Description of Sinobacter flavus gen. nov., sp. nov., and proposal of Sinobacteraceae fam. nov.

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A novel Gram-negative, non-motile, rod-shaped bacterium, designated CW-KD 4T, was isolated from a polluted soil sample collected from Jiangsu Province, China, by using a classic enrichment method. Based on 16S rRNA gene sequence analysis, the novel strain represented a deep-rooting lineage within the class Gammaproteobacteria that was clustered with the genera Hydrocarboniphaga and Nevskia and some other unidentified bacteria. Polyphasic taxonomic studies revealed that strain CW-KD 4T showed rather distant relationships to its phylogenetically closest neighbours, including the two recognized genera Hydrocarboniphaga and Nevskia. Strain CW-KD 4T showed only 89.9 % and 89.7 % 16S rRNA gene sequence similarities to the type species of the genera Hydrocarboniphaga and Nevskia, respectively. The predominant isoprenoid quinone of strain CW-KD 4T was Q-8 with minor components including Q-9, MK-7 and MK-6. The major fatty acids were C16 : 0, C18 : 1ω7c and summed feature 3. The G+C content of the DNA was 65.1 mol%. On the basis of its distinctive phenotypic and genotypic characteristics, strain CW-KD 4T represents a new genus and a novel species in the class Gammaproteobacteria, for which the name Sinobacter flavus gen. nov., sp. nov. is proposed. The type strain is CW-KD 4T (=DSM 18980T =KCTC 12881T =CCTCC AB 206145T). In addition, a new family, Sinobacteraceae fam. nov., is proposed to house the genus Sinobacter gen. nov.
species for which the name *Sinobacter flavus* gen. nov., sp. nov. is proposed.

Strain CW-KD 4\(^T\) was isolated from a farmland soil sample from Jiangsu Province, China, using a classic enrichment culture technique (Rosenberg, 1992). Modified ISP 4 medium [consisting of 200 µg ml\(^{-1}\) atrazine, 0.1 % K\(_2\)HPO\(_4\), 0.1 % MgSO\(_4\), H\(_2\)O, 0.1 % NaCl, 0.2 % (NH\(_4\))\(_2\)SO\(_4\), 0.2 % CaCO\(_3\), 0.0001 % FeSO\(_4\).H\(_2\)O and 0.0001 % MnCl\(_2\).7H\(_2\)O] in which one of the carbohydrates was substituted by atrazine as the sole source of carbon and energy, was selected as the isolation medium. Incubation was performed at 30 °C for 7 days and the strain was preserved in a 20 % (v/v) glycerol solution in distilled water at 280 °C. Biomass for molecular systematic and chemotaxonomic studies was obtained by incubation at 30 °C for 4 days in shake flasks (about 180 r.p.m.) with yeast tryptone (YT) broth for strain CW-KD 4\(^T\) and *Hydrocarboniphaga effusa* AP103\(^T\) and synthetic medium for *Nevskia ramosa* Soe 1\(^T\), as described by Stürmeyer et al. (1998).

The cellular morphology of the novel isolate was observed by scanning and transmission electron microscopy (SEM, model S-3000N, Hitachi; TEM, model H-7650, Hitachi) (Fig. 1) after incubation for 3 days at 30 °C on YT agar. Samples were prepared for SEM and TEM as described by Nedashkovskaya et al. (2005) and Busti et al. (2006). The method of Yamaguchi & Yokoe (2000) was followed to determine acid production from carbohydrates. The utilization of sole carbon sources was investigated as described by Zhou et al. (2007a). Growth was tested at 5, 10, 25, 30, 35, 37 and 40 °C on YT broth. NaCl and pH tolerance were tested using Luria–Bertani (LB) broth adjusted to various pH values (3.0, 5.0, 6.0, 7.0, 7.8, 8.0 and 10.0) and NaCl concentrations (1–5 %) (Zhou et al., 2007b). Antibiotic susceptibility was examined by placing antibiotic discs on YT agar plates as described by Nedashkovskaya et al. (2005). Gram-staining and other physiological characteristics were tested according to the methods of Gerhardt et al. (1994). The morphological, physiological and biochemical properties of the novel strain are given in detail in the species description.

