Pedobacter rhizosphaerae sp. nov. and *Pedobacter soli* sp. nov., isolated from rhizosphere soil of Chinese cabbage (*Brassica campestris*)

Soon-Wo Kwon, Jung-A Son, Soo-Jin Kim, Yi-Seul Kim, In-Cheol Park, Jeung-Im Bok and Hang-Yeon Weon

Correspondence
Hang-Yeon Weon
hyweon@rda.go.kr

Agricultural Microbiology Team, National Academy of Agricultural Science,
Rural Development Administration, Suwon 441-707, Republic of Korea

Two bacterial strains, 01-96^T and 15-51^T, isolated from rhizosphere soil of Chinese cabbage (*Brassica campestris*) were characterized by using a polyphasic approach. 16S rRNA gene sequence analysis showed that strain 01-96^T was phylogenetically related most closely to *Pedobacter suwonensis* 15-52^T and *Pedobacter roseus* CL-GP80^T (96.7 and 96.7 % similarity, respectively), and strain 15-51^T to *Pedobacter borealis* G-1^T and *P. suwonensis* 15-52^T (97.2 and 97.1 %, respectively). However, levels of DNA–DNA relatedness between strain 15-51^T and *P. borealis* KACC 14287^T and *P. suwonensis* KACC 11317^T were low (<50 %). The G + C content of the genomic DNA was 37.8 mol% for strain 01-96^T and 38.6 mol% for strain 15-51^T. The major fatty acids of the two strains were iso-C_{17:0} 3-OH, iso-C_{15:0} and summed feature 3 (iso-C_{15:0} 2-OH and/or C_{16:1} ω7c). The results of DNA–DNA hybridization and phenotypic data showed that strains 01-96^T and 15-51^T could be distinguished from their closest phylogenetic relatives, and that these strains represented two novel species of the genus *Pedobacter*, for which the names *Pedobacter rhizosphaerae* sp. nov. (type strain 01-96^T = KACC 14938^T = NBRC 107690^T) and *Pedobacter soli* sp. nov. (type strain 15-51^T = KACC 14939^T = NBRC 107691^T) are proposed.

The genus *Pedobacter* was proposed by Steyn *et al.* (1998) on the basis of the classification of heparinolytic bacteria, with the description of the type species (*Pedobacter heparinus*) and three others. Since the description of *Pedobacter cryoconitis* by Margesin *et al.* (2003), the number of recognized species has increased tremendously, with 27 novel species described up to 2010. This number reflects the easy recovery of members of the genus from the natural environment; species of the genus have been isolated from terrestrial environments (mainly soil and water) by using common media such as trypticase soy agar (TSA) or R2A agar. The genus *Pedobacter* includes Gram-negative, aerophilic or microaerophilic bacteria that are able to grow at 1–45 °C. Colonies exhibit various colours from yellow to white or pink (Gallego *et al.*, 2006), but the pigment does not exhibit the typical flexirubin reaction. Chemotaxonomically, members of the genus contain menaquinone-7 (MK-7) as the predominant menaquinone. They contain iso-C_{17:0} 3-OH, iso-C_{15:0} and summed feature 3 (iso-C_{15:0} 2-OH and/or C_{16:1} ω7c) as major fatty acids and have genomic DNA G + C contents of 33.8–44.2 mol%. In

this study, we characterized taxonomically two *Pedobacter*-like bacterial strains.

Two pink-coloured strains, designated 01-96^T and 15-51^T, were isolated from rhizosphere soil of Chinese cabbage (*Brassica campestris* L.) grown in lysimeters (37° 16' 38.50" N 126° 58' 59.60" E), which had been in continuous operation since 1994 in the National Academy of Agricultural Science. Rhizosphere soil samples were collected from the root surface. The soil samples had the following chemical properties: pH, 6.6; total organic carbon, 23 g kg⁻¹; available P₂O₅, 1184 mg kg⁻¹; exchangeable K, 0.45 cmol kg⁻¹; exchangeable Ca, 2.5 cmol kg⁻¹; exchangeable Mg, 1.5 cmol kg⁻¹. The soil texture was sandy loam. After sampling, 10 g rhizosphere soil was suspended in 90 ml distilled water containing 0.85 % NaCl (w/v), and serially diluted and plated on TSA. After incubation for 5 days at 28 °C, strains 01-96^T and 15-51^T were recovered and routine cultivation was conducted at 28 °C on TSA. Seven reference type strains of recognized *Pedobacter* species were obtained from the Korean Agricultural Culture Collection (KACC) for comparison of phenotypic and chemotaxonomic characteristics, namely *Pedobacter agri* KACC 14024^T, *P. alluvionis* KACC 14286^T, *P. borealis* KACC 14287^T, *P. roseus* KACC 11594^T, *P. sandarakinus* KACC 11593^T, *P. suwonensis* KACC 11317^T and *P. terrae* KACC 13760^T.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains 01-96^T and 15-51^T are AM279214 and AM279215, respectively.

