Chryseobacterium hungaricum sp. nov., isolated from hydrocarbon-contaminated soil

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The taxonomic position of a strain isolated from kerosene-contaminated soil in Hungary and formerly misidentified as *Brevundimonas vesicularis* was examined using a polyphasic approach. The isolate, designated CHB-20p^T, could be clearly assigned to the genus *Chryseobacterium* (family *Flavobacteriaceae*) on the basis of 16S rRNA gene sequence similarity. Strain CHB-20p^T, a moderate oil degrader, was a Gram-negative, aerobic, mesophilic microbe with a temperature optimum of 28–30 °C. Predominant fatty acids were iso-C_{15:0}, summed feature 3 (comprising C_{16:1ω7c} and/or iso-C_{15:0} 2-OH) and iso-C_{17:0} 3-OH. Menaquinone-6 (MK-6) was the predominant respiratory quinone; MK-5 was present as a minor component. The almost complete 16S rRNA gene sequence of strain CHB-20p^T shared 94–97 % similarity with sequences of the type strains of species of the genus *Chryseobacterium*. DNA–DNA relatedness between strain CHB-20p^T and its closest relative, *Chryseobacterium caeni*, was lower than 46 %. Moreover, several diagnostic phenotypic properties distinguished strain CHB-20p^T from *C. caeni*. On the basis of biochemical, chemotaxonomic and genotypic data, isolate CHB-20p^T represents a novel species within the genus *Chryseobacterium*, *Chryseobacterium hungaricum* sp. nov.; the type strain is CHB-20p^T (=NCAIM B2269^T=DSM 19684^T).

Strain CHB-20p^T, a moderate oil degrader, was originally isolated from kerosene-contaminated soil at a former military airfield in Hungary in 2003. This aerobic, Gram-negative, non-spore-forming, rod-shaped, mesophilic bacterium, which produces yellow-pigmented, slimy colonies, was first identified as *Brevundimonas vesicularis* on the basis of morphological and biochemical traits and deposited in the strain collection of Agruniver Holding Ltd, a Hungarian bioremediation company. Sequence analysis of the 16S rRNA gene of strain CHB-20p^T revealed that it actually belongs to the genus *Chryseobacterium*.

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Abbreviations: DPG, diphosphatidylglycerol; EM, electron microscopy; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PS, phosphatidylserine.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain CHB-20p^T is EF685359.

Electron micrographs of cells and API ZYM profiles of strain CHB-20p^T and other species of the genus *Chryseobacterium* are available with the online version of this paper.

The genus *Chryseobacterium*, family *Flavobacteriaceae*, phylum ‘*Bacteroidetes*’ was created by Vandamme *et al.* (1994). *Chryseobacterium miricola* and *Chryseobacterium meningosepticum* were transferred to the closely related genus *Elizabethkingia* by Kim *et al.* (2005b) and, at the time of writing, the genus contained 24 species, with *Chryseobacterium gleum* as the type species. Based on the sequences deposited in GenBank, it is expected that at least a dozen novel species of the genus will be described in the near future. *Chryseobacteria* are ubiquitous bacteria that occur in the most diverse environments such as freshwater, seawater, soil, sediment, and food, dairy, fish and clinical samples (Bernardet *et al.*, 2006). To elucidate the correct taxonomic position of strain CHB-20p^T, a polyphasic taxonomic approach was applied. It revealed that the strain actually represents a novel species in the genus *Chryseobacterium*.

The 16S rRNA gene of strain CHB-20p^T was amplified by PCR using the universal primers BSF8/20 and BSR1541/20 (Wang *et al.*, 2006). The PCR product was used as a

template for sequencing after column purification using the GFX PCR DNA Gel Band Purification kit (Amersham Biosciences). In the sequencing PCRs, the same universal primers (BSF8/20 and BSR1541/20) were used and the reactions were analysed on an ABI 3100 Genetic Analyzer (Applied Biosystems). Multiple alignments of 16S rRNA gene sequences were made by the NAST software (<http://greengenes.lbl.gov/NASt>). The MEGA4 program (Tamura *et al.*, 2007) was used to construct phylogenetic trees with the neighbour-joining (Saitou & Nei, 1987), minimum-evolution (Rzhetsky & Nei, 1992) and maximum-parsimony (Swofford, 1993) algorithms. Bootstrap values were determined based on 1000 replications.