Isoprenoid quinones were extracted from lyophilized cells and the samples were purified and analysed by HPLC using the procedures described by Hu et al. (2001). The predominant isoprenoid quinone for strain CW-KD 4\(^T\) was Q-8 (>83 %). Minor components were Q-9, MK-7 and MK-6. *H. effusa* AP103\(^T\) and *N. ramosa* Soe 1\(^T\) possessed only Q-8 as the isoprenoid quinone. Fatty acids were extracted, methylated and analysed using the standard MIDI (Microbial Identification) system as described by Sasser (1990). The major fatty acids for strain CW-KD 4\(^T\) were C\(_{16:0}\), C\(_{18:1}\)w7c and summed feature 3 (comprising i-C\(_{15:0}\)2-OH and/or C\(_{16:1}\)w7c). The major fatty acid profiles of strains CW-KD 4\(^T\), *H. effusa* AP103\(^T\) and *N. ramosa* Soe 1\(^T\) are presented in Table 1.

Genomic DNA was prepared for the determination of the base composition following the procedure of Marmur (1961). The DNA G+C content of the strain CW-KD 4\(^T\) was 65.1 mol% as determined by the thermal denaturation method (Mandel & Marmur, 1968).

PCR amplification of the 16S rRNA gene was performed as described by Li et al. (2007). The 16S rRNA gene sequence was manually aligned with reference sequences retrieved from the GenBank database following BLAST searching (some unidentified and unpublished sequences with high gene sequence similarity values to strain CW-KD 4\(^T\) were also included). Phylogenetic analysis was performed using the PHYLIP (Felsenstein, 1993) and MEGA version 3.1 (Kumar et al., 2004) software packages. Multiple alignments were performed with the CLUSTAL_X program (Thompson et al., 1997) and gaps were edited with the BioEdit program (Hall, 1999). Distances (distance options

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**Fig. 1.** SEM (a, b) and TEM (c, d) images of cells of strain CW-KD 4\(^T\) grown on LB agar for 3 days at 30 °C. Bars, 1000 nm (a, d); 2500 nm (b); 2000 nm (c).
according to the Kimura two-parameter model; Kimura, 1980, 1983) and clustering were based on the neighbour-joining (Saitou & Nei, 1987) and maximum-likelihood (Felsenstein, 1981) methods. Bootstrap analysis (1000 resamplings) was used to evaluate the topology of the neighbour-joining tree (Felsenstein, 1985).

The almost complete 16S rRNA gene sequence (1487 nt) was determined for strain CW-KD 4T. A neighbour-joining phylogenetic tree constructed based on 16S rRNA gene sequences showed that strain CW-KD 4T belongs to the class Gammaproteobacteria and clustered together with two established genera, Nevskia and Hydrocarboniphaga. The novel strain and these two genera, along with some uncultured or unidentified bacteria, formed a deep-rooting lineage within the class Gammaproteobacteria. The deep-rooting lineage was given the name ‘the HNS (Hydrocarboniphaga/Nevskia/Sinobacter) clade’. Obviously, the separated clade should not be included in the single family Xanthomonadaceae within the order Xanthomonadales (Fig. 2).

The HNS clade in the phylogenetic tree showed that strain CW-KD 4T belongs to a phylogenetic cluster mainly consisting of uncultured and unidentified bacterial strains from contaminated soil, fresh water or other polluted environments (Fig. 2). An interesting characteristic observed was that many members in the cluster showed degradation abilities for their corresponding pollutants (data were obtained from the GenBank database). The closest recognized strains were H. effusa AP103T and N. ramosa Soe 1T, but these strains showed only 89.9 % and 89.7 % 16S rRNA gene sequence similarity values to CW-KD 4T, respectively.

