**Aminipila butyrica** gen. nov., sp. nov., a strictly anaerobic, arginine-decomposing bacterium isolated from a methanogenic reactor of cattle waste

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**Abstract**

A strictly anaerobic bacterial strain (FH042\(^T\)) was isolated from a methanogenic reactor treating waste from cattle farms. Cells were stained Gram-positive, straight to gently curved rods with polar flagella. The strain was asaccharolytic. The strain fermented amino acids (L-arginine, L-lysine and L-serine) as growth substrates and produced acetate and butyrate. The optimum temperature for growth was 30°C and the optimum pH was 6.1–6.8. Oxidase, catalase and nitrate-reducing activities were negative. Hydrogen sulfide was produced. The genomic DNA G+C content of strain FH042\(^T\) was 44.7±0.2 mol%. The major cellular fatty acids were C\(_{18:1}\)ω9c DMA, C\(_{17:0}\)/C\(_{17:1}\)ω9c (as summed feature), C\(_{16:0}\) DMA and C\(_{14:0}\). The cell-wall peptidoglycan contained meso-diaminopimelic acid as a diagnostic amino acid. The most closely related described species on the basis of 16S rRNA gene sequences was *Anaerovorax odorimutans* in the family XIII *Incertae Sedis* in the order *Clostridiales* with sequence similarity of 95.1%. Based on the distinct differences in phylogenetic and phenotypic characteristics between strain FH042\(^T\) and related species, *Aminipila butyrica* gen. nov., sp. nov. is proposed to accommodate the strain. Type strain is FH042\(^T\) (=JCM 31555\(^T\)=DSM 103574\(^T\)).

In anaerobic decomposition of organic matter, protein is hydrolysed to amino acids and then the amino acids are fermented to volatile fatty acids (VFAs) such as acetate, propionate, butyrate and branched fatty acids (isobutyrate and isovalerate) as well as H\(_2\) and CO\(_2\) by anaerobic bacterial populations. Each amino acid is converted to different combinations of VFAs depending on the amino acids fermented and bacterial species involved [1–3]. Investigation into ecology or physiology of protein- or amino acid-degrading anaerobic bacteria is important to understand the methanogenic process of wastewater treatment. Recent descriptions of novel anaerobic species of amino acid-degrading bacteria isolated from methanogenic reactors [4–10] indicate that many phylogenetically diverse species are involved in degradation of proteinous compounds or amino acids. In this study, a strictly anaerobic, Gram-positive, amino acid-degrading bacterium (strain FH042\(^T\)) isolated from a methanogenic reactor is described. The strain fermented L-arginine, L-lysine and L-serine and produced acetate and butyrate. Based on the analysis of 16S rRNA gene sequence, the strain was assigned to the class *Clostridia* in the phylum *Firmicutes* and affiliated with the family XIII *Incertae Sedis* in the order *Clostridiales* [11]. We propose *Aminipila butyrica* gen. nov., sp. nov. to accommodate the strain. Type strain is FH042\(^T\) (=JCM 31555\(^T\)=DSM 103574\(^T\)).

Strain FH042\(^T\) was isolated by the anaerobic roll-tube method for the colony-counting of anaerobic fermentative bacteria [12] from a methanogenic reactor treating waste collected from cattle farms (housing up to 1000 cattle in total) in Betsukai-machi, Hokkaido, Japan, as described previously [7–10]. Strain FH042\(^T\) was one of the isolates obtained from a digester fluid sample without plant residue or other solid material collected from the reactor. The pure culture of the strain was obtained after repeats of the colony isolation using the anaerobic roll-tube method. The purity of the strain was confirmed by observing colonies on the roll tube agar and the cell morphology under a phase-contrast microscope. The purity of the strain was checked routinely by observing cells microscopically as well as by measuring fermentation products after cultivation in PY or PY–arginine medium (see below). The strain was cultivated anaerobically at 30°C unless otherwise stated by using peptone/yeast extract (PY) basal medium with oxygen-free mixed gas (95 % N\(_2\)/5 % CO\(_2\)) as the headspace as described

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**Abbreviations:** CFA, cellular fatty acid; DMA, dimethylacetate; ECL, equivalent chain length; ML, maximum-likelihood; NJ, neighbour-joining; VFA, volatile fatty acid.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain FH042\(^T\) is AB298771. Two supplementary tables and two supplementary figures are available with the online version of this article.

