Dyella soli sp. nov. and *Dyella terrae* sp. nov., isolated from soil

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Two novel strains isolated from soils, JS12-10^T and JS14-6^T, were characterized using a polyphasic approach to determine their taxonomic positions. These isolates were found to be aerobic, Gram-negative, motile with one polar flagellum, non-spore-forming and rod-shaped. Phenotypic and fatty acid data supported the affiliation of JS12-10^T and JS14-6^T to the genus *Dyella*. However, chemotaxonomic data and DNA–DNA relatedness values allowed differentiation of these strains from other *Dyella* species with validly published names. Strains JS12-10^T and JS14-6^T showed the highest 16S rRNA gene sequence similarities with *Dyella ginsengisoli* Gsoil 3046^T (98.4 %) and *Dyella japonica* XD53^T (97.9 %), respectively, and the 16S rRNA gene sequence similarity between them was 97.1 %. DNA–DNA hybridization values between the novel isolates and strains of other recognized *Dyella* species were 29–38 %. Therefore, strains JS12-10^T and JS14-6^T represent two novel species of the genus *Dyella*, for which the names *Dyella soli* sp. nov. (type strain JS12-10^T = KACC 12747^T = JCM 15423^T) and *Dyella terrae* sp. nov. (type strain JS14-6^T = KACC 12748^T = JCM 15424^T) are proposed.

Xie & Yokota (2005) isolated three bacterial strains from garden soil and assigned them to a novel genus, *Dyella*, with *Dyella japonica* as the type species. Members of the genus *Dyella* are yellow-coloured rods that are catalase- and oxidase-positive and urease-negative. These yellow-pigmented strains were shown to be distinguished from other genera, as represented by *Frateuria aurantia* (Swings *et al.*, 1980), *Rhodanobacter lindaniclasticus* (Nalin *et al.*, 1999), *Fulvimonas soli* (Mergaert *et al.*, 2002) and *Luteibacter rhizovicinus* (Johansen *et al.*, 2005), based on 16S rRNA gene sequences. In addition, the genus *Dyella* can be differentiated from *Frateuria aurantia* by the absence of cellular fatty acids C_{12:0} 2-OH, C_{12:0} 3-OH, C_{18:0} and C_{17:0} cyclo in *Dyella* species and from *Fulvimonas soli* on the basis of G+C content (63–67 compared with 71.7 mol% for *Fulvimonas soli*). At present,

the genus *Dyella* includes five species, namely *D. japonica* (Xie & Yokota, 2005), *D. koreensis* (An *et al.*, 2005), *D. yejuensis* (Kim *et al.*, 2006), *D. ginsengisoli* (Jung *et al.*, 2009) and *D. marensis* (Lee & Lee, 2009).

During a survey on cultivable bacterial communities, we isolated two yellow-coloured strains, JS12-10^T and JS14-6^T, from forest soil and soil cultivated with *Citrus* species, respectively, taken from Jeju island, Republic of Korea. These two strains were shown to be affiliated with the genus *Dyella* of the order *Xanthomonadales* and subjected to further taxonomic characterization. The results from phenotypic, chemotaxonomic and phylogenetic analyses, in combination with DNA–DNA hybridization experiments, showed the distinctiveness of strains JS12-10^T and JS14-6^T, both from each other and from the type strains of species of *Dyella*.

Soil samples (1 g) were suspended in 9 ml 0.85 % NaCl (w/v) solution and mixed in a shaker for 30 min. Aliquots of the serially diluted sample were spread on R2A agar plates (Reasoner & Geldreich, 1985) and incubated at 28 °C for 5 days. Strains JS12-10^T and JS14-6^T, which could be distinguished by their yellow-coloured colonies, were cultured and maintained on R2A agar at 28 °C and were

Abbreviations: DIG, digoxigenin–11-dUTP; ML, maximum-likelihood; MP, maximum-parsimony; NJ, neighbour-joining.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains JS12-10^T and JS14-6^T are EU604272 and EU604273, respectively.