Growth was tested on Luria–Bertani (LB) agar, nutrient agar (NA), R2A agar and MacConkey agar (all from Difco). Phenotypic characteristics, including Gram-staining, catalase and oxidase activity and hydrolysis of CM-cellulose (0.1 %, w/v), casein (10 % skimmed milk, w/v), chitin (0.5 %, w/v), hypoxanthine (0.5 %, w/v), tyrosine (0.5 %, w/v), Tween 80 (1.0 %, v/v), starch (1.0 %, w/v) and xanthine (0.5 %, w/v), were determined by using the methods of Smibert & Krieg (1994). Growth under anaerobic conditions was tested in a GasPak (BBL) jar at 28 °C for 14 days. Heparinase production was determined by the method of Joubert *et al.* (1984). Flexirubin pigments were investigated by suspending cells in 20 % KOH (Fautz & Reichenbach, 1980). Growth at pH 4.0–10.0 (at intervals of 0.5 pH units) was determined in TSA broth (TSB) that was buffered with citrate/phosphate buffer or Tris/HCl (Breznak & Costilow, 1994). Growth in the presence of 0.5, 1.0, 1.5, 2.0, 3.0 and 5.0 % (w/v) NaCl, and at 10, 15, 20, 25, 30, 35, 37 and 40 °C was investigated on TSA. Growth at 1–5 °C was also tested on TSA slants by using a bench-top incubator (e-CoolingBucket ECB; Taitec). Carbon assimilation was tested by using the API 50CH gallery as described by Kersters *et al.* (1984). Tests in the API 20E and API ZYM (bioMérieux) commercial systems were performed according to the manufacturer's instructions. API ZYM test strips were read after 4 h incubation at 37 °C, whilst API 20E strips were examined after 7 days at 28 °C. Cell morphology was observed by transmission electron microscopy (912AB; LEO) and phase-contrast microscopy (AXIO; Zeiss) by using cells grown on TSA. Motility was tested by the hanging-drop method (Skerman, 1967) with phase-contrast microscopy. Strains 01-96^T and 15-51^T grew on LB agar, NA, R2A agar and TSA, but not on MacConkey agar. Detailed characteristics for the two strains are provided in the species descriptions, and the characteristics that differentiate these strains from related type strains are summarized in Table 1.

Fatty acid methyl esters were extracted and prepared by using the standard protocol of the Microbial Identification System (MIDI, 1999) after cells were grown on TSA for 2 days at 28 °C. Isoprenoid quinones were analysed by HPLC as described by Groth *et al.* (1996). The DNA G + C content was determined by HPLC analysis of deoxyribonucleosides as described by Mesbah *et al.* (1989) by using a reversed-phase column (Supelcosil LC-18 S; Supelco). Strains 01-96^T and 15-51^T contained C_{18:1}ω7c and summed feature 3 (comprising C_{16:1}ω7c and/or iso-C_{15:0} 2-OH) as major fatty acids (Table 2). The fatty acid profiles of the two novel strains were similar to those of their closest phylogenetic neighbours, i.e. members of the genus *Pedobacter*; quantitative differences between these two strains and their closest phylogenetic neighbours are detailed in Table 2. The predominant menaquinone of the two strains was menaquinone-7 (MK-7), consistent with data for the reference *Pedobacter* species. The DNA G + C contents of strains 01-96^T and 15-51^T were 37.8 and 38.6 mol%, respectively; these values were within the range (33.8–44.2 mol%) reported for members of the genus *Pedobacter*.

