Polaromonas glacialis sp. nov. and *Polaromonas cryoconiti* sp. nov., isolated from alpine glacier cryoconite

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The taxonomic positions of two Gram-staining-negative, psychrophilic bacteria, which were isolated from alpine glacier cryoconite and designated strains Cr4-12^T and Cr4-35^T, were investigated using a polyphasic approach. Both novel strains contained ubiquinone Q-8 as the sole quinone, summed feature 3 (C_{16:1}ω7c and/or C_{16:1}ω6c) and C_{16:0} as the dominant cellular fatty acids, putrescine and 2-hydroxyputrescine as the major polyamines, and diphosphatidylglycerol, phosphatidylglycerol and phosphatidylethanolamine as the major polar lipids. The genomic DNA G + C contents of strains Cr4-12^T and Cr4-35^T were 61.3 mol% and 60.7 mol%, respectively. Phylogenetic analysis based on 16S rRNA gene sequences indicated that the two strains belonged to the genus *Polaromonas*. Although the 16S rRNA gene sequences of strains Cr4-12^T and Cr4-35^T were very similar (98.7 % sequence similarity), hybridizations indicated a DNA–DNA relatedness value of only 26.9 % between the two novel strains. In pairwise comparisons with the type strains of recognized *Polaromonas* species, strains Cr4-12^T and Cr4-35^T showed 16S rRNA gene sequence similarities of 96.4–98.5 % and 96.5–98.4 %, respectively. Based on the phenotypic and phylogenetic evidence and DNA–DNA relatedness data, strains Cr4-12^T and Cr4-35^T represent two novel species within the genus *Polaromonas*, for which the names *Polaromonas glacialis* sp. nov. and *Polaromonas cryoconiti* sp. nov., respectively, are proposed. The type strain of *Polaromonas glacialis* sp. nov. is Cr4-12^T (=DSM 24062^T =LMG 26049^T =KACC 15089^T) and that of *Polaromonas cryoconiti* sp. nov. is Cr4-35^T (=DSM 24248^T =LMG 26050^T =KACC 15090^T).

The genus *Polaromonas* was proposed by Irgens *et al.* (1996) for a species of psychrophilic, marine, gas-vacuolate bacterium isolated from Antarctica (*Polaromonas vacuolata*). At the time of writing, this genus comprised five species: *Polaromonas naphthalenivorans* (Jeon *et al.*, 2004), *Polaromonas aquatica* (Kämpfer *et al.*, 2006), *Polaromonas hydrogenivorans* (Sizova & Panikov, 2007), *Polaromonas jejuensis* (Weon *et al.*, 2008) and the type species, *P. vacuolata*.

Members of the genus *Polaromonas* have been isolated from various environmental sources, such as tap water

(Kämpfer *et al.*, 2006), marine water (Irgens *et al.*, 1996), sediment (Jeon *et al.*, 2004) and soil (Sizova & Panikov, 2007; Weon *et al.*, 2008). *Polaromonas* species have been found in contaminated environments, where they may play a role as degraders of hydrocarbons and xenobiotics (Jeon *et al.*, 2004; Mattes *et al.*, 2008; Yagi *et al.*, 2009), and in pristine environments. The geographical regions of isolation range from Antarctica (Irgens *et al.*, 1996) to Alaska (Sizova & Panikov, 2007). As members of the genus *Polaromonas* are among the dominant bacteria of glacial ice and glacial sediments worldwide, including polar and high-elevation environments (Darcy *et al.*, 2011), it is not surprising that most members are able to grow well at relatively low temperatures. *Polaromonas* phylotypes are characterized by a high local diversity (which is nearly equivalent to their global diversity) and they may be globally distributed, as dormant cells, in high-elevation air

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains Cr4-12^T and Cr4-35^T are HM583568 and HM583567, respectively.

A supplementary table and a supplementary figure are available with the online version of this paper.

currents (Darcy *et al.*, 2011). Genomic studies have revealed extreme metabolic diversity within the genus *Polaromonas*, possibly as the result of extensive horizontal gene transfer (Yagi *et al.*, 2009).

