Pigmentiphaga daeguensis sp. nov., isolated from wastewater of a dye works, and emended description of the genus Pigmentiphaga

Jung-Hoon Yoon,1 So-Jung Kang,1 Wonyong Kim2 and Tae-Kwang Oh1

1Korea Research Institute of Bioscience and Biotechnology (KIRIBB), PO Box 115, Yusong, Taejon, Korea
2Department of Microbiology, College of Medicine, Chungang University, 221 Heukseok-dong, Seoul, Korea

A Gram-negative, non-spore-forming, rod-shaped Pigmentiphaga-like bacterial strain, K110T, was isolated from wastewater collected from a dye works in Korea and was subjected to a polyphasic taxonomic analysis. Strain K110T grew optimally at pH 7.0–8.0 and 37°C in the presence of 0.5 % (w/v) NaCl. It contained Q-8 as the predominant ubiquinone and C16:0, cyclo C17:0 and cyclo C19:0 as the major fatty acids. The major polar lipids were phosphatidylglycerol, phosphatidylethanolamine and two unidentified aminolipids. The DNA G+C content was 67.4 mol%. In a neighbour-joining phylogenetic tree constructed on the basis of 16S rRNA gene sequences, strain K110T joined Pigmentiphaga kullae, the sole species of the genus, at a bootstrap confidence level of 100 %. Strain K110T exhibited a 16S rRNA gene sequence similarity of 99.4 % with respect to the type strain of P. kullae. Although strain K110T was found to be similar to P. kullae in terms of phenotypic properties, it differed in terms of motility, polar lipids, DNA–DNA relatedness and repetitive extragenic palindromic PCR genomic fingerprinting patterns. On the basis of phenotypic, phylogenetic and genetic data, strain K110T represents a novel species of the genus Pigmentiphaga, for which the name Pigmentiphaga daeguensis sp. nov. is proposed. The type strain is K110T (=KCTC 12838T =JCM 14330T).

The genus Pigmentiphaga was proposed by Blümel et al. (2001) with Pigmentiphaga kullae as the sole recognized species of the genus. Phylogenetic analysis based on 16S rRNA gene sequences showed that the genus Pigmentiphaga falls within the Betaproteobacteria (Blümel et al., 2001). In this study, we report on the taxonomic characterization of a Pigmentiphaga-like bacterial strain, K110T, which was isolated from wastewater collected from a dye works.

Wastewater collected from a dye works at Daegu, Korea, was used as the source for the isolation of bacterial strains. Strain K110T was isolated by means of the standard dilution plating technique on trypticase soy agar (TSA; Difco) at 30°C. P. kullae DSM 13608T was obtained from the Deutsche Sammlung von Mikroorganismen und Zellkulturen (Braunschweig, Germany). The morphological, physiological and biochemical characteristics of strain K110T were investigated using routine cultivation on TSA at 37°C. Cell morphology was examined by using light microscopy (E600; Nikon) and transmission electron microscopy with cells from exponentially growing cultures. Flagellation was determined by using a Philips CM-20 transmission electron microscope with cells from exponentially growing cultures: for this purpose, cells were negatively stained with 1 % (w/v) phosphotungstic acid and the grids were examined after being air-dried. The Gram reaction was determined using the bioMérieux Gram stain kit according to the manufacturer’s instructions. Growth at various temperatures (4–50°C) was measured on TSA. The pH range for growth was determined in nutrient broth (Difco) adjusted, prior to sterilization, to various pH values (pH 4.5–10.5, in increments of 0.5 pH units) by the addition of HCl or Na2CO3. Growth in the absence of NaCl and at various NaCl concentrations (0.5 %, w/v, and 1.0–10.0 %, w/v, at increments of 1.0 %) was investigated using trypticase soy broth prepared according to the formula of the Difco medium except that no NaCl was used. Growth under anaerobic conditions was determined after incubation in an anaerobic chamber on TSA and on TSA supplemented with nitrate, both of which had been prepared anaerobically under a nitrogen atmosphere. Catalase and oxidase activities and hydrolysis

Abbreviation: rep-PCR, repetitive extragenic palindromic PCR.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain K110T is EF100696.

rep-PCR fingerprints and cellular fatty acid compositions for strain K110T and P. kullae DSM 13608T are available as supplementary material with the online version of this paper.

Downloaded from www.microbiologyresearch.org by IP: 54.70.40.11
On: Fri, 23 Nov 2018 17:04:21
64901 © 2007 IUMS Printed in Great Britain
of casein, gelatin, hypoxanthine, starch, Tweens 20, 40, 60 and 80, tyrosine, urea and xanthine were determined as described by Cowan & Steel (1965). DNase activity was examined by using DNase test agar with methyl green (Difco). Hydrolysis of aesculin and nitrate reduction were studied as described previously (Lanyi, 1987). Susceptibility to antibiotics was tested on TSA plates by using antibiotic discs containing the following amounts of antibiotic: polymyxin B, 100 μU; streptomycin, 50 μg; penicillin G, 20 μg; chloramphenicol, 100 μg; ampicillin, 10 μg; cephalothin, 30 μg; gentamicin, 30 μg; novobiocin, 5 μg; tetracycline, 30 μg; kanamycin, 30 μg; lincomycin, 15 μg; oleandomycin, 15 μg; neomycin, 30 μg; and carbencillin, 100 μg. Utilization of various substrates, activities of various enzymes and other physiological and biochemical properties were tested by using the API 20E, API 20NE, API 50 CH and API ZYM systems (bioMérieux); the cells were suspended in AUX medium, according to the manufacturer’s instructions, to inoculate the API 50 CH system.

