Current Microbiology
https://doi.org/10.1007/s00284-019-01801-w

Lysobacter segetis sp. nov., Isolated from Soil

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Received: 27 July 2019 / Accepted: 22 October 2019

Abstract

A Gram-negative, aerobic, motile by gliding, rod-shaped bacterium, strain 17J68-2^T, was isolated from a soil sample taken from Jeju Island, Republic of Korea. The isolate displayed high 16S rRNA gene sequence similarity to the members of the genus *Lysobacter* in the family *Lysobacteraceae,* with *Lysobacter humi* FJY8^T (98.4% similarity), *Lysobacter xinjiangensis* RCML-52^T (98.3%), and *Lysobacter mobilis* 9NM-14^T (98.1%) as closest phylogenetic neighbors. Growth of strain 17J68-2^T occurred at 15–42 °C, pH 7–8, and in the presence of 0–1.0% NaCl. Draft genome was 2.94 Mb in size with G+C content of 70.5 mol%. The major polar lipids were phosphatidylglycerol, diphosphatidylglycerol, and phosphatidylethanolamine. Ubiquinone Q-8 was the predominant respiratory quinone and the major fatty acids were $C_{16:0}$ iso (39.4%), summed feature 3 ($C_{16:1}$ *ω7c*/$C_{16:1}$ *ω6c*) (6.6%), $C_{11:0}$ iso 3–OH (6.4%), $C_{15:0}$ iso (6.4%), and $C_{16:1}$ iso H (6.2%). The DNA–DNA relatedness between strain 17J68-2^T and *L. humi*, *L. xinjiangensis*, and *L. mobilis* were 39.9, 39.4, and 25.3%, respectively. From these results, it is concluded that the novel isolate possesses sufficient characteristics to differentiate it from the most closely affiliated *Lysobacter* species, and strain 17J68-2^T represents a novel species of the genus *Lysobacter*, for which the name *Lysobacter segetis* sp. nov. (=KCTC 62237^T = JCM 33058^T) is proposed.

Introduction

Christensen and Cook [5] proposed the genus *Lysobacter* with *Lysobacter enzymogenes* as the type species. The genus *Lysobacter* belongs to the family *Lysobacteraceae* [38] and currently (October 2019) contains 48 species with validly published names (https://www.bacterio.net/lysobacter.html). Members of this genus are Gram-stain negative, motile or non-motile, thin rods with a high G+C content (61.7–70.7 mol%) [6, 23, 43]. Predominance of iso-branched fatty acids, ubiquinone Q-8 as respiratory quinone, and phosphatidylglycerol, diphosphatidylglycerol, and phosphatidylethanolamine as the major polar lipids are the typical characteristics of the genus [4, 6, 22, 41, 46]. *Lysobacter* species have been isolated from a wide variety of ecological niches including air [41], lake fresh water from Antarctica [11], seawater [44], stream sediment [36], abandoned lead–zinc ore [43], and ginseng cultivated soil [31].

Herein, we describe bacterial strain 17J68-2^T that was recovered from a soil sample collected on Jeju Island, Republic of Korea. On the basis of 16S rRNA gene sequence analysis, this isolate was assigned to the genus *Lysobacter*. Further genomic, physiological, and chemotaxonomic characterization showed that strain 17J68-2^T represented a novel species of the genus *Lysobacter*, for which we propose the name *Lysobacter segetis* sp. nov.

The 16S rRNA gene sequence of strain 17J68-2^T has been deposited in NCBI GenBank/EMBL/DDBJ under the accession number LC434628. The draft genome sequence accession number of the strain in GenBank/EMBL/DDBJ is SMRQ00000000. The Digital Protologue Database (DPD) Taxon Number for strain 17J68-2^T is TA00939.

Electronic supplementary material The online version of this article (https://doi.org/10.1007/s00284-019-01801-w) contains supplementary material, which is available to authorized users.

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Published online: 14 November 2019

Materials and Methods

Isolation of the Bacterial Strain and Culture Conditions

Strain 17J68-2^T was isolated from a soil sample collected on Jeju Island (33°26′01.2″N 126°35′04.8″E), Republic of Korea. The soil sample (1 g) was suspended in 10 ml distilled water and serially diluted. Aliquots of 100 µl of each dilution were spread onto Reasoner's 2A agar plates (R2A; Difco) and incubated at 25 °C for 7 days. After incubation, single colony, designated 17J68-2^T, was transferred onto R2A agar plate and incubated under the same condition. Strain 17J68-2^T was cultured on trypticase soy agar plates (TSA; Difco) at 30 °C for further work and it was preserved at − 70 °C in a suspension with aqueous glycerol (20% w/v). The isolate was deposited in the Korean Collection for Type Culture (KCTC 62237^T) and the Japan collection of Microorganism (JCM 33058^T). Three reference strains used in this study, *Lysobacter humi* KCTC 42810^T, *Lysobacter xinjiangensis* KCTC 22558^T, and *Lysobacter mobilis* KCTC 52627^T, were obtained from the Korean Collection for Type Culture.