Two Gram-staining-negative, psychrophilic bacteria, designated strains Cr4-12^T and Cr4-35^T, were among the strains isolated by Zhang *et al.* (2012) from cryoconite that had been collected from the Pasterze/Großglockner glacier in the Hohe Tauern, Austria, at an altitude of 2200 m above sea level. The taxonomic positions of these two novel strains were investigated by following a polyphasic approach. Pure cultures of both strains were routinely cultured, at 20 °C, on R2A agar containing (l⁻¹) 0.5 g yeast extract, 0.5 g peptone, 0.5 g Casamino acids, 0.5 g glucose, 0.5 g starch, 0.3 g sodium pyruvate, 0.3 g K₂HPO₄, 0.05 g MgSO₄ and 15.0 g agar (pH 7; Reasoner & Geldreich, 1985). Both were also stored as suspensions in skim milk (10 %, w/v) at -80 °C. For reference, *P. naphthalenivorans* DSM 15660^T, *P. jejuensis* KACC 12508^T, *P. hydrogenivorans* KACC 12646^T and *P. aquatica* CCUG 39402^T were obtained and routinely grown on R2A agar at 20 °C.

DNA was extracted from each novel strain and purified, as described by Sambrook *et al.* (1989), so that the 16S rRNA genes could be amplified by PCR with the universal primers 27F (5'-AGAGTTTGATCCTGGCTCAG-3') and 1541R (5'-AAGGAGGTGATCCAGCCGCA-3'). Each amplification product was cloned into the pGEM-T Easy vector (Promega) before the recombinant plasmid was propagated in *Escherichia coli* according to the vector manufacturer's instructions (Zhang *et al.*, 2011). Sequencing was carried out by Eurofins MWG Operon (Ebersberg, Germany) using version 3.1 of the ABI Big Dye Terminator kit (Applied Biosystems) and the ABI PRISM 3730xl automated DNA sequencer (Applied Biosystems). Version 1.8 of CLUSTAL_X (Thompson *et al.*, 1997) was used to align the newly determined sequences with 16S rRNA gene sequences retrieved from GenBank/EMBL before phylogenetic analysis was carried out, and neighbour-joining (Saitou & Nei, 1987) and maximum-likelihood (Felsenstein, 1981) trees were constructed, using version 5.0 of the MEGA software package (Tamura *et al.*, 2011). In pairwise comparisons with the type strains of recognized *Polaromonas* species, which were made using the Kimura two-parameter model, strains Cr4-12^T and Cr4-35^T showed 16S rRNA gene sequence similarities of 96.4–98.5 % and 96.5–98.4 %, respectively. In these comparisons, strains Cr4-12^T and Cr4-35^T appeared to be least closely related to the type strain of the type species of the genus *Polaromonas*, *P. vacuolata* 34-P^T, with sequence similarities of 96.4 % and 96.5 %, respectively. The 16S rRNA genes of strains Cr4-12^T and Cr4-35^T were very similar (98.7 % sequence similarity). In the neighbour-joining phylogenetic tree, the two novel strains formed a distinct cluster in a phylogenetic line that they shared with *P. naphthalenivorans* and *P. hydrogenivorans* (Fig. 1). The maximum-likelihood tree displayed a similar topology (Fig. 1).

