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2 genus **Methyloparacoccus**

3 **Bram Vekeman**

4 Max Planck Institute for Marine Microbiology, Bremen, Germany

5

6 **Keywords:** aerobic, methanotroph, freshwater, mesophile, neutrophile

7

8 **Abstract:**

9 Cells are aerobic, Gram-negative, non-motile coccoids, 0.8-1.5 µm. Cells occur singly
10 with a diplococcoid tendency. Reproduce by normal cell division. Resting stages are
11 not observed. Obligate utilizers of methane and methanol as sole carbon and energy
12 source. Methane is oxidized by a particulate methane monooxygenase (pMMO), the
13 soluble (sMMO) and alternative particulate (pXMO) form of this enzyme are absent.
14 Cells possess the typical intracytoplasmic membrane system for
15 gammaproteobacterial methanotrophs forming bundles of membrane vesicles. No
16 growth occurs on compounds containing carbon-carbon bonds. Atmospheric nitrogen
17 is not fixed. Cells are neutrophilic, growing between pH 5.8-9, with an optimal pH of
18 6.3-6.8 and mesophilic, non-thermotolerant, growing between 20-37°C, optimal
19 growth temperature 25-33°C. The dominant cellular fatty acids are **C_{16:1w7c}** (52-54%)
20 and **C_{16:0}** (24-25%). So far only isolated from pond water in Africa and Japan.
21 Belongs to the Gammaproteobacteria as part of the Order Methylococcales, Family
22 Methylococcaceae.

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25 Defining publication: Hoefman, van der Ha, Iguchi, Yurimoto, Sakai, Boon,
26 Vandamme, Heylen and De Vos, 2014, 2105^{VP}

27 Entymology: Me.thy.lo.pa.ra.coc'cus. N.L. n. methylum (from French méthyle), the
28 methyl group; N.L. pref. methylo-, pertaining to the methyl radical; Gr. prep. para,
29 beside, alongside of, near, like; N.L. masc. n. coccus (from Gr. n. kokkos), a grain or
30 berry; N.L. masc. n. Methyloparacoccus referring to a methyl-using organism
31 resembling but clearly different from other methyl-using cocci

32

33 **Generic definition:**

34 **Strict aerobic, Gram-negative, non-motile coccoids**, 0.8-1.5 μm . Cells occur
35 singly with a **diplococcoid tendency**. Reproduce by normal cell division. **Resting**
36 **stages are not observed. Obligate utilizers of methane and methanol as sole**
37 **carbon and energy source**. Methane is oxidized by a **particulate methane**
38 **monooxygenase (pMMO)**, the soluble (sMMO) and alternative particulate (pXMO)
39 form of this enzyme are absent. Cells possess the typical intracytoplasmic membrane
40 system for gammaproteobacterial methanotrophs forming bundles of membrane
41 vesicles. **No growth occurs on compounds containing carbon-carbon bonds.**
42 The *nifH* gene is absent confirming the inability to fix atmospheric nitrogen. Cells are
43 **neutrophilic**, growing between pH 5.8-9, with an optimal pH of 6.3-6.8 and
44 **mesophilic, non-thermotolerant**, growing between 20-37°C, optimal growth
45 temperature 25-33°C. The dominant cellular fatty acids are **C_{16:1w7c}** (52-54%) and
46 **C_{16:0}** (24-25%). So far only isolated from pond water in Africa and Japan. Belongs to
47 the Gammaproteobacteria as part of the Order Methylococcales, Family
48 Methylococcaceae.

49 The mol% G+C of the DNA is: 65.6% (Tm).

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53 **Type species:**

54 Type species: **Methyloparacoccus murrellii** Hoefman, van der Ha, Iguchi,
55 Yurimoto, Sakai, Boon, Vandamme, Heylen and De Vos, 2014, 2105^{VP}

