Streptobacillus ratti sp. nov., isolated from a black rat (Rattus rattus)

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An indole-, oxidase- and catalase-negative, non-motile bacterium, strain OGS16 T, was isolated from an oral swab of a feral black rat (Rattus rattus) in 2007 in Japan. It stained Gram-negative and had pleomorphic, rod-shaped, non-spore-forming cells. Based on 16S rRNA gene sequence analyses, strain OGS16 T was assigned to the genus Streptobacillus, with 16S rRNA gene sequence similarities of 99.3, 99.0, 98.6 and 95.5 % to the type strains of Streptobacillus moniliformis, Streptobacillus notomytis, Streptobacillus felis and Streptobacillus hongkongensis, respectively. Strain OGS16 T could also be differentiated clearly from other species of the genus Streptobacillus by rpoB, groEL and recA nucleotide and deduced amino acid sequence analysis. DNA–DNA relatedness as obtained by average nucleotide identity was 89.10 % between strain OGS16 T and Streptobacillus moniliformis DSM 12112 T. Chemotaxonomic and physiological data for strain OGS16 T were congruent with results for other closely related members of the family Leptotrichiaceae, represented by highly similar enzyme profiles and fatty acid patterns. MALDI-TOF MS analysis also proved suitable in discriminating strain OGS16 T unequivocally from all currently described taxa of the genus Streptobacillus. On the basis of these data, we propose the novel species Streptobacillus ratti sp. nov., with the type strain OGS16 T (=JCM 31098 T =DSM 101843 T). The G + C content of the DNA of the type strain is 25.9 mol% and the genome size is 1.50 Mbp.

For almost a century, Streptobacillus moniliformis was a monotypic species within the genus Streptobacillus (Levaditi et al., 1925) (Streptobacillus, Leptotrichiaceae, Fusobacteriales). It causes rat bite fever and Haverhill fever (Elliott, 2007). Fever, malaise, muscle pain, arthritis and abscess formation, endocarditis, bacteraemia and

**Abbreviations:** ANI, average nucleotide identity; ML, maximum-likelihood.

The GenBank/EMBL/DDJB accession numbers for the 16S rRNA, gyrB, groEL and recA gene sequences and the complete genome sequence of strain OGS16 T are KR001922, KR001960, KR001941, KR001979 and LKKW00000000 (BioSample SAMN04099675), respectively. Complete genome sequences for Streptobacillus hongkongensis DSM 26322 T, Streptobacillus felis 131000547 T and Streptobacillus notomytis AHL 370-1 T have been deposited as BioProject PRJNA304683 (accession SAMN04306666), BioProject PRJNA304683 (accession SAMN04306665) and LJRV00000000 (BioSample SAMN04038436), respectively. Further sequences from reference strains used in this study are summarized in Table S1.

Five supplementary figures and two supplementary tables are available with the online Supplementary Material.
maculopapular, petechial or pustular rash, as well as vomiting and pharyngitis, are common symptoms of acute rat bite fever (Gaastra et al., 2009). This bacterial zoonosis is transmitted predominantly through rat bites and scratches (Gaastra et al., 2009). Haverhill fever represents a second, foodborne form of *Streptobacillus moniliformis* infection, which is transmitted by direct or indirect contact with rat urine (Bleich & Nicklas, 2008; Regnath et al., 2015). Approximately 50–100 % of wild rats usually carry *Streptobacillus moniliformis* asymptomatically in their oropharynx and shed the organism with saliva and urine (Elliott, 2007; Kimura et al., 2008). Other rodents, as well as companion and exotic animal species and livestock, are principally reported to be susceptible to clinical infection in addition to rats and mice, but mice may develop disease strain-dependently (Boyer et al., 1958; Das, 1986; Ditchfield et al., 1961; Gaastra et al., 2009; Glünder et al., 1982; Gourlay et al., 1982; Mohamed et al., 1969; Russell & Straube, 1979; Smallwood, 1929; Valverde et al., 2002; Wullenweber et al., 1990; Yamamoto & Clark, 1966).

