Archives of Microbiology
https://doi.org/10.1007/s00203-020-02032-5

ORIGINAL PAPER

Lysobacter telluris sp. nov., isolated from Korean rhizosphere soil

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Received: 1 June 2020 / Revised: 4 August 2020 / Accepted: 2 September 2020

Abstract

A Gram-stain-negative, aerobic, non-motile, non-spore-forming light-yellow-coloured rod-shaped bacterial strain, designated YJ15^T, was isolated from soil at Bigeum island in Korea. Growth was observed at 10–37 °C (optimum, 28 °C), at pH 6.0–7.5 (optimum, pH 7.0) and in the absence of NaCl. Based on 16S rRNA gene sequence analysis, strain YJ15^T was closely related to '*Lysobacter tongrenensis*' YS037^T (97.8%), *Lysobacter pocheonensis* Gsoil193^T (96.5%) and *Lysobacter daecheongensis* Dae08^T (95.8%) and phylogenetically grouped together with '*Lysobacter tongrenensis*' YS037^T, *Lysobacter dokdonensis* DS-58^T and *Lysobacter pocheonensis* Gsoil 193^T. The DNA–DNA relatedness between strain YJ15^T and '*Lysobacter tongrenensis*' KCTC 52206^T was 12% and the phylogenomic analysis based on the whole genome sequence demonstrated that strain YJ20^T formed a distinct phyletic line with *Lysobacterlter dokdonensis* DS-58^T showing average nucleotide identity (ANI) and digital DNA–DNA hybridization (dDDH) values of 76.3 and 21.3%, respectively. The predominant ubiquinone was identified as Q-8, and polar lipids were diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylglycerol and two unidentified aminolipids. The major fatty acids were iso-$C_{17:1}$ *ω9c,* iso-$C_{15:0}$, iso-$C_{16:0}$ and iso-$C_{17:0}$. The genomic DNA G + C content was 68.2 mol %. On the basis of phenotypic, chemotaxonomic properties and phylogenetic analyses in this study, strain YJ15^T is considered to represent a novel species of the genus *Lysobacter,* for which the name *Lysobacter telluris* sp. nov. is proposed. The type strain is YJ15^T (= KACC 19552^T = NBRC 113197^T).

Keywords *Lysobacter telluris* · Soil · Polyphasic taxonomy

Introduction

The genus *Lysobacter* was first described by Christensen and Cook (1978) with the type species of the genus *Lysobacter enzymogenes* and this genus was classified within the family *Xanthomonadaceae* of the class *Gammaproteobacteria* (Saddler and Bradbury 2005). The description of the genus has been subsequently emended by Park et al. (2008). At the time of writing, the genus *Lysobacter* comprised 56 recognized species with validly published names (www.bacterio.net/Lysobacter.html). Members of the genus *Lysobacter* have been isolated from diverse soil and aquatic habitats and plants (Park et al. 2008; Oh et al. 2011; Siddiqi et al. 2016; Li et al. 2018; Chhetri et al. 2019). Some members of the genus are proteolytic and have potential antibiotic compounds as new source of bioactive compounds and new antibiotics against plant and human pathogens (Ahmed et al. 2003; de Bruijn et al. 2015; Panthee et al. 2016).

During the course of a study on the isolation of rhizosphere bacteria from a farmland soil, a novel Gram-stain-negative bacterium, designated strain YJ15^T, was isolated

Communicated by Erko stackebrandt.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain YJ15T is JN848797. The whole genome sequence has been deposited at GenBank/ENA/DDBJ under the accession JAANOY000000000. The version described in this paper is version JAANOY000000000.1.

Electronic supplementary material The online version of this article (https://doi.org/10.1007/s00203-020-02032-5) contains supplementary material, which is available to authorized users.

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Published online: 12 September 2020

and identified as a member of the genus *Lysobacter*. Here, we report the taxonomic position and characterization of the bacterial strain by genotypic, chemotaxonomic and phenotypic approaches.