The almost complete 16S rRNA gene sequence (1406 bp) of strain CHB-20p^T was compared with those of the type strains of all members of the genus *Chryseobacterium* and of representative members of related genera. The highest similarity was 97.1 % with *Chryseobacterium caeni* and similarities of 94–97 % were obtained with other *Chryseobacterium* species. Moreover, several diagnostic phenotypic properties distinguished CHB-20p^T from *C. caeni*.

Fig. 1 shows the phylogenetic tree constructed by the neighbour-joining method. The topologies of the phylogenetic trees constructed by the minimum-evolution and maximum-parsimony methods were essentially the same (data not shown). In all cases, strain CHB-20p^T clustered together with *C. caeni* and formed a stable lineage within the genus *Chryseobacterium* with a bootstrap value of 97 %.

In addition to strain CHB-20p^T, *Chryseobacterium indoltheticum* LMG 4025^T, *Chryseobacterium defluvii* DSM 14219^T and *Chryseobacterium daecheongense* DSM 15235^T were used as reference strains for electron microscopy (EM) studies. These strains and *Chryseobacterium scophthalmum* LMG 13028^T were also used for the following biochemical tests: presence of urease, β -galactosidase and phenylalanine deaminase activities; reduction of nitrate and nitrite; hydrolysis of Tween 80 and starch; and acid production from L-arabinose, fructose, glycerol, lactose, maltose, trehalose and D-xylose. *C. caeni* DSM 17710^T was used for DNA–DNA hybridization experiments. Working stock cultures were maintained on TGE agar (Merck) at 28 °C.

The Gram reaction was performed as described by Gerhardt *et al.* (1994). Colony morphology was examined on cultures grown for 4 days at 28 °C on TGE agar. Flexirubin pigments were detected by the KOH test according to Bernardet *et al.* (2002). Motility of the cells grown in TGE broth for 2 days at 28 °C was examined by phase-contrast microscopy.

Cell morphology was determined by phase-contrast microscopy and EM. Samples for EM were taken from 2-day-old cultures grown in nutrient broth at 28 °C. Briefly, 10 μ l cell suspension was dropped onto a carbon-coated grid, negatively stained using 1 % uranyl acetate, dehy-

drated in an acetone/water solvent series and critical-point dried. Samples were examined using a Zeiss EM910 at 40 kV.

The growth temperature range and optimum were determined by culturing the strain in nutrient broth at 5, 28, 30, 37 and 42 °C for 7 days. The effects of pH (6.0–10.0 at 0.5 unit intervals) and NaCl (0–5 % at 0.5 % intervals) on growth were tested in nutrient broth. The pH of the medium was adjusted according to Chern *et al.* (2004). Catalase activity was detected using a 3 % (v/v) hydrogen peroxide solution. Oxidase activity was determined by the oxidation of 1 % *p*-aminomethylaniline oxalate.

Standard protocols were employed to perform tests for the presence of urease, phenylalanine deaminase and β -galactosidase activities, reduction of nitrate and nitrite, and hydrolysis of starch, tyrosine and Tween 80 (Barrow & Feltham, 1993). Utilization of various substrates as sole carbon sources and enzymic activities were assessed by using API 20NE and API ZYM strips (bioMérieux) following the manufacturer's recommendations. Acid production from carbohydrates (L-arabinose, fructose, lactose, maltose, mannitol, trehalose and D-xylose) was tested according to Barrow & Feltham (1993).

Cells of strain CHB-20p^T were non-motile when examined by phase-contrast microscopy, in accordance with all recognized species of the genus *Chryseobacterium*. It remained unclear, however, whether flagella were indeed absent since published transmission electron micrographs did not provide sufficient evidence. EM examination performed in this study on strain CHB-20p^T and the type strains of the three *Chryseobacterium* species for which no electron micrographs were available demonstrated that the four strains had totally smooth cell surfaces and were devoid of flagella (see Supplementary Fig. S1 available in IJSEM Online).

Other cultural, physiological and biochemical characteristics of strain CHB-20p^T are given in the species description and in Table 1. A unique trait of strain CHB-20p^T compared with all other *Chryseobacterium* species tested is its ability to produce acid from lactose. The results of API ZYM strips are given in Supplementary Table S1 (available in IJSEM Online).

