**INTRODUCTION**

The genera *Alcaligenes*, *Achromobacter*, *Bordetella* and *Pigmentiphaga* belong to the β-Proteobacteria and are grouped together in the family *Alcaligenaceae* (De Ley et al., 1986; Yabuuchi et al., 1998; Blümel et al., 2001). The genus *Alcaligenes* has undergone considerable changes since its creation in 1919 and is now limited to *Alcaligenes faecalis* (the type species), *Alcaligenes latus* and *Alcaligenes defragrans* (Yabuuchi et al., 1998; Foss et al., 1998; Palleroni & Palleroni, 1978). *Alcaligenes faecalis* has been isolated from a wide variety of ecological niches including soil, water and various clinical samples (Kersters & De Ley, 1984). *Alcaligenes defragrans* strains have been isolated from soil and can use alkenoic monoterpenes as sole carbon source (Foss et al., 1998). *Alcaligenes latus* was considered a species *insertae sedis* by Kersters & De Ley (1984), and recent data have shown that this organism is closely related to the genera *Rubrivivax* and *Ideonella* and thus belongs to the *Comamonadaceae* (T. Coenye and P. Vandamme, unpublished data). The taxonomy of the genus *Alcaligenes* is closely intertwined with the taxonomy of the genus *Achromobacter*, and several *Alcaligenes* species have recently been reclassified as *Achromobacter* species (Yabuuchi et al., 1998). The genus *Achromobacter* now contains three species [*Achromobacter xylosoxidans* (the type species), *Achromobacter piechaudii* and *Achromobacter ruhlandii*]. According to Yabuuchi et al. (1998), the species *Achromobacter xylosoxidans* encompasses two subspecies (*Achromobacter xylosoxidans* subsp. *denitrificans* and *Achromobacter xylosoxidans* subsp. *xylosoxidans*), but this contradicts previous work showing that there was sufficient evidence (including DNA relatedness studies) to allow the two taxa to be considered as distinct species (Vandamme et al., 1996). Below, we refer to these taxa as *Achromobacter xylosoxidans* and *Alcaligenes denitrificans*, respectively. *Achromobacter xylosoxidans* is an opportunistic human pathogen capable of causing a wide variety of infections and is widespread in oligotrophic aquatic niches (Kersters & De Ley, 1984). *Alcaligenes denitrificans* strains are found in soil but can

---

**Kerstersia gyiorum gen. nov., sp. nov., a novel *Alcaligenes faecalis*-like organism isolated from human clinical samples, and reclassification of *Alcaligenes denitrificans* Rüger and Tan 1983 as *Achromobacter denitrificans* comb. nov.**

Tom Coenye,¹ Marc Vancanneyt,² Margo C. Cnockaert,¹ Enevold Falsen,³ Jean Swings¹,² and Peter Vandamme¹

¹²Laboratorium voor Microbiologie¹ and BCCM/LMG Bacteria Collection², Universiteit Gent, Gent, Belgium
³Culture Collection, Department of Clinical Bacteriology, University of Göteborg, Göteborg, Sweden