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previously [7–10]. PY medium contained (l−1) 10 g Trypticase (BBL), 5 g yeast extract, 0.2 g Na₂CO₃, 0.3 g L-cysteine hydrochloride dihydrate (as a reducing agent) and 1 mg sodium resazurin (as a redox indicator) as well as salt solutions [12, 13]. PY medium supplemented with (l−1) 0.25 g each of glucose, cellobiose, maltose and soluble starch together with 15 g agar was designated as PY4S agar and used for isolation and maintenance of the strain in agar slants. All media were usually adjusted to pH 7.1–7.2 (before autoclaving) with 1 M NaOH.

Growth of the strain under aerobic conditions was examined as described previously [7]. Spore formation was assessed by phase-contrast microscopy and observation of cells after Gram-staining. To examine formation of thermotolerant cells, cells cultivated in PY-arginine medium or on PY4S agar slants were inoculated to PY-arginine medium, and the culture tubes were treated at 80 °C for 10 min before cultivation at 30 °C. The motility of cells was examined by phase-contrast microscopy. Flagella staining was carried out according to Blenden and Goldberg [14].

Colonies of strain FH042T were thin and translucent with a smooth surface on agar slants after 48 h of inoculation. Cells were Gram-stain-positive and straight to gently curved or sigmoid rods with flat ends, usually 0.7–1.0 µm in diameter and 3.0–8.0 µm in length. Longer rods up to 40 µm often occurred (Fig. S1a, available in the online version of this article). Cells were motile; one or two polar flagella were observed by flagella staining of cells (Fig. S1b–d). Cells of the strain did not grow in air. Spores were not observed in cells by microscopy, irrespective of the medium used for cultivation of the strain such as PY, PY-arginine and PY4S agar slants. The strain grew after heat-treatment, indicating the presence of thermostolerant cells.

Utilization of carbon sources was tested in PY liquid medium with monosaccharides, disaccharides, trisaccharides and sugar alcohols added at 10 g l−1. Polysaccharides and glycosides were added at 5 g l−1, and organic acids as well as amino acids were added at 30 mM as the final concentration in the medium. Utilization of each substrate was usually determined by growth measured by OD₆₆₀ of culture as well as measurement of pH and fermentation products after cultivation. Fermentation products (fatty acids and gases) were analysed by gas chromatography [15]. All tests were carried out in duplicate.

Strain FH042T grew in PY medium without additional substrates. The strain produced (as mean values of amounts obtained from different experiments of cultivation) acetate (7.3 mmol l−1) and butyrate (3.3 mmol l−1) after 72 h of cultivation in PY medium. Final pH after growth in PY medium was 6.6. Carbohydrates and organic acids (arabino-ose, ribose, xylose, fructose lactose, glucose, mannose, rhamnose, sorbose, cellobiose, lactose, maltose, melibiose, sucrose, trehalose, melezitose, raffinose, carboxymethylcellulose, cellulose, dextrin, glycogen, inulin, pectin, starch, xylan, dulcitol, inositol, mannitol, sorbitol, aesculin, amygdalin, salicin, glycerol, fumarate, lactate, malate, pyruvate and succinate) added to PY medium did not improve the growth and production of VFAs. Three kinds of amino acids (L-arginine, L-lysine and L-serine) enhanced the growth and production of VFAs; 12.7 mmol l−1 acetate and 12.7 mmol l−1 butyrate from L-arginine, 34.5 mmol l−1 acetate and 15.6 mmol l−1 butyrate from L-lysine, and 16.0 mmol l−1 acetate from L-serine (Table S1). A trace amount of H₂ (2.15 mmol l−1) was produced from L-arginine in PY medium. The final pH values were pH 7.7 with L-arginine and pH 5.2 with L-lysine (Table S1). We did not determine the concentrations of ammonium in the medium after cultivation, but the balance of concentrations of VFAs and ammonium generated by deamination of amino acids would affect the pH values in the medium. Although concentrations of VFAs produced were higher in the medium with L-lysine, the highest growth (OD₆₆₀) was obtained in the medium containing L-arginine. Casamino acids moderately enhanced production of acetate (10.2 mmol l−1) and butyrate (4.8 mmol l−1). Other 14 kinds of proteinogenic amino acids (L-alanine, L-aspartate, L-glutamate, glycine, L-histidine, L-isoleucine, L-leucine, L-methionine, L-phenylalanine, L-proline, L-threonine, L-tryptophane, L-tyrosine and L-valine) tested did not affect growth and products of the strain. A nonprotein amino acid, γ-aminobutyrate, did not support the growth. B-vitamin requirement was not recognized.