Isoprenoid quinones were extracted according to the method of Collins *et al.* (1977) from cells cultivated in liquid Rich medium (Yamada & Komagata, 1972) for 2 days at 28 °C and the profile was analysed by HPLC (HP 9001) (Groth *et al.*, 1997). Cellular fatty acids were extracted from cells cultured on tryptic soy agar (TSA; Difco) for 24 h at 28 °C using the method of Stead *et al.* (1992) and the extracts were analysed using the Sherlock Microbial Identification System (MIDI) according to the manufacturer's instructions. Polar lipids were determined according to the method described by Minnikin *et al.* (1979).

The main menaquinone of strain CHB-20p^T was menaquinone-6 (MK-6), with MK-5 as a minor component. The

Fig. 1. Neighbour-joining tree based on 16S rRNA gene sequences showing the phylogenetic relationships of strain CHB-20p^T, other members of the genus *Chryseobacterium* and representative members of related genera. Bootstrap percentage values >50% based on 1000 replications are indicated at branching points. Bar, 0.01 substitutions per nucleotide position.

presence of MK-5 is at variance with all other recognized *Chryseobacterium* species. The polar lipids identified were phosphatidylethanolamine (PE), phosphatidylglycerol (PG), diphosphatidylglycerol (DPG) and phosphatidylserine (PS). The fatty acid compositions of strain CHB-20p^T and closely related species are shown in Table 2. In line with other species of the genus *Chryseobacterium*, the predominant fatty acids of strain CHB-20p^T were iso-C_{15:0} (32%) and iso-C_{17:0} 3-OH (10.4%). However, strain

CHB-20p^T differed from other *Chryseobacterium* species (except *Chryseobacterium hispanicum* and *C. caeni*) in containing a very large amount of summed feature 3 (comprising C_{16:1}ω7c and/or iso-C_{15:0} 2-OH; 31.1%).

For DNA isolation, cells of strain CHB-20p^T and *C. caeni* DSM 17720^T were disrupted using a French pressure cell and DNA was purified on hydroxyapatite according to Cashion *et al.* (1977). The DNA G+C content was

Table 1. Phenotypic characteristics that differentiate strain CHB-20p^T from other species of the genus *Chryseobacterium*

Species/strains: 1, *C. hungaricum* sp. nov. CHB-20p^T (data from this study); 2, *C. caeni* N4^T (Quan *et al.*, 2007); 3, *C. gleum* (*n*=2; Vandamme *et al.*, 1994); 4, *C. balustinum* ATCC 33487^T (Vandamme *et al.*, 1994); 5, *C. indologenes* (*n*=7; Vandamme *et al.*, 1994); 6, *C. indoltheticum* LMG 4025^T (Vandamme *et al.*, 1994; this study); 7, *C. scophthalmum* (*n*=2; Vandamme *et al.*, 1994; this study); 8, *C. defluvii* B2^T (Kämpfer *et al.*, 2003; this study); 9, *C. joostei* (*n*=11; Hugo *et al.*, 2003); 10, *C. daecheongense* CPW406^T (Kim *et al.*, 2005a; this study); 11, *C. formosense* CC-H3-2^T (Young *et al.*, 2005); 12, *C. taichungense* CC-TWGS1-8^T (Shen *et al.*, 2005); 13, *C. shigense* GUM-Kaji^T (Shimomura *et al.*, 2005); 14, *C. vrystaatense* (*n*=36; de Beer *et al.*, 2005); 15, *C. soldanellicola* PSD1-4^T (Park *et al.*, 2006); 16, *C. taeanense* PHA3-4^T (Park *et al.*, 2006); 17, *C. piscium* (*n*=4; de Beer *et al.*, 2006); 18, *C. hispanicum* VP48^T (Gallego *et al.*, 2006); 19, *C. wanjuae* R2A10-2^T (Weon *et al.*, 2006). +, Positive; w, weakly positive; –, negative; v, variable; D, delayed reaction; NA, no data available.

