Chryseobacterium cucumeris sp. nov., an endophyte isolated from cucumber (Cucumis sativus L.) root, and emended description of Chryseobacterium arthrophaeae

Jin-Ju Jeong,‡ Dong Wan Lee,‡ Byeonghyeok Park, Mee Kyung Sang, In-Geol Choi and Ki Deok Kim.†

Abstract

The Gram-stain-negative, yellow-pigmented, rod-shaped bacterial strain GSE06T, isolated from the surface-sterilized root of a cucumber plant grown in a field in Gunsan, Korea, was characterized by not only cultural and morphological features but also physiological, biochemical and molecular analyses. Phylogenetic analyses based on 16S rRNA gene sequences revealed that strain GSE06T was most closely related to species of the genus Chryseobacterium. Furthermore, strain GSE06T exhibited the highest sequence similarities with the type strains Chryseobacterium indolgenes ATCC 29897T (98.9 %), Chryseobacterium gleum ATCC 35910T (98.8 %), Chryseobacterium arthrophaeae CC-VM-7T (97.7 %), Chryseobacterium contaminans C26T (98.5 %), Chryseobacterium artocarpi UTM-3T (98.3 %), and Chryseobacterium gallinarum 100T (97.9 %). Average nucleotide identity values between genome sequences of strain GSE06T and the above-mentioned reference strains ranged from 81.2 to 86.9 %, which were lower than the threshold of 95 % (corresponding to a DNA–DNA reassociation value of 70 %). The DNA G+C content of strain GSE06T was 36.1 mol%; the predominant respiratory quinone of the strain was MK-6. The major fatty acids were iso-C15:0, summed feature 9 (iso-C17:0 3ωc), summed feature 3 (C16:1ω7c and/or C16:1ω6c) and iso-C17:0 3-0H. The major polar lipids were phosphatidylethanolamine, three aminolipids, one aminophospholipid, four glycolipids and one unidentified lipid. These results of phenotypic and genotypic characteristics could differentiate strain GSE06T from closely related type strains belonging to the genus Chryseobacterium. Thus, strain GSE06T is proposed as a representative of a novel species in the genus Chryseobacterium, Chryseobacterium cucumeris sp. nov. The type strain is GSE06T (=KACC 18798T=JCM 31422T).

The genus Chryseobacterium belongs to the family Flavobacteriaceae and was emended from the genus Flavobacterium, based on the genotypic, biochemical and phenotypic characteristics of the organisms [1, 2]. In general, species of the genus Chryseobacterium are non-motile, yellow-pigmented, rod-shaped bacteria; they typically have menaquinone 6 as the predominant respiratory quinone [3]. At the time of writing, 95 species of the genus Chryseobacterium have been reported (www.bacterio.net/index.html); many of these are abundant in diverse environments, including soil, water, plants, rhizospheres, raw milk, chicken and fish [4–10]. Interestingly, several species of the genus Chryseobacterium, isolated from plants or rhizospheres, have been shown to have activities in plant growth promotion or biocontrol of plant pathogens [8, 11–15]. In an earlier study [16], the biocontrol activity of bacterial strain GSE06T was reported against Phytophthora blight of pepper (Capsicum annuum L.) caused by the destructive soilborne oomycete Phytophthora capsici [17]. Recently, the genome sequence of strain GSE06T was also reported, identifying several genes related to biocontrol activity, such as plant colonization and antimicrobial abilities (e.g. biofilm formation, enol-CoA hydratase, polyketide cyclase and thiazole) as well as abiotic or biotic stress management (e.g. superoxide dismutase, hydrogen peroxidase, catalase and peroxidase) [18]. In this study, to elucidate the taxonomic position of

Author affiliations: †Laboratory of Plant Disease and Biocontrol, College of Life Sciences and Biotechnology, Korea University, Seoul 02841, Republic of Korea; ‡Department of Biosystems and Biotechnology, Korea University, Seoul 02841, Republic of Korea; ††Department of Biotechnology, Korea University, Seoul 02841, Republic of Korea.

‡Correspondence: Ki Deok Kim, kidkim@korea.ac.kr

Keywords: Chryseobacterium strain GSE06; Chryseobacterium cucumeris; endophytic bacterium; average nucleotide identity; biocontrol agent.