Phenotypic and Biochemical Characteristics

The morphological characteristics of strain 17J68-2^T were investigated after cultivation on R2A agar for 3 days at 30 °C. Cell morphology was observed under a light microscope (Olympus, Tokyo, Japan; ×000 magnification) and a HT7700 transmission electron microscope (Hitachi, Tokyo, Japan). Gram staining of strain 17J68-2^T was performed using standard staining method [32]. Motility was examined by stabbing of semi-solid R2A medium (0.5% agar) tubes with a wire loop of culture. Gliding motility was analyzed by hanging drop technique [1]. An oxidase activity test was carried out using 1% (w/v) tetramethyl-*p*-phenylenediamine and catalase activity was tested by observing air bubble production using 3% (v/v) H_2O_2 [3]. Anaerobic growth test was performed in serum bottles containing R2A broth supplemented with thioglycolate (1 g/L) under a nitrogen atmosphere [19]. Resistance against different concentrations of NaCl [0, 0.5, 1, 2, 3, 4, 5, and 10% (w/v)] and the pH range (4, 5, 6, 7, 8, 9, and 10) for growth were determined in R2A broth (MB Cell) as the basal medium, as described by Lee et al. [21]. The ability to grow on different media was examined on R2A agar, nutrient agar (NA), TSA agar, and Luria–Bertani (LB) agar (all purchased from Difco). Growth at 4, 10, 15, 25, 30, 37, 42, and 45 °C was tested on these four media. Enzyme activities, utilization of carbon sources, and other biochemical tests were carried out using the API ZYM, API 20NE, and API 32GN systems (bioMerieux, Marcy l'Etoile, France) following the manufacturer's instructions but with increased incubation times. The API 20NE and API 32GN strips were examined after 5 days of incubation at 25 °C. The incubation time for API ZYM was 18 h at 25 °C.

Sequencing of the 16S rRNA Gene and Phylogenetic Analysis

Nearly complete stretch of 16S rRNA gene of strain 17J68-2^T was PCR amplified using universal bacterial primers 9F and 1512R [40], and the purified PCR products were sequenced by Macrogen (Seoul, South Korea). The phylogenetic neighbors were identified and pairwise 16S rRNA gene sequence similarities were calculated using the EzBioCloud server [45]. Multiple alignment with 16S rRNA gene sequences of *Lysobacter* type strains was performed using the Clustal X 2.0 program [18]. Gaps and the 5′ and 3′ ends of the alignment were edited manually using the program BioEdit [13]. Tree topologies were inferred by neighbor-joining (NJ) [29], maximum-likelihood (ML) [9], and maximum-parsimony (MP) [10] methods using the MEGA 7 program [17]. The NJ and ML phylogenetic trees were constructed using Kimura's two-parameter model [15] and the ML tree was constructed using the nearest neighbor interchange heuristic search method. The MP tree was constructed using subtree pruning and regrafting. The resultant tree topologies were evaluated by bootstrap analyses on basis of 1,000 replicates.

Draft Genome Sequencing

Draft genome sequencing of strain 17J68-2^T was performed by DNA LINK Inc (Seoul, South Korea). A DNA library was generated from extracted DNA using TruSeq Nano DNA library preparation kit (Illumina) and sequenced on an Illumina Novaseq 6000 platform. Genome assembly into contigs was carried out using MaSuRCA genome assembler (version 3.2.4) [47]. Average nucleotide identity (ANI) was calculated with OrthoANI [20] and the digital DNA–DNA hybridization (dDDH) was calculated using the Genome-to-Genome Distance Calculator (GGDC) [25]. The draft genome sequence was annotated using the NCBI prokaryotic Genome Annotation Pipeline (PGAP) [12, 35] and the Rapid Annotation using Subsystem Technology (RAST) annotation server [2].

Chemotaxonomic Analyses

The analysis of cellular fatty acid methyl esters of strain 17J68-2^T was performed following the same growth

conditions used in previous studies of the three above-mentioned references strains [22, 24, 43]. As such, strain 17J68-2^T was grown on R2A agar at 30 °C for 3 days. One loopful of bacterial colony was harvested, subjected to saponification, methylation, extraction, and separation by gas chromatography according to protocol of the Sherlock Microbial Identification System (MIDI) [30]. The fatty acid methyl esters were identified and quantified using TSBA6 database (version 6.21) of the Sherlock Microbial Identification System [30]. Isoprenoid quinones were extracted from freeze-dried cells of 17J68-2^T with chloroform/methanol (2: 1, v/v), purified by using Sep-Pak Vac Cartridges Silica (Waters) [37] and analyzed by high-performance liquid chromatography (HPLC) as described by Hiraishi et al. [14] with the following modifications. HPLC analysis was conducted on Agilent 1100 series HPLC (Agilent Technologies, Waldbronn, Germany) equipped with G1315A photodiode array detector and ChemStation software. The chromatographic separation was performed using an Atlantis T3 C_{18} column (4.6 mm × 250 mm, 5.0 µm; Waters, Milford, USA) and the mobile phase consisting methanol and isopropanol in the proportion of 7:5 (v/v) at a flow rate of 1.2 ml/min. Polar lipids of the isolate were extracted from the freeze-dried cells and analyzed by two-dimensional TLC following protocol established by Minnikin et al. [27] by using four different spray reagents [16].