Characteristic	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
Growth on/at:																			
MacConkey agar	–	–	+	+	+	+	–	–	+	–	–	–	–	–	–	–	–	–	w
5 °C	w	+	–	D	–	+	D	–	+	–	–	–	+	+	+	+	+	D	+
37 °C	+	+	+	+	–	–	–	+	–	+	–	+	–	–	+	+	–	–	+
42 °C	–	–	–	–	–	–	–	+	–	–	–	–	–	–	–	–	–	–	–
Growth in nutrient broth supplemented with 5 % NaCl	–	NA	–	–	–	–	–	–	–	NA	NA	NA	NA	–	NA	NA	+	NA	NA
Enzyme activity:																			
Urease	–	+	–	–	–	–	+	–	v	–	–	–	–	+	–	–	+	–	–
Nitrate reduction	–	–	+	+	–	–	–	–	–	+	–	–	–	–	–	–	+	+	–
Nitrite reduction	–	–	+	–	–	–	–	–	–	–	NA	NA	–	+	–	–	–	+	NA
Phenylalanine deaminase	–	NA	–	–	–	+	–	–	–	NA	NA	NA	NA	–	NA	NA	+	NA	NA
β-Galactosidase	+	+	v	–	–	–	+	NA	–	–	–	w	NA	NA	–	–	NA	+	+
Hydrolysis of:																			
Tyrosine	+	NA	+	–	–	D	+	+	+	NA	NA	NA	NA	–	NA	NA	–	NA	+
Tween 80	w	–	+	+	+	+	+	NA	+	NA	–	NA	NA	+	–	+	v	–	NA
Starch	+	–	+	–	+	–	–	+	+	+	NA	NA	+	–	NA	NA	–	+	+
Production of:																			
Indole	+	–	+	+	+	+	–	+	+	–	+	w	+	+	–	–	+	w	–
H ₂ S	–	–	–	–	–	+	–	–	–	–	–	–	+	v	–	–	–	–	NA
Acid production from:																			
L-Arabinose	–	–	+	–	–	–	–	–	–	–	–	–	–	NA	–	–	NA	+	–
Fructose	–	–	+	+	D	–	–	+	+	+	NA	NA	+	NA	–	–	NA	+	–
Glycerol	–	–	+	–	D	–	–	+	v	+	NA	NA	–	NA	–	–	NA	+	–
Lactose	+	–	–	–	–	–	–	–	–	–	NA	–	–	NA	–	–	NA	–	–
Maltose	–	–	+	–	+	+	–	+	+	+	–	+	–	NA	–	–	NA	+	–
Trehalose	+	–	+	–	+	–	+	+	+	+	+	+	–	NA	–	–	NA	–	+
D-Xylose	+	–	+	–	–	–	–	–	–	–	w	+	–	NA	–	–	NA	+	–
DNA G+C content (mol%)*	37.5	38.2	38.0	33.1	38.5	33.8	34.2	38.8	36.8	36.6	NA	NA	36.6	37.1	28.8	32.1	33.6	34.3	37.8

*DNA G+C contents shown are for type strains.

determined by HPLC (Shimadzu) according to Mesbah *et al.* (1989).

The DNA G+C content of strain CHB-20p^T was 37.5 mol%. This value is in the range of previously published DNA base compositions of chryseobacteria [from 28.8 mol% for *Chryseobacterium soldanellicola* (Park *et al.*, 2006) to 38.8 mol% for *C. defluvii* (Kämpfer *et al.*, 2003)].

DNA–DNA hybridization of strain CHB-20p^T and *C. caeni* DSM 17710^T was performed by the DSMZ identification service as described by De Ley *et al.* (1970) with the modifications of Huß *et al.* (1983) using a model Cary 100 Bio UV/VIS-spectrophotometer equipped with a Peltier-

thermostatted 6 × 6 multicell changer and a temperature controller with *in situ* temperature probe (Varian). DNA relatedness between strain CHB-20p^T and *C. caeni* DSM 17710^T was 45.7 %, thus demonstrating that strain CHB-20p^T represents an independent species (Wayne *et al.*, 1987). Strain CHB-20p^T can be differentiated from *C. caeni* DSM 17710^T by several diagnostic phenotypic properties, such as indole production, acid production from lactose and hydrolysis of Tween 80 and starch.

On the basis of physiological, chemotaxonomic and genotypic data, isolate CHB-20p^T is assigned to a novel species within the genus *Chryseobacterium* under the name *Chryseobacterium hungaricum* sp. nov.