Abbreviations: ANI, average nucleotide identity; FAME, fatty acid methyl ester; TEM, transmission electron microscopy.

†Present address: Division of Agricultural Microbiology, National Academy of Agricultural Science, Rural Development Administration, Jeonju 55365, Republic of Korea.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequence and the whole-genome shotgun projects of Chryseobacterium cucumeris GSE06T are KX144643 and BioProject accession PRJNA315066, Biosample number SAMN04544318, accession number LUVZ00000000, respectively.

Two supplementary figures and a supplementary table are available with the online Supplementary Material.
strain GSE06<sup>T</sup>, cultural, morphological, physiological and biochemical characteristics were examined, and fatty acid methyl ester (FAME) and 16S rRNA gene sequence analyses were conducted. In addition, the average nucleotide identity (ANI) between sequenced genomes of strain GSE06<sup>T</sup> and the reference strains was analysed. From these analyses, the strain could be considered a representative of a novel species belonging in the genus Chryseobacterium.

The bacterial strain GSE06<sup>T</sup> was obtained from a root of a cucumber (Cucumis sativus L.) plant grown in a field in Gunsan (35° 58′ 06″ N 126° 44′ 14″ E), Jeonbuk province, Korea, in 2002 [16]. The root sample was surface-sterilized with 1% sodium hypochlorite for 90 s, rinsed several times in sterile distilled water and then macerated with a sterile homogenizer. After shaking at 160 r.p.m. at 28°C for 30 min, the suspension was spread on tryptic soy agar (Difco) containing 50 µg cycloheximide ml<sup>-1</sup> and incubated at 28°C for 2 days. The single colony was further grown in nutrient broth (NB) (Difco) and then stored in NB amended with 20% (v/v) glycerol at −70°C until use. In this study, Chryseobacterium arthrosphaerae CCM 7645<sup>T</sup>, Chryseobacterium artecarpi KCTC 32509<sup>T</sup>, Chryseobacterium contaminans CCM 8492<sup>T</sup>, Chryseobacterium gallinarum CCM 8493<sup>T</sup>, Chryseobacterium gleum KACC 11661<sup>T</sup> and Chryseobacterium indologenes KACC 11662<sup>T</sup> were used as reference strains. These reference strains were obtained from the Korean Agricultural Culture Collection (KACC, Wanju, Korea) of the National Institute of Agricultural Biotechnology, the Korean Collection for Type Cultures (KCTC) of the Korea Research Institute of Bioscience and Biotechnology (Daejeon, Korea) and the Czech Collection of Microorganisms (CCM) of Masaryk University (Brno, Czech Republic). The strains were cultured on nutrient agar (NA) (Difco) at 28°C for 2 days before use in this study.

Genomic DNA of strain GSE06<sup>T</sup> was extracted using an i-genomic BYF DNA Extraction Mini kit (iNtRON Biotechnology) according to the manufacturer’s instructions. The 16S rRNA gene was amplified by PCR, using the conditions described by Sang et al. [19] with the universal primers 24F (5′-AGAGTTTGTATCMTGGCTCAG-3′) and 1492R (5′-TACGGYTACCTTGTTACGACTT-3′). The PCR product was purified using a MEGAquick-spin Total Fragment DNA Purification kit (iNtRON Biotechnology); this purified product was sequenced by the Cosmogenetech Sequencing Service (Cosmogenetech, Seoul, Korea). The sequenced gene was analysed with BLAST sequence analysis software (http://blast.ncbi.nlm.nih.gov/Blast.cgi) using the National Center for Biotechnology Information (NCBI) server. The 16S rRNA gene sequence (1426 nt) of strain GSE06<sup>T</sup> was aligned with sequences of related species of the genus Chryseobacterium from the NCBI’s GenBank database. Phylogenetic analysis was conducted using the PHYLIP package [20] after performing multiple alignments of the sequences using the CLUSTAL X program [21]. A phylogenetic tree was reconstructed using the neighbour-joining method [22] as well as maximum-likelihood [23] and maximum-parsimony algorithms [24] from evolutionary distances calculated with the coefficient of Jukes and Cantor [25]. The topology of the tree was assessed by performing bootstrap analysis with 1000 replications [26].

