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ORIGINAL PAPER

Lysobacter lycopersici sp. nov., isolated from tomato plant *Solanum lycopersicum*

Shih-Yao Lin · Asif Hameed · Cheng-Zhe Wen · You-Cheng Liu · Yi-Han Hsu · Wei-An Lai · Chiu-Chung Young

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Abstract A Gram-stain negative, aerobic, rod-shaped and non-spore-forming bacterium, CC-Bw-6^T was isolated from chopped tomato stems. Analysis of the 16S rRNA gene sequence of the strain CC-Bw-6^T showed its affiliation with the genus *Lysobacter* within the class *Gammaproteobacteria.* Strain CC-Bw-6^T was found to be most closely related to *Lysobacter panaciterrae* KCTC 12601^T (97.0 %) and *Lysobacter daecheongensis* KCTC 12600^T (96.8 %), and showed lower similarity (<96.5 %) to other *Lysobacter* species. DNA–DNA relatedness between strain CC-Bw-6^T and *L. panaciterrae* KCTC 12601^T was 10.8 %, the G+C content of the genomic DNA is 69.9 mol%. Strain CC-Bw-6^T was determined to possess $C_{11:0}$ iso, $C_{11:0}$ iso 3OH, $C_{14:0}$ iso, $C_{15:0}$ anteiso, $C_{15:1}$ ω5c, $C_{16:1}$ ω5c, $C_{16:0}$, $C_{15:0}$ iso, $C_{16:0}$ iso, $C_{17:0}$ iso and $C_{16:0}$ 10-methyl/$C_{17:1}$ iso ω9c as predominant fatty acids. The major polar lipid profile consists of phosphatidylethanolamine, phosphatidylglycerol, diphosphatidylglycerol and unidentified phospholipids. The predominant polyamine is spermidine, and ubiquinone-8 is the predominant respiratory quinone. Analysis of phenotypic, geno- and phylogenetic characteristics revealed a distinct taxonomic position of strain CC-Bw-6^T with respect to other *Lysobacter* species. Based on the phylogenetic, chemotaxonomic and phenotypic data presented here, we propose a novel species with the name *Lysobacter lycopersici* sp. nov. The type strain is CC-Bw-6^T (=BCRC 80612^T = JCM 19164^T).

Keywords Polyphasic taxonomy · Gammaproteobacteria · *Lysobacter lycopersici*

GenBank accession number for the 16S rRNA gene sequence of strain CC-Bw-6^T is KC820654.

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S.-Y. Lin · A. Hameed · Y.-C. Liu · Y.-H. Hsu · W.-A. Lai · C.-C. Young (✉)
Department of Soil and Environmental Sciences, College of Agriculture and Natural Resources, National Chung Hsing University, 250, Kuo Kuang Rd., Taichung 402, Taiwan
e-mail: ccyoung@mail.nchu.edu.tw

C.-Z. Wen
Bachelor Program of Bio-Industry Management, College of Agriculture and Natural Resources, National Chung Hsing University, Taichung, Taiwan

W.-A. Lai · C.-C. Young
Agricultural Biotechnology Center, National Chung Hsing University, Taichung, Taiwan

Introduction

The genus *Lysobacter* and the family *Lysobacteraceae* was proposed in 1978 (Christensen and Cook 1978). Further taxonomic studies have shown that the genus *Lysobacter* belongs to the family *Xanthomonadaceae* (Saddler and Bradbury 2005) and the description of

the genus has been emended by Park et al. (2008). There are more than thirty validly named species of the genus *Lysobacter* including four *Lysobacter* species described in 2014, *Lysobacter panacisoli* (Choi et al. 2014), *Lysobacter terrae* (Ngo et al. 2014), *Lysobacter mobilis* (Yang et al. 2014) and *Lysobacter caeni* (Ye et al. 2014). Most of *Lysobacter* species were isolated from soil samples, except for *Lysobacter spongiicola* (Romanenko et al. 2008), *Lysobacter concretionis* (Bae et al. 2005) and *L. mobilis* (Yang et al. 2014) which were isolated from deep sea sponge, sludge and abandoned lead–zinc ore, respectively.

