
Recent advance of microbial mercury methylation in the environment

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Supplementary Material

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Table S1. Confirmed mercury-methylated strains.

metabolism	Phylum	Family	strains	<i>HgcAB</i>	number	MeHg production/ (%MeHg) ^c	pmoles MeHg/mg protein ^d	References
SRB	<i>Firmicutes</i>	<i>Peptococcaceae</i>	<i>Desulfosporosinus acidiphilus</i> SJ4	+ ^a	DSM 22704	1.1%	1.0	(Gilmour et al., 2013)
			<i>Desulfitobacterium dehalogenans</i>	+	DSM 9161	0.6%	0.3	(Gilmour et al., 2013)
			<i>Desulfosporosinus youngiae</i>	+	DSM 17734	0.6%	0.6	(Gilmour et al., 2013)
	<i>Proteobacteria</i>	<i>Desulfovibrionaceae</i>	<i>Desulfovibrio</i> sp. X2	+	N.A. ^b	62.0%	N.A.	(Gilmour et al., 2011; Gilmour et al., 2013)
			<i>Desulfovibrio desulfuricans</i> ND132	+	N.A.	53.0%	22.9	(Gilmour et al., 2011; Gilmour et al., 2013)
			<i>Desulfovibrio alkalitolerans</i>	+	DSM 16529	9.0%	N.A.	(Graham et al., 2012)
			<i>Desulfovibrio aespoeensis</i> Aspo-2	+	DSM 10631	11.0%	N.A.	(Graham et al., 2012)

<i>Desulfovibrio</i>					
<i>desulfuricans</i> subsp.	N.A.	ATCC 3541	N.A.	N.A.	(King et al., 2001)
<i>desulfuricans</i>					
<i>Desulfovibrio</i>					(Compeau and
<i>desulfuricans</i> LS	N.A.	N.A.	N.A.	N.A.	Bartha, 1985)
<i>Desulfovibrio</i> sp. T2	N.A.	N.A.	27.0%	N.A.	(Graham et al., 2012)
<i>Desulfovibrio</i>					
<i>sulfodismutans</i>	N.A.	DSM 3696	1.9%	N.A.	(Graham et al., 2012)
ThAcO1					
<i>Desulfovibrio</i>					(Graham et al., 2012)
<i>psychrotolerans</i>	N.A.	DSM 19430	15.0%	N.A.	
<i>Desulfovibrio</i>					(Limper et al., 2008)
<i>intestinalis</i>	N.A.	DSM 11275	<0.1%	N.A.	
<i>Desulfovibrio</i>					(Lin and Jay, 2007)
<i>desulfuricans</i> M8	N.A.	N.A.	N.A.	N.A.	
<i>Desulfovibrio</i>					(Lin and Jay, 2007)
<i>desulfuricans</i> M9	N.A.	N.A.	N.A.	N.A.	
<i>Desulfovibrio</i>					(Bridou et al., 2011)
<i>africanus</i> ADR 13	N.A.	N.A.	N.A.	N.A.	

<i>Desulfobacteraceae</i>	<i>Desulfovibrio caledoniensis</i> BerOc1	N.A.	N.A.	N.A.	N.A.	(Bridou et al., 2011)
	<i>Desulfovibrio</i> sp. J2	+	KT 750867	N.A.	N.A.	(Cao et al., 2021; Gilmour et al., 2013)
	<i>Desulfovibrio africanus</i> str. Walvis Bay	+	ATCC 19997	N.A.	N.A.	(Brown et al., 2011)
	<i>Desulfovibrio africanus</i> Benghazi	+	DSM 2603	N.A.	8.0	(Ekstrom et al., 2003)
	<i>Desulfovibrio inopinatus</i> HHQ20	+	AF177276	1.32%	N.A.	(Goni-Urriza et al., 2020)
	<i>Desulfovibrio longus</i> SEBR2582	+	AY359867	0.51%	N.A.	(Goni-Urriza et al., 2020)
	<i>Desulfovibrio oxyclinae</i> P1B	+	U33316	0.80%	N.A.	(Goni-Urriza et al., 2020)
	<i>Desulfosarcina variabilis</i> 3be13	N.A.	DSM 2060	N.A.	N.A.	(Benoit et al., 2001)
	<i>Desulfococcus</i>	+	DSM 2059	N.A.	N.A.	(King et al., 2001)

	<i>multivorans</i> 1be1					
	<i>Desulfobacter</i> sp. BG8	N.A.	N.A.	N.A.	N.A.	(King et al., 2001)
	<i>Desulfobacterium</i> sp. BG33	N.A.	N.A.	N.A.	N.A.	(King et al., 2001)
	<i>Desulfobacterium</i> <i>autotrophicum</i> HRM 2	N.A.	DSM 3382	N.A.	N.A.	(Ekstrom et al., 2003)
	<i>Desulfobulbus</i> <i>propionicus</i> MUD	N.A.	DSM 6523	N.A.	N.A.	(Ekstrom et al., 2003)
	<i>Desulfomicrobium</i> <i>salsuginis</i> ADR 21	N.A.	DSM 19190	N.A.	N.A.	(Ranchou- Peyruse et al., 2009)
<i>Desulfomicrobia</i> <i>ceae</i>	<i>Desulfomicrobium</i> <i>salsuginis</i> ADR 28	N.A.	N.A.	N.A.	N.A.	(Ranchou- Peyruse et al., 2009)
	<i>Desulfomicrobium</i> <i>escambiense</i>	+	DSM 10707	N.A.	N.A.	(Feng et al., 2022)
	<i>Desulfomicrobium</i> <i>baculatum</i> X	+	DSM 4028	34.1%	26.6	(Gilmour et al., 2013)