Materials and methods

Bacterial strain and culture condition

Strain YJ15^T was isolated from rhizosphere soil of a farming field from Bigeum Island located in Shinan, south-west Korea (34° 44′ 23.46″ N, 125° 56′ 03.13″ E). The strain was isolated by diluting a soil sample in sterile distilled water and plating on Reasoner's 2A [R2A; Becton–Dickinson (BD)] agar with adjustment of pH to pH 7.0 using 1 M NaOH. The strain was subsequently purified three times by plating on R2A at 28 °C for 7 days and maintained on the same medium. Despite repeated attempts to isolate additional strains, only one isolate was obtained. The strain was stored at −80 °C in R2A broth supplemented with 20% (v/v) glycerol. To characterize the strain phenotypically, the isolate was routinely grown aerobically on R2A agar for 5 days at 28 °C and pH 7.0, except where indicated otherwise. The type strains, '*L. tongrenensis*' KCTC 52206^T, *L. pocheonensis* KCTC 12624^T, *L. dokdonensis* KCTC 12822^T and *L. caseinilyticus* KACC 19816^T were obtained from the culture collections indicated and used as reference strains.

Phylogenetic analysis

Genomic DNA of strain YJ15^T was extracted using the Genomic DNA Prep Kit (Biofact). The 16S rRNA gene was amplified by PCR with the forward primer 27F and the reverse primer 1492R (DeLong 1992). Direct sequence determination of the PCR-amplified DNA was carried out using an automated DNA sequencer (ABI 3730XL, Applied Biosystems). The full sequences of the 16S rRNA gene were compiled using SeqMan software (DNASTAR). The 16S rRNA gene sequence was aligned with published sequences of closely related bacteria with CLUSTAL W 2.0 software (Larkin et al. 2007). Gaps at the 5′ and 3′ ends of the alignment were omitted in further analyses. Phylogenetic trees were reconstructed using three different methods: the neighbour-joining (Saitou and Nei 1987), maximum likelihood (Felsenstein 1981) and maximum parsimony (Fitch 1971) algorithms within the MEGA7 program (Kumar et al. 2016). Evolutionary distance matrices for the neighbour-joining method were calculated using the algorithm of Kimura's two-parameter model (Kimura 1980). To evaluate the stability of the phylogenetic tree, bootstrap analysis was performed (1000 replications) (Felsenstein 1985). The 16S rRNA gene sequences used for phylogenetic comparisons were obtained from the GenBank database and their strain designations and GenBank accession numbers are shown in Fig. 1.

Phylogenomic analysis

Whole genome sequences analysis of strain YJ15^T was performed using the paired-end sequencing method with the MiSeq platform (Illumina) at ChunLab (Seoul, Republic of Korea). The resulting short sequencing reads were assembled in contigs using the SPAdes 3.13.0 program (Bankevich et al. 2012). The genome sequence was annotated with the Rapid Annotation of microbial genomes using Subsystems Technology (RAST) (Aziz et al. 2008; Overbeek et al. 2014), and the protein-coding sequences were determined using the NCBI prokaryotic genome annotation pipeline (PGAP) (Tatusova et al. 2016). The average nucleotide identity (ANI) values between strain YJ15^T and available

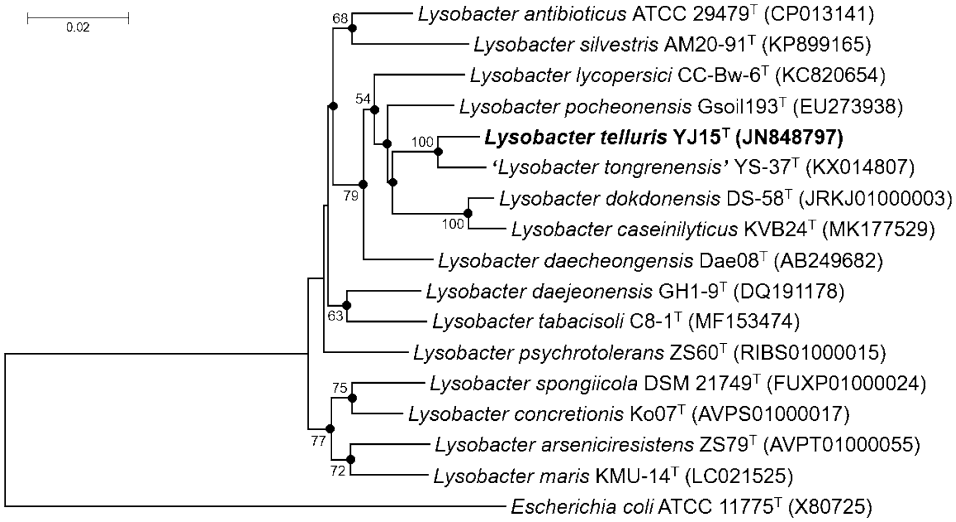

Fig. 1 Rooted neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showing the position of strain YJ15^T in the genus *Lysobacter*. Bootstrap values, expressed as a percentage of 1000 replications, are given at branching points when > 50%. Filled circles at nodes indicate generic branches that were also recovered using maximum-likelihood and maximum-parsimony algorithms. *Escherichia coli* ATCC 11775^T was used as an outgroup. Bar, 0.02 substitutes per nucleotide position

