Flavisolibacter ginsengiterrae gen. nov., sp. nov. and *Flavisolibacter ginsengisoli* sp. nov., isolated from ginseng cultivating soil

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Two strains (Gsoil 492^T and Gsoil 643^T) isolated in Pocheon Province, South Korea, from soil used for ginseng cultivation were characterized using a polyphasic approach. Both isolates comprised Gram-negative, aerobic, non-motile, rod-shaped bacteria. They had similar chemotaxonomic characteristics, e.g. containing MK-7 as the major quinone, having a DNA G + C content in the range 42.5–43.3 mol% and possessing iso-C_{15:0} and iso-C_{17:0} 3-OH as the major fatty acids. A phylogenetic analysis based on 16S rRNA gene sequences indicated that the two isolates formed a tight cluster with several uncultured bacterial clones and with the established genera *Terrimonas*, *Niastella* and *Chitinophaga* in the phylum *Bacteroidetes* but were clearly separate from these genera. The levels of 16S rRNA gene sequence similarity between the isolates and type strains of related genera ranged from 87.5 to 92.4 %. Furthermore, the results of physiological and biochemical tests allowed phenotypic differentiation of the isolates from phylogenetically closely related species with validly published names. The level of 16S rRNA gene sequence similarity between the two strains was 99.5 %, whereas the DNA–DNA relatedness value was 44 %, indicating that they represent separate species. On the basis of the polyphasic evidence, a novel genus, *Flavisolibacter* gen. nov., and two novel species, *Flavisolibacter ginsengiterrae* sp. nov. (type strain Gsoil 492^T=KCTC 12656^T=DSM 18136^T) and *Flavisolibacter ginsengisoli* sp. nov. (type strain Gsoil 643^T=KCTC 12657^T=DSM 18119^T), are proposed. *Flavisolibacter ginsengiterrae* is the type species of the genus.

During the course of a study on the culturable bacterial community in soil from a ginseng field in Pocheon Province, South Korea, a large number of novel bacterial strains were isolated (Im *et al.*, 2005). Two of these isolates, Gsoil 492^T and Gsoil 643^T, were members of the phylum *Bacteroidetes* (Garrity & Holt, 2001) and were subjected to further taxonomic investigation. On the basis of the results obtained in this study, we propose that strains Gsoil 492^T and Gsoil 643^T represent members of a novel genus.

Strains Gsoil 492^T and Gsoil 643^T were isolated from soil from a ginseng field. The soil sample was thoroughly suspended with 50 mM phosphate buffer (pH 7.0) and the suspension was spread on one-fifth-strength modified R2A agar plates (containing, l⁻¹, 0.25 g tryptone, 0.25 g peptone, 0.25 g yeast extract, 0.125 g malt extract, 0.125 g beef extract, 0.25 g Casamino acids, 0.25 g soytone, 0.5 g glucose, 0.3 g soluble starch, 0.2 g xylan, 0.3 g sodium

pyruvate, 0.3 g K₂HPO₄, 0.05 g MgSO₄, 0.05 g CaCl₂ and 15 g agar) after serial dilution with 50 mM phosphate buffer (pH 7.0). The plates were incubated at 30 °C for 1 month. Single colonies on the plates were purified by transferring them onto new plates for incubation on full-strength modified R2A or one-half-strength modified R2A. As both Gsoil 492^T and Gsoil 643^T could grow well both on full-strength modified R2A agar and on commercial R2A agar (Difco), they were routinely cultured on the latter medium at 30 °C and maintained as R2A/20 % (w/v) glycerol suspensions at –70 °C.

The Gram-stain reaction was determined using the non-staining method, as described by Buck (1982). The cell morphology was observed at ×1000 magnification with a light microscope (Nikon) using cells grown for 3 days at 30 °C on R2A agar. Catalase activity was determined by assessing bubble production in 3 % (v/v) H₂O₂, and oxidase activity was determined using 1 % (w/v) tetramethyl-*p*-phenylenediamine. Carbon-source utilization and enzyme activities were tested by using the API 20NE, API 20E, ID32 GN and API ZYM test kits (bioMérieux). Anaerobic

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains Gsoil 492^T and Gsoil 643^T are AB267476 and AB267477, respectively.

