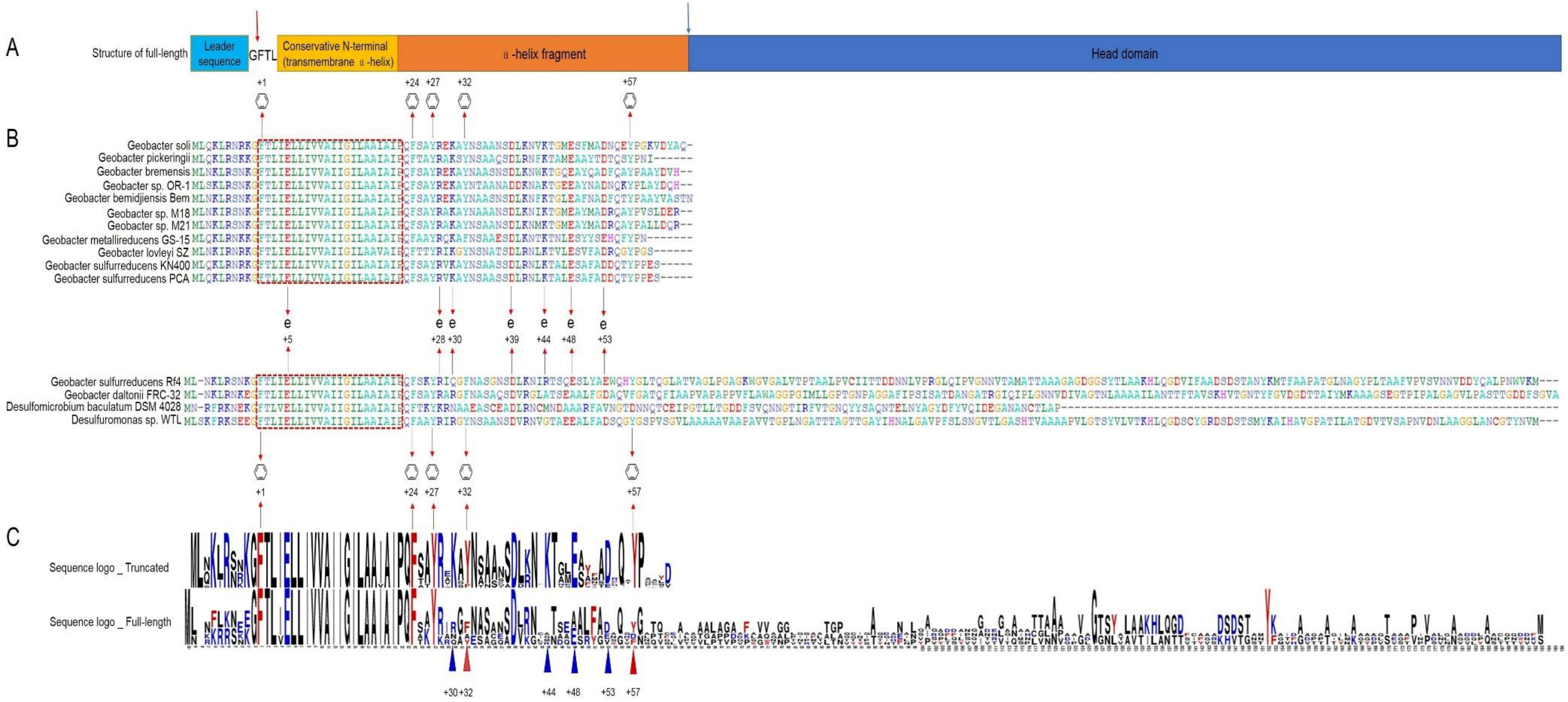


Figure S2. The conservative amino acids in GSU1496-like pilins and full-length pilins of Geobacter

A: The sequence construction of full-length pilin. The red arrow indicates the peptidase splice site, and the blue is the crack site of full-length change to truncate. B: The trans-membrane domain is shown in red dotted frame. ⬡ and **+** are employed for highlighting the sites of conserved aromatic amino acids and charged amino acids respectively. C: The sequence logo of truncated pilins (GSU1496-like) and full-length pilins in *Geobacter*. The red and blue triangles represent aromatic amino acids and charged amino acids respectively.