reference strains in the genus *Lysobacter* were calculated using the ANI Calculator (www.ezbiocloud.net/tools/ani) (Yoon et al. 2017a, b). To determine genomic relatedness, DNA–DNA hybridization (DDH) was performed using the modified method of Ezaki et al. (1989). Probe labelling for DDH was conducted using the non-radioactive DIG-High Prime system (Roche) at 50 °C; hybridized DNA was visualized using the DIG luminescent detection kit (Roche) and the level of DNA–DNA relatedness was quantified using a densitometer (Bio-Rad) and digital DDH (dDDH) values were computed using Formula 2 of the Genome-to-Genome Distance Calculator (GGDC) version 2.1 (Meier-Kolthoff et al. 2013). The genome-based phylogeny was inferred from the available type strains of species of the genus *Lysobacter* with whole genome sequences using the type strain genome server (TYGS) (Meier-Kolthoff et al. 2019). The phylogenomic tree was reconstructed using FastME (Lefort et al. 2015) from the genome BLAST distance phylogeny (GBDP) distances calculated from the genome sequences. The pairwise-genome comparisons were conducted using GBDP and intergenomic distances inferred under algorithm 'trimming' and distance formula d5 (Meier-Kolthoff et al. 2013). The trees were rooted at the midpoint (Farris 1972). Branch support was inferred from 100 pseudo-bootstrap replicates.

Morphological, physiological, and biochemical characterization

The morphology of the isolate was observed by Gram staining and transmission electron microscopy using cells from the exponential growth phase. Cells were mounted on Formvar-coated copper grids, negatively stained with 1% (w/v) potassium phosphotungstate (pH 7.0) and examined in a transmission electron microscope (CM20, Philips) operated at 80 kV, and motility was observed by phase-contrast microscopy (Eclipse 80i, Nikon) using cells from exponentially growing cultures and the hanging-drop method. Gram staining was performed by the Burke method (Murray et al. 1994). Growth of strain YJ15^T was assessed at 28 °C for 5 days on several bacteriological agar media: R2A agar, Luria–Bertani (LB; MP Biomedicals) agar, nutrient agar (NA; BD), tryptic soy agar (TSA; BD), marine agar (MA; BD), International *Streptomyces* Project 2 agar (ISP2; BD), Bennett's agar, tryptone-yeast extract agar (TYA) and potato dextrose agar (PDA; BD). Catalase and oxidase activities, nitrate reduction, hydrolysis of aesculin, casein, DNA, gelatin, Tweens 20, 40, 60 and 80, hypoxanthine, L-tyrosine, starch, xanthine, urea and tryptophan and production of indole, and methyl red and Voges–Proskauer tests were performed as recommended by Smibert and Krieg (1994). To determine the utilization of different organic substrates as carbon and energy sources, R2B (laboratory-made R2A broth without agar) medium was used from which dextrose and soluble starch, yeast extract, proteose peptone no. 3 and casamino acids were omitted and 0.5 g l^{-1} yeast extract was added as a nitrogen source. Acid production from carbohydrates was determined as described by Leifson (1963). All compounds were sterilized by filtration before adding to the medium and the cells were suspended in 0.85% (w/v) NaCl solution and inoculated. Additional biochemical characteristics were performed using API 50CH (with API 50CHB medium) and API 20NE (bioMérieux) galleries at 28 °C as recommended by the manufacturer. Enzyme activities were tested using the API ZYM kit system according to the manufacturer's instructions (bioMérieux). To determine the optimal temperature and pH for growth of strain YJ15^T, broth cultures in R2A broth (in laboratory-made R2B) were incubated at 4, 10, 15, 20, 28, 30, 35, 37, 40, 42 and 45 °C, and at pH 5–11 (at intervals of 0.5 pH units) at 28 °C. Media at pH < 6, 6–9 and > 9 were obtained using sodium acetate/acetic acid, Tris/HCl and glycine/NaOH buffers, respectively. Growth in the presence of 0, 0.5, 1, 2, 3, 4, 5, 7 and 10% NaCl (w/v) was tested in R2B at pH 7.0. Growth was monitored by turbidity at OD_{600} using a spectroscopic method (model UV-1650PC, Shimadzu). Anaerobic growth was determined by incubation in the BBL GasPak Anaerobic System (Difco) for 5 days at 28 °C on R2A agar. Antibiotic susceptibility was determined according to the conventional Kirby–Bauer method (Bauer et al. 1966), seeding with a bacterial suspension containing 1.5×10^6 c.f.u. ml^{-1} and using discs (Advantec) impregnated with various antibiotics. Susceptibility to antibiotics was tested on R2A plates using antibiotic discs containing the following (μg per disc unless otherwise stated): teicoplanin (30), amikacin (30), ampicillin (20), lincomycin (15), nalidixic acid (30), kanamycin (30), gentamicin (10), streptomycin (10), neomycin (30), penicillin G (10 U), vancomycin (30), erythromycin (15), oleandomycin (15), amoxicillin (10), spiramycin (100), rifampicin (10), polymixin B (50 U), nystatin (50), bacitracin (10 U), tetracycline (30), cycloheximide (30), roxithromycin (15), sphingomyelin (30), apramycin (30), salinomycin (30), hygromycin (30), capreomycin (30), sisomycin (10), amphotericin (2), gramicidin S (30), phosphomycin (30) and chloramphenicol (30).