Maximum-likelihood and maximum-parsimony trees based on 16S rRNA gene sequences are available with the online version of this paper.

subjected to taxonomic investigation. *D. japonica* DSM 16301^T, *D. koreensis* KCTC 12359^T, *D. yejuensis* KACC 11405^T, *Frateruia aurantia* DSM 6220^T and *L. rhizovicinus* KACC 12830^T were used as reference strains in biochemical, chemotaxonomic and DNA–DNA hybridization experiments. To investigate basic morphological, physiological and biochemical characteristics, the methods described by Smibert & Krieg (1994) were used for Gram staining, oxidase and catalase reactions and to test for hydrolysis of CM-cellulose, casein, chitin, DNA, pectin, starch, tyrosine, Tween 80 and xanthine. R2A medium was used to determine growth at various temperatures (5–45 °C at intervals of 5 °C) and requirement for NaCl (0–5 %, w/v). The pH range for growth (pH 4–10 at intervals of 1 pH unit) was determined in R2A broth adjusted with citrate-phosphate buffer or Tris/HCl buffer (Breznak & Costilow, 1994). Cell morphology was observed by transmission electron microscopy (model 912AB; LEO) and phase-contrast microscopy (Axio; Zeiss). For observation of cell morphology by TEM, cells were grown on R2A agar and suspended in physiological saline solution. A small drop of the suspension was placed on a carbon-coated copper grid and the cells were negatively stained with 0.5 % uranyl acetate. For other phenotypic tests, API 20 NE, ID 32 GN and API ZYM test kits (bioMérieux) were used according to the manufacturer's recommendations. The API ZYM tests were read after 4 h incubation at 37 °C, the other API tests after 5 days at 28 °C. Whole-cell fatty acids were analysed according to the standard protocol of the MIDI/Hewlett Packard Microbial Identification System (Sasser, 1990) after cultivation on R2A agar for 2 days at 28 °C.

Genomic DNA was isolated and purified following the method described by Ausubel *et al.* (1987). The 16S rRNA gene sequence was amplified by using the universal primers fD1 and rP2 (Weisburg *et al.*, 1991) and sequenced as described by Weon *et al.* (2005) with an automatic DNA sequencer (ABI 3100; Applied Biosystems). The 16S rRNA gene sequences were aligned with the CLUSTAL W program (Thompson *et al.*, 1994). Evolutionary distances were calculated using Kimura's two-parameter model (Kimura, 1983). Phylogenetic trees were constructed with neighbour-joining (Saitou & Nei, 1987), maximum-parsimony (Fitch, 1971) and maximum-likelihood (Felsenstein, 1981) methods using the program MEGA3 (Kumar *et al.*, 2004) and bootstrap values were calculated on the basis of 1000 replications (Felsenstein, 1985).

DNA–DNA hybridization experiments were performed using reagents from Roche Diagnostics according to the manufacturer's instructions, as follows. Chromosomal DNA of strains JS12-10^T and JS14-6^T, type strains of species of the genus *Dyella* and *Frateruia aurantia* DSM 6220^T were used to construct hybridization probes by labelling with digoxigenin-11-dUTP (DIG). DNA samples from strains JS12-10^T and JS14-6^T were loaded on to positively charged membranes as described by Seldin & Dubnau (1985). Pre-hybridization and hybridization con-

ditions for the DIG-labelled probes were as described for the DIG High Prime DNA Labeling and Detection Starter kit II. After hybridization, the blots were subjected to stringent washing steps, after which the chemiluminescence detection kit, based on CSPD, was used. Levels of relatedness were determined by scanning the X-ray membranes and slot intensities were determined by using the 1D Image Analysis Software version 3.0 (Kodak Digital Science). Self-hybridization values were considered to represent 100 % of the maximal achievable signal and values obtained with the other strains were compared with this standard. The experiments were carried out in triplicate for each sample. G + C contents were determined by HPLC analysis of deoxyribonucleosides as described by Mesbah *et al.* (1989), using a reversed-phase column (Supelcosil LC-18 S; Supelco).

Strains JS12-10^T and JS14-6^T were Gram-negative, aerobic, rod-shaped and motile with one flagellum. Both grew well on R2A agar, nutrient agar and tryptic soy agar (Difco). Strain JS14-6^T grew on MacConkey agar (Difco) but strain JS12-10^T did not. The strains could be differentiated from each other on the basis of DNA hydrolysis, nitrate reduction, arginine hydrolysis, assimilation of carbon compounds and enzyme activities. Also, the two strains could be separated from other members of genus *Dyella*, *Frateruia aurantia* and *L. rhizovicinus* on the basis of phenotypic properties (Table 1).