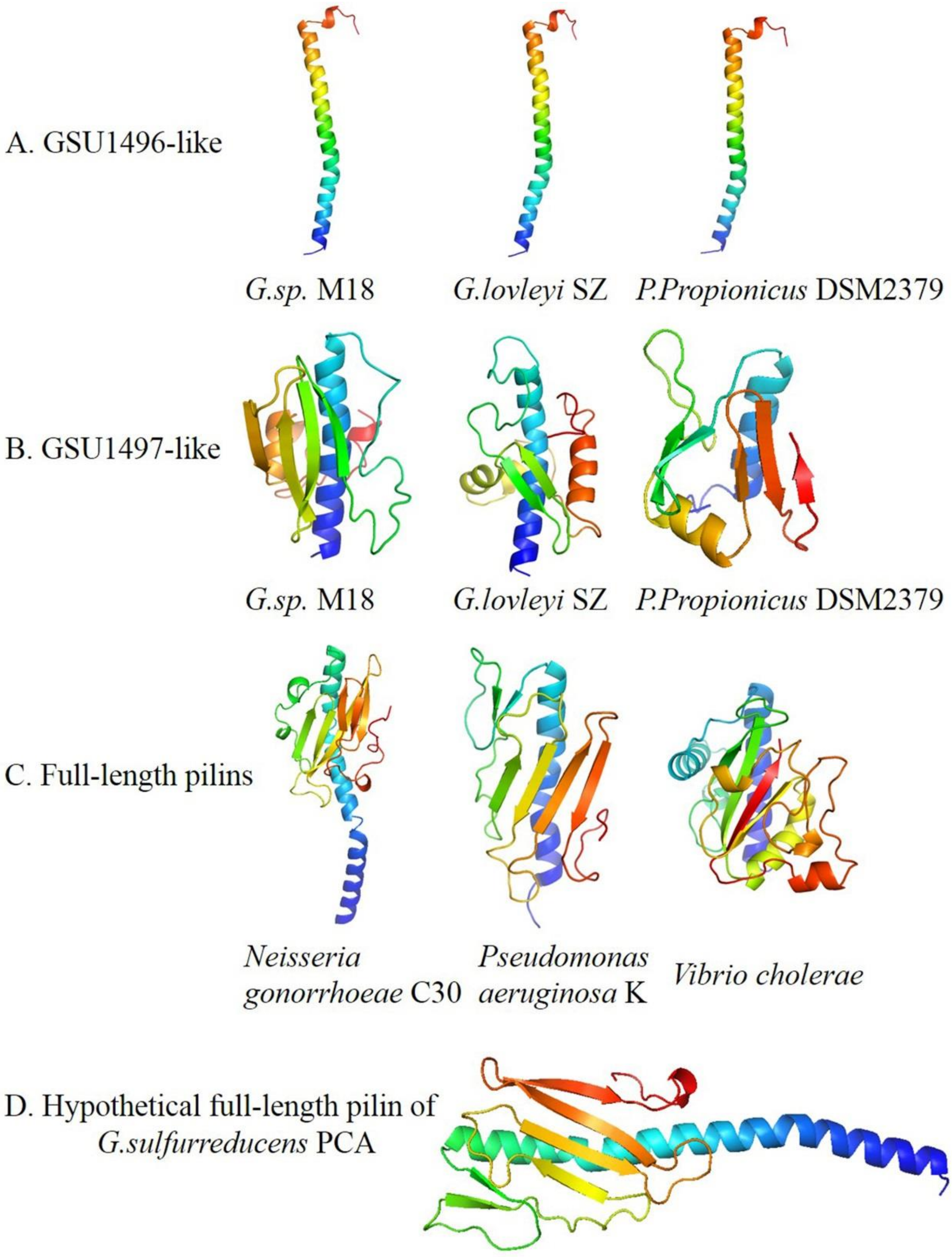


Figure S3. Structures of GSU1496-like pilins, GSU1497-like proteins, and full-length pilins

The structure of GSU1496-like pilin and GSU1497-like protein were predicted by ab initio calculations. The distribute of figureS3 as follows: The first line structures were GSU1496-like pilins, next were GSU1497-like proteins, and then were full-length pilins, last was hypothesis full-length pilin of PCA. The words were the brief name of bacteria that write in the corresponding structure directly below.