A polyphasic taxonomic study was performed on nine isolates recovered from various human clinical samples. Phenotypically, these isolates resembled *Alcaligenes faecalis*. Whole-cell protein analysis distinguished two different species, and this was confirmed by DNA–DNA hybridizations. Cellular fatty acid composition analysis and 16S rDNA sequence analysis indicated that these isolates were related to the genera *Alcaligenes*, *Bordetella*, *Achromobacter* and *Pigmentiphaga* and belonged to the family *Alcaligenaceae*. On the basis of the results of this study, the organisms were classified in a novel genus, *Kerstersia* gen. nov. This genus comprises one species, *Kerstersia gyiorum* sp. nov. (type strain LMG 5906ᵀ = API 184-2 84ᵀ = CCUG 47000ᵀ), and several unnamed isolates. The DNA G + C content of members of the genus *Kerstersia* is between 61.5 and 62.9 mol%. On the basis of previously published DNA–DNA hybridization results and data from chemotaxonomic studies, it is proposed that *Alcaligenes denitrificans* Rüger and Tan 1983 be reclassified as *Achromobacter denitrificans* comb. nov.
occasionally also be found in human clinical samples (Kersters & De Ley, 1984). *Achromobacter piechaudii* has been isolated from soil and human clinical samples, including blood (Kiredjian *et al.*, 1986). *Achromobacter ruhlandii* is a soil commensal and is not known to be pathogenic to humans (Kersters & De Ley, 1984). The genus *Bordetella* was described in 1952 (Moreno-López, 1952) and originally contained three species: *Bordetella pertussis* (the type species), *Bordetella parapertussis* and *Bordetella bronchiseptica*. *B. pertussis* is the causative agent of whooping cough, and *B. parapertussis* is closely related to *B. pertussis* but causes a milder form of disease (Pittman, 1984). *B. bronchiseptica* is traditionally isolated from the respiratory tract of wild and domestic animals, but this organism can occasionally cause respiratory tract infections in humans as well (Pittman, 1984). Several novel *Bordetella* species have been described since then: *Bordetella avium* (isolated from the respiratory tract of turkeys and other birds; Kersters *et al.*, 1984), *Bordetella holmesii* (formerly CDC group NO-2, isolated from human blood; Weyant *et al.*, 1995), *Bordetella hinzeii* (isolated from the respiratory tract of animals and humans; Vandamme *et al.*, 1995), *Bordetella trematum* (isolated from various human clinical samples, including blood and infected ears; Vandamme *et al.*, 1996) and *Bordetella petrii* (isolated from an anaerobic bioreactor; von Wintzingerode *et al.*, 2001). Recently, a novel member of the family *Alcaligenaceae* was described, *Pigmentiphaga kullae* (Blümel *et al.*, 2001). This organism was isolated from soil and is capable of the aerobic degradation of azo dyes.

We performed a polyphasic taxonomic study to elucidate the taxonomic position of nine isolates, from human clinical samples, that phenotypically resembled *Alcaligenes faecalis*, and show that these isolates belong to a novel genus, for which we propose the name *Kerstersia*. On the basis of previously published data, we also propose the formal reclassification of *Alcaligenes denitrificans* Rüger and Tan 1983 as *Achromobacter denitrificans* comb. nov.

## METHODS

### Bacterial strains and growth conditions. The *Kerstersia* strains used in this study are listed in Table 1. Reference strains of other taxa have been described previously (Vandamme *et al.*, 1995, 1996; Foss *et al.*, 1998; Yabuuchi *et al.*, 1998). All strains were grown aerobically on trypticase soy agar (BBL) at 37 °C unless otherwise indicated.

### SDS-PAGE of whole-cell proteins. Strains were grown on trypticase soy agar for 48 h at 37 °C. Preparation of whole-cell proteins and SDS-PAGE were performed as described previously (Pot *et al.*, 1994). Densitometric analysis, normalization and interpolation of the protein profiles, as well as numerical analysis using Pearson’s product-moment correlation coefficient, were performed using the GelComp 4.2 software package (Applied Maths).

### 16S rDNA sequencing. DNA was prepared by heating one or two colonies at 95 °C for 15 min in 20 μl lysis buffer containing 0.25% (w/v) SDS and 0.05 M NaOH. Following lysis, 180 μl distilled water was added to the lysate. The sequences of the 16S rDNA genes of strains LMG 5890 and LMG 5906 were determined as described previously (Coenye *et al.*, 1999). Phylogenetic analyses and bootstrap analysis (1000 replicates) was performed using the KODON 1.5 software package (Applied Maths); a phylogenetic tree was constructed using the neighbour-joining method (Saitou & Nei, 1987).