The optimum growth conditions of strain FH042T were tested in PY medium containing 30 mM L-arginine (PY-arginine medium) on temperatures at 5–45 °C (at 5 °C intervals), at pH 4.2, 5.3, 6.1, 6.8, 7.6, 8.2, 9.2 and 10.2 (as values verified after autoclaving), and by the addition of 0–50 g l−1 NaCl (at 10 g l−1 intervals with an exception of 5 g l−1) in the medium. Bicine (Good’s buffer; Dottite (20 mM) was used to adjust the pH of the medium higher than 8.0 by using N₂ gas as the headspace. The temperature range for growth was 10–35 °C with the highest growth rate at 30 °C. The strain grew at 35 °C, but growth ceased quickly and the OD₆₆₀ value declined. The strain grew at pH 5.3–8.2; optimum being pH 6.1–6.8. The strain grew in the medium containing NaCl up to 20 g l−1; the highest growth rate was obtained without NaCl addition. The specific growth rate (μ) at the optimum conditions (30 °C and pH 6.1 without added NaCl) was 0.22–0.25 h−1.

Other physiological characterization was carried out according to the methods as described by Holdeman et al. [12] and Ueki et al. [7]. Catalase, oxidase and nitrate-reducing activities were not detected. Strain FH042T produced hydrogen sulfide. Aesculin and starch were not hydrolysed. Other physiological characteristics are presented in the species description.

Cells cultivated at 30 °C for 72 h in PY-arginine medium were used for the following chemotaxonomic analyses. Genomic DNA extracted according to the method as described by Akasaka et al. [15] was digested with P1 nuclease by using a YAMASA GC kit (Yamasu Shoyu, Choshi,
Several species within the genus *Eubacterium* [27] were related to strain FH042T with sequence similarities of 91–92%. The most closely related organism, but not yet validly described species, was *Clostridium* species (*Clostridium aminobutyricum*) DSM 2634 [28] with 95.9% sequence similarity. Based on the analysis of 16S rRNA sequences, Collins et al. [29] originally classified *Clostridium aminobutyricum* in clostridia clust XI as a relatively distinct line. But almost all members in cluster XI have been renamed and currently assigned to the family *Peptostreptococcaceae* according to reclassification of *Clostridium* species that fall outside of cluster I [11, 30, 31]. Phylogenetic trees comprised of the species in the family XIII and the *Peptostreptococcaceae* as well as *Eubacterium* species related to strain FH042T were reconstructed (Figs 1 and S2). Although the positions of *Anaerovorax odorimutans* and *Clostridium aminobutyricum* were exchanged in the two trees using the NJ and ML methods, the tree topologies evaluated by the two methods were almost the same. The phylogenetic trees showed that the species in the family *Peptostreptococcaceae* formed a distinct branch from that composed of the species in the family XIII and related species.

