Archives of Microbiology
https://doi.org/10.1007/s00203-017-1457-z

ORIGINAL PAPER

Lysobacter tongrenensis sp. nov., isolated from soil of a manganese factory

Jingxin Li[1] · Yushan Han[1] · Wei Guo[1] · Qian Wang[1,3] · Shuijiao Liao[1,2] · Gejiao Wang[1]

Received: 16 August 2017 / Accepted: 15 November 2017

Abstract

A Gram-staining negative, aerobic, non-motile, rod-shaped bacterial strain, designated YS-37^T, was isolated from soil in a manganese factory, People's Republic of China. Based on16S rRNA gene sequence analysis, strain YS-37^T was most closely related to *Lysobacter pocheonensis* Gsoil 193^T (97.0%), *Lysobacter dokdonensis* DS-58^T (96.0%) and *Lysobacter daecheongensis* Dae08^T (95.8%) and grouped together with *L. pocheonensis* Gsoil 193^T and *Lysobacter dokdonensis* DS-58^T. The DNA–DNA hybridization value between strain YS-37^T and *L. pocheonensis* KCTC 12624^T was 43.3% (± 1). The major respiratory quinone of strain YS-37^T was ubiquinone-8, and the polar lipids were diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylglycerol, phospholipid, phosphatidylmethylethaolamine and two unknown lipids. Its major cellular fatty acids (> 5%) were iso-$C_{15:0}$, iso-$C_{17:1}\omega9c$, iso-$C_{16:0}$, iso-$C_{11:0}$ 3-OH and iso-$C_{11:0}$ and the G + C content of the genomic DNA was 67.1 mol%. Strain YS-37^T also showed some biophysical and biochemical differences with the related strains, especially in hydrolysis of casein. The results demonstrated that strain YS-37^T belongs to genus *Lysobacter* and represents a novel *Lysobacter* species for which the name *Lysobacter tongrenensis* sp. nov. is proposed. The type strain is YS-37^T (= CCTCC AB 2016052^T = KCTC 52206^T).

Keywords *Lysobacter tongrenensis* · Soil · Polyphasic taxonomy · 16S rRNA gene

Introduction

Genus *Lysobacter* was first described by Christensen and Cook in 1978 with *Lysobacter enzymogenes* as the type species (Christensen and Cook 1978). This genus was classified within family *Xanthomonadaceae* of *Gamma-Proteobacteria* (Saddler and Bradbury 2005) and the description was later emended by Park et al. (2008). To data, the genus *Lysobacter* consists of 43 species (http://www.bacterio.net/lysobacter.html). *Lysobacter* members are generally Gram-negative, aerobic, gliding and have a high DNA G + C contents (61.7–70.7%), and the major quinones, fatty acids and polar lipids are of ubiquinone-8 (Q-8), iso-branched fatty acids, and diphosphatidylglycerol (DPG), phosphatidylethanolamine (PE) and phosphatidylglycerol (PG), respectively (Christensen and Cook 1978; Christensen 2005; Weon et al. 2006; Ten et al. 2008, 2009; Srinivasan et al. 2010; Liu et al. 2011; Wang et al. 2011; Oh et al. 2011; Luo et al. 2012; Ye et al. 2015; Ngo et al. 2015). Here we describe the polyphasic characteristics of strain YS-37^T that related to *Lysobacter* members.

Communicated by Erko Stackebrandt.

Jingxin Li and Yushan Han contributed equally to this work.

Electronic supplementary material The online version of this article (https://doi.org/10.1007/s00203-017-1457-z) contains supplementary material, which is available to authorized users.

