Psychrobacter vallis sp. nov. and *Psychrobacter aquaticus* sp. nov., from Antarctica

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Twelve strains of psychrophilic bacteria were isolated from cyanobacterial mat samples collected from various water bodies in the McMurdo Dry Valley region of Antarctica. All the isolates were Gram-negative, non-motile, coccoid, psychrophilic, halotolerant bacteria and had C_{16:1}ω7c, C_{17:1}ω8c and C_{18:1}ω9c as the major fatty acids, ubiquinone-8 as the respiratory quinone and DNA G + C content of 41–46 mol%. Based on these characteristics, the isolates were assigned to the genus *Psychrobacter*. Based on their SDS-PAGE profiles, the 12 isolates could be categorized into three groups. Six isolates of Group I were identified as representing strains of *Psychrobacter okhotskensis*. However, using detailed phenotypic and chemotaxonomic characteristics and phylogenetic analysis based on their 16S rRNA gene sequences, strain CMS 39^T, the only strain from Group II, and strain CMS 56^T, a representative strain of Group III, were different from each other and from all recognized species of *Psychrobacter*. Therefore, it is proposed to classify CMS 39^T (= DSM 15337^T = MTCC 4208^T) and CMS 56^T (= DSM 15339^T = MTCC 4386^T) as representing the type strains of novel species of *Psychrobacter*, for which the names *Psychrobacter vallis* sp. nov. and *Psychrobacter aquaticus* sp. nov., respectively, are proposed.

Juni & Heym (1986) described the genus *Psychrobacter* to accommodate Gram-negative, cocci or rod-shaped bacteria that lacked motility and possessed strictly oxidative metabolism. The genus belongs to the family *Moraxellaceae*, which includes two other genera, *Moraxella* and *Acinetobacter* (Bowman *et al.*, 1996; Rossau *et al.*, 1991). At the time of writing, the genus *Psychrobacter* comprises 15 species (Juni & Heym, 1986; Bowman *et al.*, 1996, 1997; Maruyama *et al.*, 2000; Denner *et al.*, 2001; Romanenko *et al.*, 2002; Yoon *et al.*, 2003; Kämpfer *et al.*, 2002; Vela *et al.*, 2003; Bozal *et al.*, 2003; Yumoto *et al.*, 2003). Members of the genus *Psychrobacter* are known to be obligate or facultative psychrophiles and have been isolated from a wide range

of habitats, including food, clinical samples, skin, gills and intestines of fish, sea water, penguin colonies in Antarctica, Antarctic sea ice and Japan Trench sediments (Juni, 1991; Bowman *et al.*, 1996, 1997; Maruyama *et al.*, 2000; Yumoto *et al.*, 2003). We report here on two novel *Psychrobacter* species isolated from cyanobacterial mat samples collected from a pond, a lake and a stream in the McMurdo Dry Valley region of Antarctica.

Source of the organisms, media, growth conditions, morphology and biochemical characteristics

Twelve bacterial colonies were isolated to purity from cyanobacterial mat samples collected at three different localities in Antarctica: L3 pond in the Wright valley (strains CMS 27, CMS 28, CMS 29, CMS 30, CMS 31 and CMS 32), Adams glacier stream, Miers valley (strain CMS 39^T), and lake Canopus (strains CMS 51, CMS 52, CMS 56^T, CMS 58 and CMS 59) (Matsumoto, 1993; Matsumoto *et al.*, 1993) using Antarctic bacterial medium (ABM) agar [0.5% (w/v) peptone, 0.2% (w/v) yeast extract and 1.5% (w/v) agar, pH 7.0] as described by Reddy *et al.* (2000).

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The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains CMS 39^T and CMS 56^T are AJ584832 and AJ584833, respectively.

Tables giving additional data relating to fatty acid profiles, phospholipids, 16S rRNA gene sequence similarity and DNA–DNA relatedness are available as supplementary material in IJSEM Online.