Recently, *Streptobacillus hongkongensis* (Woo et al., 2014), *Streptobacillus felis* (Eisenberg et al., 2014, 2015b) and *Streptobacillus notomytis* (Eisenberg et al., 2015a) have been described as novel species, all of which cause considerable human or animal sequelae. Furthermore, various phenotypes of *Streptobacillus* consistent with 16S rRNA gene-based operational taxonomic units have been described from Philippine mustard, fish and microorganisms of squirrels, cotton rats, dogs, ducks, dolphins, sea lions and humans (Bik et al., 2010; Chaves-Moreno et al., 2015; Dewhirst et al., 2012; Hullar et al., 2015; Larcia et al., 2011; Maher et al., 1995; Palmer et al., 1994; Strong et al., 2013; Xenoulis et al., 2008) (Fig. S1, available in the online Supplementary Material). A series of strains of *Streptobacillus* spp., KWG2, KWG24 and OGS16T, isolated from Japanese black rats (*Rattus rattus*; Kimura et al., 2008), was recently found to represent two different species (Eisenberg et al., 2015c). The former two strains, KWG2 and KWG24, are reference strains of *Streptobacillus notomytis*, which was originally isolated from a spinnifex hopping mouse (Eisenberg et al., 2015a). Strain OGS16T gave evidence for a further novel species, and the strain is the subject of the present description.

Strain OGS16T was originally isolated from the oral cavity of a Japanese black rat (Kimura et al., 2008) in a rearing facility of a pest control company (Ikari Corporation, Chiba, Japan). The ancestors of the rats in the facility were captured in 1989 on Chichijima, one of the Ogasawara Islands (Bonin Islands), located some 1000 km south of Japan. OGS16T grew after 1–2 days of incubation at 37 °C under a capnophilic atmosphere of 10 % CO2 on Columbia agar with 5 % sheep blood (SBA; Oxoid). On this agar, strain OGS16T was also able to grow weakly at 43 °C, but not at 10, 20 or 50 °C. The strain could best be cultivated on TSA (tryptone soy agar; Oxoid) supplemented with 20 % horse serum, but also on Schaedler agar, as well as in liquid media [tryptone soy bouillon (TSB), brain heart infusion and peptone broth, supplemented with 20 % cattle or horse serum] but not on Gassner or MacConkey agar (all from Oxoid). Growth was fastidious, and colonies were indistinguishable from those of *Streptobacillus moniliformis*, displaying a butyrous, dry appearance. Gram-staining was done according to the Hucker method, as described previously (Gerhardt et al., 1994), and cell morphologies were assessed with cells grown for 3 days at 37 °C on SBA using a Leitz Dialplan light microscope at ×1000 magnification. Gram staining revealed Gram-negative, pleomorphic, fusiform to filamentous, non-spor-forming, non-encapsulated, non-acid-fast rods that sometimes displayed irregular, lateral bulbar swellings and were arranged in chains and clumps. Single rod-shaped cells were approximately 0.45 ± 0.1 μm wide and 0.83 ± 0.08 μm long.

Whole-genome sequencing was carried out with strain OGS16T. Genomic DNA was extracted from a 72 h bacterial culture with a commercial kit according to the manufacturer’s instructions [MasterPure Complete DNA and RNA Purification kit (Epicentre), distributed by Biozym Scientific]. *De novo* assembly was performed with CLC Genomics Workbench, version 7.5 (CLC Bio). For automatic annotation, we used the RAST server (Aziz et al., 2008).

For the first phylogenetic placement, phylogenetic trees based on nearly full-length 16S rRNA gene sequences were reconstructed with *MEGA*5 (Tamura et al., 2011) with the maximum-likelihood (ML) method based on the Tamura–Nei model (Tamura & Nei, 1993) and rapid bootstrap analysis and the maximum-parsimony method using the subtree-pruning-regrafting algorithm (Nei & Kumar, 2000). Both trees were based on 1108 nucleotide positions and 100 replications (bootstrap analysis) (Felsenstein, 1985).