The 16S rRNA gene sequence (1426 nt) of strain GSE06<sup>T</sup> determined in this study was compared with those of other related species of the genus Chryseobacterium. A neighbouring-joining phylogenetic tree revealed that the strain belonging to the genus Chryseobacterium formed a distinct phyletic line (Fig. 1). This relationship was also found in the trees obtained by the maximum-likelihood and maximum-parsimony algorithms. Strain GSE06<sup>T</sup> clustered with C. indologenes ATCC 29897<sup>T</sup> (98.9%), C. gleum ATCC 35910<sup>T</sup> (98.8%), C. arthrosphaerae CC-VM-7<sup>T</sup> (98.7%), C. contaminans C26<sup>T</sup> (98.5%), C. artecarpi UTM-3<sup>T</sup> (98.3%) and C. gallinarum 100<sup>T</sup> (97.9%) (Fig. 1).

The morphological features (including cell shape and size) of strain GSE06<sup>T</sup> cultured on NA at 28°C for 24 h were observed by transmission electron microscopy (TEM). The specimen for TEM was prepared as described by Sang et al. [27] and observed with a transmission electron microscope (JEM-1400 plus; JEOL). Motility of this strain was examined on motility test medium (Difco) with 2,3,5-triphenyltetrazolium chloride (TTC) [28]. Colony colour of strain GSE06<sup>T</sup> was examined on NA. In addition, growth in tryptic soy broth (TSB; Oxoid) was tested at 10, 20, 25, 28, 38 and 45°C, in which the medium was adjusted to pH 4.0, 5.0, 6.0, 7.0 or 8.0, as described by Sang et al. [27]. Growth on NA at 5, 15, 28, 37 and 45°C; growth in NB containing 1, 2, 3 or 4% (w/v) NaCl; and growth on MacConkey (Difco) agar at 5, 37 and 42°C were also tested. Other phenotypic characteristics of strain GSE06<sup>T</sup> were tested by Gram staining; hydrolysis of casein, starch, Tween 20 and Tween 80; aesculin degradation; and catalase and oxidase activity analyses based on the methods described by Gerhardt [29]. Acid production by this strain from maltose was observed according to the method of Barrow and Feltham [30]; acid production from other carbon sources (trehalose, D-fructose, cellobiose, D-mannose and D-xylose) was examined as described by Barrow and Feltham [30]. Nitrite reduction was tested based on the methods described by Gerhardt [29], and tyrosine hydrolysis was assessed on tyrosine agar medium according to the protocol of the manufacturer (Remel). Additional biochemical tests were conducted using an API 20E kit (bio-Mérieux) according to the manufacturer’s instructions. The phenotypic characteristics of strain GSE06<sup>T</sup> and other closely related species of the genus Chryseobacterium are shown in Table 1, Fig. S1 (available in online Supplementary Material) and in the species description.

For ANI analysis between strain GSE06<sup>T</sup> and the reference strains, the ANI values between sequenced genomes of the strains were calculated using ANIb based on the NCBI BLAST program [31]. Genome sequencing of strain GSE06<sup>T</sup> (GenBank accession no. LUVZ00000000) and three reference strains, C. arthrosphaerae CCM 7645<sup>T</sup> (MAYG00000000), C. artecarpi KCTC 32509<sup>T</sup> (MAYH00000000) and C.
Fig. 1. Phylogenetic neighbour-joining tree based on 16S rRNA gene sequences, showing the relationship of strain GSE06\(^T\) (GenBank accession no. KX146463) with type strains of other species of the genus Chryseobacterium and representative species of related genera. Bootstrap values of greater than 70% (expressed as the percentage of 1000 replicates) are shown at the branch points. Filled circles indicate that the corresponding nodes were also recovered in the trees generated with the maximum-likelihood and maximum-parsimony algorithms. Riemerella anatipestifer ATCC 11845\(^T\) (U60101) was used as the outgroup (not shown). Bar, 1 nucleotide substitution per 100 nt of the 16S rRNA gene sequence.
contaminans CCM 8492T (MAYF00000000), was conducted using the Illumina MiSeq platform; genome sequences of the strains were obtained by de novo genome assembly as described in a previous study [18, 32]. Additionally, the genome sequences of three other reference strains were obtained, C. gleum KACC 11661T (ACK00000000), C. indologenes KACC 11662T (BAV00000000) and C. gallinarum CCM 8493T (GenBank BioProject accession no. PRJNA265816), from the NCBI genome database.