Table 1. Phenotypic characteristics of the 12 *Psychrobacter* isolates from Antarctica

All 12 isolates are coccoid, non-motile and Gram-negative. All strains are positive for catalase, oxidase, lipase, phosphatase and nitrate reduction, but negative for H₂S production, indole production, methyl red test, Voges-Proskauer reaction, citrate utilization, hydrolysis of starch, gelatin, aesculin and arginine, arginine decarboxylase and lysine decarboxylase. Growth observed at pH 9 but not at pH 5. Growth observed at 4–30 °C but not at 37 °C and can tolerate 7.5 % NaCl. Utilize L-asparagine and L-glutamate but not D-fructose, D-mannose, sorbitol, lactose, sucrose, D-xylose, L-arabinose, inulin, dulcitol, trehalose, D-maltose, adonitol, D-melibiose, melizitol, D-mannitol, dextran, methanol, xanthine, butanol, hexadecane, L-leucine, L-isoleucine, L-methionine, L-valine, threonine, L-histidine, L-tryptophan or L-cysteine as the sole carbon source. Do not produce acid from L-arabinose, lactose or sucrose. Sensitive to chloramphenicol (30 µg), gentamicin (10 µg), polymyxin B (300 µg), nalidixic acid (30 µg), tetracycline (30 µg), tobramycin (20 µg) and rifampicin (5 µg) and resistant to lincomycin (2 µg). +, Positive; –, negative; S, sensitive; R, resistant.

Characteristic	Group I						Group II	Group III				
	CMS 27	CMS 28	CMS 29	CMS 30	CMS 31	CMS 32	CMS 39 ^T	CMS 51	CMS 52	CMS 56 ^T	CMS 58	CMS 59
Urea hydrolysis	+	+	+	+	+	+	–	+	+	+	+	+
Growth in 12 % NaCl	+	+	+	+	+	+	–	–	–	–	–	–
Carbon source utilization												
Glycerol	+	+	+	–	+	+	+	–	–	+	–	–
L-Phenylalanine	–	–	–	–	–	–	+	–	–	+	+	+
L-Alanine	–	–	–	–	–	–	+	+	+	+	+	+
L-Tyrosine	+	+	+	+	+	+	+	–	–	–	–	–
Acid production from D-glucose	+	+	+	–	+	+	+	–	–	–	–	–
Sensitivity to antibiotics (µg per disc)												
Ampicillin (10)	S	S	S	S	S	S	R	R	R	S	S	S
Amoxicillin (100)	S	S	S	S	S	S	R	R	R	S	S	S
Carbenicillin (50)	S	S	S	S	S	S	R	R	R	S	S	S
Bacitracin (10)	S	S	S	S	S	S	R	R	R	S	S	S
Colistin (10)	S	S	S	S	S	S	R	R	S	R	S	S
Co-trimoxazole (25)	S	S	S	S	S	S	R	R	R	S	S	S
Nystatin (100)	S	S	S	S	S	S	R	R	R	S	S	S
Streptomycin (10)	S	S	S	S	S	S	R	R	R	S	S	S
Nitrofurantoin (300)	S	S	S	S	S	S	R	R	R	S	S	S
Erythromycin (15)	S	S	S	S	S	S	R	R	R	S	S	S
DNA G + C content (mol%)	43.6	41.2	43.6	43.6	42.4	43.6	46	43.6	43.6	43.6	41.2	46.1

Morphological and growth characteristics were determined as described by Reddy *et al.* (2000). For biochemical tests (as listed in Table 1 and as described under the species descriptions) the cultures were grown at 22 °C on ABM and tests were performed as described by Lanyi (1987) and Smibert & Krieg (1994). The ability of the cultures to utilize a carbon compound as the sole carbon source was investigated by supplementing minimal medium [1.05 % (w/v) K₂HPO₄, 0.45 % (w/v) KH₂PO₄, 0.1 % (w/v) (NH₄)₂SO₄ and 1.5 % (w/v) agar] with 0.5 % (w/v) of the filter-sterilized carbon compound. The sensitivity of the cultures to different antibiotics was checked using antibiotic discs supplied by HiMedia pvt. Ltd.

All 12 isolates are Gram-negative, non-motile, coccoid, psychrophilic and halotolerant (up to 8 % NaCl) bacteria and possess many similar morphological and biochemical characteristics (Table 1). However, they could be differentiated based on their ability to hydrolyse urea, to tolerate 12 % NaCl, to utilize phenylalanine, alanine and tyrosine as sole carbon sources and to produce acid from glucose

and in their sensitivity to ten different antibiotics (Table 1). Chemotaxonomic grouping by SDS-PAGE analysis (Laemmli, 1970) shows that the 12 isolates can be divided into three groups (data not shown): Group I (strains CMS 27, CMS 28, CMS 29, CMS 30, CMS 31, CMS 32), Group II (strain CMS 39^T) and Group III (strains CMS 51, CMS 52, CMS 56^T, CMS 58 and CMS 59). Isolates of the same group exhibited identical protein profiles and very similar phenotypic characteristics (Table 1).