growth was tested in serum bottles by adding sodium thioglycolate (1 g l^{-1}) to R2A broth and substituting the upper airspace with nitrogen gas. Tests for the degradation of DNA [performed by flooding DNase agar (Scharlau) plates with 1 M HCl], casein, chitin, starch (Atlas, 1993), lipid (Kouker & Jaeger, 1987), xylan and cellulose (Ten *et al.*, 2004) were performed and evaluated after 5 days. Growth at different temperatures (4, 15, 20, 25, 30, 37 and 42°C) and various pH values (pH 5.0–10.0, in increments of 0.5 pH units) was assessed after 5 days incubation. Salt tolerance was tested on R2A agar supplemented with 1–10 % (w/v) NaCl after 5 days incubation. Growth on nutrient agar, trypticase soy agar (TSA) and MacConkey agar was also evaluated, at 30°C . Pigment was extracted according to a previously described method (Weeks, 1981), and a spectrum was obtained using a UV-visible spectrophotometer (Beckman). Additionally, the presence of flexirubin-type pigments was tested spectrophotometrically as described previously (Güde, 1980), using 20 % KOH.

Both strains were found to be Gram-negative, aerobic, non-motile, rod-shaped bacteria. Neither strain grew on MacConkey agar or on TSA, whereas both strains could grow on one-tenth-strength TSA. Gsoil 492^T was able to grow on nutrient agar, unlike Gsoil 643^T. On R2A agar medium, strain Gsoil 492^T grew at temperatures from 15 to 30°C and at pH values between 6.0 and 8.5, whereas strain Gsoil 643^T grew at temperatures from 15 to 37°C and at pH values between 5.5 and 8.0. For both strains, the optimal temperature and pH for growth were 30°C and pH 7.0. The NaCl tolerance range for the growth of Gsoil 492^T was 0–3.0 % (w/v), whereas that for the growth of Gsoil 643^T was 0–1.0 % (w/v). Crude extracts of strains Gsoil 492^T and Gsoil 643^T showed absorption maxima at approximately 477 and 450 nm, respectively, when extracted in ethanol. A flexirubin-like yellow-coloured pigment was not produced. Other physiological characteristics of strains Gsoil 492^T and Gsoil 643^T are summarized in the species description. Phenotypic and chemotaxonomic characteristics that serve to differentiate these strains from their closest phylogenetic relatives are listed in Table 1.

To measure the G+C content of the chromosomal DNA, genomic DNA from each of the novel strains was extracted and purified as described by Moore & Dowhan (1995) and was enzymically degraded into nucleosides for analysis by reverse-phased HPLC, as described by Mesbah *et al.* (1989). Isoprenoid quinones were extracted with chloroform/methanol (2:1, v/v), evaporated under vacuum conditions and then re-extracted in n-hexane/water (1:1, v/v). The crude n-hexane-quinone solution was purified using Sep-Pak Vac silica cartridges (Waters) and subsequently analysed by HPLC as described previously (Hiraishi *et al.*, 1996). Cellular fatty acid profiles were determined from biomass harvested from one-tenth-strength TSA (Difco) after 3 days incubation. The cellular fatty acids were saponified, methylated and extracted according to the protocol of the Sherlock Microbial Identification System (MIDI). The fatty acids were analysed by using a gas

chromatograph (model 6890; Hewlett Packard) and were identified with the Microbial Identification software package (Sasser, 1990). Polyamines were extracted and analysed according to Busse & Auling (1988) and Schenkel *et al.* (1995), respectively. DNA–DNA hybridization experiments were performed using the method described by Ezaki *et al.* (1989) with photobiotin-labelled DNA probes and micro-dilution wells.

The DNA G+C contents of strains Gsoil 492^T and Gsoil 643^T were 43.0 and 42.7 mol%, respectively. The major respiratory quinone was MK-7. As shown in Table 2, the major fatty acids in both strains were iso- $\text{C}_{15:0}$ (31.2–45.9 %), iso- $\text{C}_{17:0}$ 3-OH (11.8–13.7 %) and summed feature 4 (6.2–10.5 %). The presence of iso- $\text{C}_{17:0}$, summed feature 2 and summed feature 5, and some quantitative differences in fatty acid composition, served to distinguish strains Gsoil 492^T and Gsoil 643^T from other phylogenetically related genera (Table 2).