Cell morphology was examined under a phase-contrast light microscope (Diaplan; Leitz) and in a transmission electron microscope (Libra 120 EFTEM; Zeiss), using cells that had been grown on R2A agar at 20 °C. Motility was also investigated by light microscopy. Gram staining was performed by using a Gram staining kit (bioMérieux) according to the manufacturer's instructions. Catalase activity was evaluated as bubble production in 3 % (v/v) H₂O₂ while cytochrome *c* oxidase activity was determined using 1 % (w/v) *N,N,N',N'*-tetramethyl-*p*-phenylenediamine. Physiological and biochemical characteristics and other enzyme activities were determined by using the API 20 E, API 20 NE and API ZYM systems (bioMérieux) at 20 °C. The assimilation of glucose, maltose, sucrose, L-arabinose, mannose, D-sorbitol, *myo*-inositol, salicin, *N*-acetyl-D-glucosamine, Tween 40 and Tween 80 as sole carbon sources was also tested at 20 °C in mineral medium, as described by Zhang *et al.* (2010). To test for a vitamin requirement for growth, strains were cultured in the same mineral medium, with Tween 40 (which was utilized as a sole carbon source for growth by all the strains investigated) and with or without the vitamin solution described by Schlegel (1992). The ability to utilize naphthalene as the sole carbon and energy source was tested on mineral medium agar (Margesin & Schinner, 1997) without yeast extract. A stock solution of naphthalene (10 mg ml⁻¹) was dissolved in diethyl ether and sprayed on plates of the agar. The diethyl ether was then allowed to evaporate before the plates were inoculated with suspensions of bacterial cells in 0.9 % (w/v) NaCl. Naphthalene utilization was also tested by using the vapour-plate method (Foght & Aislabie, 2005). For this, naphthalene crystals (50 mg) were placed on a small piece of filter paper that was then placed in an inverted, inoculated agar plate. Each plate was then sealed and incubated in a sealed plastic bag, with growth evaluated regularly over an incubation period of 21 days. Amylase, lipase and protease activities were evaluated on R2A agar supplemented with the appropriate substrate (Margesin *et al.*, 2003). Growth at various temperatures (ranging from 1 °C to 42 °C) was assessed both on R2A agar and in shake cultures of R2A broth (shaken at 150 r.p.m.). Growth in medium buffered to give initial pH values varying from 5 to 10 and on R2A agar containing 0–10 % (w/v) NaCl was also evaluated. Growth on standard R2A, nutrient agar (NA) and trypticase soy agar (TSA) containing (l⁻¹) 15 g casein peptone, 5 g soy peptone, 5 g NaCl and 15 g agar, at pH 7, was compared.

All tests were carried out simultaneously with strains Cr4-12^T and Cr4-35^T and the four reference strains, with two or three replications per test. The morphological, physiological and biochemical characteristics of strains Cr4-12^T and Cr4-35^T are summarized in the species descriptions. The features that can be used to differentiate strains Cr4-12^T and Cr4-35^T from each other and from the reference strains are given in Table 1.

For fatty acid analysis, strains Cr4-12^T and Cr4-35^T and the four reference strains were grown on plates of R2A agar at

Fig. 1. Neighbour-joining tree based on 16S rRNA gene sequences showing the relationships between strains Cr4-12^T and Cr4-35^T, recognized members of the genus *Polaromonas*, and representatives of some other related taxa. Asterisks indicate that the corresponding nodes were also obtained in the maximum-likelihood tree. Bootstrap values $\geq 50\%$ (based on 1000 replications) are at branch points. Bar, 0.005 substitutions per nucleotide.

20 °C for 3 days. Under these conditions, all six strains showed similar growth behaviour and, at the end of the incubation period, sufficient cells of comparable physiological age could be harvested from the third streak quadrant on each plate. Fatty acid methyl esters were extracted, prepared and identified according to the standard protocol of version 6.1 of the Sherlock Microbial Identification System (MIDI; Sasser, 1990), using a 6890N GC (Agilent) and version 4.10 of the TSBA database. All of the analyses of cellular fatty acids were carried out by the Identification Service of the Deutsche Sammlung für Mikroorganismen und Zellkulturen (DSMZ), Braunschweig, Germany. The fatty acid profiles of strains Cr4-12^T and Cr4-35^T resembled those of members of the genus *Polaromonas* (Sizova & Panikov, 2007; Weon *et al.*, 2008; Table S1, available in IJSEM Online). The predominant cellular fatty acids of strain Cr4-12^T were summed feature 3 (C_{16:1}ω7c and/or C_{16:1}ω6c; 59.7%), C_{16:0} (15.4%) and C_{18:1}ω7c (11.9%). Those of strain Cr4-35^T were summed feature 3 (C_{16:1}ω7c and/or C_{16:1}ω6c; 60.5%) and C_{16:0} (28.0%).