For the 16S rRNA gene sequence analysis, continuous stretches of 1420 bp (strain JS12-10^T) and 1423 bp (JS14-6^T) were obtained and analysed. Strain JS12-10^T showed the highest sequence similarities to *D. ginsengisoli* Gsoil 3046^T (98.4 %) and *D. koreensis* BB4^T (98.1 %), followed by *D. japonica* XD53^T (97.9 %), *Frateruia aurantia* DSM 6220^T (97.5 %), *D. marensis* CS5-B2^T (97.2 %), strain JS14-6^T (97.1 %) and *D. yejuensis* R2A16-10^T (96.1 %). Strain JS14-6^T showed high sequence similarities to *D. japonica* XD53^T (97.9 %), *D. ginsengisoli* Gsoil 3046^T (97.3 %), *D. marensis* CS5-B2^T (97.2 %), strain JS12-10^T (97.1 %), *D. koreensis* BB4^T (96.8 %), *D. yejuensis* R2A16-10^T (96.7 %) and *Frateruia aurantia* DSM 6220^T (96.7 %). Evolutionary trees based on 16S rRNA gene sequences were constructed with the neighbour-joining (NJ), maximum-parsimony (MP) and maximum-likelihood (ML) methods (Fig. 1 and Supplementary Fig. S1, available in IJSEM Online). The overall topologies of the phylogenetic trees were similar irrespective of the phylogenetic methods used. The phylogenetic analysis revealed that the genus *Dyella* is polyphyletic and that the 16S rRNA gene sequence from *Frateruia aurantia* DSM 6220^T is similar to those of the *Dyella* species (Fig. 1). This anomaly can be explained by the high evolutionary rate of the 16S rRNA gene, meaning that multiple substitutions often occur at the same nucleotide position. This implies that there has been mutational saturation of 16S rRNA gene nucleotide sequences, which is known to confuse phylogenetic inference (Leblond-Bourget *et al.*, 1996; Dauga, 2002). This phenomenon was obvious when the addition of the

Table 1. Differential phenotypic characteristics of strains JS12-10^T and JS14-6^T and type strains of related species

Strains: 1, *Dyella soli* sp. nov. JS12-10^T; 2, *Dyella terrae* sp. nov. JS14-6^T; 3, *D. yeojuensis* KACC 11405^T; 4, *D. japonica* DSM 16301^T; 5, *D. koreensis* KCTC 12359^T; 6, *D. ginsengisoli* Gsoil 3046^T; 7, *D. marensis* CS5-B2^T; 8, *Frateruia aurantia* DSM 6220^T; 9, *Luteibacter rhizovicinus* KACC 12830^T. Unless indicated otherwise, data were obtained in this study (columns 1, 2 and 9) or taken from Kim *et al.* (2006) (columns 3–5 and 8), Jung *et al.* (2009) (column 6) and Lee & Lee (2009) (column 7). All strains are positive for alkaline phosphatase, esterase lipase (C8), leucine arylamidase, valine arylamidase and naphthol-AS-BI-phosphohydrolase (except *D. ginsengisoli* Gsoil 3046^T; data not available) and assimilate D-glucose. All strains are negative for indole production, urease, lipase (C14), trypsin, β -glucuronidase and α -mannosidase (except *D. ginsengisoli* Gsoil 3046^T; data not available) and do not assimilate L-arabinose, D-mannitol, potassium gluconate, capric acid, adipic acid, trisodium citrate or phenylacetic acid. +, Positive; (+), weakly positive; –, negative; ND, not detected/not reported.