Because of the relatively high similarity values of the 16S rRNA gene sequences, ANI values between genome sequences of strain GSE06T and the reference strains [C. indologenes KACC 11662T (81.2 %), C. gleum KACC 11661T (86.9 %), C. arthrobacter CCM 7645T (82.6 %), C. contaminans CCM 8492T (82.3 %), C. artocarpi KCTC 32509T (82.0 %) and C. gallinarum CCM 8493T (81.5 %)] were determined (Table S1). Consequently, all ANI values were lower than the threshold of 95 %, corresponding to a DNA–DNA hybridization value of 70 % (a criterion for a novel bacterial species) [33]. ANI values of over 90.0 % between strains indicate that the strains are considered to belong to the same species. Thus, these lower ANI values (81.2–86.9 %) between strain GSE06T and the reference strains indicate that strain GSE06T belongs to a distinct species in the genus Chryseobacterium.

The DNA G+C contents of strain GSE06T and the reference strains were calculated with the R package SeqinR [34], using the genome sequences obtained. The DNA G+C content of strain GSE06T was 36.1 mol%, which is in the range of those of members of the genus Chryseobacterium [35].

To analyse cellular FAMEs of strain GSE06T and the reference strains, bacterial cells were cultured on trypticase soy agar (TSA; Oxoid) at 28 °C for 24 h; harvested cells (40 mg) were then analysed by gas chromatography (7890A GC system; Agilent Technologies) using the standard protocol of the MIDI system (Sherlock Microbial Identification System, version 6.0 B). The fatty acids were identified using the Aerobie TSBA6 library according to the manufacturer’s instructions. The major fatty acids of strain GSE06T were iso-C15:0 (46.5 %), summed feature 9 (iso-C17:0 3-OH) (17.2 %), summed feature 3 (C16:1ω7c and/or C16:1ω6c) (14.3 %) and iso-C17:0 3-OH (14.2 %) (Table 2). The fatty acid composition of this strain was similar to those of closely related species of the genus Chryseobacterium (Table 2).

Major polar lipids of strain GSE06T and a reference strain (C. arthrobacter CCM 7645T) were analysed using two-dimensional TLC at MicroID (Daejeon, Korea) according to the method described by Minnikin et al. [36]. Molybdophosphoric acid, α-naphthol, ninhydrin and molybdenum blue were used for detecting total lipids, glycolipids, aminolipids and phospholipids, respectively. The major polar lipids of strain GSE06T were phosphatidylethanolamine (PE), three unidentified aminolipids (AL), one unidentified aminophospholipid (APL), four unidentified glycolipids (GL)

**Table 1. Phenotypic characteristics of strain GSE06T that differentiate this strain from the type strains of closely related species of the genus Chryseobacterium**

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Colour of colonies</strong></td>
<td></td>
<td>Y</td>
<td>Y</td>
<td>Y</td>
<td>Y</td>
<td>Y</td>
<td>Y/W</td>
</tr>
<tr>
<td><strong>Growth on MacConkey agar at:</strong></td>
<td></td>
<td>(+)</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>(+)</td>
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<tr>
<td>37 °C</td>
<td></td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
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<tr>
<td>42 °C</td>
<td></td>
<td>(+)</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>(+)</td>
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<tr>
<td><strong>Growth in NB containing 4 % NaCl</strong></td>
<td></td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td><strong>Acid production from maltose</strong></td>
<td></td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
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<tr>
<td><strong>Production of β-galactosidase</strong></td>
<td></td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
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<tr>
<td><strong>Nitrate reduction</strong></td>
<td></td>
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<td>–</td>
<td>–</td>
<td>–</td>
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<td>–</td>
</tr>
<tr>
<td><strong>Polar lipids</strong></td>
<td></td>
<td>PE, 3AL, 1APL, 6GL, 8L†</td>
<td>PE, 4AL, 7L†</td>
<td>PE, 4AL, 8L†</td>
<td>PE, 3AL, 1APL, 6GL, 8L†</td>
<td>PE, 4AL, 1APL, 6GL, 8L†</td>
<td></td>
</tr>
<tr>
<td><strong>DNA G+C content (mol%)</strong></td>
<td>36.1</td>
<td>37.2</td>
<td>36.8</td>
<td>38.3</td>
<td>35.9</td>
<td>34.8</td>
<td>37.5</td>
</tr>
</tbody>
</table>