Some bacteria of this genus exhibit robust proteolytic activity and are able to lyse certain microorganisms such as Gram-stain positive bacteria (including actinomycetes), filamentous fungi, yeasts, green algae, and some invertebrates such as nematodes (Ahmed et al. 2003; Ryazanova et al. 2005). For example, some strains of *Lysobacter enzymogenes* were shown to be used as a potential biocontrol agent for plant fungal pathogens (Folman et al. 2004; Kilic-Ekici and Yuen 2003). Typical chemotaxonomic features of the bacteria of the genus *Lysobacter* comprise Q-8 as the major respiratory quinone, iso-branched fatty acids and DPE, PE and PG as the major polar lipids.

In this study, we aimed to clarify the taxonomic status of a novel bacterium, designated CC-Bw-6^T, which was isolated from the tomato stems. In order to confirm the taxonomic position of the novel strain, comparative physiological, biochemical, chemotaxonomic, genomic and phylogenomic analyses have been performed.

Materials and methods

Bacterial strains and growth conditions

Tomato plant (*Solanum lycopersicum* L.) was collected from a greenhouse belonging Taichung senior high school of National Chung Hsing University (24°12′N, 120°68′E), Taichung, Taiwan. The chopped tomato stems were suspended in sterile water and shaken at 30 °C for 30 min. Subsequently, standard serial dilution was carried out and spread on R2A agar plates (BD, U.S.A.). Several bacterial strains were isolated, identified and preserved as glycerol suspension (30 %, v/v) at −80 °C for further characterization.

For comparative purposes, the most closely related type strains *Lysobacter panaciterrae* KCTC 12601^T (Ten et al. 2009), *Lysobacter daecheongensis* KCTC 12600^T (Ten et al. 2008), *Lysobacter ginsengisoli* KCTC 12602^T (Jung et al. 2008) and *L. enzymogenes* BCRC 11654^T (Kawamura et al. 2009) were obtained from Korean Collection for Type Cultures (KCTC, Korean) and Bioresource Collection and Research Center (BCRC, Taiwan), and used as reference strains. Due to reported phylogenetic heterogeneity of the genus *Lysobacter* (Romanenko et al. 2013), e.g., *L. panaciterrae* KCTC 12601^T was clustered with members of the genus *Luteimonas* as a separate line sharing a high 16S rRNA gene sequence similarity to *Luteimonas aquatica* LMG 24212^T (98.8 %), *L. aquatica* BCRC 17731^T (Chou et al. 2008), *Luteimonas composti* BCRC 17598^T (Young et al. 2007), *Luteimonas mephitis* BCRC 17539^T (Finkmann et al. 2000) and *Thermomonas brevis* BCRC 17538^T (Mergaert et al. 2003) were also obtained from BCRC. All reference strains were grown on R2A at 30 °C for 2 days, unless described otherwise.

Morphological tests and biochemical characterization

Colony morphology, flagellation, and morphology of the cells of strain CC-Bw-6^T were investigated using the colonies/cells grown on R2A agar for 3 days. Growth of the strain CC-Bw-6^T was also tested on nutrient agar (NA, Hi-Media) and tryptic soy broth (TSB, BD, U.S.A.) agar. Cell morphology was observed by using light microscopy (model A3000, Zeiss) and transmission electron microscopy (JEOL JEM-1400), and cells were stained with 0.2 % uranyl acetate. Gram staining was carried out using a Gram staining kit as described by Murray et al. (1994). Growth was tested using R2A broth at temperature 4, 10, 15, 20, 25, 30, 37, 40, 42, 45 and 50 °C, and pH 5–10 (1 unit increment). Salt tolerance was determined by cultivating the organism in R2A broth supplemented with NaCl at final concentrations of 0–5 % (1 % increment). The presence of flexirubin-type pigments was investigated as described by Bernardet et al. (2002). Catalase activity was determined by assessing bubble production by cells in 3 % (v/v) H_2O_2 and oxidase activity was determined by using 1 % (w/v) *N*,*N*,*N*,*N*,-tetramethyl-1,4-phenylenediamine reagent (bioMérieux). Carbon sources utilization pattern was

determined by using GN2 microplate system (Bio-Log). Nitrate reduction, indole production, activities of β-galactosidase, urease, hydrolysis of esculin and gelatin and assimilation of 12 substrates were tested with API 20 NE strips (bioMérieux). The activities of various enzymes were determined by using API ZYM system (bioMérieux).