The respiratory quinones of the novel strains were extracted and purified according to the method of Collins (1985). They were then analysed by HPLC (Wu *et al.*, 1989), with Q-8 from *P. naphthalenivorans* DSM 15660^T and *P. jejuensis*

KACC 12508^T used for reference. The only ubiquinone found in each of the novel strains was Q-8.

For polyamine analysis, strains Cr4-12^T and Cr4-35^T were grown at 20 °C in PYE medium containing (l⁻¹) 3.0 g yeast extract and 3.0 g peptone (pH 7). Polyamines were extracted as described by Busse & Auling (1988) and analysed as described by Busse *et al.* (1997), using the HPLC equipment described by Stolz *et al.* (2007). The polyamine pattern of strain Cr4-12^T consisted of [μmol (g dry mass)⁻¹] putrescine (77.2), 2-hydroxyputrescine (32.9), spermidine (3.0) and minor amounts of cadaverine (0.5) and spermine (0.3). The polyamine pattern of strain Cr4-35^T was similar, consisting of [μmol (g dry mass)⁻¹] putrescine (69.6), 2-hydroxyputrescine (26.7), spermidine (1.4) and minor amounts of cadaverine (0.6). Although both of these polyamine patterns resembled that described for *P. aquatica*, strains Cr4-12^T and Cr4-35^T contained higher amounts of putrescine and lower amounts of 2-hydroxyputrescine than detected in *P. aquatica* CCUG 39402^T (Kämpfer *et al.*, 2006).

Polar lipid profiles were analysed by the TLC method of Tindall (1990a, b), with molybdatophosphoric acid, molybdenum blue, ninhydrin and α-naphthol used to detect total lipids, phospholipids, aminolipids and glycolipids,

Table 1. Phenotypic characteristics that differentiate strains Cr4-12^T and Cr4-35^T from closely related members of the genus *Polaromonas*

Strains: 1, Cr4-12^T; 2, Cr4-35^T; 3, *P. naphthalenivorans* DSM 15660^T; 4, *P. aquatica* CCUG 39402^T; 5, *P. jejuensis* KACC 12508^T; 6, *P. hydrogenivorans* KACC 12646^T. All data from this study. All six strains were positive for growth on R2A, NA and TSA, growth in the absence of vitamins, catalase, cytochrome *c* oxidase and leucine arylamidase activities and the assimilation of Tweens 40 and 80. All were negative for motility, growth at 37 °C on R2A agar, trypsin, α -chymotrypsin, protease (skimmed milk), β -galactosidase, α -glucosidase, α -mannosidase, α -fucosidase, *N*-acetyl- β -glucosaminidase, tryptophan deaminase, lysine dihydrolase and ornithine dihydrolase activities, indole production from tryptophan, aesculin and gelatin hydrolysis, production of citrate and H₂S, glucose fermentation and the assimilation of L-arabinose, D-arabinose, D-mannose, maltose, D-mannitol, *N*-acetyl-D-glucosamine, capric acid, D-sorbitol, *myo*-inositol and salicin. +, Positive; –, negative; w, weak.