✉ Gejiao Wang
gejiao@mail.hzau.edu.cn

[1] State Key Laboratory of Agricultural Microbiology, College of Life Science and Technology, Huazhong Agricultural University, Wuhan, Hubei 430070, People's Republic of China

[2] College of Basis Science, Huazhong Agricultural University, Wuhan, Hubei 430070, People's Republic of China

[3] Department of Land Resources and Environmental Sciences, Montana State University, Bozeman, MT 59717, USA

Published online: 29 November 2017

Materials and methods

Bacterial strain and culture conditions

Strain YS-37^T was isolated from soil of a manganese factory named Guizhou Dalong Manganese Industry (109°04′E, 27°28′N) in Tongren city, Guizhou Province, People's Republic of China. The soil sample was suspended in 0.85% NaCl (w/v) and the diluted solutions were spread on R2A agar plates and incubated at 28 °C for 1 week. A total of 32 strains were isolated (data not shown) and a strain named YS-37^T was selected for this study due to the preliminary low 16S rRNA gene sequence similarity. The resistance levels of strain YS-37^T for multi-metal(loids) were tested with the minimal inhibition concentration (MIC) on R2A agar plates using $MnCl_2$, Na_3AsO_3, $K_2Sb_2(C_4H_2O_6)_2$, K_2CrO_4, $CdCl_2$ and $PbCl_2$. Strains *L. pocheonensis* KCTC 12624^T, *L. dokdonensis* KCTC 12822^T and *L. daecheongensis* KCTC 12600^T were purchased from the Korean Centre of Type Cultures and used as reference strains.

Phylogenetic analysis

Genomic DNA of strain YS-37^T was extracted according to standard procedures (Sambrook and Russell 2001). The primers 27F and 1492R were used for amplification of the 16S rRNA gene fragment as described by Brosius et al. (1978). The PCR product was purified and cloned into pGEM-T vector (Promega), subsequently PCR amplified using primers T7 and SP6 and sequenced in Tsingke Company (Beijing, China). The nearly completed 16S rRNA gene sequence (1506 bp) of strain YS-37^T was aligned with those from EzTaxon database (http://eztaxon-e.ezbiocloud.net) (Chun et al. 2007) using the CLUSTAL X program (Thompson et al. 1997). Phylogenetic analyses were performed with MEGA 6 (Tamura et al. 2013) using neighbor-joining (Saitou and Nei 1987), maximum-parsimony (Fitch 1971) and maximum-likelihood (Felsenstein 1981) algorithms. For each method, bootstrap values were calculated based on 1000 replications (Felsenstein 1985).

Morphological, physiological, and biochemical characterization

Cellular morphology was observed by scanning electron microscopy (SEM, JSM-6390; JEOL) (Fig. S1). Gram reaction was determined using a Gram-staining kit (Jiancheng Biotech, China) in combination with the 3% KOH method (Smibert and Krieg 1994). Gliding motility was tested on a fresh R2A broth culture using the hanging-drop method (Bernardet et al. 2002). Growth was assessed at various temperatures (0, 4, 16, 20, 25, 28, 32, 37, 42 and 45 °C) on R2A agar, and in various NaCl concentrations (0, 0.5, 1, 2, 3, 5, 6, and 7%, w/v) in R2A liquid medium at 28 °C. The pH range (pH 4–10) was tested in R2A liquid medium with different buffer systems (0.1 M citric acid/0.1 M sodium citrate, for pH 4.0–5.0; 0.1 M KH_2PO_4/0.1 M NaOH, for pH 6.0–8.0; 0.1 M $NaHCO_3$/0.1 M Na_2CO_3, for pH 9–10). Growth under anaerobic condition was determined by incubation in an anaerobic chamber at 28 °C for 2 weeks on R2A agar. Oxidase and catalase activities were determined using oxidase reagent and 3% (v/v) H_2O_2, respectively (Smibert and Krieg 1994). Nitrate and nitrite reduction tests were performed as described by Lányí (1987). Hydrogen sulfide production, indole test and hydrolyses of casein (5%, w/v), gelatin (15%, w/v), Tween 20, 40, 60, 80 and starch (0.2%, w/v) were determined according to Smibert and Krieg (1994). Acid production from carbohydrates were also tested (Dong and Cai 2001). The API 20 NE, API ID 32GN and API ZYM systems (bioMérieux) were used to determine biochemical properties, utilization of carbohydrates and enzyme activities according to the manufacturer's protocols, and if necessary, in combination with traditional methods.