56 Number of species with validated names: 1

57

58 **Family classification:**

59 Methylococcaceae (fbm00225)

60

61 Further Descriptive Information

62 **Cell morphology and ultrastructure.**

63 Cells of these bacteria are gram-negative, nonmotile coccoids that occur singly with a
64 diplococcoid tendency similar to what was observed by Foster and Davis (1966) in
65 *Methylococcus capsulatus* cultures (Fig. 1). They reproduce by binary fission.
66 *Methyloparacoccus* species contain standard type I intracytoplasmic membrane
67 systems appearing as bundles of vesicular disks (Fig. 1), a typical feature of the
68 gammaproteobacterial methanotrophs (Hanson and Hanson, 1996). Similarly as was
69 observed for the type strain of *Methylogaea oryzae* (Geymonat et al., 2011), cells
70 display low and high electron density inclusions (Fig. 1). These inclusions possibly
71 represent poly- β -hydroxybutyrate and glycogen granules, respectively. Both are
72 known to be produced by several methanotrophs (Helm et al., 2006; Heyer et al.,
73 2005; Whittenbury et al., 1970). *Azotobacter*-type cysts are not observed and cells
74 are neither heat resistant nor desiccation resistant.

75

76 **Colonial and cultural characteristics.**

77 Liquid cultures of *Methyloparacoccus* species display white turbidity. A surface
78 pellicle is not formed. All *Methyloparacoccus* strains available form colonies on solid

79 media made with high purity grade agar. One-week old colonies are round, convex,
80 white to creamy colored and smooth with entire edges. Older colonies remain white
81 but might display a distinct green shine. Cells exhibit catalase and cytochrome c
82 oxidase activities.

83

84 **Nutrition and growth conditions.**

85 *Methyloparacoccus* species are obligate methane oxidizing bacteria (MOB), with their
86 sole carbon and energy source restricted to methane and methanol. Medium
87 amended with 0.1% methanol does not support growth, however strains grow on
88 methanol fumes as sole carbon source when incubated on diluted Nitrate Mineral
89 Salts medium (dNMS) plates with a few drops of methanol placed on the inside lid of
90 the petri dish. Methane is oxidized to methanol by a pMMO. The genes encoding a
91 sMMO or a pXMO are absent.

92 Nitrogen sources include ammonium, nitrate, nitrite, urea, proline, aspartate, arginine
93 and yeast extract. Strains exhibit a high tolerance to the inorganic nitrogen species
94 up to 100mM, 40mM and 5mM for ammonium, nitrate and nitrite respectively
95 (Hoefman et al., 2014). The *nifH* gene could not be detected and isolates could not
96 grow in nitrogen-free medium at high (21%) or low (2.1%) oxygen tension. Strains
97 produce nitrous oxide from ammonium and nitrate (only under low oxygen tension).
98 Nitrite is only formed as an intermediate during the production of nitrous oxide from
99 nitrate (Hoefman et al., 2014).

100 Growth factors are not required for the cultivation of *Methyloparacoccus* strains,
101 however growth of some strains can be improved by the addition of cobalamin during
102 cultivation (Iguchi et al., 2011).

103 These methanotrophs are mesophilic, non thermotolerant growing at temperatures
104 between 20°C and 37°C (optimum: 25-33°C), neutrophilic with pH between 5.8 to 9

105 (optimum 6.3-6.8) and salt resistant up to additions of 100 mM NaCl. Under optimal
106 conditions in dNMS, the doubling time is in the range of 15-28h.

107

108 **Chemotaxonomic characteristics.**

109 Phospholipid fatty acid analysis identified C_{16:1}w7c and C_{16:0} as the two major fatty
110 acids. This finding is consistent with the other members of the *Methylococcus-*
111 *Methylocaldum-Methylogaea-Methylomagnum* clade. The major fatty acid of
112 *Methyloparacoccus* and *Methylomagnum* is C_{16:1}w7c, while for the other members of
113 the clade C_{16:0} is more dominant than C_{16:1}w7c (Table 1).

114

115 **Ecology.**

116 Ecological insights concerning the genus *Methyloparacoccus* are limited. Currently,
117 only one described species is reported in this genus that was isolated from pond
118 water. Based on molecular studies, using the *pmoA* gene sequences as a molecular
119 marker, members of the genus *Methyloparacoccus* are restricted to aquatic
120 ecosystems, occurring preferentially in the sediment (Knief, 2015).