### Preparation of high-molecular-mass DNA and DNA–DNA hybridization experiments. Preparation of high-molecular-mass DNA for DNA–DNA hybridization experiments and the determination of the degree of DNA–DNA binding by the initial renaturation rate method were performed as described previously (Vandamme *et al.*, 1992; De Ley *et al.*, 1970). Each value given is the mean of at least two hybridization experiments. The total DNA concentration was 65 μg ml⁻¹ and the optimal renaturation temperature in 2 × SSC (1 × SSC is 0.15 M NaCl plus 0.015 M sodium citrate, pH 7.0) was 79 °C. Alternatively, high-molecular-mass DNA was prepared as described by Pitcher *et al.* (1989), and DNA–DNA hybridizations were performed with photobiotin-labelled probes in microplate wells, as described by Ezaki *et al.* (1989), using an HTS7000 Bio

### Table 1. Strains included in this study

Abbreviations: API, Appareils et Procédés d’Identification, Montalieu-Vercieu, France; CCUG, Culture Collection, University of Göteborg, Göteborg, Sweden; LMG, BCCM/LMG Bacteria Collection, Laboratorium voor Microbiologie, Gent, Belgium.

<table>
<thead>
<tr>
<th>Strain</th>
<th>Other strain designation(s)</th>
<th>Depositor</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td><em><strong>Kerstersia gyiorum</strong></em> gen. nov., sp. nov.</td>
<td></td>
<td>Public Health Laboratory, Göteborg, Sweden</td>
<td>Human faeces (85-year-old woman, Sweden, 1995)</td>
</tr>
<tr>
<td>LMG 15979</td>
<td>CCUG 34029</td>
<td>G. L. Gilardi</td>
<td>Human leg wound (1986)</td>
</tr>
<tr>
<td>LMG 15539</td>
<td>CCUG 24721, GLG 5504</td>
<td>D. Monget</td>
<td>Human leg wound (1983)</td>
</tr>
<tr>
<td>LMG 5905†</td>
<td>API 183-2-84</td>
<td>D. Monget</td>
<td>Human ankle wound</td>
</tr>
<tr>
<td>LMG 5891</td>
<td>API 145-2-84, CCUG 46999</td>
<td>D. Monget</td>
<td>Human leg wound (USA, 1983)</td>
</tr>
<tr>
<td>LMG 5892</td>
<td>API 146-2-84, CCUG 46998</td>
<td>D. Monget</td>
<td>Human leg wound (USA, 1983)</td>
</tr>
<tr>
<td>R-2516</td>
<td>BIJL977</td>
<td>G. Claesys</td>
<td>Human sputum (Belgium, 1997)</td>
</tr>
</tbody>
</table>
Assay Reader (Perkin-Elmer) for the fluorescence measurements. The hybridization temperature was 50 °C. Reciprocal experiments were performed for every pair of strains.

**Determination of DNA base composition.** DNA (prepared as described above) was enzymically degraded into nucleosides as described by Mesbah et al. (1989). The nucleoside mixture obtained was then separated by HPLC using a Waters SymmetryShield C8 column thermostatted at 37 °C. The solvent was 0.02 M NH₄H₂PO₄ (pH 4.0) with 1.5 % acetonitrile. The detector used was a Waters model 484 UV-VIS absorbance detector set at 270 nm. Non-methylated λ phage DNA (Sigma) was used as the calibration reference.

**Fatty acid methyl ester analysis.** After an incubation period of 24 h at 35 °C, a loopful of well-grown cells was harvested and fatty acid methyl esters were prepared as described previously (Vandamme et al., 1992), separated and then identified using the Sherlock Microbial Identification System (version 3.0; MIDI).

**Phenotypic characterization.** API galleries (API 50 CH, API 50AO and API 50AA; bioMérieux) were used to determine the assimilation of 147 organic compounds as sole carbon sources, as described previously (Kersters et al., 1984). Classical phenotypic tests were performed as described by Vandamme et al. (1993). API 20NE tests were performed according to the recommendations of the manufacturer (bioMérieux). Strains LMG 5890, LMG 5891, LMG 5892, LMG 5905, LMG 5895 and LMG 5906^T were investigated with the API 50 galleries; strains LMG 5892, LMG 5905, LMG 15539 and LMG 15979 were investigated using classical phenotypic tests and API 20NE tests.