Chemotaxonomic characteristics and phylogenetic analysis

Based on the phenotypic characteristics listed in Table 1, the presence of C_{16:1}ω7c, C_{17:1}ω8c and C_{18:1}ω9c as the major fatty acids (Table A, available as supplementary material in IJSEM Online), DNA G + C content in the range 41–46 % (Table 1) and 16S rRNA gene sequence similarity ranging from 96.8 to 99.1 % (Table B, available as supplementary material in IJSEM Online) with recognized species of *Psychrobacter*, it appears that the 12 isolates

are related to members of the genus *Psychrobacter*. The six isolates in Group I, which had similar phenotypic characteristics (Table 1) and identical 16S rRNA gene sequences (CMS 27, GenBank/EMBL/DDBJ accession no. AJ748266; CMS 28, AJ748267; CMS 29, AJ748268; CMS 30, AJ584831; CMS 31, AJ748269; CMS 32, AJ748270), probably represented the same species and were closely related to *Psychrobacter okhotskensis* MD17^T based on data from 16S rRNA gene sequence similarity (98.6%) and DNA–DNA relatedness analysis (72%) (Table B). Strain CMS 30, a representative strain of Group I, shares similar phenotypic characteristics (Table 2) with *P. okhotskensis* MD17^T and differs only in a few physiological traits (Table 2) and in its polar lipid profile (Table C, available as supplementary material in IJSEM Online). Therefore, the six isolates in Group I are identified as strains representing *P. okhotskensis*. All the above phenotypic and chemotaxonomic characteristics and 16S rRNA gene sequence analysis were determined based on standard procedures as described by Shivaji *et al.* (1989, 2000) and Reddy *et al.* (2002a, 2003). The 16S rRNA gene was amplified and sequenced (Lane, 1991; Shivaji *et al.*, 2000), and the sequences were aligned using CLUSTAL W (Thompson *et al.*, 1994) and subjected to phylogenetic analysis using the PHYLIP program (Felsenstein, 1993). Evolutionary distances were calculated using Kimura's two-parameter model (Kimura, 1980) using the DNADIST program of PHYLIP (Felsenstein, 1993).

Strains CMS 39^T (Group II) and CMS 56^T (as a representative of Group III) also possess characteristics similar to those of members of the genus *Psychrobacter* (Tables 1 and 2, and Tables A and B). Riboprinting was carried out to establish the similarity of the present isolates between themselves and recognized species of *Psychrobacter* according to the protocol recommended by the manufacturer of the Riboprinting System (DuPont Qualicon). The results clearly demonstrated that strains CMS 30, CMS 39^T and CMS 56^T are different and that their riboprints do not match with those of recognized *Psychrobacter* species (Fig. 1).

16S rRNA gene sequence analysis indicated that strains CMS 30 (as a representative of Group I), CMS 39^T and CMS 56^T are closely related to each other (99.4–99.9%) and to recognized type strains of species of the genus *Psychrobacter* (96.8–99.1%) (Table B and Fig. 2). However, the three strains are more closely related to *Psychrobacter luti* LMG 21276^T with a similarity of 99% (Table B and Fig. 1). The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains for Groups II and III are as follows: CMS 39^T, AJ584832; CMS 51, AJ830004; CMS 52, AJ830005; CMS 56^T, AJ584833; CMS 58, AJ830006; CMS 59, AJ830007. Strains CMS 39^T and CMS 56^T could be differentiated from *P. luti* LMG 21276^T in that they tolerated higher NaCl concentrations, and could utilize glycerol and trehalose but not citrate, asparagine, histidine or proline as sole carbon sources (Table B). DNA–DNA hybridization was performed by the membrane filter