121 Thus, based on molecular insights and the neutrophilic, mesophilic and moderate
122 halotolerant nature of the currently available strains, it is highly probable that the
123 habitat for the genus *Methyloparacoccus* is confined to freshwater ecosystems.

124

125 **Enrichment and Isolation Procedures**

126 *Methyloparacoccus* strains can be enriched and isolated from aerobic water samples
127 in aquatic environments. Ideally a small amount of sample is collected and added to
128 NMS liquid mineral medium in serum vials (Iguchi et al., 2011). Alternatively, a diluted
129 Ammonium Mineral Salts (dAMS) medium, which is a modification of dNMS,
130 (Hoefman et al., 2012a) amended with 2 mM NH₄Cl as sole nitrogen source, 4 mM

131 phosphate buffer and 10 μM CuSO_4 can be used. Additionally cobalamin might be
132 added to stimulate the selective enrichment of *Methyloparacoccus* strains, however
133 this seems to be strain specific (Iguchi et al., 2011). After inoculation, methane
134 should be aseptically added to the headspace to achieve a headspace gas-mixing
135 ration of about 25%. Next, the serum vials should be incubated up to five weeks at
136 20°C-28°C while shaking. Alternatively a serial dilution series of the environmental
137 samples can made where the highest dilution found positive for the oxidation of
138 methane can then be used to further enrich and isolate the methane oxidizers.
139 Successful enrichments of *Methyloparacoccus* strains develop a white turbidity in
140 combination with a methane and oxygen consumption and carbon dioxide
141 production.

142 To date, MOB are still mostly isolated via the classical plate method. For this end,
143 growth from the enrichments is serially diluted onto solid media prepared with high
144 purity agar or gellum gum and incubated under a 1:1 methane/air atmosphere at 20-
145 28°C. Single colonies from these spread plates should be picked and transferred to
146 liquid media to evaluate the potential of the colony to utilize methane. Moreover, as
147 MOB cross-feed non-methanotrophs with methane-derived carbon (Krause et al.,
148 2017), methanotrophic enrichments are highly contaminated with non-
149 methanotrophic bacteria and thus one or several liquid enrichment steps, followed by
150 a serial dilution onto plates (Dedysh et al., 2004; Dunfield et al., 2003; Heyer et al.,
151 2005; Tsubota et al., 2005; Warttinen et al., 2006) are required to obtain a pure
152 culture. This makes the classical plate procedure very laborious and time consuming
153 without guarantee for successfully obtaining a pure MOB culture. Alternatively, a
154 miniaturized extinction culturing (Hoefman et al., 2012a) procedure in 96-well plates
155 can be applied. This miniaturized approach allows straightforward isolation
156 preventing the need to transfer cultures over plates and in the case of fast-growing

157 methanotrophs yielding an immediate monocultures making laborious purification
158 redundant (Hoefman et al. 2012a). MOB purity can be evaluated by (i) colony
159 morphology, (ii) phase-contrast microscopy, and (iii) absence of growth on ten-fold
160 diluted trypticase soy agar and dNMS plates supplemented with 0.1% glucose, 0.1%
161 fructose and 0.1% yeast extract under air.

162 Maintenance Procedures

163 Strains can be routinely cultured at 20°C-28°C in (d)NMS or (d)AMS medium (liquid
164 or solidified with high purity agar) with a modified copper concentration (10 μM Cu^{2+})
165 under a CH_4 :air atmosphere in gastight flasks (20% methane in air) or jars (CH_4 :air,
166 1:1). Liquid cultures are best incubated while shaking (100rpm). Periodic
167 subcultivation should be performed every 1.5-2 months. For short term storage (up to
168 several months) cultures can be kept at low metabolic rates (4°C, under a
169 methane/air atmosphere). However, continuous subcultivation and storage at low
170 temperature of the cultures requires periodic maintenance, time and physical space.
171 Therefore, mid to long term storage (>1 months) is recommended to prevent the risk
172 of contamination and loss of authenticity of the culture over time. All methanotrophic
173 strains can be long term cryopreserved without a significant loss in viability and
174 culturability using 1% trehalose in ten-fold diluted trypticase soy broth as
175 preservation medium and 5% DMSO as cryoprotectant (Hoefman et al., 2012b).
176 Additional cryopreservation and lyophilization conditions for long term storage of
177 methanotrophic bacteria are described by Hoefman et al. (2012b).