**Antimicrobial susceptibility testing.** MIC values towards levofloxacin, ciprofloxacin, ofloxacin, sparflaxacin, erythromycin, roxithromycin, clarithromycin, azithromycin, cefotaxim, cepirinom and rifampicin were determined for eight strains (R-2516 was not included in the analysis) by using the agar dilution method conforming to the guidelines of the NCCLS (1995). Strains were grown on Mueller–Hinton agar (BRL) for 16–20 h at 35 °C.

**RESULTS AND DISCUSSION**

**Phylogenetic position and structure of the genus Kerstersia**

The reproducibility of SDS-PAGE of whole-cell proteins was checked by preparing protein extracts in duplicate; the level of correlation between the patterns was more than 93 % (data not shown). After numerical analysis and visual comparison of the profiles, three clusters could be delineated, while isolate LMG 5890 and reference strains of *Bordetella*, *Alcaligenes* and *Achromobacter* species occupied separate positions in the dendrogram (Fig. 1). A first cluster contained LMG 5891 and LMG 5892. Strains LMG 15539, R-2516 and LMG 15979 formed a second cluster. Finally, LMG 5895, LMG 5905 and LMG 5906^T constituted a third cluster. Visual comparison of the patterns indicated that LMG 5890 was most similar to cluster I isolates LMG 5891 and LMG 5892 and that isolates from clusters II and III formed a second group. This discrepancy between numerical analysis and visual comparison was due to slight but reproducible variation in the position of a high-intensity band within the profile, which had a profound effect on numerical analysis (data not shown). The complete 16S rDNA sequences of isolates LMG 5890 and LMG 5906^T were determined and compared with available 16S rDNA sequences of other β-Proteobacteria (Fig. 2). The 16S rDNA sequences of LMG 5890 and LMG 5906^T were very similar to each other (98.3 %). The levels of similarity towards *Bordetella* species (93.5–96.4 %), *Achromobacter* species (91.6–95.1 %), *Alcaligenes* species (92.7–94.8 %) and *P. kulae* (92.9–93.5 %) were lower. Bootstrap analysis indicated that strains LMG 5890 and LMG 5906^T formed a stable phylogenetic group (the bootstrap value was 100 %). DNA was prepared from isolates LMG 5890, LMG 5906^T and LMG 15539 and from reference strains of *Alcaligenes faecalis*, *Alcaligenes denitrificans*, *B. hinzii*, *Achromobacter xylosoxidans*, *Achromobacter ruhlandii* and *Achromobacter piechaudii*. DNA–DNA binding values are shown in Table 2. The G+C contents of isolates LMG 5890, LMG 5906^T and LMG 15539 were respectively 61.5, 62.9 and 62.7 mol%. The cellular fatty acid compositions of all *Kerstersia* isolates were also determined (shown in Supplementary Table A in IJSEM Online). The *Kerstersia* isolates formed a homogeneous group: the predominant fatty acids were 16 : 0, 17 : 0 cyclo, 18 : 1ω7c and summed feature 2 (comprising 14 : 0 3-OH, 16 : 1 iso I, an unidentified fatty acid with an equivalent chain-length of 10-928 and/or 12 : 0 ALDE). All strains examined showed catalase activity but no oxidase, arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, β-galactosidase, gelatinase, amylase, urease or DNase activity. No reduction of nitrate or nitrite, hydrolysis of aesculin or production of acid or H₂S from triple-sugar–iron agar was observed. All strains examined were capable of growth between 28 and 42 °C and could grow with NaCl concentrations ranging from 0 to 4–5 %. Growth in 6 % NaCl and resistance to penicillin were strain dependent. All strains examined assimilated the following substrates: acetate, propionate, butyrate, n-valerate,
n-caproate, heptanoate, pelargonate, caprate, succinate, fumarate, DL-lactate, DL-lactate plus methionine, DL-3-hydroxybutyrate, D-malate, L-malate, pyruvate, citrate, phenylacetate, \( p \)-hydroxybenzoate, \( L \)\(-\)alanine, \( L \)\(-\)phenylalanine, \( L \)\(-\)tyrosine, \( L \)\(-\)aspartate, \( L \)\(-\)glutamate, \( L \)\(-\)ornithine, \( L \)\(-\)proline, DL-4-aminobutyrate, 2-aminobenzoate, 4-aminobenzoate, amylamine and DL-kynurenine. None of the strains examined assimilated erythritol, D- or L-arabinose, ribose, D- or L-xylose, adonitol, methyl \( \beta \)-D-xyloside, galactose, D-glucose, D-fructose, D-mannose, L-sorbitose, L-rhamnose, dulcitol, inositol, mannitol, sorbitol, methyl \( \alpha \)-D-mannoside, methyl \( \alpha \)-D-glucoside, N-acetylglucosamine, amygdalin, arbutin, aesculin, salicin, maltose, lactose, melibiose, sucrose, trehalose, inulin, D-melezitose, raffinose, starch, glycogen, xyitol, D-turanose, D-lyxose, D-tagatose, D- or L-fucose, D- or L-arabitol, 2- or 3-ketogluconate, oxalate, malonate, malate, glycolate, DL-glycerate, D- or L-tartrate, meso-tartrate, benzoate, o- or m-hydroxybenzoate, D- or L-mandelate, phthalate, isophthalate, terephthalate, glycine, L-serine, L-histidine, D-tryptophan, trigonelline, L-lysine, L-citrulline, L-arginine, betaine, creatine, DL-3-aminobutyrate, DL-5-aminovalerate, 3-aminobenzoate, urea, acetamide, sarcosine, ethylamine, ethanolamine, benzylation, diaminobutane, spermine, histamine or glucosamine. Assimilation of glycerol, gluconate, cellobiose, \( \beta \)-gentiobiose, isobutyrate, isovalerate, caprylate, glutarate, adipate, pimelate, suberate, azelate, sebacate, levulinate, 2-ketoglutarate, citraconate, itaconate, mesaconate, aconitate, L-leucine, L-isoleucine, DL-2-aminobutyrate, L-norleucine, L-valine, DL-norvaline, L-threonine, L-cysteine, L-methionine, L-tryptophan, tryptamine and butylamine was strain dependent. The range of MIC values and the MIC 50 and MIC 90 values of the strains are shown in Supplementary Table B in IJSEM Online.