Chemotaxonomic characterization

For whole-cell fatty acid analysis, cells of strain YS-37^T and the three reference strains were inoculated on R2A agar and harvested when the cells growth reached the exponential phase determined by the quadrant streak pattern method according to the protocol of MIDI (Sherlock Microbial Identification System, MIDI) and analyzed by gas chromatography (MIDI Sherlock version 4.5; MIDI database TSBA40 4.10) (Sasser 1990). For the extraction of respiratory quinones and polar lipids, the strains were cultured in R2A medium and freeze-dried after harvesting. Respiratory quinone analysis was performed by HPLC as described by Minnikin et al. (1984). Polar lipid analyses of strain YS-37^T and *L. dokdonensis* KCTC 12822^T were determined by two-dimensional TLC method as described by Tindall (1990). The DNA G + C content was determined by HPLC according to the method of Mesbah et al. (1989). Genomic DNA was extracted as described by Pitcher and Saunders (1989) for DNA–DNA hybridization analysis, which was performed using the thermal denaturation and renaturation method of De Ley et al. (1970).

Results and discussion

The 16S rRNA gene sequence of strain YS-37^T was closely related to *Lysobacter pocheonensis* Gsoil 193^T (97.0%), *Lysobacter dokdonensis* DS-58^T (96.0%) and *Lysobacter daecheongensis* Dae08^T (95.8%), and showed similarities less than 95.4% with the other members of the genus *Lysobacter* including the type species strain *Lysobacter enzymogenes* (93.9%). In the phylogenetic tree based on neighbor-joining algorithm, strain YS-37 ^{T} was closely related to the *Lysobacter* members and formed a branch with *L. pocheonensis* Gsoil 193^T and *L. dokdonensis* DS-58^T (Fig. 1). The phylogenetic trees based on the maximum-parsimony and maximum-likelihood algorithms showed similar relationships to those of the neighbor-joining method (marked with * in Fig. 1).

Cells of strain YS-37^T were Gram-staining-negative, aerobic, non-motile and rod-shaped (for details, see species description). In addition, strain YS-37^T is very resistant to Mn(II), As(III) and Sb(III) with MICs of 50, 2.0 and 3.0 mmol/L, respectively. The MICs for Cr(VI), Cd(II) and Pb(II) are 1.0, 0.1 and 0.8 mmol/L, respectively, indicating a certain degree of resistance. Strain YS-37^T was positive for catalase, oxidase and hydrolysis of gelatin, negative for urease activity, indole production and hydrogen sulfide production. These characteristics are consistent with the strains of the genus *Lysobacter* (Weon et al. 2006; Luo et al. 2012; Ye et al. 2015). The flexirubin-type pigment was absent. Strain YS-37^T showed some biophysical and biochemical differences with the related strains, especially in hydrolysis of casein (Table 1, supplementary material Table S1).

The DNA–DNA hybridization value between strain YS-37^T and the closely related strain *L. pocheonensis* KCTC 12624^T was 43.3% (± 1, $n = 2$), which is below the threshold value of 70% recommended for species delineation (Wayne et al. 1987). The whole-cell fatty acid compositions of strain YS-37^T, *L. pocheonensis* KCTC 12624^T, *L. dokdonensis* KCTC 12822^T, *L. daecheongensis* KCTC 12600^T and *L. enzymogenes* DSM 2043^T are shown in Table 2. The major fatty acids of strain YS-37^T were the branched compounds iso-$C_{15:0}$ (26.9%), iso-$C_{17:1}\omega9c$ (18.1%), iso-$C_{16:0}$ (9.6%), iso-$C_{11:0}$ 3-OH (13.7%) and iso-$C_{11:0}$ (8.4%). The fatty acid profile of strain YS-37^T is similar to the *Lysobacter* type strains (Weon et al. 2007; Bae et al. 2005; Ngo et al. 2015; Siddiqi and Im 2016), but a little different from the most closed *L. pocheonensis* KCTC 12624^T which has summed feature 9 (Siddiqi and Im 2016). The only respiratory quinone of strain YS-37^T was Q-8, which is typical of