Table 2. Cellular fatty acid composition of *Chryseobacterium* species

Species/strains: 1, *C. hungaricum* sp. nov. CHB-20p^T (data from this study); 2, *C. caeni* N4^T (Quan *et al.*, 2007); 3, *C. taichungense* CC-TWGS1-8^T (Shen *et al.*, 2005); 4, *C. formosense* CC-H3-2^T (Young *et al.*, 2005); 5, *C. defluvii* B2^T (Kämpfer *et al.*, 2003); 6, *C. joostei* ($n=11$; Hugo *et al.*, 2003); 7, *C. gleum* ($n=5$; Vandamme *et al.*, 1994); 8, *C. indologenes* ($n=45$; Vandamme *et al.*, 1994); 9, *C. balustinum* ATCC 33487^T (Vandamme *et al.*, 1994); 10, *C. indoltheticum* LMG 4025^T (Vandamme *et al.*, 1994); 11, *C. scopthalmum* ($n=2$; Vandamme *et al.*, 1994); 12, *C. vrystaatense* ($n=7$; de Beer *et al.*, 2005); 13, *C. daecheongense* CPW406^T (Kim *et al.*, 2005a); 14, *C. shigense* GUM-Kaji^T (Shimomura *et al.*, 2005); 15, *C. soldanellicola* PSD1-4^T (Park *et al.*, 2006); 16, *C. taeenense* PHA3-4^T (Park *et al.*, 2006); 17, *C. piscium* ($n=4$; de Beer *et al.*, 2006); 18, *C. hispanicum* VP48^T (Gallego *et al.*, 2006); 19, *C. wanjuse* R2A10-2^T (Weon *et al.*, 2006). Fatty acid percentages amounting to less than 1 % of the total fatty acids in all strains were not included. Some of the strains were grown under different culture conditions. Means $\pm$ standard deviations are given when data are available for several strains. tr, Trace (less than 1.0 %); ND, not detected; ECL, equivalent chain-length.

Fatty acid	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
iso-C _{13:0}	3.5	1.0	tr	3.6	2.8	tr	tr	tr	tr	ND	tr	1.1 $\pm$ 0.4	1.6	2.6	tr	tr	0.9 $\pm$ 0.6	2.5	tr
Unknown, ECL 13.566	tr	2.6	6.7	tr	tr	1.1 $\pm$ 0.2	1.2 $\pm$ 0.4	2.1 $\pm$ 0.7	1.6	1.7	2.9 $\pm$ 0.2	1.4 $\pm$ 0.3	1.5	2.4	2.3	3.1	tr	1.0	2.9
iso-C _{15:0}	32.0	26.4	35.4	52.2	58.5	34.6 $\pm$ 2.0	35.4 $\pm$ 2.9	34.3 $\pm$ 4.9	32.3	29.4	35.0 $\pm$ 0.7	41.8 $\pm$ 1.4	51.2	39.7	41.8	36.1	38.3 $\pm$ 5.0	26.1	40.0
iso-C _{15:0} 3-OH	4.9	3.2	4.3	1.8	2.6	2.9 $\pm$ 0.3	2.5 $\pm$ 0.1	2.6 $\pm$ 0.2	2.7	2.3	2.7 $\pm$ 0.1	2.7 $\pm$ 0.3	2.0	4.1	2.7	3.1	2.4 $\pm$ 5.0	4.0	3.7
anteiso-C _{15:0}	3.6	4.3	tr	2.1	3.2	tr	tr	tr	tr	5.9	tr	1.7 $\pm$ 0.7	1.0	tr	1.9	1.1	2.7 $\pm$ 1.9	3.6	tr
C _{16:0}	3.8	13.5	1.3	1.5	1.3	tr	1.3 $\pm$ 0.4	tr	1.6	1.0	1.2 $\pm$ 0.2	1.1 $\pm$ 0.4	1.8	tr	1.4	1.8	1.1 $\pm$ 0.2	2.4	tr
C _{16:0} 3-OH	3.6	6.7	2.6	tr	tr	1.2 $\pm$ 0.2	1.1 $\pm$ 0.1	1.0 $\pm$ 0.2	1.4	tr	1.0 $\pm$ 0.1	1.3 $\pm$ 0.4	tr	1.3	1.3	tr	1.3 $\pm$ 0.3	4.4	ND
iso-C _{16:0} 3-OH	ND	ND	1.4	1.1	tr	ND	ND	ND	tr	1.3	ND	tr	tr	tr	tr	tr	tr	ND	tr
Unknown, ECL 16.580	tr	ND	1.7	1.0	ND	1.6 $\pm$ 0.1	1.7 $\pm$ 0.1	1.7 $\pm$ 0.2	1.3	1.3	1.5 $\pm$ 0.1	1.2 $\pm$ 0.2	1.0	1.0	1.5	1.4	1.2 $\pm$ 0.2	1.9	ND
C _{17:0} 2-OH	tr	ND	ND	ND	ND	ND	ND	ND	tr	3.0	tr	ND	ND	ND	ND	ND	ND	ND	ND
iso-C _{17:0}	ND	ND	tr	2.3	2.0	tr	1.6 $\pm$ 0.6	tr	1.0	tr	tr	tr	3.0	tr	tr	1.1	1.2 $\pm$ 0.2	ND	2.9
iso-C _{17:0} 3-OH	10.4	9.8	22.4	10.9	14.1	20.1 $\pm$ 1.2	21.8 $\pm$ 0.3	19.2 $\pm$ 1.8	16.8	14.0	16.3 $\pm$ 0.1	15.4 $\pm$ 1.8	15.7	19.6	17.7	18.8	16.2 $\pm$ 3.1	17.6	21.9
iso-C _{17:1} ω 9c	1.7	ND	8.9	4.3	4.8	22.9 $\pm$ 1.9	20.2 $\pm$ 3.9	24.2 $\pm$ 3.1	27.1	25.6	24.8 $\pm$ 0.4	19.7 $\pm$ 2.3	7.6	11.9	14.6	15.8	18.7 $\pm$ 2.8	1.3	11.7
Summed feature 3*	31.1	32.4	13.8	6.5	8.4	12.1 $\pm$ 1.3	11.8 $\pm$ 0.8	11.1 $\pm$ 1.3	9.2	11.2	11.5 $\pm$ 0.3	9.1 $\pm$ 0.9	8.5	12.4	9.7	11.2	10.8 $\pm$ 1.3	26.7	11.0