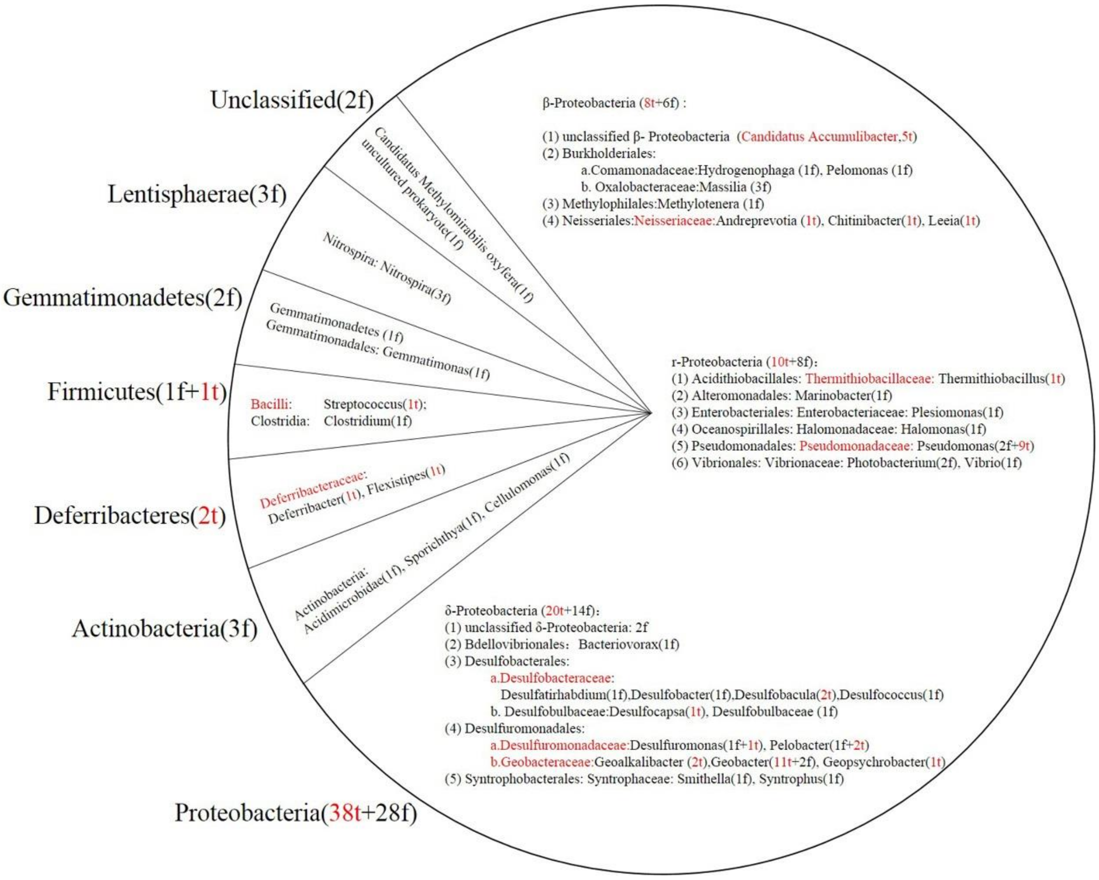