The phenotypic characteristics that differentiate strain CW-KD 4T from related type strains

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Length of rods (μm)</td>
<td>0.3–0.4 × 2.4–2.6</td>
<td>0.75–0.85 × 1.5–2.0</td>
<td>0.7–1.1 × 1.5–2.3</td>
</tr>
<tr>
<td>Cell morphology</td>
<td>Long rod</td>
<td>Rod</td>
<td>Bent Rod</td>
</tr>
<tr>
<td>Motility</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Nitrate utilization</td>
<td>–</td>
<td>+</td>
<td>(+)</td>
</tr>
<tr>
<td>Ammonium salts utilization</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Lipase (Tween 80)</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Nutritional spectrum of organic or inorganic substrates</td>
<td>Narrow</td>
<td>Wide</td>
<td>Wide</td>
</tr>
<tr>
<td>Gelatinase</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Catalase</td>
<td>–</td>
<td>(+)</td>
<td>(+)</td>
</tr>
<tr>
<td>Oxidase</td>
<td>+</td>
<td>–</td>
<td>–</td>
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<tr>
<td>Benzoate</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Ethanol</td>
<td>–</td>
<td>+</td>
<td>+</td>
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<tr>
<td>DL-lactate</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Acid production from:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Glucose</td>
<td>(+)</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Sucrose</td>
<td>(+)</td>
<td>(+)</td>
<td>+</td>
</tr>
<tr>
<td>Major cellular fatty acids</td>
<td>C18:1ω7c, C16:0 and summed feature 3</td>
<td>C18:1ω7c, i-C16:0 and summed feature 3</td>
<td>C18:1ω7c, C16:0 and i-C16:0</td>
</tr>
<tr>
<td>DNA G+C content (mol%)</td>
<td>65.1</td>
<td>60–61</td>
<td>67.8</td>
</tr>
</tbody>
</table>

Table 1. Phenotypic characteristics that differentiate strain CW-KD 4T from related type strains

Taxa: 1, strain CW-KD 4T; 2, Hydrocarboniphaga effusa AP103T; 3, Nevskia ramosa Soe 1T. +, Positive; −, negative; (+), weakly positive. Microcolonies of strain CW-KD 4T are circular, convex and smooth. Colonies of H. effusa AP103T are irregular shaped and smooth when small, but become circular later with a wrinkled and folded dome. Colonies of N. ramosa Soe 1T have a rosette-like formation. All three genera have Q-8 as their predominant isoprenoid quinone. Summed feature 3 consists of i-C15:0 2-OH and/or C16:1ω7c. Data were obtained from this study, Palleroni et al. (2004) and Stürmeyer et al. (1998).

The results of this polyphasic taxonomy study showed that the novel strain could be easily distinguished from its closest relatives both on the basis of phenotypic features and on phylogenetic position. For strain CW-KD 4T, only several carbohydrates were utilized as sole carbon or sole carbon/nitrogen sources from more than 50 carbohydrates tested; few enzyme activities were detected. The type strains of the type species of the two related genera (Hydrocarboniphaga and Nevskia) had a wide nutritional spectrum of organic or inorganic substrates. The novel isolate could not be attributed to either of these genera due to their almost complete phenotypic and phylogenetic distinctiveness. No bacterial fatty acid profile matching that of strain CW-KD 4T was found in the TSBA40 4.10 library, further supporting the placement of the novel isolate in a new genus. It is concluded that strain CW-KD 4T represents a new genus and novel species in the order
Xanthomonadales, for which the name Sinobacter flavus gen. nov., sp. nov. is proposed.

At present, the order Xanthomonadales contains only one family, the Xanthomonadaceae. The phylogenetic analysis performed in this study showed that strain CW-KD 4\textsuperscript{T} of the HNS clade represented a deep-rooting lineage in the order Xanthomonadales which clustered with the genera Hydrocarboniphaga and Nevskia and some uncultured or unidentified bacterial strains. Furthermore, the deep-rooting lineage was separated from the family Xanthomonadaceae within the class Gammaproteobacteria. The Sinobacter clade was also shown to be a well separated lineage with more than 10% 16S rRNA gene sequence dissimilarity to the recognized genera Hydrocarboniphaga and Nevskia. Thus, based on the distinct phylogenetic position and 16S rRNA gene sequence signature nucleotides of the Sinobacter lineage in the class Gammaproteobacteria, a new family, Sinobacteraceae fam. nov., is proposed to house the newly proposed genus Sinobacter.