Characteristic	1	2	3	4	5	6	7	8	9
Catalase/oxidase	+/+	+/+	+/+	–/+	+/(+)	+/+	+/-	–/+	+/+*
Motility	+	+	+	+	–	+	+	+	+*
Growth at:									
4 % NaCl	–	–	+	–	(+)	–	–	–	–*
pH 4.5	+	+	–	–	ND	–	–	+	–*
Hydrolysis of:									
Casein	–	–	+	–	+	–	–	–	ND
CM-cellulose	–	–	–	–	+	–	–	–	ND
DNA	–	+	+	+	+	–	+	+	+*
Starch	–	–	–	–	–	+	+	–	+*
Acid production from:									
Arabinose	–	–	–	+	+	–	–	+	ND
Glucose	–	–	+	+	+	+	+	+	–
Lactose	–	–	–	–	–	ND	+	+	ND
Trehalose	–	–	–	+	+	ND	+	+	ND
API 20NE tests									
Nitrate reduction	+	–	–	+	+	ND	–	–	–
Glucose fermentation	–	–	–	–	–	+	+	+	(+)
Arginine dihydrolase	+	–	–	–	–	ND	–	–	–
Aesculin hydrolysis	–	–	+	–	+	ND	ND	–	+
Gelatin hydrolysis	–	–	+	–	+	+	+	–	+
β -Galactosidase	–	(+)	+	–	+	ND	+	–	+
Assimilation of: (API 20NE)									
N-Acetylglucosamine	+	+	+	+	+	+	+	–	+
Malic acid	–	–	–	–	+	–	+	–	–
Maltose	+	+	+	+	+	+	+	–	+
D-Mannose	–	+	+	+	+	–	+	–	+
Enzyme activity (API ZYM)									
Acid phosphatase	+	+	+	+	+	ND	+	–	+
α -Chymotrypsin	–	–	–	–	–	–	+	–	–
Cystine arylamidase	–	+	+	–	–	ND	(+)	–	–
α -Fucosidase	–	–	–	–	+	ND	–	–	–
Esterase (C4)	+	+	+	+	+	+	–	+	+
α -Galactosidase	–	–	+	–	–	ND	+	–	+
α -Glucosidase	+	–	+	+	+	ND	+	–	+
β -Glucosidase	+	–	+	+	+	ND	+	–	+
N-Acetyl- β -glucosaminidase	+	–	+	–	+	ND	–	–	–
DNA G + C content (mol%)	67.0	64.0	63.0	63.5	63.8	66.6	66.2	63.5	64.3

*Data from Johansen *et al.* (2005).

sequence from *D. yeojuensis* R2A16-10^T resulted in bifurcation of the genus *Dyella*. Horizontal gene transfer may explain some of the discrepancies between the defined phylogenetic clusters and the groups described by phenotypic data (Dauga, 2002). However, as far as is known to

date, there is no report of horizontal gene transfer between *Dyella* species and *Frateruia aurantia*. The sequence from strain JS12-10^T clustered with that from *D. ginsengisoli* Gsoil 3046^T and the sequence from strain JS14-6^T clustered with that from *D. japonica* XD53^T (with bootstrap values of

Fig. 1. Neighbour-joining tree based on almost-complete 16S rRNA gene sequences showing the phylogenetic position of strains JS12-10^T and JS14-6^T. Numbers at nodes (>40%) indicate percentages of 1000 bootstrap resamplings. The outgroup is *Xanthomonas campestris* LMG 568^T. Bar, 0.01 substitutions per nucleotide position.

73, 79 and 53% and 45, 52 and 20% for the NJ, ML and MP trees, respectively). The bootstrap values of the nodes of the few clusters obtained were too low to induce much confidence and indicate that the 16S rRNA gene sequence alone cannot resolve the phylogenetic relationship among the genera *Dyella*, *Frateruia*, *Fulvimonas* and *Luteibacter* (Dauga, 2002). The NJ, ML and MP trees placed the sequence from *Frateruia aurantia* DSM 6220^T within the

cluster for *Dyella* species, which is in complete disagreement with phenotypic and fatty acid data (Tables 1 and 2). Fatty acid profiles, G+C contents and phenotypic properties may be used to differentiate these genera.

The major fatty acids (>10%) of strain JS12-10^T were iso-C_{17:1}ω9c (24.2%), iso-C_{15:0} (19.9%) and iso-C_{16:0} (17.8%) and the major fatty acids of strain JS14-6^T were

Table 2. Cellular fatty acid compositions of strains JS12-10^T and JS14-6^T and type strains of closely related species

Strains: 1, *D. soli* sp. nov. JS12-10^T; 2, *D. terrae* sp. nov. JS14-6^T; 3, *D. yeojuensis* KACC 11405^T; 4, *D. japonica* DSM 16301^T; 5, *D. koreensis* KCTC 12359^T; 6, *D. ginsengisoli* Gsoil 3046^T; 7, *Frateruia aurantia* DSM 6220^T; 8, *Luteibacter rhizovicius* KACC 12830^T. Data were obtained in this study (columns 1, 2 and 8) or were taken from Kim *et al.* (2006) (columns 3–5 and 7) and Jung *et al.* (2009) (column 6). All data were collected from cultures after 2 days on R2A agar at 28 °C. —, Not detected or <1%.