Sequencing and analysis of the 16S rRNA gene

A commercial DNA extraction kit UltraClean™ (MO BIO, USA) was used to extract the genomic DNA of CC-Bw-6^T for 16S rRNA gene amplification. The 16S rRNA gene of strain CC-Bw-6^T was amplified using the universal bacterial primers 1F and 9R as described by Edwards et al. (1989). Primers 3F, 6F and 4R were used for sequencing reaction. The amplified gene fragments were screened by 2.0 % (w/v) agarose gel electrophoresis. Gene sequencing was performed by using the Bigdye terminator kit (Heiner et al. 1998), and nucleotide sequence of PCR product was genotyped by direct sequencing in an ABI 3730 Genetic Analyzer (Applied Biosystems, Foster City, CA, USA). The DNA sequences were then assembled using the Vector NTI 9.0 software (IBI, USA) and uploaded to EzBioCloud server (EzTaxon-e Database, Kim et al. 2012) and NCBI for identification.

For the phylogenetic analysis, the almost-complete 16S rRNA gene sequence (1512 bp) of strain CC-Bw-6^T was uploaded to EzBioCloud (EzTaxon-e Database, Kim et al. 2012) and NCBI servers for BLAST search. To ascertain the phylogenetic position of the novel isolate, the 16S rRNA gene sequence of strain CC-Bw-6^T was compared with sequences obtained from GenBank. Multiple alignments of the sequences were performed using CLUSTAL_X (version 1.83) (Thompson et al. 1997). The phylogenetic analysis was performed with MEGA 6 software (Molecular Evolutionary Genetics Analysis, version 6.0; Tamura et al. 2013) and the topology of the resultant neighbor-joining (Saitou and Nei 1987), maximum likelihood (Felsenstein 1981) and maximum-parsimony (Fitch 1971) trees were evaluated by bootstrap analyses (Felsenstein 1985) after 1000 replications.

DNA–DNA hybridization

DNA–DNA hybridization (Graham et al. 1991; Wayne et al. 1987) is considered to be a standard method for species definition. DNA-DNA hybridisation was performed between strain CC-Bw-6^T and *L. panaciterrae* KCTC 12601^T (97.0 % 16S rRNA gene sequences similarity) using the DIG-High Prime DNA Labelling and Detection Starter kit II according to the manufacturer's instructions (Roche). DNA samples were loaded on to positively charged membranes as described by Seldin and Dubnau (1985). Chromosomal DNA of strain CC-Bw-6^T and *L. panaciterrae* KCTC 12601^T were used to construct hybridization probes by labelling with digoxigenin–11-dUTP (DIG). Hybridization was conducted in triplicate with reciprocal probes.

DNA base composition

For the analysis of DNA G+C content, DNA samples were prepared as described by Mesbah et al. (1989). The nucleoside mixtures obtained were then separated and analyzed via HPLC [Hitachi L-2130 chromatograph equipped with a Hitachi L-2200 autosampler, Hitachi L-2455 Diode array detector, and a reverse-phase C18 column (Phenomenex® Synergi 4 µ Fusion-RP80 250 × 4.60 mm)].

Determination of the predominant quinones and polar lipids

For the investigation of chemotaxonomic characteristics, strain CC-Bw-6^T and the reference strains were grown on R2A agar plates for 2 days at 30 °C and cells of these strains were harvested at a similar physiological age given that all strains showed similar growth kinetics. Isoprenoid quinones were purified according to the methods of Minnikin et al. (1984) and analysed by HPLC as described by Collins (1985). Biomass subjected to polar lipid analysis was grown on R2A broth and harvested at the stationary growth phase. Polar lipids were extracted according to the procedures described by Minnikin et al. (1984) and analyzed by two-dimensional TLC followed by spraying with appropriate detection reagents. Phospholipids were detected with the Zinzadze reagent of Dittmer and Lester (1964). Whole lipid profiles were detected by spraying with molybdophosphoric acid followed by heating at 150 °C (Worliczek et al. 2007). Determination of the respiratory quinone system was carried out as described by Collins (1985).