Chemotaxonomic characterization

For analysis of fatty acids, strain YJ15^T was cultured on R2A agar at 28 °C for 5 days and the related type strains were cultured under the same conditions. Cellular fatty acids were extracted and analysed by GC (6890 N, Agilent Technologies) according to the standard protocol of the Sherlock Microbial Identification System (version 4.5; MIDI database TSBA40 4.10) (Sasser 1990). For the analyses of isoprenoid quinones and polar lipids, cells were harvested in the late-exponential phase and freeze-dried. Isoprenoid

quinones were extracted and analysed by HPLC (SPD-10AV, Shimadzu), as described by Collins and Jones (1981). For polar lipid analysis, the cellular lipids were extracted, washed aând hydrolyzed with 0.5 M NaOH as described by Yabuuchi et al. (1990, 1995). The total lipids were separated on silica-gel plates by two-dimensional TLC with a solvent system composed of chloroform/methanol/water (65:25:4, by vol.) in the first direction and chloroform/methanol/acetic acid/water (80:15:12:4, by vol.) in the second direction. To detect spots and their colour reaction, 5% ethanolic molybdo-phosphoric acid, molybdenum blue, ninhydrin solution and α-naphthol reagent were used for total lipids, phospholipids, aminolipids and glycolipids, respectively.

Results and discussion

The almost-complete 16S rRNA gene sequence (1488 bp) of strain YJ15^T was obtained and used for initial BLAST searches of the GenBank database and for phylogenetic analyses. The 16S rRNA gene sequences of related taxa were obtained from GenBank and the EzBioCloud server and the identification of phylogenetic neighbours and calculation of pairwise 16S rRNA gene sequence similarity were achieved using the EzBioCloud server (www.ezbiocloud.net) (Yoon et al. 2017a, b). Results of phylogenetic analyses based on 16S rRNA gene sequences showed highest 16S rRNA gene sequence similarity to '*L. tongrenensis*' YS-37^T (97.8%), *L. pocheonensis* Gsoil193^T (96.5%), *L. dokdonensis* Dae08^T (95.3%) and *L. caseinilyticus* KVB24^T (95.0%), whereas the other members in the genus showed similarity below 96.0% using the neighbour-joining algorithm (Fig. 1). Strain YJ15^T formed a stable cluster with '*L. tongrenensis*' YS-37^T, *L. dokdonensis* Dae08^T, *L. caseinilyticus* KVB24^T and *L. pocheonensis* Gsoil193^T in the genus *Lysobacter.* Furthemore, highly similar relationships were also recovered in phylogenetic trees reconstructed with the maximum-likelihood and maximum-parsimony algorithms with high bootstrap values (Figs S1 and S2). To determine genomic relatedness, DDH was performed between strain YJ15^T and '*L. tongrenensis*' KCTC 52206^T as the closest phylogenetic neighbours which shows > 97% 16S rRNA gene sequence similarity and a genome sequence is not available (Li et al. 2018). The DDH value between strain YJ15^T and '*L. tongrenensis*' KCTC 52206^T was 12%, and this value was significantly lower than 70%, the threshold value recommended for the assignment of genomic species (Wayne et al. 1987).

