**Vicinamibacteraceae fam. nov., the first described family within the subdivision 6 Acidobacteria**

Katharina J. Huber¹,* and Jörg Overmann¹,²

**Abstract**

*Acidobacteria* constitute a globally widespread phylum and mainly inhabit soil environments. Despite their high abundance and activity, only 60 species from seven of the 26 acidobacterial subdivisions (sds; corresponding to class level) are (validly) described. Thus, only a low number of higher taxonomic ranks is currently distinguished within the *Acidobacteria*. Additionally, the distribution of the known acidobacterial species within the described families of the *Acidobacteria* (sd1), *Bryobacteraeae* (sd3), *Blastocatellaceae* (sd6), *Pyrinomonadaceae* (sd4), *Holophagacaeae* (sd8) and *Acanthopleuribacteraceae* (sd8) is extremely biased as most strains are affiliated with the *Acidobacteria*. Members of this family are characteristic for acidic soils. In contrast, culture-independent analysis of microbial communities worldwide revealed that sd6 *Acidobacteria* prevail in soils with neutral pH. To improve the existing acidobacterial taxonomy, we here formally describe the first family within sd6 *Acidobacteria*, the *Vicinamibacteraceae*. Members of the *Vicinamibacteraceae* are aerobic, neutrophilic, psychrotolerant to mesophilic chemoheterotrophs. Their cells stain Gram-negative, do not form capsules or spores, and are non-motile. They occur as single cells or in aggregates and divide by binary fission. Growth occurs on sugars or complex proteinaceous compounds. MK-8 is the major quinone. Major fatty acids are isom-C<sub>15</sub>:0, summed feature 3 (C<sub>16:1</sub>ω7c/C<sub>16:1</sub>ω6c), C<sub>18:1</sub>ω7c or ω9c, iso-C<sub>17:1</sub>ω9c, C<sub>16:0</sub> and iso-C<sub>17:0</sub>. Diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylcholine and phosphatidylglycerol are the major polar lipids. Unidentified glycolipids or unknown phospholipids might also be present. The G+C content of the DNA ranges from 64.7 to 65.9 mol%. Within the *Vicinamibacteraceae* fam. nov., *Vicinamibacter* and *Luteitalea* are the only genera described so far.

*Acidobacteria* mainly inhabit soil environments, but also some extreme habitats like cave paintings [1], Arctic deserts [2], wastewaters [3] and hot springs [4]. In volcanic, tundra/peatland, semiarid savannah or temperate soils, members of this phylum constitute up to 70% of the bacterial diversity, only 60 species of *Acidobacteria* were initially divided in 26 different subdivisions (sds), corresponding to class level [10]. Only the three classes *Acidobacteria* (former sd1) [11], *Blastocatellae* (former sd4) [12] and *Holophagae* (former sd8) [13] have been formally described so far. Six acidobacterial families are distinguished: the *Acidobacteriaceae* [14] and *Bryobacteraeae* [15] within the class *Acidobacteria*, the *Blastocatellaceae* [12] and *Pyrinomonadaceae* [16] within the class *Blastocatellae*, and the *Holophagacaeae* [13] and the *Acanthopleuribacteraceae* [13] within the class *Holophagae*.

Most of the isolated strains are affiliated with the families *Acidobacteriaceae* (37 species) and *Blastocatellaceae* (eight species), while only four species belong to the *Pyrinomonadaceae*, three to the *Bryobacteraeae*, two to the *Holophagaeae* and one species to the *Acanthopleuribacteraceae*. In addition, ‘*Chloracidobacterium thermophilum*’ B [17], ‘*Thermostomaculum hydrothermale*’ AC55 [18] and *Thermoaerobaculum aquaticum* MP-01<sup>T</sup> [19] are not affiliated with any acidobacterial family so far. Of the entire sd6, however, only the two cultivated representatives *Vicinamibacter silvestris* DSM 29464<sup>T</sup> [20] and *Luteitalea pratensis* DSM 100886<sup>T</sup> [21] have just recently been described, and no higher taxonomic rank has been proposed for this bacteria. However, sd6 *Acidobacteria* are highly abundant in non-acidic soils [7, 22, 23], are highly diverse (3942 different sequence types of the total 14534 for the phylum *Acidobacteria*), and were also reported to be successfully cultivated in the past [24]. Therefore, a description of many additional
species is to be expected for the near future, requiring a more detailed nomenclature below class level. Accordingly, we here propose the first family *Vicinamibacteracea* fam. nov. of the sd6 *Acidobacteria*.