DNA–DNA Hybridization and Determination of DNA G+C Content

The genomic DNA of strain 17J68-2^T and reference strains *L. humi* KCTC 42810^T, *L. xinjiangensis* KCTC 22558^T, and *L. mobilis* KCTC 52627^T were extracted according to a standard protocol of Wilson [42]. DNA–DNA hybridization was conducted using the microplate method described by Ezaki et al. [8]. The highest and lowest values from five independent repetitions of the same hybridization reaction were excluded, and the mean of the remaining three values was recorded as the DNA–DNA hybridization value. The genomic DNA G+C content of strain 17J68-2^T was calculated from the draft genome sequence.

Results and Discussion

Phylogenetic Analysis

The results of the phylogenetic analysis based on the almost complete 16S rRNA gene sequence of strain 17J68-2^T (1468 bp) revealed that it belongs to the genus *Lysobacter*. The isolate shared highest sequence similarity with *L. humi* FJY8^T (98.4%), *L. xinjiangensis* RCML-52^T (98.3%), and *L. mobilis* 9NM-14^T (98.1%). The sequence similarities between strain 17J68-2^T and other recognized *Lysobacter* species were less than 96.7%. The phylogenetic position of 17J68-2^T, determined by three tree-making algorithms, revealed that the novel isolate appeared within the genus *Lysobacter* and clustered with the three above-mentioned reference strains in the ML, NJ, and MP trees, with high bootstrap values of 98–100%. A threshold of 97% similarity in 16S rRNA gene sequence was first proposed for bacterial species delineation [33], later, based on a broader dataset, it was re-evaluated to 98.7% by Stackebrandt and Ebers [34] and Chun et al. [7]. Based on the re-evaluated threshold value, the above data indicate that strain 17J68-2^T represents a novel species of the genus *Lysobacter*. To confirm the results of 16S rRNA gene sequence similarity analysis, DNA–DNA hybridizations were performed between the novel isolate and the three above-mentioned closest relatives (Fig. 1).

Draft Genome Sequencing Analysis

The raw reads (82,815,012) of strain 17J68-2^T were assembled into 133 contigs with a coverage of 2845.82 × and N50 of 42,536 bp. The draft genome of the isolate was 2,939,468 bp in length with DNA G+C content of 70.5 mol%, which lies within the range observed for recognized members of the genus *Lysobacter* (61.7–70.7 mol%) [6, 23, 43]. Annotation with the NCBI predicted 2913 genes, including 2847 coding DNA sequences (CDSs), 66 RNA genes, and 111 pseudogenes. The draft genome of strain 17J68-2^T analyzed by the RAST server revealed that the most abundant genes can be classified in the following categories: amino acids and derivatives (170 genes), protein metabolism (150 genes), co-factors, vitamins, prosthetic groups, pigments (138 genes), carbohydrates (104 genes), DNA metabolism (91 genes), nucleosides and nucleotides (51 genes) (Supplementary Fig. S1). The ANI and dDDH values between strain 17J68-2^T and *Lysobacter enzymogenes* ATCC 29487^T (FNOG00000000), the type species of the genus, and most closely related strain of *Lysobacter* (95.5% of 16S rRNA gene sequence similarity), whose genome was available at the time of this study, were calculated to be 76.3% and 22.0%, respectively. These values were significantly lower than the accepted threshold values for delineating prokaryotic species using ANI (94–96%) and in silico DDH (70%) [26, 28], providing further evidence for assignment of the strain to a novel species of the genus *Lysobacter*.

Morphological and Phenotypic Characteristics

Cells of strain 17J68-2^T were observed to be Gram-stain negative, aerobic, motile by gliding, yellow pigment-producing rods (0.4–0.6 µm wide and 1.7–3.6 µm long) (Supplementary Fig. S2). The strain grew at 15–42 °C (optimum