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182 Differentiation of the genus *Methyloparacoccus* from other genera

183 Phenotypic characteristics distinguishing *Methyloparacoccus* from other members of
184 the *Methylococcus-Methylocaldum-Methylogaea-Methylomagnum* clade are shown in
185 table2.

186 The cells of *Methyloparacoccus murrellii* are clearly different in appearance when
187 compared to *Methylogaea*, *Methylocaldum* and *Methylomagnum* cells, since rod-
188 shapes, pleomorphism and motility are absent for all *Methyloparacoccus* strains. The
189 non-motile cocci most closely resemble the appearance of cells of *Methylococcus*
190 strains. Although *Methylococcus* and *Methylocaldum* strains are thermotolerant,
191 *Methyloparacoccus* strains, *Methylogaea oryzae* E10^T and *Methylomagnum*
192 *ishizawai* RS11D-Pr^T are not. Further distinctions between *Methyloparacoccus*
193 strains and *Methylococcus* strains include the sensitivity to 1% NaCl, sensitivity to
194 0.1% methanol and the absence of the *nifH* and *mmoX* genes, respectively, for
195 *Methyloparacoccus*. Further, *Methyloparacoccus* strains seem to be capable of
196 nearly complete methane oxidation when 1%, 0.1% or 0.01% methane are amended
197 to the headspace. In contrast, Knief and Dunfield (2005) found that the strains
198 *Methylococcus capsulatus* Bath and *Methylocaldum* sp. E10a, lost their methane
199 oxidation activity when incubated with 0.1% CH₄ in the headspace.

200

201 Taxonomic comments

202 16S rRNA gene based phylogenetic analysis indicates that *Methyloparacoccus*
203 *murrellii* is a member of the deep lineage of the *Methylococcus-Methylocaldum-*
204 *Methylogaea-Methylomagnum* clade included among gammaproteobacterial
205 methanotrophs within the family *Methylococcaceae* (Bowman et al., 1993). The
206 closest phylogenetic neighbors of *Methyloparacoccus* are methanotrophs belonging
207 to the genus *Methylomagnum* (93.8-94.4% sequence similarity). Despite their close

208 phylogenetic relationship they are phenotypically clearly distinct. The 16S rRNA gene
209 sequence results are in line with the phylogenetic analysis of the *pmoA* gene,
210 confirming that members of the genus *Methyloparacoccus* form a line of descent
211 different from members of the *Methylococcus-Methylocaldum-Methylogaea-*
212 *Methylomagnum* clade (Fig. 3).

213

214 **List of species of the genus *Methyloparacoccus***

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216 **1. *Methyloparacoccus murrellii***

217 Hoefman, van der Ha, Iguchi, Yurimoto, Sakai, Boon, Vandamme, Heylen and De
218 Vos, 2014, 2105^{VP}

219 *murrellii* of Murrell, named in honor of the British microbiologist Colin
220 Murrell, for his numerous contributions to expanding the knowledge on methanotroph
221 physiology, biochemistry, diversity and molecular ecology.

222 Displays all properties described for the genus *Methyloparacoccus*. In addition, cocci
223 have a diameter of 0.8 to 1.5 μm . Cells still display methane oxidation activity with
224 0.01 % CH_4 amended to the headspace. Cells grow optimally between 25°C to 33°C
225 at a pH between 6.3 and 6.8 and can utilize ammonium, nitrate, nitrite, urea, proline,
226 aspartate, arginine and yeast extract as sole nitrogen source. Cells grow with 0.58%
227 NaCl amended to the medium, but are sensitive to 1% NaCl additions.

228 Two currently available strains, R-49797^T (= LMG 27482^T = JCM 19379) and OS501
229 (=LMG 27483), of this species are isolated from a facultative waste stabilization, high
230 inorganic nitrogen containing pond in South Africa and the Inukai pond in Suita City,
231 Osaka, Japan respectively.