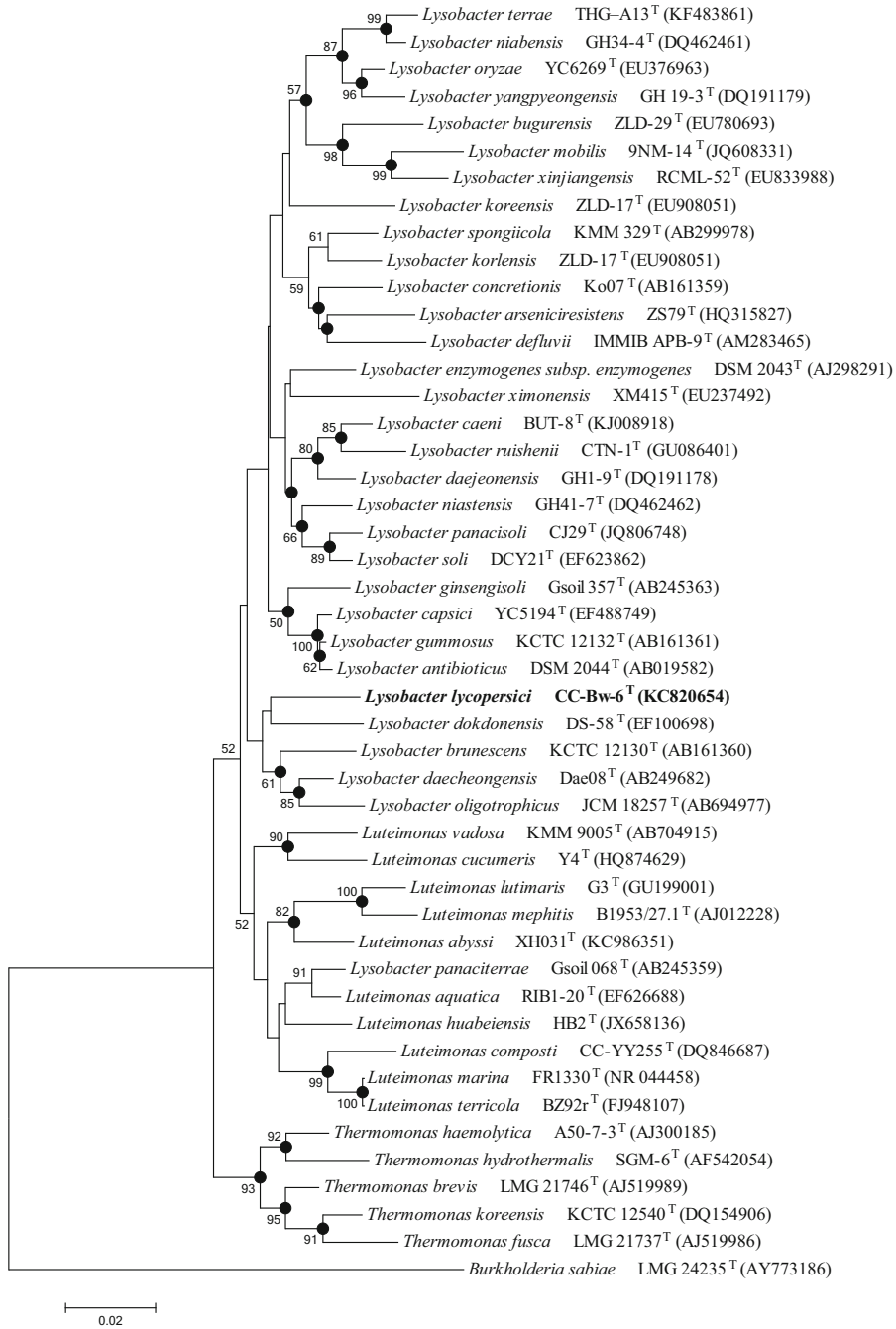

Fig. 1 Neighbor-joining phylogenetic tree showing taxonomic position of strain CC-Bw-6^T and other closely related species of the genus *Lysobacter* based on 16S rRNA gene sequences. *Filled circles* indicate that the corresponding nodes were also recovered in the tree constructed based on maximum parsimony and maximum likelihood algorithm. Bootstrap values (>50 %) based on 1000 replications are listed as percentages at the branching points