The 16S rRNA gene sequences of the two strains were determined by PCR amplification (Kwon *et al.*, 2003) and direct sequencing (Hiraishi, 1992). Nearly complete 16S rRNA gene sequences were determined for strains 01-96^T (1486 bp) and 15-51^T (1487 bp). Identification of phylogenetic neighbours and calculation of pairwise levels of 16S rRNA gene sequence similarity were achieved by using the EzTaxon server (<http://www.eztaxon.org/>; Chun *et al.*, 2007). The program CLUSTAL W version 1.8 (Thompson *et al.*, 1994) was used to align the sequences of strains 01-96^T and 15-51^T with those of related taxa retrieved from public databases. Phylogenetic analysis was performed via the software package MEGA version 4.1 (Tamura *et al.*, 2007), by using the neighbour-joining (Saitou & Nei, 1987) and maximum-parsimony (Fitch, 1971) methods with bootstrap values based on 1000 replications (Felsenstein, 1985). To determine genomic relatedness, the filter hybridization method was performed according to Seldin & Dubnau (1985). Probe labelling was conducted by using the non-radioactive DIG-High prime system (Roche); hybridized DNA was visualized with the DIG luminescent detection kit (Roche). Levels of DNA–DNA relatedness were quantified by using Bio-1D Image analysis software (Vilber Lourmat). The neighbour-joining phylogenetic tree based on 16S rRNA gene sequences revealed that strains 01-96^T and 15-51^T were members of the family *Sphingobacteriaceae* of the phylum *Bacteroidetes*. The two strains formed a cluster (bootstrap value 83 %) with *P. agri* PB92^T, *P. alluvionis* NWER-III1^T, *P. borealis* G-1^T, *P. roseus* CL-GP80^T, *P. sandarakinus* DS-27^T, *P. suwonensis* 15-52^T and *P. terrae* DS-57^T (Fig. 1). Similar results were also obtained with the maximum-parsimony algorithm. Levels of 16S rRNA gene sequence similarity between strain 01-96^T and the type strains of all recognized *Pedobacter* species were <96.7 %, whereas levels of similarity between strain 15-51^T and *P. borealis* G-1^T and *P. suwonensis* 15-52^T were 97.2 and 97.1 %, respectively. 16S rRNA gene sequence similarity between strains 01-96^T and 15-51^T was 96.2 %.

To clarify the taxonomic position of strain 15-51^T at the species level, DNA–DNA hybridization was performed. Levels of DNA–DNA relatedness between strain 15-51^T and *P. suwonensis* KACC 11317^T and *P. borealis* KACC 14287^T were 49.4 % (reciprocal, 45.2 %) and 40.9 % (reciprocal, 30.2 %), respectively. The 16S rRNA gene-based phylogeny and DNA–DNA hybridization results thus revealed that strains 01-96^T and 15-51^T could be classified as novel members of the genus *Pedobacter*. Strains 01-96^T and 15-51^T were found to share many physiological and morphological characteristics with each other. However, they could be differentiated from each other on the basis of their DNA G + C content, assimilation patterns of five carbon sources and temperature ranges for growth (Table 1). Strains 01-96^T and 15-51^T could be differentiated from their phylogenetically closest relatives based on hydrolysis of casein, CM-cellulose and gelatin, assimilation patterns and enzyme activities (API ZYM). On the basis of data from the present polyphasic taxonomic study, strains 01-96^T and 15-51^T are

Table 1. Differential phenotypic characteristics between strains 01-96^T and 15-51^T and the type strains of closely related *Pedobacter* species

Strains: 1, 01-96^T; 2, 15-51^T; 3, *P. agri* KACC 14024^T; 4, *P. alluvionis* KACC 14286^T; 5, *P. borealis* KACC 14287^T; 6, *P. roseus* KACC 11594^T; 7, *P. sandarakinus* KACC 11593^T; 8, *P. suwonensis* KACC 11317^T; 9, *P. terrae* KACC 13760^T. Unless otherwise indicated, data for reference type strains were compiled from Gordon *et al.* (2009), Hwang *et al.* (2006), Kwon *et al.* (2007), Roh *et al.* (2008) and Yoon *et al.* (2006, 2007). All strains are positive for aerobic growth, hydrolysis of starch, tyrosine and Tween 80, assimilation of D-xylose, galactose, glucose, mannose, methyl α -D-glucoside, N-acetylglucosamine, arbutin, aesculin, salicin, cellobiose, maltose, lactose, melibiose, sucrose, trehalose, starch, gentiobiose and turanose and enzyme activities of catalase, oxidase, alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, acid phosphatase, naphthol-AS-BI-phosphohydrolase and α -glucosidase, but negative for assimilation of glycerol, erythritol, ribose, L-xylose, sorbose, inositol, mannitol, D-tagatose, D- and L-arabitol and 2-ketogluconate and enzyme activities of lipase (C14) and α -chymotrypsin. +, Positive; (+), weakly positive; v, variable; –, negative.