PCR-mediated amplification of the 16S rRNA genes and sequencing of the purified PCR products were carried out according to Kim *et al.* (2005). Full sequences of the 16S rRNA genes were compiled using SeqMan software (DNASTAR). The 16S rRNA gene sequences of related taxa were obtained from GenBank. Multiple alignments were performed using the CLUSTAL_X program (Thompson *et al.*, 1997). Gaps were edited in the BioEdit program (Hall, 1999). Evolutionary distances were calculated using the Kimura two-parameter model (Kimura, 1983). Phylogenetic trees were constructed by using a neighbour-joining method (Saitou & Nei, 1987) with the MEGA3 program (Kumar *et al.*, 2004); bootstrap values were based on 1000 replications (Felsenstein, 1985).

Almost-complete 16S rRNA sequences for strains Gsoil 492^T and Gsoil 643^T were determined and subjected to comparative analysis. A phylogenetic analysis based on 16S rRNA gene sequences indicated that the two isolates were clustered with several uncultured bacterial clones and with established genera (*Terrimonas*, *Niastella* and *Chitinophaga*) in the phylum *Bacteroidetes* but were clearly separated from these genera (Fig. 1). Strains Gsoil 492^T and Gsoil 643^T showed the highest levels of 16S rRNA gene sequence similarity (91.9–92.4 %) with respect to the type strains of the genus *Terrimonas*, followed by the type strains of *Niastella* species (91.1–91.8 %) and *Chitinophaga* species (87.5–89.5 %) with their unique phylogenetic position. The level of 16S rRNA gene sequence similarity between the two strains was 99.5 % and the DNA–DNA relatedness value was 44 %, which is below the threshold (70 %) recommended for the assignment of strains to the same bacterial species (Wayne *et al.*, 1987). It is clear from the DNA–DNA relatedness value that strains Gsoil 492^T and Gsoil 643^T represent two distinct genomic species.

On the basis of the data and observations described above, it is appropriate to conclude that strains Gsoil 492^T and Gsoil 643^T represent members of a novel genus within the phylum *Bacteroidetes*, for which the name *Flavisolibacter*

Table 1. Phenotypic characteristics of strains Gsoil 492^T and Gsoil 643^T and related type strains

Strains: 1, Gsoil 492^T; 2, Gsoil 643^T; 3, *Terrimonas lutea* DY^T; 4, *Terrimonas ferruginea* ATCC 13524^T; 5, *Niastella koreensis* GR20-10^T; 6, *Niastella jeongjuensis* GR20-13^T; 7, *Chitinophaga japonensis* IFO 16041^T; 8, *Chitinophaga arvensicola* IAM 12650^T; 9, *Chitinophaga sancti* IFO 15057^T; 10, *Chitinophaga filiformis* IFO 15056^T; 11, *Chitinophaga skermanii* SG-1B^T; 12, *Chitinophaga pinensis* ACM 2034^T. Data in columns 3–12 are from Xie & Yokota (2006), Weon *et al.* (2006) and Kämpfer *et al.* (2006). None of the strains assimilate inositol. +, Positive; –, negative; w, weak reaction; v, variable among studies; ND, no data available.