Cellular polyamines and fatty acid methyl ester (FAME) analyses

Biomass subjected to polyamine analysis was grown on R2A and harvested at the late exponential growth phase. Polyamines were extracted as described by Scherer and Kneifel (1983), analyzed by using HPLC. The dansyl derivatives were separated by using a Hitachi L-2130 equipped with a Hitachi L-2200 autosampler, Hitachi L-2485 fluorescence detector (excitation at 360 nm and emission at 520 nm), and a reverse-phase C18 column (Phenomenex® Synergi Fusion-RP80, 250 × 4.60 mm, 4 μm particle size). For the extraction of fatty acid methyl esters (FAMEs), strain CC-Bw-6^T and reference type strains were cultured simultaneously on R2A agar for 48 h at 30 °C (the type strains exhibited similar growth rates). Samples were prepared, separated and identified according to the standard protocol (Paisley 1996) of the Microbial Identification System (MIDI) (Sasser 1990) by gas chromatograph (Agilent 7890A) fitted to a flame ionization detector. Harvested biomasses were subjected to saponification, methylation and extraction (Miller 1982). Identification and comparison were made by using the Aerobe (RTSBA6) database of the MIDI System (Sherlock version 6.0).

Results and discussion

Analysis of the 16S rRNA gene sequences indicated that strain CC-Bw-6^T shows the highest similarity to *L. panaciterrae* KCTC 12601^T (97.0 %) followed by *L. daecheongensis* KCTC 12600^T (96.8 %) and other recognized species of the genus *Lysobacter* (<96.8 %). The similarity values of the 16S rRNA gene suggested that strain CC-Bw-6^T could be considered as a novel species since sequence divergence values of ≥3 % are recommended for the species delineation (Stackebrandt and Goebel 1994). DNA–DNA hybridization value between strain CC-Bw-6^T and *L. panaciterrae* KCTC 12601^T was found to be 10.8 ± 1.5 % (reciprocal value was 5.1 ± 0.9 %). This value is below the 70 % cut-off recommended for genomic species discrimination (Wayne et al. 1987), clearly suggesting that strain CC-Bw-6^T represents a novel species of the genus *Lysobacter*.

The 16S rRNA gene sequence similarities between strain CC-Bw-6^T and other related species of the genera *Lysobacter* (25 species), *Luteimonas* (10 species) and *Thermomonas* (5 species) were found to be 93–97, 95–97 and 93–96 %, respectively, which is at the interspecies level. The phylogenetic position of strain CC-Bw-6^T is shown in Fig. 1. Similar topology of the phylogenetic trees was obtained using neighbor-joining, maximum likelihood and maximum-parsimony algorithms.

Colonies of strain CC-Bw-6^T were observed to be circular, smooth and yellow-colored after three-days of incubation on R2A agar. Cell morphology of strain CC-Bw-6^T is presented in Fig. 2. Strain CC-Bw-6^T was found to produce flexirubin-type pigments. In the biochemical tests, strains CC-Bw-6^T, *L. enzymogenes* subsp. *enzymogenes* BCRC 11654^T and *L. panaciterrae* KCTC 12601^T utilize glycogen, Tween 40, pyruvic acid methyl ester, acetic acid, formic acid, β-hydroxybutyric acid, α-keto butyric acid, α-keto glutaric acid, α-keto valeric acid, propionic acid, L-glutamic acid, glycyl-L-aspartic acid, L-serine, L-threonine and urocanic acid as carbon sources; positive for β-glucosidase and protease (hydrolysis of gelatin); activity of alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase, α-chymotrypsin, acid phosphatase and Naphthol-AS-BI-phosphohydrolase were detected; but negative for α-galactosidase, β-galactosidase and β-glucuronidase.