232 DNA G+C content (mol %): 65.6% (Tm).

233 Type strain: R-49797, LMG 27482, JCM 19379.

234 The EMBL/GenBank accession (16S rRNA gene): HF558990

235

236 **TABLES**

237

238 **Table 1:** Composition of cellular fatty acids distinguishing *Methyloparacoccus* strains from other genera within the *Methylococcus*-
 239 *Methylocaldum*-*Methylogaea*-*Methylomagnum* clade. Values are percentages of the total fatty acids.

Fatty acid	<i>Methyloparacoccus</i>	<i>Methylococcus</i>	<i>Methylogaea</i>	<i>Methylocaldum</i>	<i>Methylomagnum</i>
	<i>murrellii</i>	spp.*	<i>oryzae</i> [†]	spp. [‡]	<i>ishizawai</i> [§]
C _{12:0}	-	NR	2.11	0-0.10	NR
C _{14:0}	3.77-4.71	0.8-6.2	5.84	1.8-3.26	15.8
C _{15:1} W8c	0.29-0.34	NR	NR	NR	0.22
C _{15:0}	3.19-3.34	0-12.7	1.03	2.49-3.51	1.6
C _{16:1} W9c	5.14-6.45	-	7.36	NR	NR
C _{16:1} W7c [§]	52.4-54.2	10.6-45.9	10.33	43-46.8	47.3
C _{16:1} W5c	4.17-5.70	0-9.0	NR	0-0.24	-

C _{16:1}	-	-	-	11.9-46.77	-
C _{16:0}	23.7-24.8	33.5-56	62.05	43.22-64.99	19.6
C _{16:0} 3-OH	2.61-2.72	NR	2.93	0-0.37	1.8
iso-C _{16:0} 3-OH	-	NR	3.69	NR	NR
C _{17:0} cyclo	-	0-15.1	-	1.3-8.99	NR

-, not detected; NR, not reported

Data was extracted from * Bowman et al. (1993), † Geymonat et al. (2011), ‡ Knief et al. (2003), Eshinimaev et al. (2004), Takeuchi et al. (2014) and § Khalifa et al. (2015)

§ This peak in the chromatogram represents C_{16:1}w7c and/or iso-C_{15:0} 2-OH according to the MIDI system, however in this study the peak is assigned to C_{16:1}w7c since this fatty acid is common among the studied methanotrophs

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244 **Table 2:** Phenotypic characteristics distinguishing *Methyloparacoccus* strains from other genera within the *Methylococcus*-
 245 *Methylocaldum*-*Methylogaea*-*Methylomagnum* clade.

Characteristic	<i>Methyloparacoccus</i> <i>murrellii</i>	<i>Methylococcus</i> spp.*	<i>Methylogaea</i> <i>oryzae</i>[†]	<i>Methylocaldum</i> spp.[‡]	<i>Methylomagnum</i> <i>ishizawai</i>[§]
Cell shape	Cocci	Cocci-rods	Curved rods	Rods-pleomorphic	Rods
Cell size (µm)	0.8-1.5	0.8-1.5 x 1.0-1.5	0.5-0.7 x 2.0-2.2	0.4-1.2 x 1.0-2.0	2.0-4.0 x 1.5-2.0
Pigmentation	White	White to brown	White	Cream to Brown	White
Motility	-	Variable	-	+/-	+
Chain formation	-	-	NR	Variable	-
Cyst formation	-	+	-	+	+
Temperature range (°C)	20-37	28-55	20-37	20-62	20-37

Temperature					31-33
optimum (°C)	25-33	37-50	30-35	42-55	
pH range	5.8-9	5.5-9.0	5-8	6-8.5	5.5-9.0
pH optimum	6.3-6.8	NR	6.5-6.8	7.1-7.2	6.8-7.4
Tolerance to 1% NaCl	-	+	-	+/-	-
<i>nifH</i> presence	-	+	+	+ [§]	-
N ₂ Fixation	-	+	-	NR	-
sMMO	-	+	-	-	+
Methanol 0.1%	-	+	+	-	-
G+C content (mol%)	65.6	59-66	63.1	57-59.7	64.1

+, positive result; -, negative result; +/-, strain dependent result; NR, not reported

Data was extracted from * Bowman et al. (1993), † Geymonat et al. (2011), ‡ Bodrossy et al. (1997), Eshinimaev et al.