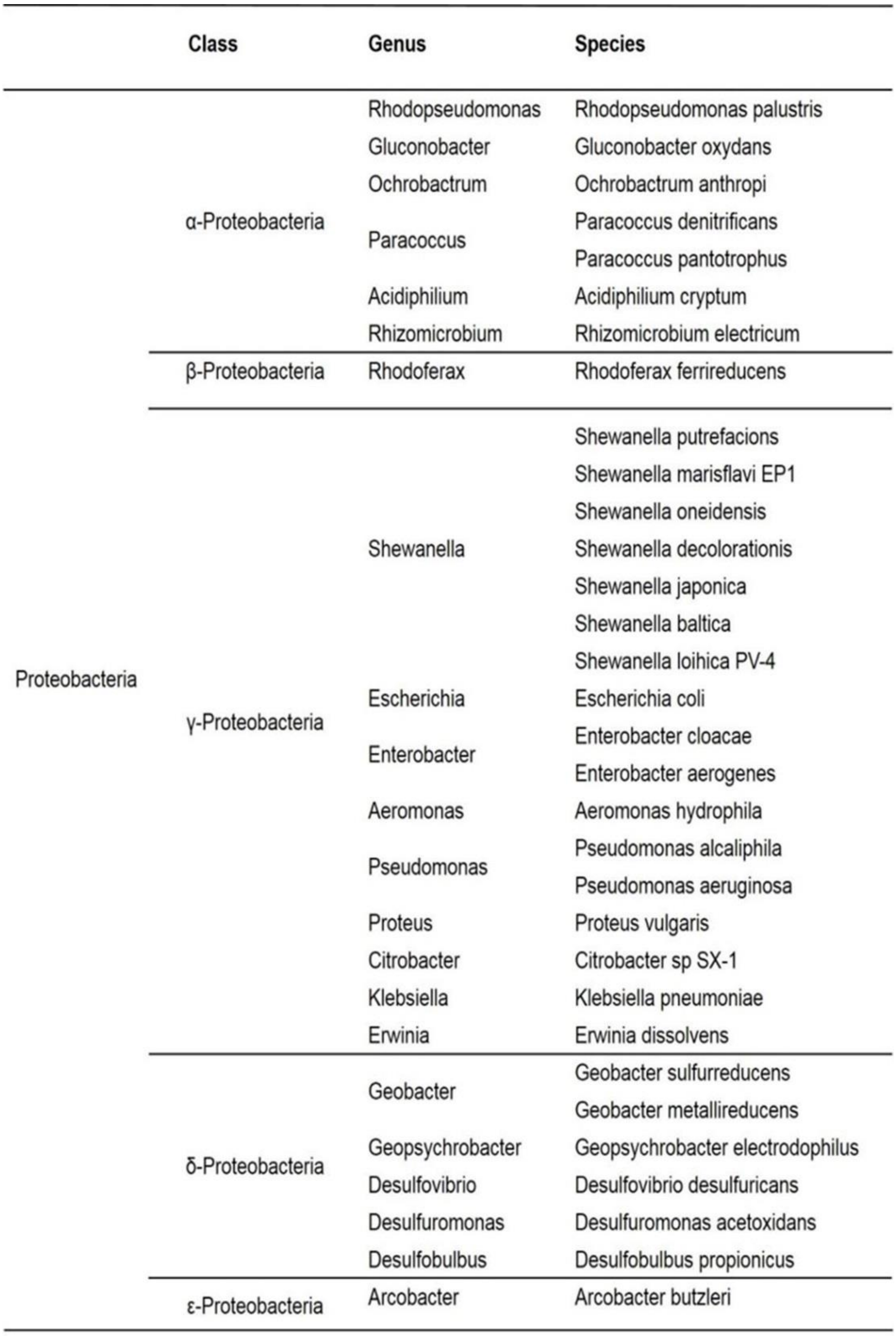