Characteristic	1	2	3	4	5	6	7	8	9	10	11	12
Pigment	Yellow	Yellow	Red or yellow	Yellowish orange	Light yellow	Milky white	Yellowish orange	Yellowish orange	Golden yellow	Golden yellow	Yellow	Yellow
Cell length (µm)	0.3–1.0	0.3–6.0	1–2	0.6–4.0	10–50	10–40	2–18	0.6–4.0	2–15	30–80	1–2	<40
Gliding movement	–	–	–	–	+	+	+	–	+	+	–	+
Major fatty acids (>20 %)	iso-C _{15:0}	iso-C _{15:0}	iso-C _{15:0} , iso-C _{15:1}	iso-C _{15:0} , iso-C _{15:1}	iso-C _{15:0} , iso-C _{17:0}	iso-C _{15:0} , iso-C _{17:0}	iso-C _{15:0} , C _{16:1} ω5c	iso-C _{15:0} , C _{16:1} ω5c	iso-C _{15:0}	iso-C _{15:0} , C _{16:1} ω5c	iso-C _{15:0} , C _{16:1} ω5c	iso-C _{15:0} , C _{16:1} ω5c
Oxidase	+	–	+	+	–	+	+	+	ND	+	+	+
Catalase	–	+	w	+	–	–	+	+	–	+	+	–
Hydrolysis of:												
Starch	–	–	ND	+	–	–	–	v	+	–	ND	–
Chitin	–	–	–	–	+	+	–	ND	–	–	ND	+
Casein	–	–	ND	–	+	+	–	ND	ND	–	ND	+
Gelatin	+	+	+	–	+	+	+	v	+	w	+	+
Urea	–	–	–	–	–	–	ND	–	ND	ND	–	+
DNA	–	–	ND	–	–	–	+	+	ND	+	ND	–
Growth at 37 °C	–	+	+	+	+	–	+	–	–	+	+	+
Highest NaCl conc. (%) tolerated	3.0	1.0	1.0	1.0	ND	ND	2.0	2.0	1.0	0.3	ND	ND
Assimilation of:												
N-Acetyl-D-glucosamine	+	–	+	–	–	–	+	+	–	–	+	+
L-Arabinose	+	–	+	–	–	–	+	+	+	–	–	+
Gluconate	+	–	–	–	–	–	–	–	+	–	–	–
D-Mannose	+	–	+	+	–	–	+	+	+	+	+	+
D-Maltose	+	–	+	+	–	–	+	+	+	+	+	+
α-D-Melibiose	+	–	+	–	–	–	+	+	+	+	+	–
L-Rhamnose	+	–	–	+	–	–	+	+	–	–	–	+
D-Ribose	–	–	–	–	–	–	–	+	–	–	–	–
Sucrose	+	+	+	–	–	–	+	+	–	+	–	+
Salicin	+	–	–	–	–	–	+	+	–	+	+	+
Nitrate reduction	–	–	–	–	–	–	+	v	+	+	ND	–
DNA G + C content (mol%)	43.0	42.7	47.2	48.9	45.8	44.3	49.8	43–46	46–47	46–47	40.7	42–46

Table 2. Major fatty acids of strains Gsoil 492^T, Gsoil 643^T and related taxa

Strains: 1, Gsoil 492^T; 2, Gsoil 643^T; 3, *T. lutea* DY^T; 4, *T. ferruginea* ATCC 13524^T; 5, *N. koreensis* GR20-10^T; 6, *N. jeongjuensis* GR20-13^T; 7, *C. japonensis* IFO 16041^T; 8, *C. arvensicola* IAM 12650^T; 9, *C. sancti* IFO 15057^T; 10, *C. filiformis* IFO 15056^T; 11, *C. skermanii* SG-1B^T; 12, *C. pinensis* ACM 2034^T. Data for taxa 3–12 are from Xie & Yokota (2006), Weon *et al.* (2006) and Kämpfer *et al.* (2006). Fatty acids that account for <1.0 % of the total are not shown. Summed feature 2 comprises any combination of C_{12:0} aldehyde, C_{14:0} 3-OH and/or iso-C_{16:1}; summed feature 3 comprises any combination of iso-C_{15:0} 2-OH and/or C_{16:1}ω7c; summed feature 4 comprises any combination of iso-C_{17:1} I and/or anteiso-C_{17:1} B; summed feature 5 comprises iso-C_{17:1} I and/or anteiso-C_{17:1} B; summed feature 6 comprises C_{18:2}ω6,9c and/or anteiso-C_{18:0}; summed feature 7 comprises C_{18:1}ω7c, C_{18:1}ω9t or C_{18:1}ω12t or any combination of these isomers. –, Not detected.