The assembled genome sequence of strain YJ15^T was found to be 2860800 bp long, composed of 121 contigs with an N50 value of 84537 bp and sequencing coverage of 70-fold. The NCBI PGAP revealed a copy of the 5S, 16S and 23S rRNA gene, respectively, and 52 RNA genes (three rRNA, 45 tRNA and four ncRNA). Among a total 2653 predicted genes, 2537 genes were identified as protein-coding sequences. Of the 2537 genes, 24 genes attributable to plant growth promotion were found in the genome of strain YJ15^T (Table S1). The 16S rRNA gene sequence of YJ15^T obtained from the genome was compared with that determined by PCR, at the NCBI server BLAST-N site (www.ncbi.nlm.nih.gov/BLAST). The BLAST result showed that the two sequences were highly similar (99.7%). The DNA G + C content of the genome was found to be 68.2 mol %, which was in the range (61.7–70.7 mol %) with those reported for other species in the genus *Lysobacter* (Table 1). The comparison of ANI and dDDH values between genome of strain YJ15^T and other related members in the genus *Lysobacter* and *Luteimonas* was in the range of 78.0–74.4% and 22.2–20.6%, respectively, far below the cut-off points for the novel species (< 95% ANI, < 70% dDDH) (Wayne et al. 1987; Goris et al. 2007; Meier-Kolthoff et al. 2013) and showed high similarity to *L. dokdonensis* DS-58^T with 76.3% which is one of the closest strain in the cluster in which the strain YJ15^T is located (Table S2). With the result of DNA–DNA relatedness between strain YJ15^T and '*L. tongrenensis*' KCTC 52206^T, based on genome analysis, phylogenomic analyses based on whole genome sequences showed strain YJ15^T was located in the genus *Lysobacter,* forming a distinct phyletic lineage separated clearly from the closest strains '*L. tongrenensis*' YS-37^T and *L. dokdonensis* DS-58^T indicating a novel line of species in the genus *Lysobacter* (Fig. 1 and Fig. S3).

Strain YJ15^T formed non-motile rods when grown for 5 days at 28 °C on R2A agar (Fig. S4). Other cultural, physiological and biochemical properties of strain YJ15^T are summarized in the species descriptions. Differential phenotypic characteristics among strain YJ15^T and its closely related members of the genus *Lysobacter* are summarized in Table 1. Strain YJ15^T was susceptible to teicoplanin, amikacin, nalidixic acid, kanamycin, gentamicin, streptomycin, neomycin, erythromycin, oleandomycin, amoxicillin, spiramycin, bacitracin, cycloheximide, roxithromycin, tetracycline, apramycin, hygromycin, sisomycin, gramicidin S, phosphomycin, capreomycin, amphotericin and chloramphenicol, but resistant to ampicillin, lincomycin, penicillin G, vancomycin, rifampicin, polymixin B, nystatin, sphingomyelin, salinomycin.

The major fatty acids (> 10%) of strain YJ15^T were identified as iso-$C_{17:1}$ $\omega 9c$ (26.8%), iso-$C_{15:0}$ (23.0%), and $C_{16:0}$ (13.2%) and $C_{17:0}$ (13.4%). Moderate amounts of $C_{16:0}$ (6.9%) and iso-$C_{11:0}$ (5.7%) were also present (Table 2). These are common characteristics of members of the genus *Lysobacter*, although there were differences in the abundance of iso-$C_{17:0}$ and iso-$C_{17:1}$ $\omega 9c$ of strain YJ15^T higher than those of the other type strains. The predominant isoprenoid quinones was determined to be ubiquinone-8 (Q-8) same as known members of the genus *Lysobacter* (Park et al.

