Anaeromassilibacillus senegalensis gen. nov., sp. nov., isolated from the gut of a child with kwashiorkor

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Abstract

We report the main characteristics of *Anaeromassilibacillus senegalensis* strain mt9^T (= CSUR P1511) isolated from the stool of a 1-year-old kwashiorkor patient from Senegal.

Keywords: *Anaeromassilibacillus senegalensis*, culturomics, genomics, taxonogenomics, taxonomy
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Using culturomics [1], a culture-based technique that aims to characterize the microbial diversity of stool samples collected from patients with kwashiorkor, we report the isolation in January 2015 of the strain mt9^T from the stool specimen of a 1-year-old Senegalese kwashiorkor patient. The patient's parents provided signed informed consent, and the agreements of the National Ethics Committee of Senegal and the local ethics committee of the IFR48 (Marseille, France) were obtained under numbers 11-017 and 09-022, respectively. Using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF) (http://www.mediterranee-infection.com/article.php?laref=256&titre=urms-database) analysis on a MicroFlex spectrometer (Bruker Daltonics, Leipzig, Germany), we were not able to obtain an identification score of >1.9, which would have allowed a correct identification for this strain [2]. The isolate of the strain mt9^T was obtained by anaerobic culture at 37°C on a 5% sheep's blood–enriched Columbia agar (COS) (bioMérieux, Marcy l'Etoile, France) after a thermic shock and 15-day preincubation in a blood culture bottle. The pure culture of this bacterium grew anaerobically after 72-hour incubation at 37°C. Strain mt9^T was catalase and oxidase negative. Colonies grown on COS medium were white, opaque and 1 to 2 mm in diameter. Bacterial cells were Gram-negative, motile, spore-forming, rod-shaped bacilli with a length of 2.4 µm and a diameter of 0.9 µm. The 16S rRNA gene was sequenced using the fD1–rP2 primers as previously described [3], using a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France). Strain mt9^T exhibited 93.6% sequence similarity with *Clostridium leptum* DSM 753 (GenBank accession no. NR114789), the phylogenetically closest valid species with standing in nomenclature (Fig. 1), which putatively classifies it as a member of a new genus within the family Clostridiaceae in the Firmicutes phylum [4]. In contrast with *C. leptum,* described in 1973 [5] as a Gram-positive bacterium, strain mt9^T is Gram negative.

Because the strain mt9^T exhibited a 16S rRNA sequence divergence of >5% with its phylogenetically closest validated species [6], we propose the creation of the new genus *Anaeromassilibacillus* gen. nov. with the strain mt9^T as the type strain of *Anaeromassilibacillus senegalensis* gen. nov., sp. nov., as the first cultivated representative of this new genera.

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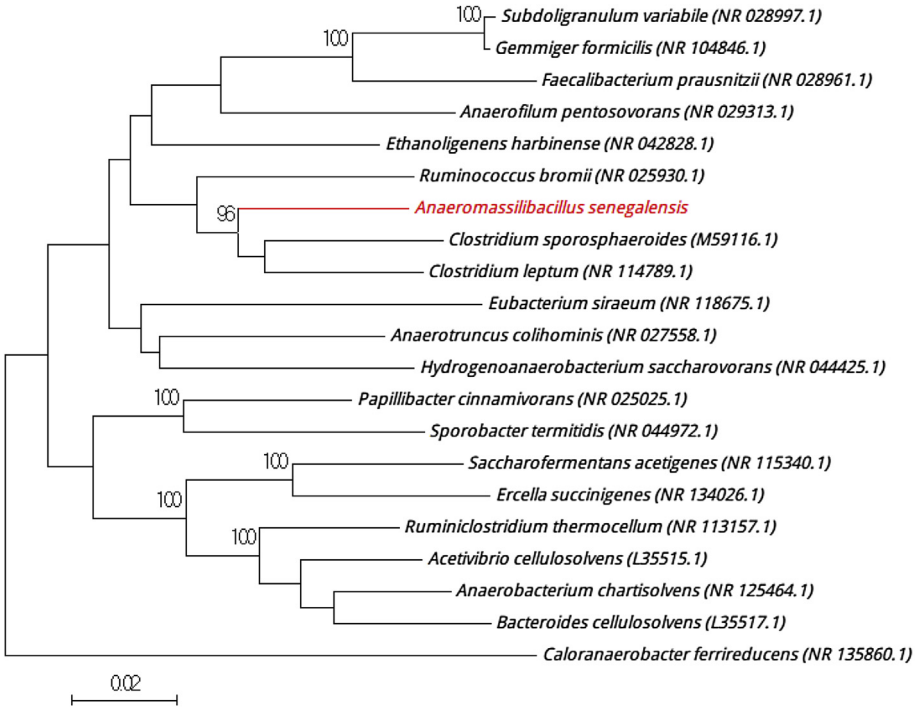

FIG. 1. Phylogenetic tree showing position of *Anaeromassilibacillus senegalensis* strain mt9^T relative to other phylogenetically close members of family Clostridiaceae. GenBank accession numbers are indicated in parentheses. Sequences were aligned using CLUSTALW, and phylogenetic inferences were obtained using maximum-likelihood method within MEGA software. Numbers at nodes are percentages of bootstrap values (≥95%) obtained by repeating analysis 500 times to generate majority consensus tree. Scale bar = 2% nucleotide sequence divergence.

Nucleotide sequence accession number

The 16S rRNA gene sequence was deposited in GenBank under accession number LN866991.

Deposit in a culture collection

Strain mt9^T was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under accession number P1511.

Conflict of Interest

None declared.

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