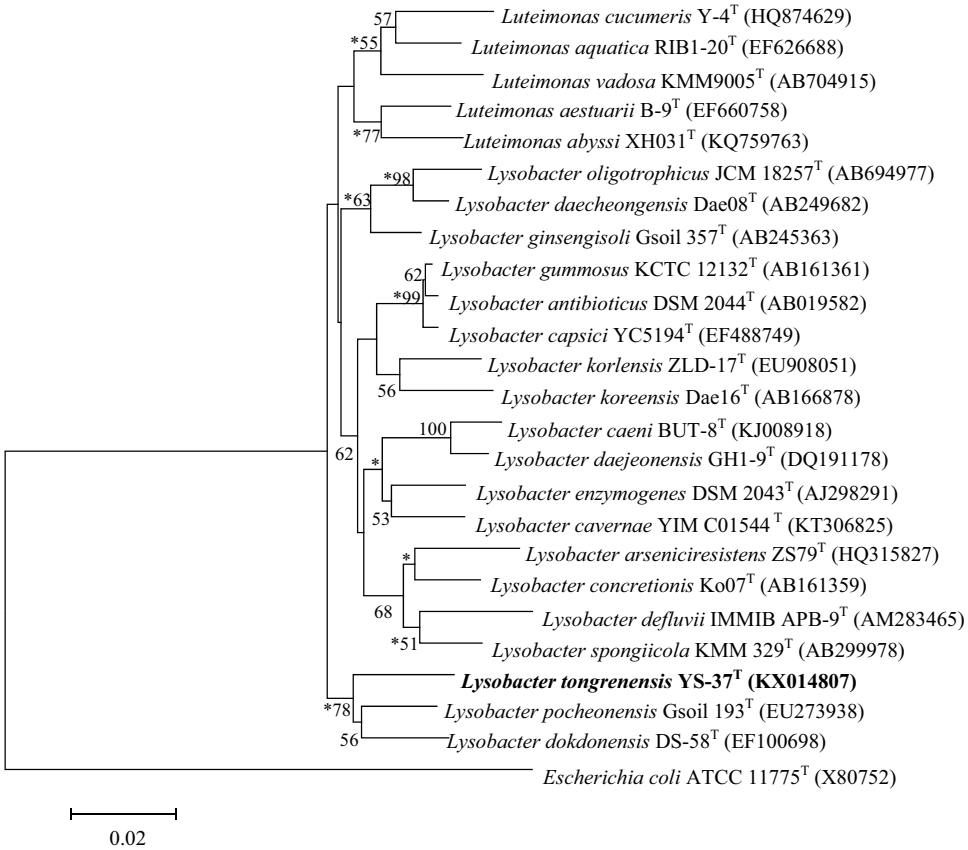

Fig. 1 Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the positions of strain YS-37^T and closely related strains. Bootstrap values > 50% (based on 1000 replications) are shown at branching points. *Bar* 0.02 substitutions per nucleotide position. The asterisk (*) indicates identical branch topologies of the maximum-parsimony and maximum-likelihood trees

Table 1 Differential phenotypic characteristics of strain YS-37^T and related *Lysobacter* strains