Some characteristics of strain FH042T were compared with those of the species in the family XIII (*Anaerovorax odorimutans* and *Mogibacterium* species) including four *Eubacterium* species related to the family XIII and *Clostridium aminobutyricum* (Table 1). Cells of strain FH042T are straight or gently curved to sigmoid rods in various sizes (Fig. S1), whereas cells of *Anaerovorax odorimutans* are typical curved or crescent-shaped rods with an approximately uniform size. Cells of strain FH042T have polar flagella, while *Anaerovorax odorimutans* have 3–5 lateral flagella on the concave side of the cell [24]. Thus, the cell type of strain FH042T is essentially different from that of *Anaerovorax odorimutans*. *Anaerovorax odorimutans* does not utilize carbohydrates, organic acids, alcohols and proteinogenic amino acids as growth substrates and only utilizes putrescine (a kind of polyamines), γ-aminobutyrate (a nonprotein amino acid) and 4-hydroxybutyrate. The genomic DNA G+C content of *Anaerovorax odorimutans* is 29.6% [25], which is a similar level as those of the species in the *Peptostreptococcaceae* (26–34%) [11]. These data indicated that it is not correct to assign strain FH042T to the genus *Anaerovorax*. *Mogibacterium* species are anaerobic, nonspore-forming, nonmotile short rods and asaccharolytic. The genomic DNA G+C contents of the five species in the genus are 41–50 mol% [11]. Cells of the four *Eubacterium* species related to the family XIII are all anaerobic, non-spore-forming, nonmotile short rods. They are asaccharolytic and the genomic DNA G+C contents are 38–48% [27]. All species in the two genera *Mogibacterium* and *Eubacterium* have common cellular and physiological characteristics and similar values of the genomic DNA G+C contents. The genomic DNA G+C content of strain FH042T is also within the range observed for species of these genera. Cells of *Clostridium aminobutyricum* are spore-forming, motile small rods. It is saccharolytic, and produces acids (acetate and butyrate) and...
gas from various carbohydrates [28]. The saccharolytic property of ‘Clostridium aminobutyricum’ is exceptional in the species within the family XIII including strain FH042\(^T\) and the related Eubacterium species.

In addition to low 16S rRNA gene sequence similarities with all related validly described species, phenotypic characteristics of the closest species, Anaerovorax odorimutans, were distinctly different from those of strain FH042\(^T\). It has been proposed that the genus Clostridium should be restricted to species belonging to clostridial cluster I (Clostridium sensu stricto) (Clostridium butyricum and related species) [11, 29, 32]. The 16S rRNA gene sequence similarity (95.1%) between FH042\(^T\) and Anaerovorax odorimutans DSM 5092\(^T\) is almost within the threshold value for defining bacterial genera (94.5–95.0%) recommended by Yarza et al. [33]. Thus, based on the data, we propose the novel genus Aminipila gen. nov. in the family XIII in the order Clostridiales to accommodate strain FH042\(^T\) as Aminipila butyrica. The novel species expanded the diversity of the members in the Clostridiales as well as insight for the proteolytic or aminolytic bacterial consortium in anaerobic digestion of organic matter.

**DESCRIPTION OF AMINIPILA GEN. NOV.**

Aminipila (A.mi.ni.pi’la. N.L. neut. n. aminum amine; L. fem. n. pila pillar; N.L. fem. n. Aminipila an amino acid-decomposing pillar).

Table 1. Differential characteristics of the species in the family XIII in the Clostridiales