Table 1 Differential phenotypic and genotypic characteristics of strain YJ15^T and type strains of closely related species of the genus *Lysobacter*

Characteristic	1	2	3	4	5
Colony size (mm)	0.5–2.0	0.5–1.0	0.3–1.0	1.0–2.0	0.5–1.5
Cell width (μm)	0.8–1.0	0.3–0.4[a]	0.3–0.4[b]	0.4–0.8[c]	0.4–0.8[e]
Cell length (μm)	1.4–2.0	0.6–1.5[a]	2.5–5.0[b]	1.0–5.0[c]	1.4–2.3[e]
Temperature range (optimum) (°C)	10–37 (28)	4–32 (28)	20–30 (30)	4–38 (30)	10–37 (30)
pH range (optimum)	6.0–7.5 (7.0)	6.5–7.5 (7.0)	5.0–9.0 (7.0)	6.5–8.0 (7.0)	6.0–8.0 (7.0)
Oxidase/catalase	+/+	+/+	–/–	+/+	+/+
Hydrolysis of urea	–	–	+	+	–
Assimilation of:					
D-Trehalose	+	–	–	–	–
Glycogen	+	–	–	+	–
L-Arginine	–	–	+	–	–
Malic acid	–	–	–	+	–
Citric acid	+	+	–	–	–
Phenyl-acetic acid	+	+	+	–	–
Enzyme activity (API ZYM):					
Alkaline phosphatase	–	w	+	+	+
Esterase (C4)	–	w	+	+	+
Esterase lipase (C8)	–	w	+	+	+
Lipase (C14)	+	–	–	–	–
Crystine arylamidase	–	w	+	w	w
Trypsin	–	+	w	+	w
α-Chymotrypsin	+	–	–	+	–
α-Glucosidase	–	–	–	+	+
DNA G+C content (mol %)	68.2	67.1[a]	64.8[b]	67.2[d]	67.8[e]

Strains: 1, Strain YJ15^T; 2, '*L. tongrenensis*' KCTC 52206^T; 3, *L. pochonensis* KCTC 12624^T; 4, *L. dokdonensis* KCTC 12822^T; *L. caseinilyticus* KACC 19816^T. All data were obtained from this study except indicated otherwise. Strains were shared the following characteristics: positive for activity of tryptophane deaminase, gelatin hydrolysis and nitrate reduction but negative for H_2S and indole production, glucose acidification, aesculin hydrolysis and assimilation of arabinose, mannose, mannitol, *N*-acetylglucosamine, maltose, gluconate, caprate and adipate. In API ZYM test strips, all strains were positive for leucine arylamidase, valine arylamidase, acid phosphatase and Naphtol-AS-BI-phosphohydrolase, but negative for α- and β-galactosidase, β-glucuronidase, β-glucosidase, *N*-acetyl-β-glucosamininase, α-mannosidase, α-fucosidase and acylamidase

+, Positive; –, negative; w, weakly positive

[a]Data from Li et al. 2008

[b]Data from Siddiqi and Im 2016

[c]Data from Oh et al. 2011

[d]Data from whole genome sequence in NCBI bacterial database

[e]Data from Chhetri et al. 2019

2008; Oh et al. 2011; Siddiqi et al. 2016; Li et al. 2018; Chhetri et al. 2019). The polar lipids were found to be comprised of diphosphatidylglycerol (DPG), phosphatidylethanolamine (PE), phosphatidylglycerol (PG) and two unidentified aminolipids (ALs) (Fig. S5). The presence of DPG, PE, PG and some unidentified amino group-containing lipids is common characteristic feature of members of the genus *Lysobacter* (Park et al. 2008).

All the chemotaxonomic data are consistent with the assignment of strain YJ15^T to the genus *Lysobacter*. Strain YJ15^T could be distinguished from its closely related members by several phenotypic characteristics (Table 1) such as temperature range for growth, assimilation of D-trehalose. Moreover, different enzyme activities of alkaline phosphatase, esterase, esterase lipase, lipase, crystine arylamidase, trypsin α-chymotrypsin and α-glucosidase could also distinguish the isolate from closely related members in the genus *Lysobacter*. Based on its distinct phylogenetic position within the genus *Lysobacter*, together with physiological and chemotaxonomic properties, it is concluded that strain YJ15^T represents a novel species in the genus *Lysobacter*, for which the name *Lysobacter telluris* sp. nov. is proposed.