Characteristic	1	2	3	4	5
Colony color	LY	LY	LY	C	DY-C
NaCl tolerance (%, w/v)	0-0.5	0-0.5	0-0.5	0–7	0–2
pH range	6.5–7.5	5.0–9.0	6.5-8.0	6.0–8.0	6.0–10.0
Catalase	+	−	+	−	+
Hydrolysis of					
Casein	−	+	+	+	+
Gelatin	+	+	+	−	+
Aesculin	−	−	−	+	+
Esculin ferric citrate	−	−	+	+	ND
Urea	−	+	−	−	−
Assimilation of					
L-proline	+	−	−	−	+
L-arginine	−	+	−	−	−
Glycogen	−	−	+	+	+
Caprate	−	−	−	+	ND
N-acetylglucosamine	−	−	−	+	+
Maltose	−	−	+	−	+
Alanine	−	−	+	−	ND
Enzyme activities					
Valine arylamidase	+	+	+	−	ND
Cystine arylamidase	w	+	w	−	ND
α-glucosidase	−	−	w	−	+
Lipaes (C14)	−	−	−	+	ND
α-chymotrypsin	−	+	−	−	ND
DNA G + C content (mol%)	67.1	64.8[a]	68.1[b]	69.3[c]	69.0[d]

Strains: 1, strain YS-37^T; 2, *L. pocheonensis* KCTC 12624^T; 3, *L. dokdonensis* KCTC 12822^T; 4, *L. daecheongensis* KCTC 12600^T; 5, *L. enzymogenes* DSM 2043^T (Christensen and Cook 1978). These data of 1, 2, 3 and 4 are from this study except for the G + C% contents. Data of 5 are from Christensen and Cook 1978; Bae et al. 2005; Ten et al. 2009

+ positive, − negative, *w* weakly positive, *ND* no data available, *LY* light yellow, *DY* deep yellow, *C* cream

[a]Data from Siddiqi and Im 2016

[b]Data from Oh et al. 2011

[c]Data from Ten et al. 2008

[d]Data from Christensen and Cook 1978

the *Lysobacter* strains (Christensen and Cook 1978; Yassin et al. 2007; Choi et al. 2014; Ngo et al. 2015; Siddiqi and Im 2016). The polar lipids of strain YS-37^T were DPG, PE, PG, phosphatidylmethylethaolamine (PME), phospholipid (PL) and two unknown polar lipids (ND) (Fig. S2A). The polar lipids of *L. dokdonensis* KCTC 12822^T were DPG, PE, PG, P, PL, aminolipid (AL) and phosphoaminolipid (PN) (Fig. S2B). The present of PME and the two NDs and the absent of PN and AL could differentiate strain YS-37^T with the related strain *L. dokdonensis* KCTC 12822^T. In addition, the polar lipids of *L. daecheongensis* KCTC 12600^T were DPG, PE, PG, PME and unknown aminolipid (Ten et al. 2008), strain KCTC 12600^T did not contain PL which is different from strain YS-37^T. The DNA G + C content of strain YS-37^T is 67.1 mol%, which is within the range described for the genus *Lysobacter* (61.7–70.7 mol%) (Christensen and Cook 1978; Weon et al. 2006; Park et al. 2008; Luo et al. 2012; Liu et al. 2015).

These data indicate that strain YS-37^T belongs to genus *Lysobacter*, but can be differentiated from the related *Lysobacter* members by DNA–DNA hybridization, fatty acids and biochemical and physiological characteristics. Based on the polyphasic taxonomic results described in this study, strain YS-37^T represents a novel species of the genus *Lysobacter*, for which the name *Lysobacter tongrenensis* sp. nov. is proposed.

Description of *Lysobacter tongrenensis* sp. nov

Lysobacter tongrenensis (tong.ren.en'sis. N.L. masc. adj. *tongrenensis* pertaining to Tongren, a city of Guizhou

Table 2 Cellular fatty acid composition of strain YS-37^T and related *Lysobacter* strains