(2004), Takeuchi et al. (2014) and * Khalifa et al. (2015)

§ Data on *nifH* presence of type strains of *Methylocaldum* has not been reported, however *nifH* sequences of strains reported in (Eshinimaev et al., 2004) are available

247 **FIGURE CAPTIONS**

248

249 **Figure 1.** Electron micrographs of ultrathin sections of methane growing cells of
250 strain R-49797^T showing a cell shape resembling *Methylococcus* cultures. ICM,
251 intracytoplasmic membranes; PHB, poly-β-hydroxybutyrate. Bar, 0.2 μm.

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254 **Figure 2.** 16SrRNA gene-based neighbor joining tree (1348 nt alignment), showing
255 the position of *Methyloparacoccus murrellii* relative to other gammaproteobacterial
256 methanotrophs. An alphaproteobacterial methanotroph, *Methylocystis parvus* OBBP^T
257 (GenBank accession number Y18945), was used as an outgroup. Bootstrap values
258 (1000 data resamplings) lower than 50 % are not shown. Scale bar indicates the
259 evolutionary distance.

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262 **Figure 3.** *pmoA* gene-based neighbor joining tree (146 nt alignment), showing the
263 position of *Methyloparacoccus murrellii* relative to other gammaproteobacterial
264 methanotrophs. An alphaproteobacterial methanotroph, *Methylocystis parvus* OBBP^T
265 (GenBank accession number U31651), was used as an outgroup. Bootstrap values
266 (1000 data resamplings) lower than 50 % are not shown. Scale bar indicates the
267 evolutionary distance.

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299 **REFERENCES**

- 300 Bodrossy L, Holmes EM, Holmes AJ, Kovács KL and Murrell JC (1997) Analysis of
301 16S rRNA and methane monooxygenase gene sequences reveals a novel group
302 of thermotolerant and thermophilic methanotrophs, *Methylocaldum* gen. nov.
303 *Arch. Microbiol.* **168**: 493–503.
- 304 Bowman JP, Sly LI, Nichols PD and Hayward AC (1993) Revised Taxonomy of the
305 Methanotrophs: Description of *Methylobacter* gen. nov., Emendation of
306 *Methylococcus*, Validation of *Methylosinus* and *Methylocystis* Species, and a
307 Proposal that the Family *Methylococcaceae* Includes Only the Group I
308 Methanotrophs. *Int. J. Syst. Bacteriol.* **44**: 375–375.
- 309 Dedysh SN, Berestovskaya YY, Vasylieva LV, Belova SE, Khmelenina VN, Suzina
310 NE, Trotsenko YA, Liesack W and Zavarzin GA (2004) *Methylocella tundrae* sp.
311 nov., a novel methanotrophic bacterium from acidic tundra peatlands. *Int. J.*
312 *Syst. Evol. Microbiol.* **54**: 151–156.
- 313 Dunfield PF, Khmelenina VN, Suzina NE, Trotsenko YA and Dedysh SN (2003)
314 *Methylocella silvestris* sp. nov., a novel methanotroph isolated from an acidic
315 forest cambisol. *Int. J. Syst. Evol. Microbiol.* **53**: 1231–1239.
- 316 Eshinimaev BT, Medvedkova KA, Khmelenina VN, Suzina NE, Osipov GA, Lysenko
317 AM and Trotsenko YA (2004) New thermophilic methanotrophs of the genus
318 *Methylocaldum*. *Microbiology* **73**: 448–456.
- 319 Foster JW and Davis RH (1966) A methane-dependent coccus, with notes on
320 classification and nomenclature of obligate, methane-utilizing bacteria. *J.*
321 *Bacteriol.* **91**: 1924–1931.
- 322 Geymonat E, Ferrando L and Tarlera SE (2011) *Methylogaea oryzae* gen. nov., sp.
323 nov., a mesophilic methanotroph isolated from a rice paddy field. *Int. J. Syst.*
324 *Evol. Microbiol.* **61**: 2568–2572.

325 Hanson RS and Hanson TE (1996) Methanotrophic bacteria. *Microbiol. Rev.* **60**:
326 439–71.

327 Helm J, Wendlandt KD, Rogge G and Kappelmeyer U (2006) Characterizing a stable
328 methane-utilizing mixed culture used in the synthesis of a high-quality
329 biopolymer in an open system. *J. Appl. Microbiol.* **101**: 387–395.