*Fatty acids that could not be separated by GC using the Sherlock Microbial Identification System (MIDI) software were considered summed features. Summed feature 3 contains C_{16:1} ω 7c and/or iso-C_{15:0} 2-OH.

Description of *Chryseobacterium hungaricum* sp. nov.

Chryseobacterium hungaricum (hun.ga'ri.cum. L. neut. adj. *hungaricum* from Hungary).

Cells are Gram-negative, non-spore-forming, non-motile rods with rounded ends, devoid of flagella, approximately 0.5 µm in diameter and 0.9 µm in length. Aerobic. Oxidase- and catalase-positive. Good growth is observed on TGE, TSA and nutrient agars, but not on MacConkey agar. Colonies are shiny, 3–4 mm in diameter, circular with entire edges and creamy in consistency, becoming mucous after 2 days incubation on nutrient agar. Bright yellow flexirubin-type pigments are produced (KOH-test-positive). Growth occurs at 5–37 °C (optimum, 28–30 °C), but not at 42 °C. The pH range for growth is 6.0–10.0 (optimum, pH 6.5–7.5). Growth occurs with 0–2 % NaCl (optimum, 0–1 %). Acid is produced from lactose, maltose, trehalose and D-xylulose, but not from L-arabinose, fructose, glycerol or mannitol. Glucose, mannose and maltose are utilized as sole carbon sources, but arabinose, mannitol, N-acetylglucosamine, gluconate, caprate, adipate, malate, citrate and phenylacetate are not. Indole is produced. β-Glucosidase activity is present, but urease activity is absent. Nitrate and nitrite are not reduced. The predominant fatty acids are iso-C_{15:0}, summed feature 3 (comprising C_{16:1ω7c} and/or iso-C_{15:0} 2-OH) and iso-C_{17:0} 3-OH. MK-6 is the predominant respiratory quinone; MK-5 occurs in small amounts. PE, PG, DPG and PS are present as polar lipids.

The type strain is CHB-20p^T (=NCAIM B2269^T=DSM 19684^T), isolated from hydrocarbon-contaminated soil in Hungary. The DNA G+C content of the type strain is 37.5 mol%.

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