Fatty acid	1	2	3	4	5	6	7	8
iso-C _{11:0}	3.4	3.8	3.7	5.0	4.5	4.9	—	3.8
iso-C _{11:0} 3-OH	3.8	5.2	4.2	6.0	5.5	4.0	—	3.4
C _{12:0} 2-OH	—	—	—	—	—	—	2.2	—
C _{12:0} 3-OH	—	—	—	—	—	—	5.7	—
iso-C _{12:0} 3-OH	—	1.6	1.0	1.4	1.4	—	—	—
iso-C _{13:0} 3-OH	2.6	2.8	2.4	4.0	2.3	2.8	1.2	2.6
C _{14:0}	—	—	—	—	—	—	3.1	—
C _{14:1} ω5c	—	—	—	—	—	—	1.0	—
iso-C _{14:0}	—	1.2	1.1	—	1.1	—	—	1.4
anteiso-C _{15:0}	4.9	3.1	6.9	5.1	3.6	4.1	2.4	8.8
iso-C _{15:0}	19.9	18.2	14.5	14.6	11.1	14.6	41.2	25.4
C _{16:0}	1.9	1.8	1.8	1.5	2.5	3.4	7.5	8.8
iso-C _{16:0}	17.8	21.6	21.3	17.5	19.2	5.1	—	8.4
iso-C _{16:1} H	1.1	1.1	—	—	—	—	—	—
C _{17:0} cyclo	—	—	—	—	—	—	9.8	8.3
C _{17:1} ω6c	—	1.4	—	—	—	—	—	—
anteiso-C _{17:0}	1.8	1.1	1.6	1.8	2.9	0.8	—	—
iso-C _{17:0}	8.3	5.0	7.9	8.5	6.7	29.2	5.3	8.8
iso-C _{17:0} 3-OH	—	—	—	1.5	—	—	—	—
iso-C _{17:1} ω9c	24.2	18.9	21.5	20.3	19.0	28.2	1.8	8.8
C _{18:0}	—	—	—	—	—	—	1.2	—
iso-C _{18:0}	—	1.0	1.2	1.3	2.6	—	—	—
Unknown 11.799	2.0	2.6	2.3	3.1	2.5	1.1	—	2.0
Summed feature 3*	4.2	8.5	5.2	5.0	7.9	2.0	10.5	6.6

*Summed feature 3 contains iso-C_{15:0} 2-OH and/or C_{16:1}ω7c.

iso-C_{16:0} (21.6 %), iso-C_{17:1}ω9c (18.9 %) and iso-C_{15:0} (18.2 %) (Table 2). The fatty acid profiles of the *Dyella* species and the novel isolates differed from *Frateruia aurantia* DSM 6220^T and *L. rhizovicinus* KACC 12830^T in the absence of C_{17:0} cyclo, C_{12:0} 2-OH, C_{12:0} 3-OH, C_{14:0} and C_{14:1}ω5c, the presence of anteiso-C_{17:0} and a larger proportion of iso-C_{17:1}ω9c. Strains JS12-10^T and JS14-6^T could be differentiated from the other strains tested on the basis of the presence of iso-C_{16:1} H in the novel isolates. Strain JS14-6^T contained iso-C_{12:0} 3-OH, iso-C_{14:0}, C_{17:1}ω6c and iso-C_{18:0}, which strain JS12-10^T did not. Only *D. japonica* DSM 16301^T contained iso-C_{17:0} 3-OH and *D. ginsengisoli* Gsoil 3046^T contained a larger percentage of iso-C_{17:0} than the other strains tested.

The DNA G + C contents of strains JS12-10^T (67.0 mol%) and JS14-6^T (64.0 mol%) are close to the G + C contents reported for *D. ginsengisoli* (66.6 mol%), *D. marenensis* (65.7–66.7 mol%), *D. japonica* (63.4–64.0 mol%) and *D. koreensis* (63.8 mol%). The DNA–DNA hybridization values for strain JS12-10^T with respect to *D. koreensis* KCTC 12359^T, *D. japonica* DSM 16301^T, strain JS14-6^T and *Frateruia aurantia* DSM 6220^T were 35, 32, 29 and 26 %, respectively. The levels of DNA–DNA relatedness for strain JS14-6^T with respect to *D. japonica* DSM 16301^T, *D. yeosuensis* KACC 11405^T, strain JS12-10^T and *Frateruia aurantia* DSM 6220^T were 38, 30, 30 and 26 %, respectively. DNA–DNA hybridization results revealed that strains JS12-10^T and JS14-6^T were genotypically distant from each other and the type strains of *Dyella* and *Frateruia*. A bacterium that shows a 16S rRNA gene sequence similarity of 98 % or below to its closest relatives is generally considered to belong to a different species, and this relatively low level of similarity usually indicates that the DNA–DNA reassociation level is lower than 50 % (Wayne *et al.*, 1987).