330 Heyer J, Berger U, Hardt M and Dunfield PF (2005) *Methylohalobius crimeensis* gen.
331 nov., sp. nov., a moderately halophilic, methanotrophic bacterium isolated from
332 hypersaline lakes of Crimea. *Int. J. Syst. Evol. Microbiol.* **55**: 1817–1826.

333 Hoefman S, Van Der Ha D, Boon N, Vandamme P, De Vos P and Heylen K (2014)
334 Niche differentiation in nitrogen metabolism among methanotrophs within an
335 operational taxonomic unit. *BMC Microbiol.* **14**: 1–11.

336 Hoefman S, van der Ha D, De Vos P, Boon N and Heylen K (2012a) Miniaturized
337 extinction culturing is the preferred strategy for rapid isolation of fast-growing
338 methane-oxidizing bacteria. *Microb. Biotechnol.* **5**: 368–378.

339 Hoefman S, van Hoorde K, Boon N, Vandamme P, de Vos P and Heylen K (2012b)
340 Survival or revival: Long-term preservation induces a reversible viable but non-
341 culturable state in methane-oxidizing bacteria. *PLoS One* **7**.

342 Iguchi H, Yurimoto H and Sakai Y (2011) Stimulation of methanotrophic growth in
343 cocultures by cobalamin excreted by rhizobia. *Appl. Environ. Microbiol.* **77**:
344 8509–8515.

345 Khalifa A, Lee CG, Ogiso T, Ueno C, Dianou D, Demachi T, Katayama A and
346 Asakawa S (2015) *Methylomagnum ishizawai* gen. nov., sp. nov., a mesophilic
347 type i methanotroph isolated from rice rhizosphere. *Int. J. Syst. Evol. Microbiol.*
348 **65**: 3527–3534.

349 Knief C (2015) Diversity and habitat preferences of cultivated and uncultivated
350 aerobic methanotrophic bacteria evaluated based on *pmoA* as molecular marker.

351 *Front. Microbiol.* **6**:1346

352 Knief C and Dunfield PF (2005) Response and adaptation of different methanotrophic
353 bacteria to low methane mixing ratios. *Environ. Microbiol.* **7**: 1307–1317.

354 Knief C, Lipski A and Dunfield P (2003) Diversity and activity of methanotrophic
355 bacteria in different upland soils. *AEM* **69**: 6703-6714

356 Krause SMB, Johnson T, Karunaratne YS, Fu Y, Beck DAC, Chistoserdova L and
357 Lidstrom ME (2017) Lanthanide-dependent cross-feeding of methane-derived
358 carbon is linked by microbial community interactions. *PNAS* **114**: 358-363.

359 Takeuchi M, Kamagata Y, Oshima K, Hanada S, Tamaki H, Marumo K, Maeda H,
360 Nedachi M, Hattori M, Iwasaki W and Sakata S (2014) *Methylocaldum marinum*
361 sp. nov., a thermotolerant, methane-oxidizing bacterium isolated from marine
362 sediments, and emended description of the genus *Methylocaldum*. *IJSEM* **64**:
363 3240-3246

364 Tsubota J, Eshinimaev BT, Khmelenina VN and Trotsenko YA (2005)
365 *Methylothermus thermalis* gen. nov., sp. nov., a novel moderately thermophilic
366 obligate methanotroph from a hot spring in Japan. *Int. J. Syst. Evol. Microbiol.*
367 **55**: 1877–1884.

368 Warttinen I, Hestnes AG, McDonald IR and Svenning MM (2006) *Methylobacter*
369 *tundripaludum* sp. nov., a methane-oxidizing bacterium from Arctic wetland soil
370 on the Svalbard islands, Norway (78 degrees N). *Int. J. Syst. Evol. Microbiol.* **56**:
371 109–113.

372 Whittenbury R, Davies SL and Davey JF (1970) Exospores and Cysts Formed by
373 Methane-utilizing Bacteria. *J. Gen. Microbiol.* **61**: 219–226.

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