Characteristic	1	2	3	4	5	6
Isolation source	Glacier cryoconite	Glacier cryoconite	Contaminated sediment	Tap water	Soil	Forest soil
Growth on R2A agar:						
Slime production	+	–	+	–	–	+
Growth at 1 °C	+	+	+	–	–	+
Growth at 30 °C	–	–	–	+	+	–
Growth at pH 8	–	–	–	+	–	w
Growth with 1 % (w/v) NaCl	+	–	w	w	w	w
Nitrate reduction	+	+	+	–	–	+
Enzyme activity:						
Alkaline phosphatase	w	+	–	+	+	+
Lipase (C14)	w	+	–	w	+	w
α -Galactosidase	–	–	w	–	–	–
Valine arylamidase	w	w	–	w	+	+
Amylase	w	–	–	w	w	–
Assimilation of:						
D-Glucose	–	–	+	–	–	+
Sucrose	–	–	+	–	–	+
Potassium gluconate	–	w	–	–	+	–
Adipic acid	–	w	–	+	–	–
Malic acid	–	w	–	+	–	–
Trisodium citrate	–	–	–	–	+	–
Phenylacetic acid	–	–	–	–	+	–
Utilization of naphthalene*	–	–	+	–	–	–

*As sole carbon and energy source.

respectively. The polar lipid profile of strain Cr4-12^T comprised phosphatidylglycerol, diphosphatidylglycerol, phosphatidylethanolamine, an unidentified aminolipid, three unidentified phospholipids and five unidentified polar lipids. The corresponding profile of strain Cr4-35^T comprised phosphatidylglycerol, diphosphatidylglycerol, phosphatidylethanolamine, three unidentified aminolipids and one unidentified polar lipid. Thus, the polar lipid profile of strain Cr4-12^T contained three unidentified phospholipids not seen in strain Cr4-35^T, as well as at least four more unidentified polar lipids (Fig. S1).

For DNA–DNA hybridization experiments and the determination of genomic DNA G+C content, DNA was isolated from each novel strain using a French pressure cell (Thermo Spectronic) and was then purified by chromatography on hydroxyapatite, as described by Cashion *et al.* (1977).

The genomic DNA G+C contents of strains Cr4-12^T and Cr4-35^T, which were determined by the Identification

Service of the DSMZ using standard HPLC (Mesbah *et al.*, 1989), were 61.3 mol% and 60.7 mol%, respectively.

DNA–DNA hybridization was carried out in 2 × SSC buffer with 10 % (v/v) formamide at 68 °C, as described by De Ley *et al.* (1970) with the modifications described by Huß *et al.* (1983). A Cary 100 Bio UV/visible spectrophotometer (Varian) equipped with a Peltier-thermostatted 6 × 6 multi-cell changer and a temperature controller with *in situ* temperature probe was used. The mean DNA–DNA relatedness values recorded in duplicate reassociation experiments of strain Cr4-12^T with *P. aquatica* CCUG 39402^T, *P. naphthalenivorans* DSM 15660^T, *P. hydrogenivorans* KACC 12946^T, *P. jejuensis* KACC 12508^T and strain Cr4-35^T were 23.7, 32.7, 5.8, 24.1 and 27.0 %, respectively. When the recommendation of a threshold DNA–DNA relatedness value of 70 % for the definition of a bacterial species (Wayne *et al.*, 1987) is considered, these results (together with those of the phylogenetic analysis based on 16S rRNA gene sequences) indicate that strain Cr4-12^T does not belong either to any established

member of the genus *Polaromonas* or to the same species as strain Cr4-35^T.

When, in similar experiments, the DNA from strain Cr4-35^T was hybridized with DNA samples from *P. aquatica* CCUG 39402^T, *P. naphthalenivorans* DSM 15660^T, *P. hydrogenivorans* KACC 12946^T and *P. jejuensis* KACC 12508^T, mean DNA–DNA relatedness values of 11.9, 25.2, 26.3 and 11.8 % were recorded, respectively. These results (together with those of the phylogenetic analysis based on 16S rRNA gene sequences) indicate that strain Cr4-35^T does also not belong to any established member of the genus *Polaromonas*.

The data presented in this article indicate that strains Cr4-12^T and Cr4-35^T are two psychrophilic members of the genus *Polaromonas* that, like their phylogenetic neighbours *P. naphthalenivorans* DSM 15660^T and *P. hydrogenivorans* KACC 12646^T, exhibit good growth over a temperature range of 1–25 °C. The word 'psychrophilic' is here used only to describe a micro-organism that can grow in a cold environment, since the definition of psychrophilic given by Morita (1975), which was based on temperature ranges over which growth occurs and on optimum growth temperatures evaluated via growth rates, has been shown to be ambiguous and inappropriate (Feller & Gerday, 2003; Margesin, 2009).