**Description of Sinobacter flavus sp. nov.**

Sinobacter flavus (fla’vus. L. masc. adj. flavus yellow, the colour of colonies or pigment that the bacterium produces).

The following properties are also observed in addition to those given in the genus description. Cells are Gram-negative, long rods, non-endospore-forming and non-motile. Aerobic and chemo-organotrophic. Oxidase positive and catalase negative. The major fatty acids are C\textsubscript{16:0}, C\textsubscript{18:1}ω7c and summed feature 3. The predominant isoprenoid quinone is Q-8. The DNA G+C content is 65 mol%. The type and only species is Sinobacter flavus sp. nov.
Acid is produced from cellobiose, L-threomannose, D-ribose and sucrose, but not from D-arabinose, adonitol, dulcitol, D-fructose, L-fucose, D-galactose, D-glucose, inositol, D-lactose, maltose, D-mannitol, D-melibiose, D-melezitose, L-raffinose, D-sorbitol, L-sorbose, trehalose or D-xylene. N-acetylglucosamine, cellobiose, D-glucose, glucosamine, D-ribose, starch and sucrose are utilized. Acetate, adonitol, adenosine, aesculins, D-arabinose, dextrin, dulcitol, D-erythrose, D-fructose, D-galactose, gelatin, inulin, inositol, D-lactose, D-mannose, maltose, malonate, D-mannitol, D-melezitose, melibiose, muconic acid, pyruvate, raffinose, salicin, D-sorbitol, D-sorbose, sucrose, trehalose, Tween 80, turanose, tartrate, xylitol and D-xylose are not utilized. Oxidase and weak urease activities are present. Arginine decarboxylase, arginine dihydrolase, catalase, DNase, β-galactosidase, leucine decarboxylase, lipase (Tween 80 hydrolysis activity), methyl α-D-glucosidase, ornithine decarboxylase and phenylalanine decarboxylase activities are absent. Nitrate and nitrite are not reduced. H₂S (TSI reaction) is not produced. Methyl red and Voges–Proskauer tests are negative. KCN (0.0075 %) is not tolerated. Susceptible to ampicillin, carbenicillin, chloramphenicol, doxycycline, erythromycin, kanamycin, lincomycin, neomycin, polymixin B, rifampicin, streptomycin and tetracycline. Resistant to gentamicin, penicillin G and vancomycin. The predominant isoprenoid quinone is Q-8; Q-9, MK-7 and MK-6 are present as minor components. The fatty acid profile contains C₁₈:1ω7c (28.92 %), C₁₆:0 (19.83 %), summed feature 3 (12.04 %, comprising i-C₁₅:0 2-OH and/or C₁₆:1ω7c), i-C₁₆:0 (6.75 %), C₁₆:1ω5c (5.8 %), C₁₄:0 (4.97 %), C₁₂:0 (4.08 %), c-C₁₉:0ω5c (1.48 %) and C₁₂:0 2-OH (1 %). The DNA G+C content is 65.1 mol%.

The type strain, CW-KD 5^T (=DSM 18980^T=KCTC 12881^T=CCTCC AB 206145^T), was isolated from the surface layer of a polluted farmland soil from Nanjing, Jiangsu Province, China.

**Description of Sinobacteraceae fam. nov.**

Sinobacteraceae (Si.no.bac’ter.a.ce.ae). N.L. masc. n. Sinobacter type genus of the family; suff. -aceae ending to denote a family; N.L. fem. pl. n. Sinobacteraceae the Sinobacter family.

Cells are Gram-negative, non-motile and non-endospore-forming. Obligate aerobes with Q-8 as the predominant isoprenoid quinone and C₁₆:0ω6c C₁₈:1ω7c and summed feature 3 as the major fatty acids. Oxidase positive and catalase negative. The pattern of 16S rRNA gene signatures of members of the family consists of nucleotides at positions 143 (C), 220 (A), 289–311 (A–U), 317–336 (C–G), 369–392 (G–A), 514–537 (U–A), 560 (U), 580–761 (U–A), 778–804 (U–U), 1129–1143 (C–A), 1163–1173 (A–U) and 1268 (A). The family is a member of the class Gammaproteobacteria, order Xanthomonadales. The type genus is Sinobacter.

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**References**