Isolates LMG 5906\(^T\) and LMG 5890 (representatives of the two major protein electrophoretic groups) formed a single and stable phylogenetic lineage. The closest related genera are Bordetella, Achromobacter, Alcaligenes and Pigmentiphaga, but 16S rDNA sequence similarities with these genera.

### Table 2. DNA–DNA binding values of all strains examined

Asterisks indicate values obtained using the initial renaturation rate method; other values were obtained using the microplate method.

| Strain | DNA–DNA binding (%) with strain:
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>1. <strong>K. gyiorum</strong> LMG 5906(^T)</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>2. <strong>K. gyiorum</strong> LMG 15539</td>
<td>91*</td>
<td>100</td>
</tr>
<tr>
<td>3. <strong>Kerstersia</strong> sp. LMG 5890</td>
<td>267/38</td>
<td>28*</td>
</tr>
<tr>
<td>4. <strong>Alcaligenes faecalis</strong> LMG 1229(^T)</td>
<td>1</td>
<td>–</td>
</tr>
<tr>
<td>5. <strong>B. hinzii</strong> LMG 13501(^T)</td>
<td>8</td>
<td>–</td>
</tr>
<tr>
<td>6. <strong>Achromobacter xylosoxidans</strong> LMG 1863(^T)</td>
<td>9</td>
<td>–</td>
</tr>
<tr>
<td>7. <strong>Achromobacter piechaudii</strong> LMG 1873(^T)</td>
<td>17</td>
<td>–</td>
</tr>
<tr>
<td>8. <strong>Achromobacter ruhlandii</strong> LMG 1866(^T)</td>
<td>9</td>
<td>–</td>
</tr>
<tr>
<td>9. <strong>Achromobacter denitrificans</strong> LMG 1231(^T)</td>
<td>6</td>
<td>–</td>
</tr>
</tbody>
</table>