Strain CC-Bw-6^T can be distinguished from other phylogenetically related species by its ability to utilize of α-keto valeric acid, L-alanine, L-phenylalanine, L-histidine, L-leucine, L-ornithine and L-proline; negative for lipase, cystine arylamidase, trypsin and *N*-

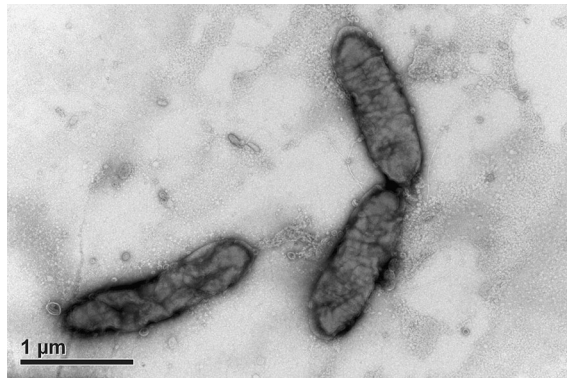

Fig. 2 Transmission electron micrograph of a negatively stained cell of strain CC-Bw-6^T. The cells appeared as short rods (0.3–0.4 × 1.5–1.7 μm) with a single polar flagellum. *Bar* 1.0 μm

Table 1 Phenotypic characteristics of strain CC-Bw-6^T and closely related species

Characteristic	1	2	3	4	5	6	7
Ranges for growth							
pH	5.0–8.0	6.0–8.0	5.0–9.0	5.0–9.0	6.0–8.0	5.0-9.0	5.0–9.0
NaCl (%, w/w)	<1.0	<1.0	<1.0	<1.0	0–0.5	0–2.0	0–1.0
Temperature (°C)	20–37	20–37	20–37	20–30	4–38	2–40	20–30
Reduction							
NO^{3-} to NO^{2-}	+	−	−	−	−	+	−
NO^{3-} to N_2	−	+	−	−	ND	ND	+
Carbon source utilization							
Dextrin	−	+	−	+	+	−	+
D-Cellobiose	−	+	+	+	−	+	+
D-Fructose	−	+	−	+	−	+	+
α-D-Glucose	−	+	−	+	−	+	+
Maltose	−	+	+	+	w	+	+
α-Keto valeric acid	+	+	−	−	−	+	+
L-Alanine	+	−	−	−	+	+	+
L-Aspartic acid	−	+	−	−	−	+	+
L-Phenylalanine	+	−	−	−	−	ND	−
L-Histidine	+	−	−	−	−	+	+
L-Leucine	+	−	−	+	+	ND	+
L-Ornithine	+	−	−	−	−	+	+
L-Proline	+	−	−	+	−	+	+
Glycerol	−	+	+	−	ND	ND	+
Enzymatic activities							
Lipase (C14)	−	−	−	−	−	ND	+
Cystine arylamidase	−	+	+	−	−	ND	+
Trypsin	−	+	−	−	−	ND	+
N-acetyl-*β*-glucosaminidase	−	+	−	−	ND	ND	+
Assimilation							
D-Glucose	−	+	−	−	−	+	+
D-Mannose	−	−	−	−	−	+	+
N-acetyl glucosamine	−	+	−	−	−	+	+
D-Maltose	−	−	−	−	w	+	+
Malic acid	−	w	−	−	ND	+	+
DNA G+C content	69.9	67.0[a]	69.3[a]	69.3[a]	68.1[a]	69.2[a]	69.0[a]

Data were obtained in this study unless indicated otherwise

1 strain CC-Bw-6^T; *2 Lysobacter panaciterrae* KCTC 12601^T; *3 Lysobacter daecheongensis* KCTC 12600^T; *4 Lysobacter ginsengisoli* KCTC 12602^T; *5 Lysobacter dokdonensis* DS-58^T (Oh et al. 2011); *6 Lysobacter antibioticus* BCRC 11653^T (Weon et al. 2007); *7 Lysobacter enzymogenes* subsp. *enzymogenes* BCRC 11654^T (type species)