Characteristic	1	2	3	4	5	6	7	8	9
Source of isolation	Cabbage rhizosphere	Cabbage rhizosphere	Soil	Floodplain sediment	Soil	Hypertrophic freshwater	Soil	Cabbage rhizosphere	Soil
Growth on MacConkey agar	–	–	–	–	–	+	–	–	–
Temperature range for growth (°C)	2–37	4–35	10–30	4–30	4–30	5–33	4–33	1–37	4–35
DNA G + C content (mol%)	37.8	38.6	41.4	39.3	39.7	41.3	39.7	44.2	39.7
Colony colour	Pinkish yellow	Pinkish yellow	Yellow	Reddish pink	Reddish pink	Pink	Orange	Pinkish yellow	Orange
Hydrolysis of:									
Casein*	+	+	–	+	+	+	–	+	+
CM-cellulose*	–	–	–	–	–	–	–	+	–
Gelatin	+	+	–	+	+	+	–	+	+
Assimilation of:*									
D-Arabinose	(+)	–	–	–	–	–	–	–	–
L-Arabinose	+	+	+	+	–	+	+	+	+
Adonitol	–	–	(+)	–	–	–	–	–	–
Methyl β -D-xyloside	–	–	–	–	–	–	+	–	–
Fructose	(+)	+	–	+	+	+	+	(+)	+
Rhamnose	+	+	(+)	+	–	+	+	+	–
Dulcitol	–	–	–	–	–	–	+	–	–
Sorbitol	(+)	–	–	–	–	–	+	–	–
Methyl α -D-mannoside	–	+	–	(+)	–	–	(+)	+	+
Amygdalin	+	+	+	+	–	+	+	+	+
Inulin	–	–	–	+	+	+	–	–	+
Melezitose	–	+	+	–	–	(+)	+	+	–
Raffinose	+	+	+	+	–	+	+	+	+
Glycogen	+	+	+	–	+	+	+	+	+
Xylitol	–	–	–	–	–	–	+	–	–
D-Lyxose	–	–	–	–	–	–	+	–	–
D-Fucose	–	–	–	–	–	–	+	–	–
L-Fucose	–	–	–	–	–	+	–	–	–
Gluconate	(+)	–	–	–	+	(+)	+	–	–
5-Ketogluconate	–	–	–	–	–	–	+	–	–
Enzyme activity* (API ZYM)									
Valine arylamidase	+	+	+	+	+	+	–	+	+
Cystine arylamidase	(+)	(+)	–	(+)	(+)	–	(+)	–	–
Trypsin	+	+	+	+	+	+	+	+	–
α -Galactosidase	+	+	–	–	+	+	–	–	–
β -Galactosidase	+	+	–	+	+	v	+	+	+
β -Glucuronidase	–	–	–	–	+	–	–	–	–
β -Glucosidase	+	+	+	+	v	–	+	+	+
N-Acetyl- β -glucosaminidase	+	+	–	+	+	+	+	+	+
α -Mannosidase	+	+	–	+	+	+	+	–	(+)
α -Fucosidase	(+)	(+)	–	(+)	+	–	–	+	–

*Data from this study except those for *P. suwonensis* KACC 11317^T.

Table 2. Cellular fatty acid profiles of strains 01-96^T and 15-51^T and the type strains of related *Pedobacter* species

Strains: 1, 01-96^T; 2, 15-51^T; 3, *P. agri* KACC 14024^T; 4, *P. alluvionis* KACC 14286^T; 5, *P. borealis* KACC 14287^T; 6, *P. roseus* KACC 11594^T; 7, *P. sandarakinus* KACC 11593^T; 8, *P. suwonensis* KACC 11317^T; 9, *P. terrae* KACC 13760^T. Data were obtained in this study except those for *P. suwonensis* KACC 11317^T, which was taken from Kwon *et al.* (2007). Prior to fatty acid extraction, all strains were grown on TSA (Difco) at 28 °C for 2 days. Values are percentages of the total fatty acids, and only fatty acids representing more than 1 % for at least one of the strains are shown. –, Not detected; tr, trace amounts (<1 %).