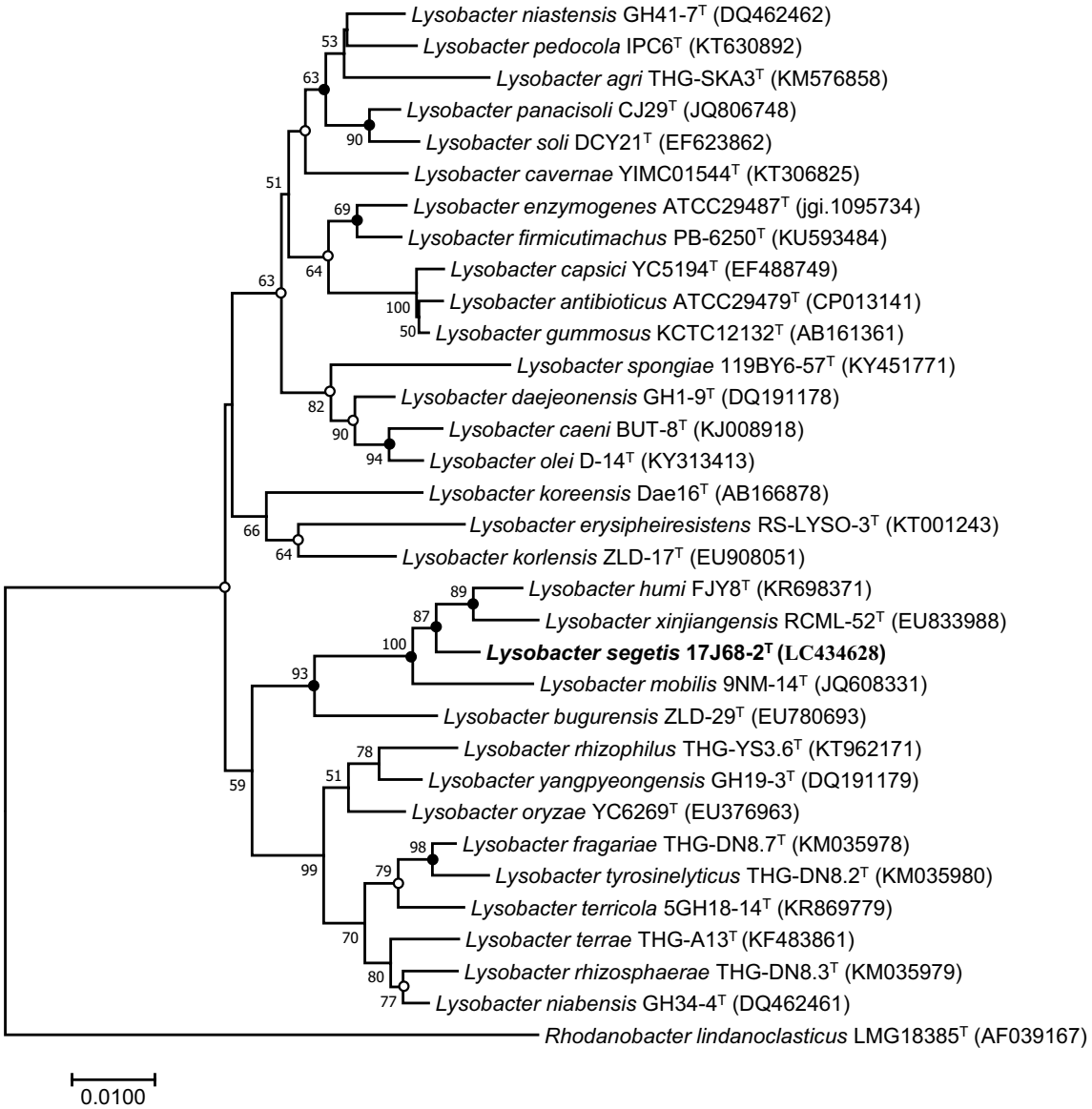

Fig. 1 Neighbor-joining phylogenetic tree, based on 16S rRNA gene sequences, showing the position of strain 17J68-2^T within the genus *Lysobacter*. Bootstrap values (based on 1000 replications) greater than 50% are shown at branch points. Filled circles indicate that the corresponding nods were also recovered in trees generated using the maximum-likelihood and maximum-parsimony algorithms. Open circles indicate that the corresponding nods were also recovered in the trees generated using the maximum-likelihood or maximum-parsimony algorithms. Accession numbers are shown in parenthesis. *Rhodanobacter lindanoclasticus* LMG 18385^T was used as an outgroup. Bar = 0.01 substitutions per nucleotide position

30 °C) but not at 10 or 45 °C. The pH range for growth was pH 7–8 (optimum pH 7). The strain was found to grow in the presence of 0–1% NaCl (w/v) but not in 2% NaCl (w/v). Growth occurred on R2A, TSA, and NA but not on LB agar. The results of other physiological and biochemical analyses are summarized in the species description and negative characteristics of strain 17J68-2^T in API ZYM, API 20NE, and API 32GN tests are given in Supplementary Table S1. The morphological, physiological, and biochemical characteristics differentiating the novel strain from *L. humi* KCTC 42810^T, *L. xinjiangensis* KCTC 22558^T, and *L. mobilis* KCTC 52627^T are listed in Table 1.

Chemotaxonomic Characteristics

The major fatty acids of strain 17J68-2^T were identified as $C_{16:0}$ iso (39.4%), summed feature 3 ($C_{16:1}$ ω7*c*/$C_{16:1}$ ω6*c*) (6.6%), $C_{11:0}$ iso 3–OH (6.4%), $C_{15:0}$ iso (6.4%), and $C_{16:1}$ iso H (6.2%). These results are similar to the previously described cellular fatty acids profiles of other members

Table 1 Differential phenotypic characteristics of strain 17J68-2^T and its phylogenetically closely related species in the genus *Lysobacter*