Table 2 Cellular fatty acid composition (%) of strain YJ15^T and type species of the genus *Lysobacter*

Fatty acid	1	2	3	4	5
$C_{14:0}$	tr	1.0	tr	tr	tr
$C_{16:0}$	6.9	3.6	1.0	5.6	3.8
iso-$C_{10:0}$	tr	1.0	tr	tr	tr
iso-$C_{11:0}$	5.7	4.5	9.8	5.0	5.3
iso-$C_{11:0}$ 3-OH	2.5	3.8	7.8	4.6	5.4
iso-$C_{12:0}$	–	1.4	tr	tr	tr
iso-$C_{14:0}$	tr	2.6	2.4	2.6	2.1
iso-$C_{15:0}$	**23.0**	**18.3**	**23.6**	**17.8**	**13.7**
iso-$C_{16:0}$	**13.2**	**22.4**	**28.2**	**19.3**	**20.2**
iso-$C_{17:0}$	**13.4**	3.4	3.4	3.4	4.2
iso-$C_{15:1}$ F	tr	2.0	tr	tr	–
iso-$C_{16:1}$ H	–	1.5	1.6	tr	tr
iso-$C_{16:1}$ $\omega 7c$ alcohol	–	6.9	–	–	–
iso-$C_{17:1}$ $\omega 9c$	**26.8**	**18.6**	**13.4**	**14.5**	**14.3**
anteiso-$C_{11:0}$	tr	tr	tr	tr	1.1
anteiso-$C_{15:0}$	2.6	2.8	3.2	**13.6**	**18.5**
anteiso-$C_{17:0}$	tr	tr	tr	2.1	3.6
Summed feature 3*	2.7	1.9	1.0	4.6	3.2

Strains: 1, Strain YJ15^T; 2, '*L. tongrenensis*' KCTC 52206^T; 3, *L. pocheonensis* KCTC 12624^T; 4, *L. dokdonensis* KCTC 12822^T; 5, *L. caseinilyticus* KACC 19816^T; All data were obtained from this study. The data shown in this table are more than 1% for all strains. Major fatty acids components (> 10.0%) are highlighted in bold. –, Not detected; tr, trace amount (< 1%)

*Summed features represent groups of two or three fatty acids which could not be separated by GLC with MIDI system. Summed feature 3 comprised $C_{16:1}$ $\omega 7c$ and/or iso-$C_{15:0}$ 2-OH

Description of *Lysobacter telluris* sp. nov

Lysobacter telluris (tel.lu'ris. L. gen. n. *telluris* from soil)

Colonies are light yellow in colour, 0.5–2.0 mm, smooth, circular and convex with entire margins when grown for 5 days at 28 °C on R2A agar. Cells are Gram-stain-negative, non-motile, non-spore forming aerobic rods measuring 0.8–1.0 × 1.4–2.5 μm in size. Grows at 10–37 °C (optimum, 28 °C), pH 6.0–7.5 (optimum, pH 7.0) and in the absence of NaCl. Does not grow under anaerobic conditions. Positive for catalase and oxidase. Nitrate is reduced to nitrate and nitrate is not reduced to nitrogen. Negative for methyl red and Voges–Proskauer tests and indole and H_2S production. Hydrolyses casein, skim milk gelatin and tryptophan but does not hydrolyses aesculin, urea, DNA, Tweens 20, 40, 60 and 80, hypoxanthine, L-tyrosine, starch and xanthine. Using the API kit (API 50CH, API 50CHB, API 20NE and API ZYM), assimilates D-trehalose, glycogen, citric acid, phenyl-acetic acid, gluconic acid and propionic acid, and acid is produced from D-fructose, L-sorbose, aesculin, D-tagatose and potassium 5-keto-gluconate, and positive for leucine arylamidase, valine arylamidase, acid phosphatase and naphtol-AS-BI-phosphohydrolase. List of all negative traits of commertial kit is given in Table S3. The major fatty acids are iso-$C_{17:1}$ $\omega 9c$, iso-$C_{15:0}$, iso-$C_{16:0}$ and iso-$C_{17:0}$. The predominant isoprenoid quinone is ubiquinone Q-8. Polar lipids are diphosphatidylglycerol, phosphatidyl-ethanolamine, phatidylglycerol and two unidentified aminolipids. The genomic DNA G + C content is 68.2 mol %.

The type strain, YJ15^T (= KACC 19552^T = NBRC 113197^T) was isolated from a farming field located in Bigeum Island at Shinan, south-west Korea.

Funding This work was funded by the Strategic Initiative for Microbiomes in Agriculture and Food, Ministry of Agriculture, Food and Rural Affairs, Republic of Korea (as part of the Genome Technology to Business Translation Program). grant number 918016-4.

Compliance with ethical standards

Conflict of interest The authors declare that there are no conflicts of interest.

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