Fatty acid	1	2	3	4	4	6	7	8	9
Straight-chain saturated									
C _{14:0}	tr	tr	1.8	tr	1.0	tr	tr	tr	tr
C _{16:0}	7.7	4.1	6.9	2.2	2.0	3.2	tr	1.6	1.8
C _{14:0} 2-OH	tr	tr	1.0	tr	tr	tr	–	–	tr
C _{16:0} 3-OH	3.1	2.1	4.7	2.0	2.2	1.7	1.1	tr	1.1
C _{17:0} 2-OH	tr	tr	tr	tr	tr	1.0	tr	–	tr
Mono-unsaturated									
C _{15:1ω6c}	tr	tr	tr	tr	tr	tr	1.5	–	tr
C _{16:1ω5c}	2.1	1.4	3.5	2.0	2.7	1.4	1.4	1.4	1.5
C _{17:1ω8c}	tr	–	tr	–	–	–	1.0	–	–
C _{18:1ω5c}	tr	tr	–	tr	1.3	tr	tr	tr	tr
iso-C _{17:1ω9c}	5.1	6.9	1.3	4.3	6.6	5.9	3.8	7.4	7.1
Branched saturated									
anteiso-C _{15:0}	tr	tr	2.1	tr	1.1	1.9	tr	tr	tr
iso-C _{11:0}	1.0	tr	–	tr	–	tr	tr	–	tr
iso-C _{15:0}	23.1	29.6	23.7	28.9	25.4	32.0	37.1	35.4	31.4
iso-C _{17:0}	1.2	tr	tr	tr	tr	tr	tr	–	tr
iso-C _{15:0} 3-OH	2.5	2.0	2.0	3.5	3.3	2.5	3.3	2.4	2.9
iso-C _{16:0} 3-OH	tr	tr	1.4	tr	tr	tr	tr	tr	tr
iso-C _{17:0} 3-OH	15.7	12.3	10.7	14.6	14.6	16.4	18.0	15.8	17.0
Summed features*									
1	tr	tr	tr	tr	1.1	tr	tr	tr	tr
3	28.6	33.1	35.2	30.4	30.6	26.8	22.9	27.2	29.8
4	1.7	1.0	–	3.5	2.3	tr	–	tr	1.2
Unknown fatty acids†									
ECL 13.565	tr	tr	tr	tr	tr	tr	tr	1.3	tr
ECL 16.582	1.5	1.3	1.2	1.1	1.3	1.3	1.6	1.5	1.0

*Summed feature 1 comprises C_{13:0} 3-OH and/or iso-C_{15:1} I, summed feature 3 comprises iso-C_{15:0} 2-OH and/or C_{16:1ω7c} and summed feature 4 comprises anteiso-C_{17:1} B and/or iso-C_{17:1} I.

†Unknown fatty acids have no name listed in the peak library file of the MIDI system and therefore cannot be identified; equivalent chain-lengths are given.

thus considered to represent novel species of the genus *Pedobacter*, for which the names *Pedobacter rhizosphaerae* sp. nov. and *Pedobacter soli* sp. nov. are proposed, respectively.

Description of *Pedobacter rhizosphaerae* sp. nov.

Pedobacter rhizosphaerae [rhi.zo.sphae'rae. Gr. fem. n. *rhiza* root; L. fem. n. *sphaera* -ae (from Gr. fem. n. *sphaira* -as) ball, any globe, sphere; N.L. gen. fem. n. *rhizosphaerae* of the rhizosphere].

Cells are strictly aerobic, Gram-stain-negative, non-motile, non-spore-forming rods, 0.7–0.8 µm in diameter and 1.4–2.2 µm long after 2 days at 28 °C on TSA. Colonies are 0.4–1.0 mm in diameter, smooth, circular, convex and pink after 2 days at 28 °C on TSA. Grows on LB agar, NA, R2A agar and TSA, but not on MacConkey agar. Catalase- and