+ positive; - negative; *w* weak reaction, *ND* no data available

[a] Data obtained from Mergaert et al. (2003); Weon et al. (2007); Young et al. (2007); Chou et al. (2008); Park et al. (2008); Ten et al. (2009); Zhang et al. (2011); Oh et al. (2011)

acetyl-*β*-glucosaminidase in enzymatic activities; reduction of nitrate (NO^{3-}) to nitrite (NO^{2-}). The detail phenotypic characteristics of strain CC-Bw-6^T are given in the species description. Additionally, strain CC-Bw-6^T showed several distinct physiological and biochemical characteristics, a comparison of the

Table 2 Cellular fatty acid composition (%)

Fatty acid	1	2	3	4	5	6	7
$C_{11:0}$ iso	5.8	12.8	6.0	3.4	5.9	3.3	9.7
$C_{11:0}$ iso 3OH	8.0	28.3	9.7	6.6	7.8	7.3	22.6
$C_{12:0}$ iso 3OH	tr	2.7	tr	tr	–	–	tr
$C_{14:0}$ iso	2.3	tr	3.6	1.6	4.6	tr	tr
$C_{14:0}$	–	–	tr	tr	–	tr	–
$C_{15:1}$ iso F*	tr	1.2	tr	tr	–	–	tr
$C_{15:0}$ iso	15.7	11.7	24.4	4.8	18.7	28.3	32.3
$C_{15:0}$ anteiso	2.9	1.9	3.0	4.6	4.9	3.6	tr
$C_{15:1}\omega 5c$	3.6	3.8	6.0	tr	–	4.3	8.9
$C_{16:1}$ iso H	tr	1.1	tr	1.6	1.1	tr	tr
$C_{16:0}$ iso	27.5	8.0	22.4	35.0	30.5	6.1	1.6
$C_{16:1}\omega 5c$	4.8	1.6	4.9	6.0	–	tr	tr
$C_{16:0}$	2.0	tr	1.4	3.5	1.9	5.8	2.0
$C_{15:0}$ iso 3OH	tr	tr	tr	1.1	–	2.1	1.7
$C_{17:0}$ iso	5.4	3.0	2.9	2.9	2.5	3.4	2.0
$C_{17:0}$ anteiso	–	–	–	1.3	–	tr	–
$C_{17:0}$ cyclo	–	1.3	–	–	–	1.4	1.5
$C_{18:0}$ iso	–	–	tr	1.2	–	tr	–
Summed feature 1	–	–	tr	tr	–	tr	–
Summed feature 2	1.9	–	–	–	–	–	–
Summed feature 3	1.4	1.7	1.3	4.5	–	11.7	5.7
Summed feature 8	–	–	–	tr	–	1.7	–
Summed feature 9	13.0	11.8	8.5	13.7	14.0	8.6	5.1

Data were obtained in this study unless indicated otherwise

1 strain CC-Bw-6^T; *2 Lysobacter panaciterrae* KCTC 12601^T; *3 Lysobacter daecheongensis* KCTC 12600^T; *4 Lysobacter ginsengisoli* KCTC 12602^T; *5 Lysobacter dokdonensis* DS-58^T (Oh et al. 2011); *6 Lysobacter antibioticus* BCRC 11653^T (Weon et al. 2007); *7 Lysobacter enzymogenes* subsp. *enzymogenes* BCRC 11654^T (type species)

tr trace (<1 %), – not detected

Fatty acids found in amounts <1.0 % in all strains are not shown

$C_{15:1}$ iso F* should correspond to either $C_{15:1}$ iso v6c and/or $C_{15:1}$ iso v5c. The double bond position is presumptive (Yassin et al. 2007)

Summed features represent groups of two or three fatty acids that cannot be separated by GLC with the MIDI system

Summed feature 1 $C_{15:1}$ iso H/$C_{13:0}$ 3-OH, *Summed feature 2* $C_{14:0}$ 3-OH/$C_{16:1}$ iso I, *Summed feature 3* $C_{16:1}\omega 7c$/$C_{16:1}\omega 6c$, *Summed feature 8* $C_{18:1}\omega 7c$/$C_{18:1}\omega 6c$, *Summed feature 9* $C_{16:0}$ 10-methyl/$C_{17:1}$ iso

phenotypic properties between strain CC-Bw-6^T and the type strains of validly named species in the genus *Lysobacter* is given in Table 1.