Fatty acid	1	2	3	4	5
$C_{14:0}$	1.0	–	1.1	0.8	1.2
$C_{16:0}$	2.1	0.7	4.5	1.7	5.1
iso-$C_{11:0}$	8.4	5.8	6.2	11.2	4.3
iso-$C_{11:0}$ 3OH	13.7	8.3	8.2	11.2	6.0
iso-$C_{13:0}$	1.1	–	–	–	–
iso-$C_{14:0}$	2.7	6.6	2.9	4.9	1.4
iso-$C_{15:0}$	26.9	30.4	28.5	43.2	43.0
iso-$C_{15:1}$ F	4.8	1.8	0.9	2.0	–
anteiso-$C_{15:0}$	0.8	3.8	3.4	0.8	3.8
iso-$C_{16:0}$	9.6	20.6	15.1	7.2	3.0
$C_{16:0}$ N alcohol	–	–	3.3	–	–
$C_{17:0}$ cyclo	–	–	–	–	10.6
iso-$C_{16:1}$ H	–	1.6	–	0.6	–
iso-$C_{17:0}$	1.6	0.9	2.3	0.7	4.4
$C_{16:1}\omega7c$ alcohol	1.5	–	–	–	–
$C_{16:1}\omega11c$	1.5	–	–	–	–
iso-$C_{17:1}\omega9c$	18.1	–	15.4	8.5	8.8
Summed features*					
1	–	1.2	0.7	1.2	–
3	2.5	2.1	4.0	4.4	–
4	–	–	–	–	8.3
9	–	15.3	–	–	–

Strains: 1, strain YS-37^T; 2, *L. pocheonensis* KCTC 12624^T; 3, *L. dokdonensis* KCTC 12822^T; 4, *L. daecheongensis* KCTC 12600^T; 5, *L. enzymogenes* DSM 2043^T (Christensen and Cook 1978). Data of 1, 2, 3 and 4 are from this study. Data of 5 are from Christensen and Cook 1978; Bae et al. 2005; Ten et al. 2009

– less than 0.5% or not detected

*Summed features combine groups of two or more fatty acids that cannot be separated by GLC with the MIDI system. Summed feature 1 comprised iso-$C_{15:1}$ H and/or $C_{13:0}$ 3OH; Summed feature 3 comprised $C_{16:1}\omega7c$ and/or $C_{15:0}$ 2OH; Summed feature 4 comprised iso-$C_{15:0}$ 2-OH and/or $C_{16:1}\omega7c$; Summed feature 9 comprised iso-$C_{17:1}$ $\omega9c$/$C_{16:0}$ 10-methyl

Province in Southwest People's Republic of China, from where the type strain was isolated).

Cells are Gram-staining-negative, strictly aerobic, non-motile and rod-shaped (0.3–0.4 × 0.6–1.5 μm). Colonies grown on R2A plates are 0.5–1.0 mm in diameter, circular, smooth, convex and light yellow-colored. Growth occurs at 4–32 °C (optimum 28 °C), at pH 6.5–7.5 (optimum pH 7.0) and NaCl concentrations in the range 0–0.5% (optimum, 0%). Positive for oxidase, catalase, hydrolysis of gelatin and assimilation of L-proline. The leucine arylamidase, valine arylamidase and trypsin are positive, and alkaline phosphatase, esterase (C4), esterase lipase (C8), cystine arylamidase, acid phosphatase and naphthol-AS-BI-phosphohydrolase are weakly positive. The major fatty acids are iso-$C_{15:0}$, iso-$C_{17:1}\omega9c$, iso-$C_{16:0}$, iso-$C_{11:0}$, and iso-$C_{11:0}$ 3-OH. The only respiratory quinone is ubiquinone Q-8, and the polar lipids are diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylglycerol, phosphatidylmethylethaolamine, phospholipid and two unknown lipids. The G + C content of the genomic DNA of the type strain is 67.1 mol%.

The type strain is YS-37^T (= CCTCC AB 2016052^T = KCTC 52206^T), was isolated from soil of a manganese factory in Tongren city, Guizhou Province, People's Republic of China. The Digital Protologue database TaxonNumber for strain YS-37^T is TA00250. The GenBank accession number for the 16S rRNA gene sequence of strain YS-37^T is KX014807.

Acknowledgements We are grateful to Dr. Bernhard Schink for the etymology of the strain's name and Penghao Cai for technique assistance. The analyses of quinone, polar lipid and DNA G + C content were performed by DSMZ. This work was supported by National Key Research and Development Program of China (2016YFD0800702) and China Postdoctoral Science Foundation Special Funding (2015T80814).