Strains Cr4-12^T and Cr4-35^T could be easily differentiated from each other by their growth characteristics (growth of strain Cr4-35^T was significantly delayed compared with that of strain Cr4-12^T), colony morphology (strain Cr4-35^T formed much smaller colonies than strain Cr4-12^T), several physiological properties (Table 1) and polar lipid profiles (see above). Phenotypic characteristics that can be used to distinguish the two novel strains and their four closest phylogenetic neighbours are shown in Table 1. Unfortunately, little is currently known about the polyamines and polar lipids of three of the four species used for reference in this study (i.e. *P. naphthalenivorans*, *P. hydrogenivorans* and *P. jejuensis*). Both strain Cr4-12^T and strain Cr4-35^T did, however, contain more putrescine and less 2-hydroxyputrescine than *P. aquatica* CCUG 39402^T. The polar lipid profile of strain Cr4-12^T contained fewer unidentified aminolipids than that of *P. aquatica* CCUG 39402^T, whereas the polar lipid profile of strain Cr4-35^T contained none of the unidentified phospholipids found in *P. aquatica* CCUG 39402^T. Based on the phenotypic and phylogenetic evidence and DNA–DNA relatedness data, strains Cr4-12^T and Cr4-35^T represent two novel species within the genus *Polaromonas*, for which the names *Polaromonas glacialis* sp. nov. and *Polaromonas cryoconiti* sp. nov., respectively, are proposed.

Description of *Polaromonas glacialis* sp. nov.

Polaromonas glacialis (gla.ci.a'lis. L. fem. adj. *glacialis* icy, frozen, full of ice, referring to the frozen, icy environment from which the species was isolated).

Cells are aerobic, Gram-staining-negative, non-motile and coccoid (measuring 0.6–0.8 × 0.8–1.0 µm and often

occurring in chains after 7 days at 20 °C on R2A agar). Colonies on R2A agar are creamy white, slimy, convex and round with entire margins and measure 1.0–1.5 mm in diameter after 14 days at 20 °C. Grows well at 1–25 °C but does not grow at 30 °C. Grows at pH 6–7 and with 0–1 % (w/v) NaCl. Grows on R2A agar, NA and TSA. Vitamins are not required for growth. Positive for catalase, cytochrome *c* oxidase, acid phosphatase, naphthol-AS-BI-phosphohydrolase and leucine arylamidase activities and nitrate reduction. Weakly positive for alkaline phosphatase, lipase (C14), valine arylamidase and amylase activities. Negative for indole production from tryptophan, aesculin and gelatin hydrolysis, H₂S production, utilization of citrate, and urease, trypsin, α-chymotrypsin, protease (skimmed milk), α-galactosidase, β-galactosidase, α-glucosidase, β-glucosidase, α-mannosidase, α-fucosidase, *N*-acetyl-β-glucosaminidase, tryptophan deaminase, arginine dihydrolase, lysine dihydrolase and ornithine dihydrolase activities. Assimilates Tween 40 and Tween 80 but not D-glucose, sucrose, L-arabinose, D-arabinose, D-mannose, maltose, D-mannitol, *N*-acetyl-D-glucosamine, malic acid, adipic acid, capric acid, phenylacetic acid, D-sorbitol, *myo*-inositol, salicin, potassium gluconate or trisodium citrate. Negative for fermentation of D-glucose, D-mannitol, sucrose, inositol, sorbitol, L-rhamnose, melibiose, amygdalin and L-arabinose. The predominant cellular fatty acids are summed feature 3 (C_{16:1}ω7c and/or C_{16:1}ω6c), C_{16:0} and C_{18:1}ω7c. The sole ubiquinone is Q-8. The polar lipid profile comprises phosphatidylglycerol, diphosphatidylglycerol, phosphatidylethanolamine, one unidentified aminolipid, three unidentified phospholipids and five unidentified polar lipids. The major polyamines are putrescine and 2-hydroxyputrescine.