Strain CC-Bw-6^T was determined to possess 69.9 ± 0.4 mol% DNA, which is within the range described for the genus *Lysobacter* (61.7–70.1 mol%). Similar polyamine patterns with spermidine as the major compound, were also observed for several type strains of species of the genera *Lysobacter*, *Luteimonas* and *Thermomonas*. The major polar lipids were identified as phosphatidylethanolamine (PE), phosphatidylglycerol (PG), diphosphatidylglycerol (DPG), unidentified phospholipids (PL1-6), unidentified aminophospholipids (APL1-3); a moderate amount of phosphatidylmethylethanolamine (PME) was also identified (Supplementary data Fig. S1). The major fatty acids in strain CC-Bw-6^T were determined to be $C_{11:0}$ iso, $C_{11:0}$ iso 3OH, $C_{15:0}$ iso, $C_{16:0}$ iso, $C_{17:0}$ iso and $C_{16:0}$ 10-methyl/$C_{17:1}$ iso ω9c, which are commonly detected in *Lysobacter* species lipids (Table 2).

Based on the results of the polyphasic taxonomic study, strain CC-Bw-6^T is proposed to represent a novel species *Lysobacter lycopersici* sp. nov. CC-Bw-6^T (=BCRC 80623^T = JCM 19164^T) within the genus *Lysobacter*.

Description of *Lysobacter lycopersici* sp. nov

Lysobacter lycopersici (ly.co.per'si.ci N.L. gen. neut. n. lycopersici of *Lycopersicon*, the systematic name of the tomato).

Cells are Gram-stain negative, rod-shaped, 1.5–1.7 μm in length and 0.3–0.4 μm in diameter. Colonies are circular, smooth and yellow-colored after three-days of incubation on R2A agar. The growth temperature ranges from 20 to 37 °C, pH 5.0–8.0 but tolerates less than 1 % (w/v) NaCl concentration. Oxidase and catalase tests give a positive reaction. The flexirubin pigments are produced. Nitrates are reduced to nitrites, but nitrites are not reduced. The following carbon sources are utilized in the BioLog GN2 system: glycogen, Tween 40, pyruvic acid methyl ester, acetic acid, formic acid, β-hydroxybutyric acid, α-keto butyric acid, α-keto glutaric acid, α-keto valeric acid, propionic acid, L-alaninamide, L-alanine, L-alanyl-glycine, L-asparagine, L-glutamic acid, glycyl-L-aspartic acid, glycyl-L-glutamic acid, L-histidine, hydroxy-L-proline, L-leucine, L-ornithine, L-phenylalanine, L-proline, L-serine, L-threonine and urocanic acid. Alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase, α-chymotrypsin, acid phosphatase and naphthol-AS-BI-phosphohydrolase are positive in the API-ZYM system. The fatty acid profiles consists of $C_{11:0}$ iso, $C_{11:0}$ iso 3OH, $C_{14:0}$ iso, $C_{15:0}$ anteiso, $C_{15:1}$ ω5c, $C_{16:1}$ ω5c, $C_{16:0}$, $C_{15:0}$ iso, $C_{16:0}$ iso, $C_{17:0}$ iso and $C_{16:0}$ 10-methyl/$C_{17:1}$ iso ω9c. The polar lipid profile constitutes PE, PG and DPG as major lipids. The predominant polyamine is spermidine (Spd) and the predominant ubiquinone is (Q-8). The DNA G+C content is 69.9 ± 0.4 mol%.

The type strain is CC-Bw-6^T (=BCRC 80612^T = JCM 19164^T), isolated from chopped tomato stems, in Taiwan.

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