Fatty acid	1	2	3	4	5	6	7	8	9	10	11	12
iso-C _{14:0}	–	–	4.3	1.1	–	–	–	–	–	–	–	–
C _{14:0}	–	–	–	–	–	–	–	1.4	–	–	1.8	–
iso-C _{15:0} 3-OH	1.4	1.0	2.3	2.2	1.3	1.9	2.4	3.0	3.4	3.3	2.6	3.1
iso-C _{15:0}	45.9	31.2	34.8	28.4	26.8	30.6	40.0	35.3	44.0	37.3	47.3	30.4
anteiso-C _{15:0}	5.9	5.0	–	–	4.9	3.3	–	–	–	–	–	–
iso-C _{15:1}	5.3	4.4	21.8	26.2	15.6	14.7	–	–	–	–	–	–
C _{15:0}	–	–	–	2.7	–	–	–	–	–	–	–	–
iso-C _{17:1} ω9c	1.3	–	–	–	–	–	–	–	1.1	–	–	–
C _{16:1} ω11c	–	–	–	–	–	–	1.0	–	–	–	–	1.9
C _{16:1} ω5c	–	–	–	–	–	1.2	22.2	33.6	13.5	25.5	24.4	33.2
C _{16:0} 2-OH	–	–	–	–	–	–	3.0	–	–	1.1	–	–
C _{16:0}	5.5	7.5	1.1	1.7	2.6	2.9	3.0	5.1	4.2	4.3	3.5	4.2
iso-C _{16:0}	–	–	–	1.4	1.0	–	–	0.3	–	–	–	–
C _{16:0} 10-methyl	–	2.6	–	–	–	–	–	–	–	–	–	–
C _{16:0} 2-OH	–	2.9	–	–	–	–	–	–	–	–	–	–
C _{16:0} 3-OH	–	–	3.3	2.5	1.3	2.3	–	1.7	–	1.2	1.6	1.2
iso-C _{17:0}	3.1	9.1	–	–	1.6	–	–	–	–	–	–	–
anteiso-C _{17:0}	–	1.0	–	–	–	–	–	–	–	–	–	–
C _{17:0} 2-OH	–	–	–	–	3.5	2.6	–	–	–	–	–	–
C _{17:0} 3-OH	–	–	–	–	1.2	–	–	–	–	–	–	–
iso-C _{17:0} 3-OH	13.7	11.8	14.2	15.3	29.4	27.1	13.0	5.9	9.1	11.8	5.0	11.5
C _{18:0}	–	2.0	–	–	–	–	–	–	–	–	–	–
Unknown	–	–	–	–	–	–	–	–	–	–	–	–
Equivalent chain-length 13.565	–	–	3.2	1.3	–	–	3.1	3.6	3.2	2.5	4.4	2.6
Equivalent chain-length 16.582	–	–	1.8	1.3	1.4	1.6	1.1	–	1.3	0.9	–	1.1
Summed features												
2	2.7	2.5	–	–	–	–	–	–	–	–	–	–
3	–	–	14.9	11.2	4.3	5.3	3.3	3.7	16	11.2	3.5	7.7
4	10.5	6.2	–	–	–	–	1.3	–	–	–	–	–
5	1.4	3.1	–	–	–	–	1.3	–	–	–	–	–
6	–	1.7	–	–	–	–	1.3	–	–	–	–	–
7	–	1.2	–	–	–	–	1.3	–	–	–	–	–

nov. is proposed. Strains Gsoil 492^T and Gsoil 643^T should be classified within this genus as *Flavisolibacter ginsengiterrae* sp. nov. and *Flavisolibacter ginsengisoli* sp. nov., respectively.

Description of *Flavisolibacter* gen. nov.

Flavisolibacter (Fla.vi.so.li.bac'ter. L. adj. *flavus* yellow; L. n. *solum* soil; N.L. masc. n. *bacter* a rod; N.L. masc. n. *Flavisolibacter* a yellow, rod-shaped bacterium from soil).

Gram-negative, aerobic, non-motile and chemoheterotrophic. Nitrate is not reduced under aerobic conditions.

The major fatty acids are iso-C_{15:0} and iso-C_{17:0} 3-OH. The major respiratory quinone is MK-7. Homospermidine is the major polyamine component. Positioned phylogenetically within the phylum *Bacteroidetes*. The type species is *Flavisolibacter ginsengiterrae*.

Description of *Flavisolibacter ginsengiterrae* sp. nov.

Flavisolibacter ginsengiterrae (gin.sen.gi.te.r'rae. N.L. n. *ginsengum* ginseng; L. n. *terra* soil; N.L. gen. n. *ginsengiterrae* of soil from a ginseng field).

Fig. 1. Rooted phylogenetic tree based on the 16S rRNA gene sequences of strains Gsoil 492^T and Gsoil 643^T and related bacteria in the phylum *Bacteroidetes*. This tree was constructed using the neighbour-joining method (Saitou & Nei, 1987) with a two-parameter Kimura (1983) distance matrix and pairwise deletion. Bootstrap percentages (from 1000 replications) greater than 70% are shown at the branch points. Bar, 20 nucleotide substitutions per 1000 nucleotides.