Characteristic	1	2	3	4
Cell size (μm)				
Width	0.4–0.6	0.7–1.0[a]	0.5–0.7[b]	0.4–0.6[c]
Length	1.7–3.6	1.3–1.5[a]	1.1–2.1[b]	0.8–1.0[c]
Growth on/at				
15 °C	+	−	−	+
42 °C	+	+	+	−
pH 10	−	+	+	−
1% NaCl	+	−	+	−
Motility	+	−	−	+
Catalase	−	+	+	−
Nitrate reduction	−	−	−	+
Aesculin hydrolysis	−	+	+	−
Enzyme activity (API ZYM)				
α-Chymotrypsin	w	w(+)[a]	+	−
Cystine arylamidase	+	−	+	+
α-Glucosidase	w	−	−	−
β-Glucuronidase	−	−	−	+
Lipase (C14)	−	+	+	w(−)[a]
Trypsin	−	+	+ (−)[b]	+
Assimilation of (API 20NE, API 32GN)				
N-Acetyl-D-glucosamine	−	−	+ (−)[b]	−
L-Arabinose, D-melibiose	−	−	−	+ (−)[a]
L-Histidine	−	−	−	w
4-Hydroxybenzoate	−	−	w	+
L-Proline	−	−	+	+ (−)[a]
D-Ribose	−	+	+	−
G+C content (mol%)	70.5	68.0[a]	69.7[b]	70.7[c]

Strains: 1, 17J68-2^T; 2, *L. humi* KCTC 42810^T; 3, *L. xinjiangensis* KCTC 22558^T; 4, *L. mobilis* KCTC 52627^T

All data obtained in this study, unless otherwise noted

All strains were positive for gelatin hydrolysis, oxidase, acid phosphatase, alkaline phosphatase, esterase (C4), esterase (C8), leucine arylamidase, naphthol-AS-BI-phosphohydrolase, and valine arylamidase, but negative for acid production from glucose, indole production, *N*-acetyl-*β*-glucosaminidase, arginine dihydrolase, *α*-fucosidase, *α*-galactosidase, *β*-galactosidase, *β*-glucosidase, *α*-mannosidase, and assimilation of acetate, adipate, L-alanine, caprate, citrate, L-fucose, gluconate, D-glucose, glycogen, 3-hydroxybenzoate, DL-3-hydroxybutrate, inositol, itaconate, 2-ketogluconate, 5-ketogluconate, DL-lactate, L-malate, malonate, D-maltose, D-mannitol, D-mannose, phenylacetate, propionate, L-rhamnose, L-serine, salicin, D-sorbitol, D-sucrose, suberate, and *n*-valerate

+ positive reaction, − negative reaction, *w* weak positive reaction

Results deviating from published data are shown within parentheses

[a]Data from Ref [22]

[b]Data from Ref [24]

[c]Data from Ref [43]

Table 2 Fatty acids composition of strain 17J68-2^T and closely related *Lysobacter* species

Fatty acids	1	2	3	4
Saturated				
$C_{10:0}$ iso	2.1	1.1	2.3	–
$C_{11:0}$ iso	4.0	5.3	12.4	7.0
$C_{12:0}$ iso	3.1	tr	1.7	–
$C_{14:0}$ iso	3.4	–	–	–
$C_{15:0}$ iso	6.4	13.7	11.0	18.2
$C_{15:0}$ anteiso	2.3	tr	tr	tr
$C_{16:0}$	3.9	2.1	2.3	3.3
$C_{16:0}$ iso	39.4	26.9	24.3	7.9
$C_{17:0}$ iso	tr	3.4	4.3	7.9
$C_{18:0}$	1.6	–	–	–
Hydroxy				
$C_{11:0}$ iso 3–OH	6.4	4.8	7.7	10.0
$C_{12:0}$ 3–OH	1.5	–	–	–
$C_{16:0}$ N alcohol	–	tr	tr	2.1
$C_{17:0}$ 3–OH	–	tr	tr	4.9
Unsaturated				
$C_{14:1}$ *ω5c*	tr	tr	tr	5.8
$C_{16:1}$ iso H	6.2	1.3	tr	–
Summed feature 3[a]				
($C_{16:1}$ *ω7c*/$C_{16:1}$ *ω6c*)	6.6	6.3	3.3	2.3
Summed feature 9[a]				
($C_{17:1}$ iso *ω9c*/$C_{16:0}$ 10-methyl)	4.8	26.2	19.9	27.8

Strains: 1, 17J68-2^T; 2, *L. humi* FJY8^T [22]; 3, *L. xinjiangensis* RCML-52^T [24]; 4, *L. mobilis* 9NM-14^T [43]

All strains were grown on R2A agar for 3 days at 30 °C. Values are percentage of total fatty acids, and only fatty acids accounting for more than 1.0% in at least one strain of the strains are indicated

– not detected, *tr* trace (<1.0%)