Members of the genera *Vicinamibacter* and *Luteitalea* are aerobic chemoorganoheterotrophs that grow on different sugars but prefer complex proteinaceous compounds [20, 21]. Growth on organic acids and nucleic acids might occur. The degradation of some complex organic compounds was detected by tests with ApiZYM galleries [20, 21]. Additionally, functional genes potentially involved in chitin degradation were detected in the 7.4 Mb large genome of *Luteitalea pratensis* DSM 100886\(^ \text{I} \) but the corresponding enzyme activities could not be detected [21, 25]. While most exoenzyme activities were similar in both genera, the species *Vicinamibacter silvestris* DSM 29464\(^ \text{I} \) differed from *Luteitalea pratensis* DSM 100886\(^ \text{I} \) by the activity of the cysteine and valine arylaminidase and aesculine and gelatin hydrolysis (Table 1) [20, 21]. Cells of both genera stain Gram-negative, divide by binary fission, do not form spores or capsules and are non-motile. They occur either as single cells or in aggregates. Catalase activity can be detected and the activity of cytochrome c oxidase varies [20, 21].

While the two strains available were isolated from semiarid riparian forest soil with a neutral pH and from a mown pasture grassland soil with slightly acidic pH, respectively, they were isolated from riparian forest soil with a neutral pH and from a mown pasture grassland soil with slightly acidic pH, respectively, they tolerate a broader pH range of 4.7–9.0 and of 5.3–8.3, respectively [20, 21]. Both strains are also adapted to a broader range of temperature values (12–40°C or rather 0–36°C) and are resistant to a variety of antibiotics. Both species grow at NaCl concentration up to 1% (w/v) (Table 1) [20, 21]. MK-8 is the major respiratory quinone.

Diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylcholine, phosphatidylglycerol, two unknown phospholipids or one unidentified glycolipid are the polar lipids detected. The major fatty acids are iso-C\(_{15:0}\), C\(_{16:0}\), iso-C\(_{17:0}\), summed feature 3 (C\(_{16:1}\)ω6c/C\(_{16:1}\)ω7c), iso-C\(_{17:1}\)ω9c, C\(_{18:1}\)ω7c or ω9c. The G+C content of DNA varies between 64.7 and 65.9 mol% [20, 21].

Phylogenetic analysis of the 16S rRNA gene sequences performed with the ARB program [26] show that *Vicinamibacter silvestris* DSM 29464\(^ \text{I} \) and *Luteitalea pratensis* DSM 100886\(^ \text{I} \) share a 16S rRNA gene sequence identity of 93.7% to each other [20, 21] and hence represent two genera of the same family [27]. In addition, 16S rRNA gene sequence identities of 79.1–85.2% with the other *Acidobacteria* clearly place both species outside the (validly) described families *Acidobacteriaceae* [14], *Bryobacteraceae* [15], *Blastocatellaceae* [12], *Pyrinomonadaceae* [16], *Holophagaceae* [13] and *Acanthopleuribacteriaceae* [13] (Fig. 1).

Based on this clearly separated phylogenetic cluster and the similarity values between the genera *Vicinamibacter* and *Luteitalea*, we here propose the first family within sd6 *Acidobacteria*, *Vicinamibacteracea* fam. nov.

**DESCRIPTION OF VICINAMIBACTERACEA FAM. NOV.**

*Vicinamibacteracea* (Vi.ci.na.mi.bac.ter.rac.eae. – N.L. masc. n. *Vicinamibacter* type genus of the family; suff. -aceae ending to denote a family; N.L. fem. pl. n. *Vicinamibacteracea*, the *Vicinamibacter* family).