The type strain, Cr4-12^T (=DSM 24062^T =LMG 26049^T =KACC 15089^T), was isolated from alpine glacier cryoconite collected from the Pasterze/Großglockner glacier in the Hohe Tauern, Austria. The genomic DNA G + C content of the type strain is 61.3 mol%.

Description of *Polaromonas cryoconiti* sp. nov.

Polaromonas cryoconiti (cry.o.co.ni'ti. N.L. gen. n. *cryoconiti* from cryoconite, the material from which the species was isolated).

Cells are aerobic, Gram-staining-negative, non-motile and small, oval, short rods that measure 0.7–0.9 × 1.1–1.4 µm after 7 days at 20 °C on R2A agar. Colonies on R2A agar are creamy white, convex and round with entire margins and measure <1.0 mm in diameter after 21 days at 20 °C. Grows slowly but well at 1–25 °C (cell yields are highest at 1–10 °C) and does not grow at 30 °C. Grows well at pH 7 but only weakly at pH 6 and does not grow in the presence of 1 % (w/v) NaCl. Grows on R2A agar, NA and TSA. Vitamins are not required for growth. Positive for catalase, cytochrome *c* oxidase, alkaline phosphatase, esterase lipase (C8), lipase (C14) and leucine arylamidase activities and nitrate reduction. Weakly positive for acid phosphatase, valine arylamidase and naphthol-AS-BI-phosphohydrolase

activities. Negative for indole production from tryptophan, aesculin and gelatin hydrolysis, H₂S production, utilization of citrate, and urease, trypsin, α -chymotrypsin, protease (skimmed milk), amylase, α -galactosidase, β -galactosidase, α -glucosidase, β -glucosidase, β -glucuronidase, α -mannosidase, α -fucosidase, *N*-acetyl- β -glucosaminidase, tryptophan deaminase, arginine dihydrolase, lysine dihydrolase and ornithine dihydrolase activities. Assimilates Tween 40 and Tween 80 well but the assimilation of potassium gluconate, adipic acid and malic acid is weak. Negative for the assimilation of D-glucose, sucrose, L-arabinose, D-arabinose, D-mannose, maltose, D-mannitol, *N*-acetyl-D-glucosamine, capric acid, phenylacetic acid, D-sorbitol, *myo*-inositol, salicin and trisodium citrate. Negative for the fermentation of D-glucose, D-mannitol, sucrose, inositol, sorbitol, L-rhamnose, melibiose, amygdalin and L-arabinose. The predominant cellular fatty acids are summed feature 3 (C_{16:1} ω 7c and/or C_{16:1} ω 6c) and C_{16:0}. The sole ubiquinone is Q-8. The polar lipid profile comprises phosphatidylglycerol, diphosphatidylglycerol, phosphatidylethanolamine, three unidentified aminolipids and one unidentified polar lipid. The major polyamines are putrescine and 2-hydroxyputrescine.

The type strain, Cr4-35^T (=DSM 24248^T =LMG 26050^T =KACC 15090^T), was isolated from alpine glacier cryoconite collected from the Pasterze/Großglockner glacier in the Hohe Tauern, Austria. The genomic DNA G + C content of the type strain is 60.7 mol%.

Acknowledgements

The authors are grateful to W. Salvenmoser (Institute of Zoology, University of Innsbruck) for performing the transmission electron microscopy. We thank P. Thurnbichler, J. Mair (University of Innsbruck), B. Sträubler and B. Grün (DSMZ) for technical assistance and Dr Hang-Yeon Weon (KACC) for providing us with the type strains of *P. hydrogenivorans* and *P. jejuensis*. R.M. is grateful for financial support from an 'Aktion D. Swarovski & Co. 2009' grant from the University of Innsbruck.

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