Cell biomass for DNA extraction and for isoprenoid quinone and polar lipid analyses was obtained from cultivation in trypticase soy broth (Difco) at 37°C. Chromosomal DNA was isolated and purified according to the method described by Yoon et al. (1996), with the exception that RNase T1 was used in combination with RNase A to minimize contamination with RNA. The 16S rRNA gene was amplified by a PCR using two universal primers as described previously (Yoon et al., 1998). Sequencing of the amplified 16S rRNA gene and phylogenetic analysis were performed as described by Yoon et al. (2003). Isoprenoid quinones were extracted according to the method of Komagata & Suzuki (1987) and analysed using reversed-phase HPLC and a YMC ODS-A (250 × 4.6 mm) column. For cellular fatty acid analysis, cell mass of strain K110T and P. kullae DSM 13608T was harvested from TSA plates after incubation for 3 days at 37°C. The fatty acids were extracted and the fatty acid methyl esters prepared according to the standard protocol of the MIDI/Hewlett Packard Microbial Identification System (Sasser, 1990). Polar lipids were extracted according to the procedures described by Mintikin et al. (1984) and then identified by two-dimensional TLC followed by spraying with appropriate detection reagents (Mintikin et al., 1984; Komagata & Suzuki, 1987). The DNA G+C content was determined by the method of Tamaoka & Komagata (1984), with the modification that the DNA was hydrolysed and the resulting nucleotides analysed by reversed-phase HPLC. DNA–DNA hybridization was performed fluorometrically by the method of Ezaki et al. (1989), using photobiotin-labelled DNA probes and microdilution wells. Hybridization was performed with five replications for each sample. The highest and lowest values obtained for each sample were excluded and the means for the remaining three values are quoted as the DNA–DNA relatedness values. Repetitive extragenic palindromic PCR (rep-PCR) genomic fingerprinting using REP, BOX and (GTG)₅ PCR primers was performed as described by Rademaker et al. (1998). Computer-assisted analysis of the genomic fingerprints was performed by using GelCompar II software, version 1.5 (Applied Maths).

Morphological, cultural, physiological and biochemical characteristics of strain K110T are given in the species description (see below) or are shown in Table 1. The almost-complete 16S rRNA gene sequence of strain K110T determined in this study comprised 1486 nt, representing approximately 96.8% of the Escherichia coli 16S rRNA gene sequence. Comparative 16S rRNA gene sequence analysis showed that strain K110T was most closely related phylogenetically to the genus Pigmentiphaga (Fig. 1). In the neighbour-joining phylogenetic tree based on 16S rRNA gene sequences, strain K110T joined the type strain of P. kullae at a bootstrap resampling value of 100% (Fig. 1). Strain K110T exhibited a 16S rRNA gene sequence similarity value of 99.4% with respect to the type strain of P. kullae and showed less than 96.4% similarity with respect to other species included in the phylogenetic analysis.

The predominant isoprenoid quinone detected in strain K110T was Q-8 (peak area ratio, approx. 94%). Strain

Table 1. Differential phenotypic characteristics of strain K110T and P. kullae DSM 13608T

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Strain K110T</th>
<th>P. kullae DSM 13608T</th>
</tr>
</thead>
<tbody>
<tr>
<td>Motility</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Susceptibility to:</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Tetracycline</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>Carbenicillin</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Major polar lipid(s)*</td>
<td>PE</td>
<td>PE</td>
</tr>
<tr>
<td>DNA G+C content</td>
<td>67.4</td>
<td>68.5 ± 0.3 (67.9)†</td>
</tr>
</tbody>
</table>

*AL, Unidentified aminolipids; PE, phosphatidylethanolamine; PG, phosphatidylylycerol.
†Data from this study for strain DSM 13608T obtained using HPLC.
K110<sup>T</sup> had a cellular fatty acid profile that contained large amounts of straight-chain and hydroxy fatty acids; the major components (>10% of total fatty acids) were C<sub>16:0</sub>, cyclo C<sub>17:0</sub> and cyclo C<sub>19:0</sub>8c (see Supplementary Table S1, available in IJSEM Online). This fatty acid profile was similar to that of the type strain of <i>P. kullae</i>, although there were differences in the proportions of some fatty acids (Supplementary Table S1). The major polar lipids detected in strain K110<sup>T</sup> were phosphatidylglycerol, phosphatidylethanolamine and two unidentified aminolipids; minor amounts of diphasatidylglycerol and an unidentified phospholipid were also present. The DNA G+C content of strain K110<sup>T</sup> was 67.4 mol%. These chemotaxonomic properties supported the result of the monothetic phylogenetic classification, namely that strain K110<sup>T</sup> could be a member of the genus <i>Pigmentiphaga</i>. Therefore, on the basis of the phenotypic, phylogenetic and genetic classification, namely that strain K110<sup>T</sup> could be a member of the genus <i>Pigmentiphaga</i> <i>sp. nov.</i> is proposed.

**Description of Pigmentiphaga daeguensis sp. nov.**

<i>Pigmentiphaga daeguensis</i> (dae.gu.en’sis. N.L. fem. adj. daeguensis of Daegu, Korea, from where the type strain was isolated).

**Acknowledgements**

This work was supported by the 21C Frontier Program of Microbial Genomics and Applications (grant MG05-0401-2-0) and the Support and Application Project of Biological Resources (grant M10508050004-06N0805-00410) from the Ministry of Science and Technology (MOST) of the Republic of Korea.

**References**


Ezaki, T., Hashimoto, Y. & Yabuuchi, E. (1989). Fluorometric deoxyribonucleic acid-deoxyribonucleic acid hybridization in microdilution wells as an alternative to membrane filter hybridization in


**Pigmentiphaga daeguensis** sp. nov.