Figure S4. The species of bacterium for phylogenetic analysis

The names of phylum are marked on the outside of circle. The pie chart shows the detailed classification information. Numbers in brackets represent the strain distribution. In brackets, how many t mean how many truncated pilins, the number of f means that the number of full-length pilins. Red letters indicate the distribution of truncated pilins.

Table S2. The species of electricigens in Proteobacteria



	Class	Genus	Species	
Proteobacteria	α-Proteobacteria	Rhodopseudomonas	Rhodopseudomonas palustris	(1)
		Gluconobacter	Gluconobacter oxydans	(2)
		Ochrobactrum	Ochrobactrum anthropi	(3)
		Paracoccus	Paracoccus denitrificans	(4)
			Paracoccus pantotrophus	(5)
		Acidiphilium	Acidiphilium cryptum	(6)
		Rhizomicrobium	Rhizomicrobium electricum	(7)
	β-Proteobacteria	Rhodoferax	Rhodoferax ferrireducens	(8)
	γ-Proteobacteria	Shewanella	Shewanella putrefacions	(9)
			Shewanella marisflavi EP1	(10)
			Shewanella oneidensis	(11)
			Shewanella decolorationis	(12)
			Shewanella japonica	(13)
			Shewanella baltica	(14)
			Shewanella loihica PV-4	(15)
		Escherichia	Escherichia coli	(3)
		Enterobacter	Enterobacter cloacae	(16)
			Enterobacter aerogenes	(17)
		Aeromonas	Aeromonas hydrophila	(8)
		Pseudomonas	Pseudomonas alcaliphila	(18)
			Pseudomonas aeruginosa	(3)
		Proteus	Proteus vulgaris	(19)
		Citrobacter	Citrobacter sp SX-1	(20)
		Klebsiella	Klebsiella pneumoniae	(21)
		Erwinia	Erwinia dissolvens	(22)
	δ-Proteobacteria	Geobacter	Geobacter sulfurreducens	(23)
			Geobacter metallireducens	(24)
		Geopsychrobacter	Geopsychrobacter electrodophilus	(3)
		Desulfovibrio	Desulfovibrio desulfuricans	(3)
		Desulfuromonas	Desulfuromonas acetoxidans	(8)
		Desulfobulbus	Desulfobulbus propionicus	(25)
	ε-Proteobacteria	Arcobacter	Arcobacter butzleri	(26)

Table S3. The detail of truncated pilins in phylogenetic tree

Function	Genus/ species	Strains	Isolated from	Aerobism	Cluster	Class
phosphorus removal	Candidatus Accumulibacter sp. (27)	SK-02	wastewater	Anaerobic	2	β
		BA-94	wastewater	Anaerobic	2	β
		BA-92	wastewater	Anaerobic	2	β
		phosphatis	wastewater	Anaerobic	2	β
sulfate reducer	Desulfobacula	toluolica Tol2 (28)	marine sediment	Anaerobic	2	δ
		sp. TS(29)	oil-contaminated tidal flat	Anaerobic	3	δ
	Desulfocapsa sulfexigens	DSM 10523(30)	tidal flat	Anaerobic	3	δ
	Desulfuromonas sp.(31)	TF	marine sediments	Anaerobic	4	δ
		WTL	marine sediments	Anaerobic	4	δ
	Desulfomicrobium baculatum	DSM 4028(32)	water-saturated manganese carbonate ore	Anaerobic	4	δ
	Thermithiobacillus(33)	tepidarius	industrial anaerobic sludge pool	Anaerobic	2	γ
naphthalene degrader, crude oil hydrocarbons degrader	Pseudomonas(34)	stutzeri CCUG 29243	polluted marine sediments	facultative anaerobic	3	γ
		Stutzeri MF28	Mantle fluid	facultative anaerobic	3	γ
		stutzeri	polluted marine sediments	facultative anaerobic	3	γ
	Pseudomonas	sp. 10B238(35)	deep-sea sediment	Anaerobic	3	γ
		sp. ML96(36)		Aerobic	3	γ
		sp. BAY1663			3	γ
		mendocina(37)		Aerobic	3	γ
nitrogen oxides remover	Pseudomonas	mendocina DLHK(38)	Biotrickling reactor	Aerobic	3	γ