method of Reddy *et al.* (2002b) and the results indicate that CMS 39^T and CMS 56^T share a DNA–DNA relatedness of only 25% between themselves and of 34 and 10%, respectively, with *P. luti* LMG 21276^T, indicating that the two isolates are distinctly different from *P. luti* LMG 21276^T (Table B). Strains CMS 39^T and CMS 56^T can also be differentiated from the other closely related species of the genus *Psychrobacter* in that they varied in their riboprint profiles (Fig. 2), in their phenotypic characteristics (Table 2) and in their fatty acid composition (Tables C and D). Furthermore, CMS 39^T and CMS 56^T exhibited less than 70% DNA–DNA relatedness with 16 of the 17 species that exhibited greater than 97% 16S rRNA gene sequence similarity (Table B). Therefore, it is proposed to assign strains CMS 39^T and CMS 56^T to two novel species, for which the names *Psychrobacter vallis* sp. nov. and *Psychrobacter aquaticus* sp. nov., respectively, are proposed.

Description of *Psychrobacter vallis* sp. nov.

Psychrobacter vallis [val'lis. L. n. *vallis* (or *valles*) a valley, vale; L. gen. n. *vallis* of a valley].

On Zobell Marine 2296 agar, forms circular, convex, smooth and opaque colonies with a diameter of 2–3 mm. Cells are Gram-negative, non-motile, coccoid and psychrophilic (growth observed at 4–30 °C). Negative for urease. Utilizes erythritol, D-glucose, inositol, pyruvate, D-ribose, L-arginine, L-glutamine, L-phenylalanine, L-serine and L-tyrosine as sole carbon source but not acetate, fumaric acid, hydroxybutyric acid, lactic acid, L-asparagine or L-valine. Produces acid from D-glucose but not from D-mannose. Sensitive to chlortetracycline (30 µg) and trimethoprim (5 µg). Resistant to bacitracin (10 µg), carbenicillin (50 µg), colistin (10 µg), erythromycin (15 µg), furazolidone (50 µg), furoxone (100 µg), kanamycin (30 µg) and nitrofurantoin (300 µg). Table B (available in IJSEM Online) lists phenotypic characteristics common to the two novel species. Fatty acids present include C_{10:0} (1.1%), C_{16:0} (1.4%), C_{17:0} (0.2%), C_{18:0} (0.9%), iso-C_{16:0} (0.2%), C_{14:1} (0.2%), C_{16:1ω7c} (19.5%), C_{17:1ω8c} (9.3%) and C_{18:1ω9c} (65.7%). Ubiquinone-8 is the respiratory quinone and phosphatidylethanolamine, phosphatidylglycerol and diphosphatidylglycerol are the major polar lipids present.

The type strain is CMS 39^T (=DSM 15337^T=MTCC 4208^T).

Description of *Psychrobacter aquaticus* sp. nov.

Psychrobacter aquaticus (a.qua.ti'cus. L. masc. adj. *aquaticus* living, growing or found in or by the water, aquatic).

On Zobell Marine 2296 agar, forms circular, convex, smooth and opaque colonies with a diameter of 2–3 mm. Cells are Gram-negative, non-motile, coccoid and psychrophilic (growth observed at 4–30 °C). Positive for urease and negative for β-galactosidase. Utilizes L-phenylalanine as sole carbon source but not acetate, cellulose, erythritol,

Table 2. Phenotypic characteristics that differentiate *Psychrobacter okhotskensis* CMS 30, *Psychrobacter vallis* CMS 39^T and *Psychrobacter aquaticus* CMS 56^T between themselves and recognized species of the genus *Psychrobacter*