oxidase-positive. Growth occurs at 2–37 °C, at pH 5.5–8.0 and with NaCl concentrations of 0–1.5 %. Hydrolyses casein, gelatin, starch, tyrosine and Tween 80, but not chitin, CM-cellulose, heparin, hypoxanthine, urea or xanthine. Positive (in API ZYM strips) for alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, acid phosphatase, naphthol-AS-BI-phosphohydrolase, α-galactosidase, β-galactosidase, α-glucosidase, β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase, but negative for lipase (C14), α-chymotrypsin and β-glucuronidase activities. Assimilates D- and L-arabinose, D-xylose, galactose, glucose, fructose, mannose, rhamnose, sorbitol, methyl α-D-glucoside, N-acetylglucosamine, amygdalin, aesculin, salicin, cellobiose, maltose, lactose, melibiose, sucrose, trehalose, raffinose, starch, glycogen, gentiobiose, turanose and gluconate, but

Fig. 1. Neighbour-joining phylogenetic dendrogram constructed from a comparative analysis of 16S rRNA gene sequences showing the relationships between strains 01-96^T and 15-51^T and related species. Bootstrap values (expressed as percentages of 1000 replications) of >50 % are shown at branch points. Filled circles indicate that the corresponding branches were also recovered in the maximum-parsimony tree. Bar, 2 substitutions per 100 nucleotide positions.

not glycerol, erythritol, ribose, L-xylose, adonitol, methyl β -D-xyloside, sorbose, dulcitol, inositol, mannitol, methyl α -D-mannoside, inulin, melezitose, xylitol, D-lyxose, D-tagatose, D- or L-fucose, D- or L-arabitol or 2- or 5-ketogluconate. The predominant menaquinone is MK-7. The major fatty acids are iso-C_{17:0} 3-OH, iso-C_{15:0} and summed feature 3 (iso-C_{15:0} 2-OH and/or C_{16:1} ω 7c). The DNA G + C content of the type strain is 37.8 mol%.

The type strain, 01-96^T (=KACC 14938^T =NBRC 107690^T), was isolated from the rhizosphere of Chinese cabbage (*Brassica campestris* L.).

Description of *Pedobacter soli* sp. nov.

Pedobacter soli (so'li. L. gen. n. *soli* of soil, the source of the type strain).

Cells are strictly aerobic, Gram-stain-negative, non-motile, non-spore-forming rods, 0.7–0.8 μ m in diameter and 1.4–3.0 μ m long after 2 days at 28 °C on TSA. Colonies are 0.4–0.5 mm in diameter, smooth, circular, convex and pink after 2 days at 28 °C on TSA. Grows on LB agar, NA, R2A agar

and TSA, but not on MacConkey agar. Catalase- and oxidase-positive. Growth occurs at 4–35 °C, at pH 5.5–8.0 and with NaCl concentrations of 0–1.5 %. Hydrolyses casein, gelatin, starch, tyrosine and Tween 80, but not chitin, CM-cellulose, heparin, hypoxanthine, urea or xanthine. Positive (in API ZYM strips) for alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, acid phosphatase, naphthol-AS-BI-phosphohydrolase, α -galactosidase, β -galactosidase, α -glucosidase, β -glucosidase, *N*-acetyl- β -glucosaminidase, α -mannosidase and α -fucosidase, but negative for lipase (C14), α -chymotrypsin and β -glucuronidase activities. Assimilates L-arabinose, D-xylose, galactose, glucose, fructose, mannose, rhamnose, methyl α -D-mannoside, methyl α -D-glucoside, *N*-acetylglucosamine, amygdalin, arbutin, aesculin, salicin, cellobiose, maltose, lactose, melibiose, sucrose, trehalose, melezitose, raffinose, starch, glycogen, gentiobiose and turanose, but not glycerol, erythritol, D-arabinose, ribose, L-xylose, adonitol, methyl β -D-xyloside, sorbose, dulcitol, inositol, mannitol, sorbitol, inulin, xylitol, D-lyxose, D-tagatose, D- or L-fucose, D- or L-arabitol, gluconate or 2- or 5-ketogluconate. The

predominant menaquinone is MK-7. The major fatty acids are iso-C_{17:0} 3-OH, iso-C_{15:0} and summed feature 3 (iso-C_{15:0} 2-OH and/or C_{16:1}ω7c). The DNA G+C content of the type strain is 38.6 mol%.

The type strain, 15-51^T (=KACC 14939^T =NBRC 107691^T), was isolated from the rhizosphere of Chinese cabbage (*Brassica campestris* L.).

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