Degradation of the steroid compound cholate	Pseudomonas	sp. Chol1(39)	soil	facultative anaerobic	3	γ
Metal-reducing bacterium	Geobacter	metallireducens GS-15(40)	freshwater sediments of the Potomac River	Anaerobe	4	δ
		lovleyi SZ(41)	creek sediment	Anaerobe	4	δ
		pickeringii(42)	Sedimentary Kaolin Deposits	Anaerobe	4	δ
		sulfurreducens KN400(43)	a fuel cell	Anaerobe	4	δ
		sulfurreducens PCA(44)	surface sediments	Anaerobe	4	δ
		bremensis(45)	freshwater mud samples	Anaerobe	4	δ
		bemidjiensis Bem(46)	subsurface sediments	Anaerobe	4	δ
		sp. OR-1(47)	paddy soil	Anaerobe	4	δ
		soli(48)	forest soil	Anaerobe	4	δ
		sp. M21(49)	experiment	Anaerobic	4	δ
		sp. M18		Anaerobic	4	δ
	Pelobacter	seleniigenes(50)	wetland	Anaerobic	4	δ
		propionicus DSM 2379(51)	Marine muds	Anaerobic	4	δ
	Geoalkalibacter	ferrihydriticus DSM 17813(52)	bottom sediments of soda lakes	Anaerobic	4	δ
		subterraneus(53)	production water of oilfield	Anaerobic	4	δ
	Geopsychrobacter	Electrodiphilus (54)	Marine Sediment	Anaerobic	4	δ
	Andreprevotia chitinilytica(55)		forest soil	aerobic	2	β
	Leeia oryzae(56)		rice-field soil	aerobic	2	β
	Chitinibacter sp. ZOR0017(57)		soil	aerobic	2	β
	Streptococcus pneumoniae(58)		blood	facultative anaerobic	3	

sulfur-, nitrate- and arsenate-reducing thermophile	Deferribacter	Flexistipes sinusarabici DSM 4947(59)	sea water	anaerobic	4	
	Deferribacter	Deferribacter desulfuricans SSM1(60)	deep-sea	anaerobic	4	
Denitrification, phosphorus removal	Candidatus Accumulibacter sp.	SK-12(61)	wastewater	Anaerobic	5	β

Table S4. The detail of full-length pilins in phylogenetic tree

Function	Genus/ species	Strains	Isolated from	Aerobism	Lineage/cluster	Class
moderately halophilic	Halomonadaceae	Halomonas salina(62)	hypersaline soil	aerobic	L1	γ
	Oxalobacteraceae(63)	Massilia sp.Root335	Soil/air/water	aerobic	L1	β
		Massilia sp. JS1662	Soil/air/water	aerobic	L1	β
		Massilia sp. Root1485	Soil/air/water	aerobic	L1	β
degrade starch	Alteromonadaceae	Marinobacter salarius(64)	sea water	aerobic	L1	γ
denitrificans	Methylophilaceae	Methylotenera sp. L2L1(65)	lake	aerobic	L1	β
conditioned pathogen	Pseudomonas(66)	Pseudomonas aeruginosa CI27	widely distributed in nature	aerobic	L1	γ
		Pseudomonas aeruginosa C3719	widely distributed in nature	aerobic	L1	γ
Reduces Fe(III) Indirectly via Sulfide Production	Desulfuromonadales	Pelobacter carbinolicus DSM 2380(67, 68)	freshwater sediments, sewage sludge	anaerobic	L1	δ
Degradation of chlorobenzene	Enterobacteriaceae	Plesiomonas sp. ZOR0011(69)	freshwater	aerobic	L1	γ
bioluminescent microbe	Vibrionaceae	Photobacterium leiognathi(70)	warm tropical waters	facultative anaerobe	L1	γ
bioluminescent microbe	Vibrionaceae	Photobacterium angustum(71)	Sea Water	aerobic	L1	γ
Hydrogen-Oxidizing Bacteria	Comamonadadeae	Hydrogenophaga sp. Root209(72)	activated sludge	aerobic	L1	β
convert nitrite into nitrogen gas	Comamonadaceae	Pelomonas sp. Root1237(73)	water	aerobic	L1	β
acetate-oxidizing bacterium	Clostridiales	Clostridium homopropionicum DSM 5847	anoxic digested sludge	anaerobic(74)	L2/cluster 1	