CMS 30, CMS 39^T and CMS 56^T have the following identical phenotypic characteristics: grow at 4–30 °C, tolerate 10% NaCl and grow optimally at pH 7. The three species are positive for catalase, oxidase, lipase and alkaline phosphatase and reduce nitrate to nitrite. Negative for gelatinase, arginine dihydrolase, arginine decarboxylase, lysine decarboxylase, indole production and Voges–Proskauer test and do not hydrolyse aesculin, starch or cellulose. Utilize trehalose and L-glutamic acid as sole carbon source but not L-arabinose, D-cellobiose, citrate, dextran, dulcitol, D-fructose, D-galactose, inulin, lactose, D-mannose, D-mannitol, D-maltose, melizitose, D-melibiose, D-raffinose, L-rhamnose, D-sorbose, sorbitol, sucrose, succinic acid, thioglycolate, D-xylose, L-alanine, L-aspartic acid, cysteine, L-glycine, L-histidine, L-leucine, L-isoleucine, L-lysine, L-methionine, L-proline, L-tryptophan or threonine. Do not produce acid or gas from L-arabinose, D-fructose, D-galactose, D-maltose, D-melibiose or lactose. The three isolates are sensitive to ampicillin (10 µg), amoxicillin (100 µg), chloramphenicol (30 µg), co-trimoxazole (25 µg), gentamicin (10 µg), nalidixic acid (30 µg), nystatin (100 µg), polymyxin B (300 µg), rifampicin (5 µg), streptomycin (10 µg), tetracycline (30 µg) and tobramycin (20 µg) and resistant to lincomycin (2 µg). Ubiquinone-8, phosphatidylethanolamine, phosphatidylglycerol and diphosphatidylglycerol are present. The predominant fatty acid is C_{18:1}ω₉c.

Taxa: 1, *P. okhotskensis* (CMS 30); 2, *P. vallis* (CMS 39^T); 3, *P. aquaticus* (CMS 56^T); 4, *P. luti* (LMG 21276^T)¹; 5, *P. marincola* (DSM 14160^T)²; 6, *P. submarinus* (DSM 14161^T)²; 7, *P. proteolyticus* (DSM 13887^T)³; 8, *P. faecalis* (DSM 14664^T)⁴; 9, *P. jeotgali* (YKJ-103^T)⁵; 10, *P. frigidicola* (ACAM 304^T)⁶; 11, *P. glacincola* (ATCC 700754^T)⁶; 12, *P. urativorans* (ATCC 15174^T)⁷; 13, *P. immobilis* (DSM 7229^T)⁷; 14, *P. pacificensis* (IFO 16270^T)⁸; 15, *P. phenylpyruvicus* (ATCC 23333^T)⁶; 16, *P. fozii* (LMG 21280^T)¹; 17, *P. okhotskensis* (JCM 11840^T)⁹; 18, *P. pulmonis* (CECT 5989^T)¹⁰. Data from: ¹Bozal *et al.* (2003), ²Romanenko *et al.* (2002), ³Denner *et al.* (2001), ⁴Kämpfer *et al.* (2002), ⁵Yoon *et al.* (2003), ⁶Bowman *et al.* (1996, 1997), ⁷Juni & Heym (1986), ⁸Maruyama *et al.* (2000), ⁹present study and ¹⁰Vela *et al.* (2003). +, Positive; –, negative; ND, not done; V, variable; w+, weak positive.