[a]Summed feature contained two or three fatty acids that could not be separated by gas liquid chromatography (GLC) using the Sherlock Microbial Identification (MIDI) System

of the genus *Lysobacter*, which are known to contain iso-branched chain fatty acids as major components [22, 46]. However, strain 17J68-2^T can be clearly differentiated from the three reference strains by the presence of $C_{14:0}$ iso, $C_{18:0}$, and $C_{12:0}$ 3–OH, higher content of $C_{16:1}$ iso H, lower content of summed feature 9 ($C_{17:1}$ iso *ω9c*/$C_{16:0}$ 10-methyl), and the absence of $C_{16:0}$ N alcohol and $C_{17:0}$ 3–OH, as shown in Table 2. The quinone analysis showed that strain 17J68-2^T contained ubiquinone Q-8 as the predominant quinone, which is the major respiratory quinone found in other members of the genus *Lysobacter* [4, 6, 41]. The major polar lipids in strain 17J68-2^T were observed to be phosphatidylglycerol (PG), diphosphatidylglycerol (DPG), and phosphatidylethanolamine (PE) (Supplementary Fig. S3), which have been identified as the main polar lipids in other *Lysobacter* species [23, 37, 43]. In addition, the polar lipid profile of the

isolate included two unidentified aminophospholipids (APL_1 and APL_2), four unidentified phospholipids (PL_1–PL_4), and five unidentified lipids (L_1–L_5).

DNA–DNA Hybridization Results

DNA–DNA hybridization values for strain 17J68-2^T with *L. humi* KCTC 42810^T, *L. xinjiangensis* KCTC 22558^T, and *L. mobilis* KCTC 52627^T were 39.9, 39.4, and 25.3%, respectively. All DNA–DNA pairing values are below the threshold value of 70% recommended for the delineation of novel bacterial species [39]. Thus, the results of 16S rRNA gene sequence similarity analysis and DNA–DNA hybridization data are consistent with the contention that strain 17J68-2^T forms a new species not currently recognized within the genus *Lysobacter*.

Taxonomic Conclusion

The combined results obtained in the current study demonstrate that it is reasonable to classify strain 17J68-2^T as a member of the genus *Lysobacter*. However, based on its phylogenetic distance from currently recognized species within the genus *Lysobacter*, low levels of DNA relatedness shared with closely related species, and its specific combination of phenotypic and chemotaxonomic characteristics (Table 1), it is clear that strain 17J68-2^T is not affiliated with any recognized species in the genus *Lysobacter*. Therefore, strain 17J68-2^T should be classified as a representative of a novel species within the genus *Lysobacter*, for which the name *Lysobacter segetis* sp. nov. is proposed.

Description of Lysobacter segetis sp. nov.

Lysobacter segetis (se.ge'tis. L. n. *seges* soil; L. gen. n. *segetis* of the soil).

Cells are Gram-negative, motile by gliding, aerobic rods, 0.4–0.6 μm wide and 1.7–3.6 μm long. Colonies grown on TSA agar after 48 h of incubation are circular, convex, yellow in color with a mean diameter of 1–2 mm. Optimum temperature for growth is 30 °C; growth occurs at 15–42 °C on TSA, NA, and R2A agar. Cells grow at pH 7–8 and with 0–1% NaCl. No growth is observed under anaerobic conditions. Tests for oxidase activity and gelatin hydrolysis are positive. Catalase is absent, indole is not produced, and nitrate is not reduced. Negative results in tests for arginine dihydrolase, urease, hydrolysis of aesculin, and acid production from glucose. In API ZYM tests, the strain is positive for acid phosphatase, alkaline phosphatase, α-chymotrypsin (weakly, w), cystine arylamidase, esterase (C4), esterase (C8), α-glucosidase (w), leucine arylamidase, naphthol-AS-BI-phosphohydrolase (w), and valine arylamidase activities. In API 32GN and API 20NE tests, all substrates are not utilized. The fatty acid profile consists predominantly of iso-branched acids with the major components $C_{16:0}$ iso, $C_{11:0}$ iso 3–OH, $C_{15:0}$ iso, and $C_{16:1}$ iso H. Phosphatidylglycerol, diphosphatidylglycerol, and phosphatidylethanolamine are major polar lipids. Two unidentified aminophospholipids, four unidentified phospholipids, and five unidentified lipids are present in moderate to minor amounts. The predominant respiratory isoprenoid quinone is ubiquinone Q-8.

The type strain 17J68-2^T (=KCTC 62237^T = JCM 33058^T) was isolated from a soil sample collected on Jeju Island (33°26′01.2″N 126°35′04.8″E), Republic of Korea. The genomic DNA G+C content of the type strain is 70.5 mol%.

Acknowledgements This work was supported by the Brain Pool Program (Grant No. 2019H1D3A2A01061406) through the National Research Foundation (NRF) funded by the Ministry of Science and ICT, Republic of Korea.