							(King et al., 2001;
		<i>Desulfobulbus propionicus</i> 1pr3	+	DSM 2032	N.A.	N.A.	Moreau et al., 2015)
	<i>Desulfohalobiacae</i>	<i>Desulfonatronospira thiodismutans</i> ASO3-1	+	DSM 19093	29.6%	N.A.	(Gilmour et al., 2013)
	<i>Syntrophobacteraceae</i>	<i>Desulfacinum hydrothermale</i>	N.A.	DSM 13146	N.A.	N.A.	(Malcolm et al., 2010)
IRB	<i>Proteobacteria</i>	<i>Geobacter sulfurreducens</i> PCA	+	DSM 12127	14.0%	N.A.	(Kerin et al., 2006)
		<i>Geobacter metallireducens</i> GS-15	+	DSM 7210	5.0%	N.A.	(Kerin et al., 2006)
	<i>Geobacteraceae</i>	<i>Geobacter bemidjiensis</i> Bem	+	DSM 16622	74.9%	625.0	(Gilmour et al., 2013)
		<i>Geobacter daltonii</i> FRC-32	+	DSM 22248	30.0%	N.A.	(Gilmour et al., 2013)
		<i>Geobacter</i> sp. strain CLFeRB	N.A.	N.A.	N.A.	N.A.	(Fleming et al., 2006)

<i>Firmicutes</i>	<i>Desulfuromonadaceae</i>	<i>Geobacter hydrogenophilus</i> H2	N.A.	DSM 13691	0.5%	N.A.	(Kerin et al., 2006)
		<i>Geobacter anodireducens</i> SD-1	N.A.	CP0 14963	N.A.	N.A.	(Liu et al., 2018)
		<i>Desulfuromonas</i> sp. DDH964	+	CPO 15080	N.A.	N.A.	(Guo et al., 2021; Liu et al., 2018)
	<i>Peptococcaceae</i>	<i>Desulfuromonas palmitatas</i>	+	DSM 12391	N.A.	N.A.	(Kerin et al., 2006)
Methanogens	<i>Euryarchaeota</i>	<i>Methanolobus tindarius</i>	+	DSM 2278	3.6%	1.5	(Gilmour et al., 2013)
		<i>Methanomethylovorans hollandica</i>	+	DSM 15978	3.0%	10.4	(Gilmour et al., 2013)
		<i>Methanomicrobium liminatans</i> GKZPZ	+	DSM 4140	0.6%	N.A.	(Gilmour et al., 2018)
		<i>Methanoregula palustris</i> E1-9c	+	DSM 19958	15.0%	N.A.	(Gilmour et al., 2018)
		<i>Methanomassiliicoccus luminyensis</i> B10	+	DSM 25720	53.4%	N.A.	(Podar et al., 2015)
		<i>Methanocella paludicola</i> SANAE	+	DSM 17711	8.6%	N.A.	(Gilmour et al., 2018)

		<i>Methanocorpusculaceae</i>	<i>Methanocorpusculum bavaricum</i>	+	DSM 4179	0.2%	N.A.	(Gilmour et al., 2018)
		<i>Methanospirillaceae</i>	<i>Methanospirillum hungatei</i> JF-1	+	DSM 864	64.2%	0.1	(Gilmour et al., 2018; Yu et al., 2018)
Others	Firmicutes	<i>Ruminococcaceae</i>	<i>Ethanoligenens harbinense</i> YUAN-3	+	DSM 18485	0.9%	1.2	(Gilmour et al., 2013)
		<i>Syntrophomonadaceae</i>	<i>Dethiobacter alkaliphilus</i> AHT 1	+	DSM 19026	5.4%	46.4	(Gilmour et al., 2013)
		<i>Veillonellaceae</i>	<i>Acetoneuma longum</i> APO-1	+	DSM 6540	7.8%	0.9	(Gilmour et al., 2013)
	Proteobacteria	<i>Syntrophaceae</i>	<i>Syntrophus aciditrophicus</i> SB	+	DSM 26646	20.5%	191.1	(Gilmour et al., 2013)
		<i>Pseudomonadaceae</i>	<i>Pseudomonas fluorescens</i> TGRB2	+	KU 954349	1.4%	N.A.	(Cao et al., 2021)
			<i>Pseudomonas putida</i> TGRB4	-	MF 996382	0.9%	N.A.	(Cao et al., 2021; Xiang et al., 2020)
		<i>Enterobacteriaceae</i>	<i>Raoultella terrigena</i> TGRB3	- ^e	MK 102091	0.4%	N.A.	(Feng et al., 2022)

	<i>Syntrophobacter</i>	+	DSM 2805	N.A.	4.4	(Yu et al., 2018)
<i>Syntrophobacter</i>	<i>wolinii</i>					
<i>aceae</i>	<i>Syntrophobacter</i>	+	DSM 16706	N.A.	N.A.	(Yu et al., 2018)
	<i>sulfatireducens</i>					

- a. The *hgcAB* gene was confirmed by the molecular biological method.
- b. Data not available.
- c. %MeHg: The percentage of MeHg production in pure medium.
- d. pmoles MeHg/mg protein: Mercury methylation potential normalized to protein content.
- e. Strains do not with the *hgcAB* gene

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