Characteristic	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
Growth temperature (°C)																		
4	+	+	+	+	–	–	ND	ND	+	+	+	+	+	–	+	+	+	ND
25	+	+	+	+	+	+	+	+	+	–	–	+	+	+	+	+	+	+
30	+	+	+	+	+	+	ND	+	+	–	–	V	+	+	+	+	+	+
37	–	–	–	–	–	–	–	–	–	–	–	–	+	+	+	–	+	+
Optimum	22	22	22	15	25	28	25	15–30	25–30	14–16	13–15	18–20	27–31	25	32	15	25	ND
Tolerance to NaCl (%)																		
0	+	+	+	+	–	–	ND	ND	+	+	+	+	+	–	+	+	+	+
8	+	+	+	+	+	+	+	+	+	+	+	V	+	+	+	+	+	–
10	+	+	W+	–	+	+	+	+	+	–	+	–	V	–	–	+	+	–
12	+	–	–	–	+	+	+	+	–	–	V	–	V	–	–	+	W+	–
15	+	–	–	–	+	+	ND	–	–	–	–	–	–	–	–	–	–	–
Enzymology																		
Lipase (Tween 80)	+	+	+	+	+	+	W+	ND	+	–	+	–	+	–	+	–	+	–
Nitrate reduction	+	+	+	+	–	–	–	ND	+	–	V	+	–	–	+	–	ND	+
Alkaline phosphatase	+	+	+	+	ND	ND	+	+	+	–	–	–	ND	ND	+	+	+	–
Urease	+	–	+	–	–	–	+	–	+	–	+	+	V	+	+	+	+	–
Acid production																		
L-Arabinose	+	–	–	–	–	+	+	–	–	–	–	–	–	+	–	–	+	–
D-Fructose	–	–	–	–	–	+	ND	ND	–	–	–	–	ND	+	ND	–	–	ND
D-Glucose	–	+	–	–	–	–	ND	–	–	–	–	–	–	ND	ND	–	–	–
D-Xylose	+	–	–	–	–	–	ND	–	–	–	–	–	ND	+	–	–	+	ND
Carbon source utilization																		
Acetate	+	–	–	+	–	–	–	+	+	+	+	+	+	V	+	+	+	ND
D-Glucose	+	+	–	–	–	–	–	W+	–	–	–	–	–	–	–	–	–	–
Citrate	–	–	–	+	–	–	+	+	–	–	+	–	–	–	+	–	–	–
Glycerol	–	+	+	–	–	–	ND	–	ND	–	–	–	–	ND	–	–	–	ND
β-Hydroxybutyric acid	–	–	–	ND	ND	ND	+	ND	ND	–	+	+	+	V	+	ND	–	ND
Inositol	+	+	–	ND	–	–	ND	–	ND	ND	–	ND	ND	–	ND	ND	+	ND
Pyruvate	+	+	–	ND	ND	ND	ND	+	+	–	+	+	+	ND	+	ND	+	ND
Trehalose	+	+	+	–	–	+	+	ND	ND	+	+	+	–	ND	ND	–	–	ND
L-Asparagine	+	–	–	+	ND	ND	+	ND	ND	+	+	+	–	ND	ND	+	+	ND
L-Arginine	+	+	–	+	ND	ND	–	ND	ND	–	+	+	–	ND	–	+	+	ND
L-Histidine	–	–	–	+	–	–	+	+	ND	–	V	–	+	+	–	+	–	ND
L-Proline	–	–	–	+	–	–	ND	–	ND	+	+	+	+	+	+	+	ND	ND
L-Phenylalanine	–	+	+	–	ND	ND	–	–	ND	+	–	+	+	ND	+	–	–	ND
DNA G+C content (mol%)	43.6	46.1	43.6	45	50.7	46.7	43.6	ND	43–44	41–42	43–44	44–46	44–47	44–45	43	44	47	ND

Fig. 1. Comparison of riboprints of *Psychrobacter vallis* sp. nov. (CMS 39^T) and *Psychrobacter aquaticus* sp. nov. (CMS 56^T) with those of other closely related species of the genus *Psychrobacter*.

fumaric acid, glucose, *meso*-inositol, lactic acid, pyruvate, D-ribose, L-arginine, L-asparagine, L-glutamine, L-serine, L-tyrosine or L-valine. Produces acid from D-mannose but does not produce acid or gas from D-glucose. Sensitive to bacitracin (10 µg), carbenicillin (50 µg), chlortetracycline (30 µg), erythromycin (15 µg), nitrofurantoin (300 µg),

nitrofurazone (10 µg), oxytetracycline (30 µg), penicillin (10 µg) and trimethoprim (5 µg). Resistant to colistin (10 µg), furazolidone (50 µg), furoxone (100 µg) and kanamycin (30 µg). Table B (available in IJSEM Online) lists phenotypic characteristics common to the two novel species. The fatty acids present are common to all the

Fig. 2. Phylogenetic relationship between *Psychrobacter vallis* sp. nov. (CMS 39^T) and *Psychrobacter aquaticus* sp. nov. (CMS 56^T) and other closely related species of the genus *Psychrobacter* based on UPGMA analysis of 16S rRNA gene sequences. Bootstrap values are given at the nodes. *Acinetobacter calcoaceticus* was used as an outgroup.

strains of the species and vary quantitatively as follows: C_{10:0} (0.3–2.0%), C_{12:0} (0.1–0.4%), C_{16:0} (0.3–2.4%), C_{18:0} (0.5–1.2%), iso-C_{16:0} (0.1–0.4%), C_{14:1} (0.5–1.3%), C_{16:1}ω7c (12.4–23%), C_{17:1}ω8c (11.2–20%) and C_{18:1}ω9c (58–64.3%). Ubiquinone-8 is the respiratory quinone and phosphatidylethanolamine, phosphatidylglycerol and diphosphatidylglycerol are the major polar lipids present.

The type strain is CMS 56^T (=DSM 15339^T=MTCC 4386^T).

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