The sequenced 16S rRNA gene fragment of strain OGS16T represents a stretch of 1482 unambiguous nucleotides between sequence positions 28 and 1499 (*Escherichia coli* numbering; Brosius et al., 1978). The 16S rRNA gene sequence identity of strain OGS16T was highest with the type strains of *Streptobacillus moniliformis* (99.3 %), *Streptobacillus notomytis* (99.0 %), *Streptobacillus felis* (98.6 %) and *Streptobacillus hongkongensis* (95.5 %), followed by *Sneathia sanguinegens* (93.0 %). Lower (<92 %) sequence similarities were observed to all other taxa. ML as well as maximum-parsimony treeing revealed a distinct cluster (98 % bootstrap support) of strain OGS16T with the type strains of all other species of the genus *Streptobacillus* (Fig. 1), clearly separated from the genera *Sneathia*, *Sebadella* and *Leptotrichia*. The closest similarities were observed between strain OGS16T and seven strains of *Streptobacillus moniliformis* from different sources (Table S2) including the type strain, which was supported by a bootstrap value of 78 %. Two previously designed PCR assays for the detection of *Streptobacillus moniliformis* also resulted in characteristic amplicon sizes of approximately
Fig. 1. ML tree showing the phylogenetic position of *Streptobacillus ratti* sp. nov. OGS16T within the family *Leptotrichiaceae*. The tree was reconstructed with MEGAS (Tamura et al., 2011) with the ML method based on the Tamura–Nei model (Tamura & Nei, 1993) and rapid bootstrap analysis (100 bootstraps) and is based on a 16S rRNA gene sequence alignment of 1108 nucleotide positions. GenBank accession numbers are given in brackets. Numbers at branch nodes refer to bootstrap values >70 (100 replicates). Bar, 0.02 substitutions per site.

For a more detailed view of the phylogenetic relationships of strain OGS16T and closely related species of the genus *Streptobacillus*, the criteria of Woo et al. (2014) were considered. Phylogenetic analyses based on both partial nucleotide and deduced amino acid sequences of the *gyrB*, *groEL* and *recA* genes were performed to take into account non-synonymous substitutions (Glaeser & Kämpfer, 2015). Nucleotide and deduced amino acid sequences were aligned using CLUSTAL W (Thompson et al., 1994) implemented in MEGAS (Tamura et al., 2011). Pairwise sequence similarities were calculated based on p-distances (calculated without an evolutionary model). Phylogenetic trees were generated using the ML method with a discrete Gamma distribution (+G) with five rate categories and by assuming that a certain fraction of sites are evolutionary invariant (+I) (for nucleotide sequences) and the Jones–Thornton–Taylor model (JTT; Jones et al., 1992) +G+I (for deduced amino acid sequences). All trees were based on 100 replications (bootstrap analysis).

Based on the partial nucleotide sequences and the more-conserved deduced amino acid sequences of *gyrB, groEL* and *recA*, phylogenetic trees showed the formation of monophyletic clusters including all species of *Streptobacillus* in all but the *GyrB* (deduced amino acid sequence) tree. Strain OGS16T clustered (with high bootstrap support) closest to, but on a distinct branch between, strains of *Streptobacillus moniliformis* and *Streptobacillus notomytis* (Figs S2–S4). In the *GyrB* deduced amino acid sequence tree, strain OGS16T clustered together with all strains of *Streptobacillus moniliformis* in one clade. The clear genetic distinction of strain OGS16T was supported by a comparison of nucleotide and deduced amino acid sequence differences, which were always considerably lower between strain OGS16T and strains of the other species of the genus *Streptobacillus* (Table S2).