References

1. Agarwal S, Hunnicutt DW, McBride MJ (1997) Cloning and characterization of the *Flavobacterium johnsoniae* (*Cytophaga johnsonae*) gliding motility gene, *gldA*. Proc Natl Acad Sci USA 94:12139–12144
2. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F et al (2008) The RAST Server: rapid annotations using subsystems technology. BMC Genom 9:75
3. Cappuccino JG, Sherman N (2010) Microbiology: a laboratory manual, 9th edn. Benjamin Cummings, San Francisco
4. Chen W, Zhao YL, Cheng J, Zhou XK, Salam N, Fang BZ, Li QQ, Hozzein WN, Li WJ (2016) *Lysobacter cavernae* sp. nov., a novel bacterium isolated from a cave sample. Antonie Van Leeuwenhoek 109:1047–1053
5. Christensen P, Cook FD (1978) *Lysobacter*, a new genus of non-fruiting, gliding bacteria with a high base ratio. Int J Syst Evol Microbiol 28:367–393
6. Christensen P (2005) Genus IV. *Lysobacter* Christensen and Cook 1978 372^{AL}. In: Brenner DJ, Krieg NR, Staley JT, Garrity GM (eds) Bergey's Manual of systematic bacteriology, vol 2, 2nd edn. Springer, New York, pp 95–101
7. Chun J, Oren A, Ventosa A, Christensen H, Arahal DR, da Costa MS, Rooney AP, Hana Y, Xu XW, De Meyer S, Trujillo ME (2018) Proposed minimal standards for the use of genome data for the taxonomy of prokaryotes. Int J Syst Evol Microbiol 68:461–466
8. Ezaki T, Hashimoto Y, Yabuuchi E (1989) Fluorometric DNA–DNA hybridization in microdilution wells as an alternative to membrane filter hybridization in which radioisotopes are used to determine genetic relatedness among bacterial strains. Int J Syst Bacteriol 39:224–229
9. Felsenstein J (1981) Evolutionary trees from DNA sequences: a maximum likelihood approach. J Mol Evol 17:368–376
10. Fitch WM (1971) Toward defining the course of evolution: minimum change for a specific tree topology. Syst Zool 20:406–416
11. Fukuda W, Kimura T, Araki S, Miyoshi Y, Atomi H, Imanaka T (2013) *Lysobacter oligotrophicus* sp. nov., isolated from an Antarctic freshwater lake in Antarctica. Int J Syst Evol Microbiol 63:3313–3318