*PE, phosphatidylethanolamine; AL, unidentified aminolipid; APL, unidentified aminophospholipid; GL, unidentified glycolipid; L, unidentified lipid.
†Data taken from: a, Montero-Calasanz et al. [8]; b, Nguyen et al. [40]; c, Kämpfer et al. [9]; d, Venil et al. [41].
Table 2. Cellular fatty acid contents (percentages) of strain GSE06\textsuperscript{T} and the type strains of closely related species of the genus Chryseobacterium

<table>
<thead>
<tr>
<th>Fatty acid</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
</tr>
</thead>
<tbody>
<tr>
<td>iso-C\textsubscript{15:0}</td>
<td>1.3</td>
<td>1.3</td>
<td>TR</td>
<td>–</td>
<td>–</td>
<td>2.9</td>
<td>–</td>
</tr>
<tr>
<td>iso-C\textsubscript{15:0}</td>
<td>46.5</td>
<td>50.9</td>
<td>44.4</td>
<td>42.1</td>
<td>42.2</td>
<td>47.1</td>
<td>46.1</td>
</tr>
<tr>
<td>iso-C\textsubscript{15:0, 3-OH}</td>
<td>4.3</td>
<td>3.3</td>
<td>4.1</td>
<td>6.1</td>
<td>5.6</td>
<td>5.3</td>
<td>5.4</td>
</tr>
<tr>
<td>C\textsubscript{16:0}</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>–</td>
<td>–</td>
<td>2.7</td>
<td>–</td>
</tr>
<tr>
<td>C\textsubscript{16: 3-OH}</td>
<td>–</td>
<td>TR</td>
<td>TR</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>iso-C\textsubscript{16:0}</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>iso-C\textsubscript{18: 3-OH}</td>
<td>–</td>
<td>1.0</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>iso-C\textsubscript{17: 0}</td>
<td>1.4</td>
<td>TR</td>
<td>1.3</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>iso-C\textsubscript{17:0, 3-OH}</td>
<td>14.2</td>
<td>10.0</td>
<td>13.6</td>
<td>13.7</td>
<td>15.5</td>
<td>13.2</td>
<td>15.0</td>
</tr>
<tr>
<td>Summed feature 3\textsuperscript{*}</td>
<td>14.3</td>
<td>9.4</td>
<td>15.3</td>
<td>18.6</td>
<td>20.2</td>
<td>14.0</td>
<td>17.2</td>
</tr>
<tr>
<td>Summed feature 4\textsuperscript{*}</td>
<td>–</td>
<td>TR</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Summed feature 9\textsuperscript{*}</td>
<td>17.2</td>
<td>20.6</td>
<td>18.5</td>
<td>19.5</td>
<td>16.5</td>
<td>14.8</td>
<td>16.3</td>
</tr>
</tbody>
</table>

*As indicated by Montero-Calasanz et al. [8], summed features are groups of two or three fatty acids that are treated together for the purpose of evaluation in the MIDI system and include both peaks with discrete ECLs as well as those where the ECLs are not reported separately. Summed feature 3 was listed as C\textsubscript{16:1ω7c} and/or C\textsubscript{16:1ω6c}; summed feature 4 was listed as iso-C\textsubscript{17:1} and/or anteiso-C\textsubscript{17:1}; B; and summed feature 9 was listed as iso-C\textsubscript{17:1ω9c}.

and one unidentified lipid (Table 1, Fig. S2). The PE and AL of strain GSE06\textsuperscript{T} were also observed in all other closely related species (except AL in C. artocarpi KCTC 32509\textsuperscript{T}) of the genus Chryseobacterium; however, APL and GL of strain GSE06\textsuperscript{T} were detected only in C. arthrophaeræa CCM 7645\textsuperscript{T}, C. contaminans CCM 8492\textsuperscript{T} and C. gallinarum CCM 8493\textsuperscript{T} (Table 1). In addition, various unidentified lipids were detected in all strains examined including strain GSE06\textsuperscript{T} (Table 1).