DNA–DNA hybridization (DDH) of strains of *Streptobacillus* has been shown to give weak results (Eisenberg et al.,
2015c). Instead, average nucleotide identity (ANI) was determined according to the method described by Goris et al. (2007). The overall DNA–DNA relatedness between strain OGS16\textsuperscript{T} and Streptobacillus moniliformis DSM 12112\textsuperscript{T} was 89.10 % as determined by ANI, and it is therefore evident that they represent separate species (Richter & Rosselló-Móra, 2009). The same assertion was supported by a comparison of genomes with the type strains of the remaining species of the genus Streptobacillus, in that ANI between OGS16\textsuperscript{T} and Streptobacillus notomytis AHL 370-1\textsuperscript{T}, Streptobacillus felis 131000547\textsuperscript{T} and Streptobacillus hongkongensis DSM 26322\textsuperscript{T} was calculated as 89.00, 81.96 and 74.77 %, respectively. As a countercheck, and to avoid statistical uncertainty, we also confirmed these results by using the in-silico genome-to-genome comparison tool (GGDC 2.0; http://ggdc.dsmz.de/), which works independently of ANI and was found to yield higher correlations with conventional DDH (Meier-Kolthoff et al., 2013). Strain OGS16\textsuperscript{T} consistently displayed DDH estimate levels of <40.40 % (bootstrap confidence intervals 20.4–38.0 %) to strains of all other species of the genus Streptobacillus using formula 2 [identities/high-scoring pair (HSP) length] (data not shown).

Strain OGS16\textsuperscript{T} displayed three conserved signature indels in the amino acid sequences of an MreB/MrI family protein (MreB/MrI; 2 aa deletion), alanine-tRNA ligase (AlaS; 5 aa insertion) and RecA (2 aa insertion) that were recently found to be specific for the Leptotrichiaceae (Gupta & Sethi, 2014) (data not shown).

It is evident from the results of 16S rRNA, gyrB, groEL and recA gene sequence analysis, and also from ANI, that strain OGS16\textsuperscript{T} is different from members of the genera Sneathia, Sebaldella and Leptotrichia and from the species Streptobacillus moniliformis, Streptobacillus hongkongensis, Streptobacillus felis and Streptobacillus notomytis.

Physiological results are considered as weak for the unequivocal discrimination of species of the genus Streptobacillus (Eisenberg et al., 2015c). The physiological characterization of strain OGS16\textsuperscript{T} is given in the species description and in Table 1. Biochemical profiling was carried out according to the manufacturer’s instructions using the commercial test systems VITEK2-compact with the NHI card and API ZYM (both from bioMérieux). VITEK NHI identified strain OGS16\textsuperscript{T} as Neisseria cinerea or Neisseria elongata (bioprofile 022200000 or 027300000) and Streptobacillus moniliformis DSM 12112\textsuperscript{T}, Streptobacillus hongkongensis DSM 26322\textsuperscript{T} and Streptobacillus felis 131000547\textsuperscript{T} as Neisseria cinerea with 98 % (023200000), 93 % (022300000) and 99 % (022200000) confidence and Streptobacillus notomytis AHL 370-1\textsuperscript{T} as Neisseria elongata (bioprofile 023300000). Physiological characteristics alone did not possess sufficient discriminatory power to differentiate strain OGS16\textsuperscript{T} from Streptobacillus moniliformis DSM 12112\textsuperscript{T}, Streptobacillus hongkongensis DSM 26322\textsuperscript{T}, Streptobacillus felis 131000547\textsuperscript{T} and Streptobacillus notomytis AHL 370-1\textsuperscript{T}. In the absence of validated clinical breakpoints, antimicrobial susceptibility testing was limited to the assessment of the MIC as obtained by broth microdilution testing (Merlin Diagnostika, as described previously (Eisenberg et al., 2015c). Strain OGS16\textsuperscript{T} displayed MICs as follows (µg ml\textsuperscript{-1}): amoxicillin/clavulanic acid (<2/1), colistin (≥1), florfenicol (<1), trimethoprim/sulfamethoxazole (<0.25/4.75), tetracycline (≤0.125), cephalothin (<1), enrofloxacin (≥2), erythromycin (≥1), penicillin G (<0.0625), tiamulin (<8), tilmicosin (<1), ceftiofur (≤0.25), gentamicin (≥0.5), spectinomycin (≥4), tularthromycin (<2) and ampicillin (≥0.25).

For matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF MS), strains incubated for 24 h were selected from SBA plates and subsequently transferred to steel targets using the direct transfer protocol according to the manufacturer’s instructions (MALDI Biotyper; Bruker Daltonics). Analysis was performed on a MALDI-TOF MS Biotyper version 3.3.1.0. The database used (DB 5627; Bruker Daltonics) included only one entry from Streptobacillus moniliformis DSM 12112\textsuperscript{T}. With this database alone, strain OGS16\textsuperscript{T} could not be identified, yielding score levels only between 1.3 and 1.5. Following the manual inclusion of spectra from strain OGS16\textsuperscript{T} as well as the type strains of other species of the genus Streptobacillus to the database, all species of Streptobacillus could be differentiated based on spectral differences. Furthermore, MALDI-TOF mass spectra of strain OGS16\textsuperscript{T} turned out to be most closely related to the database, all species of Streptobacillus could be differentiated based on spectral differences.

Table 1. Physiological characteristics of Streptobacillus ratti sp. nov. OGS16\textsuperscript{T} and strains of other species of the genus Streptobacillus

<table>
<thead>
<tr>
<th>Characteristic</th>
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<th>6</th>
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<tbody>
<tr>
<td>Haemolysis on SBA\textsuperscript{*}</td>
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<td>+</td>
<td>+</td>
<td>+</td>
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<td>+</td>
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<tr>
<td>Phosphatase (unspecified)\textsuperscript{b}</td>
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<td>–</td>
<td>+</td>
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<tr>
<td>Phenolalanine arylamidase\textsuperscript{b}</td>
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<tr>
<td>Ala-Phe-Pro arylamidase\textsuperscript{b}</td>
<td>+</td>
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<tr>
<td>Alkaline phosphatase\textsuperscript{c}</td>
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<td>w</td>
<td>v</td>
<td>+</td>
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<tr>
<td>Esterase (C4)\textsuperscript{c}</td>
<td>–</td>
<td>w</td>
<td>v</td>
<td>w</td>
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<tr>
<td>Esterase lipase (C8)\textsuperscript{c}</td>
<td>+</td>
<td>+</td>
<td>w/+</td>
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<tr>
<td>Leucine arylamidase\textsuperscript{c}</td>
<td>–</td>
<td>–</td>
<td>v</td>
<td>–</td>
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<tr>
<td>2-Chymotrypsin\textsuperscript{c}</td>
<td>+</td>
<td>w/+</td>
<td>w</td>
<td>–</td>
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<tr>
<td>Acid phosphatase\textsuperscript{c}</td>
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<tr>
<td>Naphthol-AS-BI-phosphohydrolase\textsuperscript{c}</td>
<td>–</td>
<td>–</td>
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<td>–</td>
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</table>

\textsuperscript{*}Results were obtained with: a, classical reactions; b, VITEK-compact with the NHI card; c, API ZYM [scores 0–5 indicate the intensity of enzymatic reactions (0–2; –; 3; w; 4–5; +)].
to those of *Streptobacillus notomytis* and *Streptobacillus moniliformis*. A dendrogram including selected main spectra peak (msp) lists of the family *Leptotrichiaceae* from the Bruker database as well as manual database entries for strain OGS16T, six further reference strains of *Streptobacillus moniliformis*, *Streptobacillus hongkongensis* DSM 26322T, *Streptobacillus felis* 131000547T, *Streptobacillus notomytis* ATCC 33386T is depicted in Fig. S5; it shows a separate position of spectra from strain OGS16T from those from other members of the genus *Streptobacillus*.