12. Haft DH, DiCuccio M, Badretdin A, Brover V, Chetvernin V et al (2018) RefSeq: an update on prokaryotic genome annotation and curation. Nucleic Acids Res 46(D1):D851–D860
13. Hall TA (1999) BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symp Ser 41:95–98
14. Hiraishi A, Ueda Y, Ishihara J, Mori T (1996) Comparative lipoquinone analysis of influent sewage and activated sludge by high performance liquid chromatography and photodiode array detection. J Gen Appl Microbiol 42:457–469
15. Kimura M (1980) A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. J Mol Evol 16:111–120
16. Komagata K, Suzuki KI (1987) Lipid and cell-wall analysis in bacterial systematics. Methods Microbiol 19:161–205
17. Kumar S, Stecher G, Tamura K (2016) MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. Mol Biol Evol 33:1870–1874
18. Larkin MA, Blackshields G, Brown NP, Chenna R, McGettigan PA, McWilliam H, Valentin F, Wallace IM, Wilm A, Lopez R, Thompson JD, Gibson TJ, Higgins DG (2007) Clustal W and Clustal X version 2.0. Bioinformatics 23:2947–2948
19. Lee M, Woo SG, Chae M, Shin MC, Jung HM, Ten LN (2011) *Stenotrophomonas daejeonensis* sp. nov., isolated from sewage. Int J Syst Evol Microbiol 61:598–604
20. Lee I, Kim YO, Park SC, Chun J (2016) OrthoANI: an improved algorithm and software for calculating average nucleotide identity. Int J Syst Evol Microbiol 66:1100–1103
21. Lee JJ, Lee YH, Park SJ, Lee SY, Kim BO, Ten LN, Kim MK, Jung HY (2017) *Spirosoma knui* sp. nov., a radiation-resistant bacterium isolated from the Han River. Int J Syst Evol Microbiol 67:1359–1365
22. Lee D, Jang JH, Cha S, Seo T (2017) *Lysobacter humi* sp. nov., isolated from soil. Int J Syst Evol Microbiol 67:951–955
23. Li J, Han Y, Guo W, Wang Q, Liao S, Wang G (2018) *Lysobacter tongrenensis* sp. nov., isolated from soil of a manganese factory. Arch Microbiol 200:439–444
24. Liu M, Liu Y, Wang Y, Luo X, Dai J, Fang C (2011) *Lysobacter xinjiangensis* sp. nov., a moderately thermotolerant and alkalitolerant bacterium isolated from a gamma-irradiated sand soil sample. Int J Syst Evol Microbiol 61:433–437
25. Meier-Kolthoff JP, Auch AF, Klenk HP, Göker M (2013) Genome sequence-based species delimitation with confidence intervals and improved distance functions. BMC Bioinform 14:60
26. Meier-Kolthoff JP, Klenk HP, Göker M (2014) Taxonomic use of DNA G+ C content and DNA–DNA hybridization in the genomic age. Int J Syst Evol Microbiol 64:352–356
27. Minnikin DE, O'Donnell AG, Goodfellow M, Alderson G, Athalye M, Schaal A, Parlett JH (1984) An integrated procedure for the extraction of bacterial isoprenoid quinones and polar lipids. J Microbiol Methods 2:233–241
28. Richter M, Rossello-Mora R (2009) Shifting the genomic gold standard for the prokaryotic species definition. Proc Natl Acad Sci USA 106:19126–19131
29. Saitou N, Nei M (1987) The neighbor-joining method: a new method for reconstructing phylogenetic trees. Mol Biol Evol 4:406–425
30. Sasser M (1990) Identification of bacteria by gas chromatography of cellular fatty acids. MIDI Technical Note 101. MIDI Inc, Newark
31. Siddiqi MZ, Im WT (2016) *Lysobacter pocheonensis* sp. nov., isolated from soil of a ginseng field. Arch Microbiol 198:551–557
32. Smibert RM, Krieg NR (1994) Phenotypic characterization. In: Gerhardt P, Murray RGE, Wood WA, Krieg NR (eds) Methods for general and molecular bacteriology. American Society for Microbiology, Washington, DC, pp 607–654
33. Stackebrandt E, Goebel BM (1994) Taxonomic note: a place for DNA–DNA reassociation and 16S rRNA sequence analysis in the present species definition in bacteriology. Int J Syst Bacteriol 44:846–849
34. Stackebrandt E, Ebers J (2006) Taxonomic parameters revisited: tarnished gold standards. Microbiol Today 33:152–155
35. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J (2016) NCBI prokaryotic genome annotation pipeline. Nucleic Acids Res. 44:6614–6624
36. Ten LN, Jung HM, Yoo SA, Im WT, Lee ST (2008) *Lysobacter daecheongensis* sp. nov., isolated from sediment of stream near the Daechung dam in South Korea. J Microbiol 46:519–524
37. Ten LN, Jung HM, Im WT, Yoo SA, Oh HM, Lee ST (2009) *Lysobacter panaciterrae* sp. nov., isolated from soil of a ginseng field. Int J Syst Evol Microbiol 59:958–963
38. Tindall BJ (2014) The family name Solimonadaceae Losey et al. 2013 is illegitimate, proposals to create the names 'Sinobacter soli'comb. nov. and 'Sinobacter variicoloris' contravene the Code, the family name Xanthomonadaceae Saddler and Bradbury 2005 and the order name Xanthomonadales Saddler and Bradbury 2005 are illegitimate and notes on the application of the family names Solibacteraceae Zhou et al. 2008, Nevskiaceae Henrici and Johnson 1935 (Approved Lists 1980) and Lysobacteraceae Christensen and Cook 1978 (Approved Lists 1980) and order name Lysobacteriales Christensen and Cook 1978 (Approved Lists 1980) with respect to the classification of the corresponding type genera Solibacter Zhou et al. 2008, Nevskia Famintzin 1892 (Approved Lists 1980) and Lysobacter Christensen and Cook 1978 (Approved Lists 1980) and importance of accurately expressing the link between a taxonomic name, its authors and the corresponding description/circumscription/emendation. Int J Syst Evol Microbiol 64 293–297
39. Wayne LG, Brenner DJ, Colwell RR, Grimont PAD, Kandler O et al (1987) Report of the ad hoc committee on reconciliation of approaches to bacterial systematics. Int J Syst Bacteriol 37:463–464
40. Weisburg WG, Barns SM, Pelletier DA, Lane DJ (1991) 16S ribosomal DNA amplification for phylogenetic study. J Bacteriol 173:697–703
41. Wen C, Xi L, She R, Zhao S, Hao Z, Luo L, Liao H, Chen Z, Han G, Cao S, Wu R, Yan Q, Hou R (2016) *Lysobacter chengduensis* sp. nov. isolated from the air of captive *Ailuropoda melanoleuca* enclosures in Chengdu China. Curr Microbiol 72:88–93
42. Wilson K (1997) Preparation of genomic DNA from bacteria. In: Ausubel FM et al (eds) Current protocols in molecular biology, no. supplement 27. Wiley, New York, pp. 2.4.1–2.4.5
43. Yang SZ, Feng GD, Zhu HH, Wang YH (2015) *Lysobacter mobilis* sp. nov., isolated from abandoned lead-zinc ore. Int. J. Syst. Evol. Microbiol. 65:833–837
44. Yoon J (2016) Polyphasic characterization of *Lysobacter maris* sp. nov., a bacterium isolated from seawater. Curr Microbiol 72:282–287
45. Yoon SH, Ha SM, Kwon S, Lim J, Kim Y, Seo H, Chun J (2017) Introducing EzBioCloud: a taxonomically united database of 16S rRNA and whole genome assemblies. Int J Syst Evol Microbiol 67:1613–1617
46. Zhang XF, Wang HH, Sun XY, Pan CM (2017) *Lysobacter zhanggongensis* sp. nov. isolated from a pit mud. Curr Microbiol 74:1389–1393
47. Zimin AV, Marçais G, Puiu D, Roberts M, Salzberg SL, Yorke JA (2013) The MaSuRCA genome assembler. Bioinformatics 29:2669–2677