In addition, the respiratory quinones of strain GSE06\textsuperscript{T} (harvested cells from 400 ml NB culture) were examined using reverse-phase HPLC [flow rate of 1.0 ml min\textsuperscript{-1}]; solvent, methanol/isopropyl ether (4:1; v/v)] at the Korean Culture Center of Microorganisms (KCCM; Seoul, Korea) [37, 38]. The predominant respiratory quinone of the strain was MK-6.

Based on the results of 16S rRNA gene sequence and ANI analyses as well as phenotypic characterization, strain GSE06\textsuperscript{T} is proposed as a representative of a novel species in the genus Chryseobacterium under the name of Chryseobacterium cucumeris sp. nov.

EMENDED DESCRIPTION OF CHRYSEOBACTERIUM ARTHROPHAERAE

Kämpfer et al. 2010

The description is as given for the species by Kämpfer et al. [39], with the following amendment. The major polar lipids are phosphatidylethanolamine, three unidentified aminolipids, one unidentified aminophospholipid, four unidentified glycolipids and one unidentified lipid.

DESCRIPTION OF CHRYSEOBACTERIUM CUCUMERIS SP. NOV.

Chryseobacterium cucumeris (cu.cu’m.e.ris. L. masc. gen. n. cucumeris of a cucumber).

Cells are Gram-stain-negative, short rods (0.5–0.8 μm wide and 1.1–2.0 μm long), without flagella or motility. Colonies are yellow, circular, and pulvinate with entire margins on NA. Cells grow at 10–38 °C (optimum, 25 °C) and at pH 5.0–8.0 (optimum, pH 6.0–8.0) in TSB and in NB containing 1–3 % NaCl (optimum, 1–2 % NaCl), and grow weakly on MacConkey agar at 37 and 42 °C. Casein, starch, tyrosine, Tween 20, and Tween 80 are hydrolysed; aesculin degradation and oxidase and catalase activities are positive, but nitrite reduction is negative. Acids are produced from D-fructose, maltose and trehalose, but not those from cellobiose, D-mannose or D-xylose. With the API 20E kit (bioMérieux), β-galactosidase, urease and gelatinase activities and indole production are positive. However, arginine dihydrolase, lysine and ornithine decarboxylase, citrate utilization, H\textsubscript{2}S production, tryptophan deaminase, acetoin production, and nitrate reduction are negative. Acids are not produced from D-glucose, D-mannitol, inositol, D-sacrose, amygdalin, L-arabinose, D-melibiose, L-rhamnose or D-sorbitol. Major fatty acids are iso-C\textsubscript{15:0}, summed feature 9 (iso-C\textsubscript{17:1ω9c}), summed feature 3 (C\textsubscript{16:1ω7c} and/or C\textsubscript{16:1ω6c}) and iso-C\textsubscript{17:0 3-OH}. Cells contain MK-6 as the predominant respiratory quinone. The major polar lipids are phosphatidylethanolamine, three unidentified aminolipids, one unidentified aminophospholipid, four unidentified glycolipids and one unidentified lipid.
The type strain, GSE06\(^{T}\) (=KACC 18798\(^{T}\)=JCM 31422\(^{\prime}\)), was isolated from the surface-sterilized root of cucumber (Cucumis sativus L.) in Gunsan, Jeonbuk Province, Korea. The DNA G+C content of strain GSE06\(^{T}\) is 36.1 mol%.

Funding information
J.-J. J. was supported by the Global PhD program through the National Research Foundation of Korea, funded by the Ministry of Education (2015-034526), Korea.

Acknowledgements
We thank J. Y. Oh for assistance with the collection of the reference strains used in this study.

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

References


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