Gram-negative, non-sporing nor capsule-forming (short) rods, which either occur as single cells or in aggregates. Cells

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**Table 1.** Distinguishing characteristics of the genera *Vicinamibacter* and *Luteitalea* of the family *Vicinamibacteracea*

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Vicinamibacter</th>
<th>Luteitalea</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cell size (µm)</td>
<td>1.3–2.0×0.6–0.7</td>
<td>0.9–1.4×0.6–0.75</td>
</tr>
<tr>
<td>Arrangement of cells</td>
<td>Single or in aggregates</td>
<td>Single, in pairs or in chains</td>
</tr>
<tr>
<td>NaCl optimum for growth (% w/v)</td>
<td>0</td>
<td>0.25</td>
</tr>
<tr>
<td>Temperature range for growth (°C)</td>
<td>12–40</td>
<td>0–36</td>
</tr>
<tr>
<td>Temperature optimum for growth (°C)</td>
<td>26–31</td>
<td>20–30</td>
</tr>
<tr>
<td>pH range for growth</td>
<td>6.0–9.0</td>
<td>4.0–9.0</td>
</tr>
<tr>
<td>pH optimum for growth</td>
<td>7.0–8.5</td>
<td>5.5–9.0</td>
</tr>
<tr>
<td>DNA G+C content (mol%)</td>
<td>65.9</td>
<td>64.7</td>
</tr>
<tr>
<td>Cytochrome c oxidase</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>Doubling time (h)</td>
<td>17.4</td>
<td>29.8</td>
</tr>
<tr>
<td>ApiZYM</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cysteine arylaminidase</td>
<td>(+)</td>
<td>–</td>
</tr>
<tr>
<td>Valine arylaminidase</td>
<td>(+)</td>
<td>–</td>
</tr>
<tr>
<td>Api20 NE</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Gelatinase</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>Aesculin hydrolysatation</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>Genome size (Mb)</td>
<td></td>
<td>7.4</td>
</tr>
</tbody>
</table>

ND, no data available.
divide by binary fission. Catalase-positive. Cytochrome c oxidase variables. Aerobic chemoorganoheterotrophs that grow on different simple sugars but prefer complex proteinaceous compounds. Growth on organic acids and nucleic acids might occur. Enzyme activities for alkaline and acid phosphatase, naphthol-AS-BI-phosphohydrolase, α-chymotrypsin, trypsin and esterase C4 can be observed. Additionally, the activity of esterase lipase C8 and leucine arylaminidase is detectable. Psychrotolerant to mesophilic acidobacteria. Key features of the type species include: 

- Gram-positive rods/shortly coccoid, 0.5–1 x 1–2 μm
- Catalase positive
- Cytochrome c oxidase variable
- Catalase- and oxidase-positive
- Cytochrome variables
- Aerobic chemoorganoheterotrophs that tolerate a broader range of pH values. 
- NaCl concentrations up to 1 % are tolerated. 
- MK-8 is the major quinone. 
- Major fatty acids are iso-C₁₅:₀, C₁₆:₀, summed feature 3 (C₁₆:₁ω₆c/C₁₆:₁ω₇c), iso-C₁₇:₀, iso-C₁₇:₁ω₉c, C₁₈:₁ω₇c or ω₉c. Diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylcholine, phosphatidylglycerol, one unidentified glycolipid or two unknown phospholipids are the major polar lipids. The family accommodates the genera Vicinamibacter and Luteitalea. The type genus is Vicinamibacter. The G+C content of the DNA ranges from 64.7 to 65.9 mol%.

**References**


13. Fukunaga Y, Kurahashi M, Yanagi K, Yokota A, Harayama S. *Acanthopleuribacter pedis* gen. nov., *Acanthopleuribacter* species nov. and *Acanthopleuribacterium* fam. nov., *Acanthopleuribacteriales* ord. nov., *Holophagales* fam. nov., *Holophagaceae* ord. nov. and *Holophagaceae* classis nov. in the
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