---

**Fig. 2.** Phylogenetic tree based on 16S rDNA sequences showing the position of *Kerstersia* gen. nov. The scale bar represents 10% sequence dissimilarity.
were below 96.4, 95.1, 94.8 and 93.5%, respectively. The stability of the cluster (indicated by a bootstrap value of 100%) and the relatively low similarity values towards the closest related genera warrant the inclusion of these isolates in a novel genus, for which we propose the name *Kerstersia*. Numerical analysis and visual comparison of the protein profiles suggested that there were two different genomic groups present within the genus *Kerstersia*. Since the similarity of the 16S rDNA of representative isolates of the two protein electrophoretic groups was above 98.3%, DNA–DNA hybridizations were performed to clarify their relatedness (Stackebrandt & Goebel, 1994). The results from these DNA–DNA hybridization experiments confirmed that the two major protein electrophoretic groups (one containing the strains belonging to cluster I and one containing the strains belonging to clusters II and III) formed two separate genomic species. Biochemically, the two genomic species were indistinguishable. At this time, we propose the formal binomial name *Kerstersia gyiorum* gen. nov., sp. nov. for the isolates belonging to protein electrophoretic clusters II and III. Pending the availability of a formal binomial name, we propose the name *Kerstersia gyiorum* comb. nov., sp. nov. for the isolates belonging to clusters II and III. The formal binomial name *Kerstersia gyiorum* gen. nov., sp. nov. is the same as *K. gyiorum* gen. nov., sp. nov. for the isolates belonging to clusters II and III. The formal binomial name *Kerstersia gyiorum* gen. nov., sp. nov. is the same as *K. gyiorum* gen. nov., sp. nov. for the isolates belonging to clusters II and III.

Identification of members of the genus *Kerstersia*

Several previous studies have shown that species of the genera *Alcaligenes*, *Achromobacter* and *Bordetella* can be identified using SDS-PAGE of whole-cell proteins (Vancanneyt et al., 1995; Vandamme et al., 1995, 1996). This was confirmed in the present study. In addition, our data also indicated that SDS-PAGE of whole-cell proteins can be used to distinguish the two genomic groups present in the genus *Kerstersia* from each other and from related taxa. Using whole-cell fatty acid analysis, *Kerstersia* can be separated from other members of the *Alcaligenaceae* by the absence of 12:0 2-OH and by the large relative amounts of 18:1o7c. Biochemically, members of the genus *Kerstersia* are difficult to separate from other members of the *Alcaligenaceae*. In contrast to *Kerstersia* spp., most *Achromobacter* strains are oxidase-positive and assimilate aesculin and meso-tartrate, while most *Bordetella* strains are oxidase-positive and do not assimilate caprate. *P. kulae* does not assimilate phenylacetate but does assimilate adipate. Phenotypic characteristics useful for the differentiation of *K. gyiorum* from related taxa are shown in Table 3.

**Taxonomic status of *Alcaligenes denitrificans***

Rüger and Tan 1983

According to Yabuuchi et al. (1998), *Alcaligenes denitrificans* should be classified as a subspecies of *Achromobacter xylosoxidans*, based on intermediate DNA–DNA binding values between the two type strains and the results of 16S rDNA sequence analysis. However, previous work (Kiredjian et al., 1981; Vandamme et al., 1995, 1996) has shown clearly that strains of the two subspecies of *Achromobacter xylosoxidans* can be easily differentiated by DNA–DNA relatedness studies, whole-cell protein and fatty acid analysis as well as by phenotypic characteristics. These conclusions are again substantiated in the present study. It is therefore justified to reclassify *Alcaligenes denitrificans* Rüger and Tan 1983 as *Achromobacter denitrificans* comb. nov.