References

Bae HS, Im WT, Lee ST (2005) *Lysobacter concretionis* sp. nov., isolated from anaerobic granules in an upflow anaerobic sludge blanket reactor. Int J Syst Evol Microbiol 55(3):1155–1161

Bernardet JF, Nakagawa Y, Holmes B (2002) Subcommittee on the taxonomy of *Flavobacterium* and Cytophaga-like bacteria of the International Committee on Systematics of Prokaryotes. Proposed minimal standards for describing new taxa of the family *Flavobacteriaceae* and emended description of the family. Int J Syst Evol Microbiol 52:1049–1070

Brosius J, Palmer ML, Kennedy PJ, Noller HF (1978) Complete nucleotide sequence of a 16S ribosomal RNA gene from *Escherichia coli*. Proc Natl Acad Sci USA 75:4801–4805

Choi JH, Seok JH, Cha JH, Cha CJ (2014) *Lysobacter panacisoli* sp. nov., isolated from ginseng soil. Int J Syst Evol Microbiol 64:2193–2197

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. Springer, New York, pp 95–101

Christensen P, Cook FD (1978) *Lysobacter*, a new genus of nonfruiting, gliding bacteria with a high base ratio. Int J Syst Bacteriol 28:367–393

Chun J, Lee JH, Jung Y, Kim M, Kim S, Kim BK, Lim YW (2007) EzTaxon: a web-based tool for the identification of prokaryotes based on 16S ribosomal RNA gene sequences. Int J Syst Evol Microbiol 57:2259–2261

De Ley J, Cattoir H, Reynaerts A (1970) The quantitative measurement of DNA hybridization from renaturation rates. Eur J Biochem 12:133–142

Dong XZ, Cai MY (2001) Determinative manual for routine bacteriology. Scientific Press, Beijing

Felsenstein J (1981) Evolutionary trees from DNA sequences: a maximum likelihood approach. J Mol Evol 17:368–376

Felsenstein J (1985) Confidence limit on phylogenies: an approach using the bootstrap. Evolution 39:783–791

Fitch WM (1971) Toward defining the course of evolution: minimum change for a specific tree topology. Syst Zool 20:406–416

Lányí B (1987) Classical and rapid identification methods for medically important bacteria. Methods Microbiol 19:1–67

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

Liu L, Zhang S, Luo M, Wang G (2015) Genomic information of the arsenic-resistant bacterium *lysobacter arseniciresistens* type strain ZS79 and comparison of *lysobacter* draft genomes. Stand Genomic Sci 10:1–7

Luo G, Shi Z, Wang G (2012) *Lysobacter arseniciresistens* sp. nov., an arsenite-resistant bacterium isolated from iron-mined soil. Int J Syst Evol Microbiol 62:1659–1665

Mesbah M, Premachandran U, Whitman WB (1989) Precise measurement of the G + C content of deoxyribonucleic acid by highperformance liquid chromatography. Int J Syst Bacteriol 39:159–167

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

Ngo HTT, Won K, Du J, Son HM, Park Y, Kook M, Kim KY, Jin FX, Yi TH (2015) *Lysobacter terrae* sp. nov., isolated from *Aglaia odorata* rhizosphere soil. Int J Syst Evol Microbiol 65:587–592

Oh KH, Kang SJ, Jung YT, Oh TK, Yoon JH (2011) *Lysobacter dokdonensis* sp. nov., isolated from soil. Int J Syst Evol Microbiol 61:1089–1093

Park JH, Kim R, Aslam Z, Jeon CO, Chung YR (2008) *Lysobacter capsici* sp. nov., with antimicrobial activity, isolated from the rhizosphere of pepper, and emended description of the genus *Lysobacter*. Int J Syst Evol Microbiol 58:387–392

Pitcher DG, Saunders NA (1989) Rapid extraction of bacterial genomic DNA with guanidium thiocyanate. Lett Appl Microbiol 8:151–156