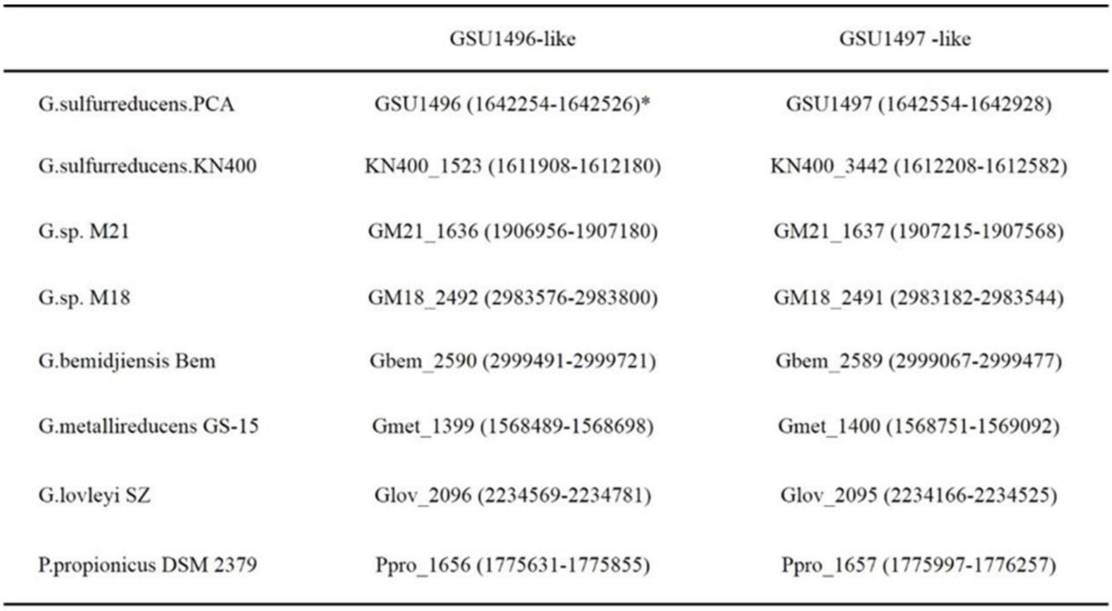
unreported	Gemmatimonadetes	Gemmatirosa kalamazoonesis	soil(75)	aerobic	L2/cluster 1	
polyphosphate-accumulating micro-organism	Gemmatimonadetes(76)	Gemmatimonas sp. SG8 28	soil	aerobic	L2/cluster 1	
Nitrite oxidation into nitrates	Nitrospiraceae	Nitrospira defluvii(77)	marine recirculation aquaculture system/water	aerobic	L2/cluster 1	
iron-oxidizing	Actinobacteria	Ferrimicrobium acidiphilum DSM 19497	Acid mine drainage waters	aerobic(78)	L2/cluster 1	
unreported	Sporichthyaceae	Sporichthya polymorpha	soil(79)	facultative anaerobic	L2/cluster 1	
cellulose-degrading	Cellulomonadaceae	Cellulomonas sp. FA1(80)	plant material	facultative anaerobic	L2/cluster 1	
biocontrol agent	Bacteriovoracaceae	Bacteriovorax sp. Seq25 V	Marine/salt-water	aerobic(81)	L2/cluster 1	δ
butyrate-oxidizing, sulfate-reducing	Desulfobacteraceae	Desulfatirhabdium butyrativorans(82)	anaerobic bioreactor	anaerobic	L2/cluster 1	δ
sulfate-reducing	Desulfobacteraceae	Desulfococcus multivorans DSM 2059	soil	anaerobic(83)	L2/cluster 1	δ
Nitrite oxidation into nitrates	Nitrospiraceae	Nitrospira moscoviensis	water(84)	aerobic	L2/cluster 1	
		Nitrospira sp. 2	water(85)	aerobic	L2/cluster 1	
sulfate reducer	Desulfobacteraceae	Desulfobacter postgatei 2ac9	brackish water	anaerobe(86)	L2/cluster 2	δ
oxidation of sulfide to sulfate	proteobacterium	delta proteobacterium MLMS-1	Mono Lake(87)	anaerobe	L2/cluster 2	δ
Sulfidogenic activity	Deltaproteobacteria	Desulfurivibrio alkaliphilus AHT 2	Natrun lakes(88)	anaerobe	L2/cluster 2	δ
unknown	Deltaproteobacteria	Deltaproteobacteria bacterium SM23 61	unknown	anaerobic	L2/cluster 2	δ
hydrogen-using microorganism	syntrophaceae	Syntrophus aciditrophicus SB(89)	sewage treatment plant	anaerobic	L2/cluster 2	δ