On the basis of the data from polyphasic studies, including analyses of biochemical properties, fatty acid composition, 16S rRNA gene sequences and DNA–DNA hybridization values, it is shown that strains JS12-10^T and JS14-6^T represent two novel species within the genus *Dyella*, for which the names *Dyella soli* sp. nov. and *Dyella terrae* sp. nov., respectively, are proposed.

Description of *Dyella soli* sp. nov.

Dyella soli (so'li. L. gen. n. *soli* of soil).

Cells are Gram-negative, aerobic, rod-shaped, 0.4–0.5 µm wide and 0.9–5.0 µm long, and motile with one polar flagellum. After growth on R2A medium at 28 °C for 2 days, colonies are yellow and irregular. Grows well on R2A agar, nutrient agar and tryptic soy agar and does not grow on MacConkey agar. Positive for nitrate reduction and methyl red tests and negative for Voges–Proskauer test, H₂S production and phenylalanine deaminase. Grows at 10–35 °C (optimum 28–30 °C), pH 4–8 (optimum pH 6–7) and 0–2 % (w/v) NaCl (optimum 0–1 %). Tween 80 and tyrosine are hydrolysed, but casein, chitin, CM-cellulose, DNA, pectin, starch and xanthine are not. Positive for

arginine dihydrolase, but negative for indole production, glucose fermentation, urease, aesculin hydrolysis, gelatin hydrolysis and β-galactosidase (API 20NE). In addition to the data shown in Table 1, sodium acetate is weakly assimilated but L-rhamnose, D-ribose, inositol, sucrose, itaconic acid, suberic acid, sodium malonate, lactic acid, L-alanine, potassium 5-ketogluconate, glycogen, 3-hydroxybenzoic acid, L-serine, salicin, melibiose, L-fucose, D-sorbitol, propionic acid, valeric acid, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid, 4-hydroxybenzoic acid and L-proline are not assimilated (API ID 32 GN). Major fatty acids (>5 %) are iso-C_{17:1}ω9c, iso-C_{15:0}, iso-C_{16:0} and iso-C_{17:0}. The DNA G + C content of the type strain is 67.0 mol%.

The type strain, JS12-10^T (=KACC 12747^T =JCM 15423^T), was isolated from forest soil taken from Jeju island, Republic of Korea.

Description of *Dyella terrae* sp. nov.

Dyella terrae (ter'rae. L. gen. n. *terrae* of the soil).

Cells are Gram-negative, aerobic, rod-shaped, 0.4–0.5 µm wide and 1.0–5.0 µm long, and motile with one polar flagellum. After growth on R2A medium at 28 °C for 2 days, colonies are yellow and irregular. Grows well on R2A agar, nutrient agar, tryptic soy agar and MacConkey agar. Positive for methyl red test and negative for nitrate reduction, Voges–Proskauer, H₂S production and phenylalanine deaminase. Grows at 10–35 °C (optimum 28–30 °C), pH 4–9 (optimum pH 6–7) and 0–3 % (w/v) NaCl (optimum 0–1 %). DNA and tyrosine are hydrolysed, Tween 80 is weakly hydrolysed, but casein, chitin, CM-cellulose, pectin, starch and xanthine are not. Weakly positive for β-galactosidase, but negative for indole production, glucose fermentation, arginine dihydrolase, urease, aesculin hydrolysis and gelatin hydrolysis (API 20NE). In addition to the data shown in Table 1, sodium acetate, L-serine and 3-hydroxybutyric acid are assimilated, but L-rhamnose, D-ribose, inositol, sucrose, itaconic acid, suberic acid, sodium malonate, lactic acid, L-alanine, potassium 5-ketogluconate, glycogen, 3-hydroxybenzoic acid, salicin, melibiose, L-fucose, D-sorbitol, propionic acid, valeric acid, L-histidine, potassium 2-ketogluconate, 4-hydroxybenzoic acid and L-proline are not (API ID 32 GN). Major fatty acids (>5 %) are iso-C_{16:0}, iso-C_{17:1}ω9c, iso-C_{15:0}, summed feature 3 (iso-C_{15:0} 2-OH and/or C_{16:1}ω7c), iso-C_{11:0} 3-OH and iso-C_{17:0}. The DNA G + C content of the type strain is 64.0 mol%.

The type strain, JS14-6^T (=KACC 12748^T =JCM 15424^T), was isolated from soil cultivated with *Citrus* species on Jeju island, Republic of Korea.

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