Romanenko LA, Uchino MN, Tanaka N, Frolova GM, Mikhailov VV (2008) *Lysobacter spongiicola* sp. nov., isolated from a deep-sea sponge. Int J Syst Evol Microbiol 58:370–374

Saddler GS, Bradbury JF (2005) Family I. *Xanthomonadaceae* fam. nov. In: Brenner DJ, Krieg NR, Staley JT, Garrity GM (eds) Bergey's manual of systematic bacteriology. Springer, New York, p 63

Saitou N, Nei M (1987) The neighbor-joining method: a new method for reconstructing phylogenetic trees. Mol Biol Evol 4:406–425

Sambrook J, Russell D (2001) Molecular cloning: a laboratory manual, 3rd edn. Cold Spring Harbor, New York

Sasser M (1990) Identification of bacteria by gas chromatography of cellular fatty acids. MIDI Technical Note 101, MIDI Inc., Newark

Siddiqi MZ, Im WT (2016) *Lysobacter pocheonensis* sp. nov., isolated from soil of a ginseng field. Arch Microbiol 198(6):551–557

Smibert RM, Krieg NR (1994) Phenotypic characterization. In: Gerhardt P, Murray RGE, Woods WA, Krieg NR (eds.) Methods for general and molecular bacteriology. American Society for Microbiology, Washington, pp 607–654

Srinivasan S, Kim MK, Sathiyaraj G, Kim HB, Kim YJ, Yang DC (2010) *Lysobacter soli* sp. nov., isolated from soil of a ginseng field. Int J Syst Evol Microbiol 60:1543–1547

Tamura K, Stecher G, Peterson D, Filipski A, Kumar S (2013) Mega6: molecular evolutionary genetics analysis version 6.0. Mol Biol Evol 30(4):2725–2729

Ten LN, Jung HM, Im WT, Yoo SA, Lee ST (2008) *Lysobacter daecheongensis* sp. nov., isolated from sediment of stream near the daechung dam in South Korea. J Microbiol 46:519–524

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

Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F, Higgins DG (1997) The CLUSTAL_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. Nucleic Acids Res 25:4876–4882

Tindall BJ (1990) Lipid composition of *Halobacterium lacusprofundi*. FEMS Microbiol Lett 66:199–202

Wang GL, Wang L, Chen HH, Shen B, Li SP, Jiang JD (2011) *Lysobacter ruishenii* sp. nov., a chlorothalonil-degrading bacterium isolated from a long-term chlorothalonil-contaminated soil. Int J Syst Evol Microbiol 61:674–679

Wayne LG, Brenner DJ, Colwell RR et al (1987) International Committee on Systematic Bacteriology. Report of the ad hoc committee on reconciliation of approaches to bacterial systematics. Int J Syst Bacteriol 37:463–464

Weon HY, Kim BY, Baek YK, Yoo SH, Kwon SW, Stackebrandt E, Go SJ (2006) Two novel species, *Lysobacter daejeonensis* sp. nov. and *Lysobacter yangpyeongensis* sp. nov., isolated from Korean greenhouse soils. Int J Syst Evol Microbiol 56:947–951

Weon HY, Kim BY, Kim MK, Yoo SH, Kwon SW, Go SJ, Stackebrandt E (2007) *Lysobacter niabensis* sp. nov. and *lysobacter niastensis* sp. nov., isolated from greenhouse soils in korea. Int J Syst Evol Microbiol 57:548–551

Yassin AF, Chen WM, Hupfer H, Siering C, Kroppenstedt RM, Arun AB, Lai WA, Shen FT, Rekha PD, Young CC (2007) *Lysobacter defluvii* sp. nov., isolated from municipal solid waste. Int J Syst Evol Microbiol 57:1131–1136

Ye XM, Chu CW, Shi C, Zhu JC, He Q, He J (2015) *Lysobacter caeni* sp. nov., isolated from the sludge of a pesticide manufacturing factory. Int J Syst Evol Microbiol 65:845–850