Fatty acid composition analysis followed Kämpfer & Kropfenstedt (1996) (Table 2). The major fatty acids C16:0, C18:0, C18:1 C9c and C18:2 (summed feature 5), as reported by Pins et al. (1996), Rowbotham (1983) and Rygg & Bruun (1992), could also be detected in our study, thereby confirming the affiliation of OGS16T to *Streptobacillus*.

The separate position of strain OGS16T as a member of a distinct species of *Streptobacillus* is well supported by the molecular differences obtained by ANI, phylogenetic analyses of established housekeeping genes (Figs 1 and S2–S4) and differences based on MALDI-TOF MS (Fig. S5). Its growth characteristics are in full agreement with those of other members of the genus. In particular, this includes the fastidious growth of strain OGS16T and its dependence on a capnophilic environment with 10% CO2 in the presence of blood or serum, its negative reactivity for cytochrome oxidase, catalase, nitrate and indole, the production of a cotton-ball-like appearance in liquid media, its inducible L-forms in addition to ‘normal’ small butyrous colonies, its Gram-negative, filamentous, rod-shaped cell morphology arranged in chains and clumps with irregular bulbar swellings, and its presumed broad antimicrobial susceptibilities (Table 1). These characteristics also justify the placement of strain OGS16T in the genus *Streptobacillus* and distinguish it from *Sneathia sanguinegens* and *Sneathia amnii* (Woo et al., 2014). In summary, genotypic and phenotypic differences prove that strain OGS16T represents a novel species different from *Streptobacillus moniliformis*, *Streptobacillus hongkongensis*, *Streptobacillus felis* and *Streptobacillus notomytis*, for which we propose the name *Streptobacillus ratti* sp. nov.

**Description of *Streptobacillus ratti* sp. nov.**

*Streptobacillus ratti* (rat’ti. L. gen. n. ratti of the rat).

Growth can be observed after 1–2 days at 37 °C and depends on a capnophilic atmosphere of 5–10% CO2 on SBA or TSA or in TSB with 20% horse serum, but only weak growth is observed on Schaedler and chocolate agar, and no growth is observed on Gassner or MacConkey agar. In an anaerobic environment, reduced growth can be observed. Colonies are tiny, dry, butyrous and slightly opaque, 0.1–0.4 mm in diameter. Colonies are initially non-haemolytic on SBA but, in aged cultures (> 10 days), a weak zone of χ-haemolysis can be observed. Conversion to L-phase or transitional phase variant may rarely occur spontaneously during cultivation. In liquid media, streptobacillary growth can be detected after 2–5 days as a typical ‘cotton ball’- or ‘bread crumb’-like appearance. Microscopic morphological features are indicative of Gram-negative, pleomorphic, fusiform to filamentous, non-spor-forming, non-encapsulated, non-acid-fast rods, 0.45 ± 0.1 µm wide and 0.83 ± 0.08 µm long, that are arranged in chains and clumps, also sometimes displaying irregular, lateral bulbar swellings. Positive for esterase lipase (C8) and χ-chymotrypsin. Negative for motility, acid and alkaline phosphatase, esterase (C4), lipase (C14), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, naphthol-AS-BI-phosphohydrolase χ-galactosidase, β-galactosidase, χ-glucosidase, β-glucosidase, β-glucuronidase, N-acetyl-β-glucosaminidase, χ-mannosidase, χ-fucosidase, cytochrome oxidase, catalase, nitrate reductase and indole production. The major fatty acids are C16:0 (palmitic acid), C18:0 (stearic acid) and C18:1 C9c (oleic acid).

The type strain, OGS16T (=JCM 31098T=DSM 101843T), was isolated from the oral cavity of an asymptomatic black rat (*Rattus rattus*). The G+C content of the DNA of the type strain is 25.9 mol% and the genome size is 1.50 Mbp.

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