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cell morphology</td>
<td>Straight to gently curved rods</td>
<td>Curved or crescent-shaped rods with rounded ends</td>
<td>Short rods</td>
<td>Short rods</td>
<td>Small rods</td>
</tr>
<tr>
<td>Cell size (µm)</td>
<td>0.7-1.0×3.0-40</td>
<td>0.7-0.8×1.9-2.7</td>
<td>0.2-0.8×1.0-3.1</td>
<td>0.4-1.0×1.0-7.0</td>
<td>0.4-0.8×1.2-1.7</td>
</tr>
<tr>
<td>Gram-staining</td>
<td>+</td>
<td>– (Gram-positive type cell wall)</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Motility</td>
<td>+ (1-2 polar flagella)</td>
<td>+ (3-5 lateral flagella on the concave side of the cell)</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Spore</td>
<td>– (†)</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Utilization of growth substrate</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Carbohydrates</td>
<td>–</td>
<td>–</td>
<td>NR</td>
<td>NR</td>
<td>+</td>
</tr>
<tr>
<td>Proteinogenic amino acids</td>
<td>t-Arginine, t-Lysine, t-Serine</td>
<td>–</td>
<td>NR</td>
<td>NR</td>
<td>–</td>
</tr>
<tr>
<td>γ-Aminobutyrate</td>
<td>–</td>
<td>+</td>
<td>NR</td>
<td>NR</td>
<td>+</td>
</tr>
<tr>
<td>Major products</td>
<td>Acetate, butyrate</td>
<td>Acetate, butyrate</td>
<td>Phenylacetate</td>
<td>Acetate, butyrate</td>
<td>Acetate, butyrate</td>
</tr>
<tr>
<td>Major CFAs</td>
<td>C₁₈ : ₁ω⁹c DMA, C₁₇ : ₂ω⁹c</td>
<td>NR</td>
<td>NR</td>
<td>NR</td>
<td>NR</td>
</tr>
<tr>
<td>Genomic DNA G+C content (mol%)</td>
<td>44.7</td>
<td>29.6</td>
<td>41-50</td>
<td>38-48</td>
<td>NR</td>
</tr>
</tbody>
</table>

†Thermotolerant cells.

One species (E. sulci) utilizes L-threonine.

Aminipila butyrica (bu.ty’ri.ca. N.L. neut. n. acidum butyricum butyric acid; N.L. fem. adj. butyrica pertaining to production of butyric acid).

Cells are straight or slightly curved to sigmoid rods with flat ends, 0.7-1.0 µm in diameter and 3.0-8.0 µm in length. Longer rods up to 40 µm often occur. Motile with polar flagella. Spore formation is not observed, but thermotolerant cells are present. Colonies on PY4S agar are translucent with smooth surface. B-vitamins are not required for growth. Grows at 10-35 °C (optimum 30 °C), pH 5.3-8.2 (optimum pH 6.1-6.8) and 0-20 g l⁻¹ of NaCl (optimum 0 g l⁻¹). Grows in PY medium and produces acetate and butyrate. Does not utilize carbohydrates and organic acids (arabinose, ribose, xylose, fructose galactose, glucose, mannose, rhamnose, sorbose, cellobiase, lactose, maltose, melibiose, sucrose, trehalose, melezitose, raffinose, carboxymethylcellulose, cellulose, dextrin, glycogen, inulin, pectin, starch, xylan, dulcitol, inositol, mannitol, sorbitol, ascinus, amygdalin, salicin, fumarate, lactate, malate, pyruvate and succinate). Utilizes L-arginine, L-lysine and L-serine. Weakly utilizes casamino acids. Produces acetate and butyrate from L-arginine and L-lysine, and acetate from L-serine. Produces a trace amount of H₂ from L-arginine. Does not utilize other amino acids (L-alanine, L-aspartate, L-glutamate, glycine, L-histidine, L-isoleucine, L-leucine, L-methionine, L-phenylalanine, L-proline, L-threonine, L-tryptophane, L-tyrosine, L-valine and L-γ-aminobutyrate). Final pH values after growth with L-arginine are 7.7 and 5.2 with L-lysine. Oxidase, catalase and nitrate-reducing activities are negative. Hydrogen sulfide is produced. Aesculin, starch and gelatin are not hydrolysed. Indole, lecithinase and lipase are not produced. Milk is unchanged and no growth occurs in chopped meat broth. The genomic DNA G+C content is 44.7±0.2 mol%. C₁₈ : ₁ω⁹c DMA, C₁₇ : ₂ω⁹c, ω⁹c (as summed feature), C₁₆ : ₀ DMA and C₁₄ : ₀ are detected as major components by the cellular fatty acid analysis. The cell-wall peptidoglycan contains meso-diaminopimelic acid as a diagnostic amino acid. Does not have any respiratory quinones.

The type strain, FH042ᵀ (≡JCM 31555ᵀ=DSM 103574ᵀ) was isolated from a methanogenic reactor treating waste from cattle farms in Japan.

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

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