Possesses the following properties in addition to those given in the genus description. Cells are $0.3\text{--}0.7 \times 0.6\text{--}1.0\text{ }\mu\text{m}$. Colonies grown on R2A agar plates are smooth, circular, convex, opaque and yellow in colour within 5 days at $30\text{ }^{\circ}\text{C}$. Optimal growth temperature and pH are $30\text{ }^{\circ}\text{C}$ and pH 7.0. *N*-acetyl-D-glucosamine, L-arabinose, L-fucose, glycogen, glucose, histidine, maltose, D-mannose, D-melibiose, L-proline, rhamnose, salicin and D-sucrose are assimilated. Positive for hydrolysis of aesculin and gelatin and for β -galactosidase activity. Negative reactions are observed for hydrolysis of urea, indole production, glucose fermentation, arginine dihydrolase, H_2S production and assimilation of acetate, adipate, L-alanine, n-caprate, citrate, gluconate, 3-hydroxybenzoate, 4-hydroxybenzoate, 3-hydroxybutyrate, inositol, itaconate, 2-ketogluconate, 5-ketogluconate, lactate, DL-malic acid, malonate, mannitol, phenylacetate, propionate, D-ribose, L-serine, D-sorbitol, suberate and valerate. With the API ZYM gallery, positive for *N*-acetyl- β -glucosaminidase, acid phosphatase, alkaline phosphatase, α -chymotrypsin, cystine arylamidase, esterase (C4), esterase lipase (C8), α -galactosidase, β -galactosidase, β -glucosidase, leucine arylamidase and valine arylamidase, and weakly positive for α -fucosidase. Negative for α -glucosidase, β -glucuronidase, lipase (C14), α -mannosidase, naphthol-AS-BI-phosphohydrolase and trypsin. The DNA G+C content is 43.0 mol%.

The type strain, Gsoil 492^T (=KCTC 12656^T=DSM 18136^T), was isolated from soil from a ginseng field in Pocheon Province, South Korea.

Description of *Flavisolibacter ginsengisoli* sp. nov.

Flavisolibacter ginsengisoli (gin.sen.gi.so'li. N.L. n. *ginsengum* ginseng; L. n. *solum* soil; N.L. gen. n. *ginsengisoli* of soil from a ginseng field).

Possesses the following properties in addition to those given in the genus description. Cells are $0.3\text{--}0.7 \times 3.0\text{--}6.0\text{ }\mu\text{m}$. Colonies grown on R2A agar plates are circular, convex, opaque and yellow. Optimal growth temperature and pH are $30\text{ }^{\circ}\text{C}$ and pH 7.0. 3-Hydroxybenzoate, L-fucose, 5-ketogluconate, mannitol, L-proline and D-sucrose are assimilated. Positive for hydrolysis of aesculin and for β -galactosidase activity. Negative reactions are observed for hydrolysis of urea and gelatin, indole production, glucose fermentation, arginine dihydrolase, H_2S production and assimilation of acetate, *N*-acetyl-D-glucosamine, adipate, L-alanine, L-arabinose, n-caprate, citrate, gluconate, glucose, glycogen, histidine, 4-hydroxybenzoate, 3-hydroxybutyrate, inositol, itaconate, 2-ketogluconate, lactate, DL-malic acid, malonate, maltose, D-mannose, D-melibiose, phenylacetate, propionate, rhamnose, D-ribose, salicin, L-serine, D-sorbitol, suberate and valerate. With the API ZYM gallery, positive for *N*-acetyl- β -glucosaminidase, acid phosphatase, alkaline phosphatase, α -chymotrypsin, cystine arylamidase, esterase (C4), esterase lipase (C8), α -galactosidase, α -glucosidase, β -glucosidase, leucine arylamidase and valine arylamidase, and weakly positive for α -fucosidase. Negative for β -galactosidase, β -glucuronidase, lipase (C14), α -mannosidase, naphthol-AS-BI-phosphohydrolase and trypsin. The DNA G+C content is 42.7 mol%.

The type strain, Gsoil 643^T (=KCTC 12657^T=DSM 18119^T), was isolated from soil from a ginseng field in Pocheon Province, South Korea.

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