unknown	syntrophaceae	Smithella sp. F21	unknown	anaerobic(90)	L2/cluster 2	δ
sulfate-reducing	Desulfuromonas	Desulfuromonas sp. WTL(91)	marine sediments	anaerobic	L2/cluster 4	δ
Metal-reducing bacterium	Geobacter	Geobacter uraniireducens Rf4(92)	subsurface sediment	anaerobic	L2/cluster 4	δ
sulfur-reducing	Desulfomicrobiaceae	Desulfomicrobium baculatum DSM 4028(93)	water-saturated manganese carbonate ore	anaerobic	L2/cluster 4	δ
Metal-reducing bacterium	Geobacter	Geobacter daltonii FRC-32(94)	contaminated subsurface	anaerobic	L2/cluster 4	δ
Methanotroph; nitrite-reducing Denitrification	unclassified	Candidatus Methylomirabilis oxyfera(95)	freshwater	anaerobic	L2/cluster 5	

Table S5. The homology gene of GSU1497 predicted by PSI-BLAST

	gene	length	score	consistency%	similarity%	E-values
G.sulfurreducens PCA	GSU1497	124	357	100.0	100.0	7.0e-32
G.sulfurreducens KN400	KN400_3442	124	357	100.0	100.0	7.0e-32
G.sp. M18	GM18_2491	120	280	20.0	40.0	6.0e-23
G.bemidjiensis Bem	Gbem_2589	136	270	21.0	42.0	8.0e-22
G.sp.M21	GM21_1637	117	268	18.0	39.0	1.0e-21
G.lovleyi SZ	Glov_2095	119	236	20.0	45.0	7.0e-18
G.metallireducens GS-15	Gmet_1400	113	232	27.0	43.0	2.0e-17
P.propionicus DSM 2379	Ppro_1657	86	201	19.0	43.0	8.0e-14

Table S6. Locus tags and location of GSU1496-like pilins and GSU1497-like proteins



	GSU1496-like	GSU1497 -like
G.sulfurreducens.PCA	GSU1496 (1642254-1642526)*	GSU1497 (1642554-1642928)
G.sulfurreducens.KN400	KN400_1523 (1611908-1612180)	KN400_3442 (1612208-1612582)
G.sp. M21	GM21_1636 (1906956-1907180)	GM21_1637 (1907215-1907568)
G.sp. M18	GM18_2492 (2983576-2983800)	GM18_2491 (2983182-2983544)
G.bemidjiensis Bem	Gbem_2590 (2999491-2999721)	Gbem_2589 (2999067-2999477)
G.metallireducens GS-15	Gmet_1399 (1568489-1568698)	Gmet_1400 (1568751-1569092)
G.lovleyi SZ	Glov_2096 (2234569-2234781)	Glov_2095 (2234166-2234525)
P.propionicus DSM 2379	Ppro_1656 (1775631-1775855)	Ppro_1657 (1775997-1776257)

*The value in bracket represent the location in genome of nucleotide acid that encoding GSU1496-like pilin or GSU1497-like protein.

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