**Description of *Achromobacter denitrificans*** comb. nov.

The description of *Achromobacter denitrificans* is the same as the description given by Kersters & De Ley (1984) for *Alcaligenes xylosoxidans* subsp. *denitrificans*.

**Table 3.** Phenotypic characteristics useful for the differentiation of *K. gyiorum* from related taxa

<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>
<th>8</th>
<th>9</th>
<th>10</th>
<th>11</th>
<th>12</th>
<th>13</th>
<th>14</th>
<th>15</th>
<th>16</th>
</tr>
</thead>
<tbody>
<tr>
<td>Growth at 42°C</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>ND</td>
<td>+</td>
<td></td>
</tr>
<tr>
<td>Oxidase activity</td>
<td>-</td>
<td>+</td>
<td>ND</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>ND</td>
<td>+</td>
<td></td>
</tr>
<tr>
<td>Assimilation of:</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>D-Glucose</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>ND</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td>D-Xylose</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>ND</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Caprate</td>
<td>+</td>
<td>+</td>
<td>ND</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>ND</td>
</tr>
<tr>
<td>Adipate</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>ND</td>
</tr>
<tr>
<td>L-Malate</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>V</td>
<td>-</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>ND</td>
<td>+</td>
</tr>
<tr>
<td>Phenylacetate</td>
<td>+</td>
<td>V</td>
<td>ND</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>ND</td>
</tr>
<tr>
<td>Aesculin</td>
<td>-</td>
<td>-</td>
<td>ND</td>
<td>ND</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>ND</td>
</tr>
</tbody>
</table>
**Description of Kerstersia gen. nov.**

*Kerstersia* (Kers.ters’i.a. N.L. fem. n. *Kerstersia* in honour of K. Kersters, an eminent Belgian microbiologist, for his contributions to polyphasic taxonomy and to the introduction of computerized protein gel electrophoresis).

Gram-negative, small (1–2 μm long), coccoid cells that occur as single units, in pairs or in short chains. Motility is strain dependent. On nutrient agar, colonies are flat or slightly convex with smooth margins with a colour ranging from white to light brown. Catalase activity, but not oxidase, urease or β-galactosidase activity, is observed. Growth is observed at 28 and 42 °C. Additional biochemical characteristics are given above (see Results). MIC values for a number of antibiotics are shown in Supplementary Table B in IJSEM Online. The following fatty acid components are present: 14:0, 14:0 2-OH, 16:0, 17:0 cyclo, 18:0, 18:1ω7c, 19:0 cyclo ω8c, summed feature 2 and summed feature 3. The G+C content is 61.5–62.9 mol%. Strains of this genus have been isolated from various human clinical samples. The type species is *Kerstersia gyiorum*.

**Description of Kerstersia gyiorum sp. nov.**

*Kerstersia gyiorum* (gy.i.o’rum. Gr. n. gyior limb; N.L. gen. n. *gyiorum* from the limbs, referring to the fact that the majority of strains were isolated from human leg wounds).

The description is the same as for the genus. Additional characteristics are the assimilation of caprylate and the absence of assimilation of isobutyrate, isovalerate, glutarate, adipate, pimelate, suberate, azelate, sebacate, levulinate, 2-ketoglutarate, citraconate, itaconate, mesaconate, aconitate, L-leucine, L-isoleucine, L-valine, DL-norvaline, L-threonine, L-cysteine and L-methionine. The G+C content is 62.7–62.9 mol%. The type strain, LMG 5906^T (= API 184-2-84^T = CCUG 47000^T), was isolated from a human ankle wound. Characteristics for the type strain are the same as described above for the species. In addition, the type strain can use L-norleucine. The G+C content of the type strain is 62.9 mol%. All *K. gyiorum* strains reported in this study have been deposited in the BCCM/LMG Bacteria Collection (Laboratorium voor Microbiologie, Gent, Belgium) and the CCUG (Department of Clinical Microbiology, Göteborg, Sweden).

**REFERENCES**


