

## NEW SPECIES

# '*Lachnoclostridium massilosenegalense*', a new bacterial species isolated from the human gut microbiota

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## Abstract

We report the main characteristics of '*Lachnoclostridium massilosenegalense*' strain mt23<sup>T</sup> (=CSUR P299 =DSM 102084), a new bacterial species isolated from the gut microbiota of a healthy young girl from Senegal.

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As part of the 'culturomics' exploration of the gut microbiota [1,2], a stool sample was collected from a 38-month-old healthy girl from Senegal. Her weight-for-height z-score was -0.12. Oral consent was obtained from the parents, and the ethics committee of the Institut Federatif de Recherche IFR48 validated this study. After a 7-day anaerobic pre-incubation of the stool sample in a marine broth and seeding on 5% sheep-blood-enriched Colombia agar (bioMérieux, La Balme-les-Grottes, France), strain mt23<sup>T</sup> was isolated in October 2015. Colonies were translucent with a mean diameter of 2 mm on 5% sheep-blood-enriched Colombia agar. Cells were Gram-positive rods and showed a mean length of 2.5 µm and a mean diameter of 0.5 µm on electron microscopy. Strain mt23<sup>T</sup> was catalase and oxidase negative. Routine identification of colonies was carried out using matrix-assisted laser desorption-ionization time-of-flight mass spectrometry (MALDI-TOF MS) on a Microflex spectrometer (Bruker Daltonics, Bremen, Germany) [3,4], which failed to identify strain mt23<sup>T</sup>. Therefore, the 16S rRNA gene was sequenced with fD1-rP2 primers as previously

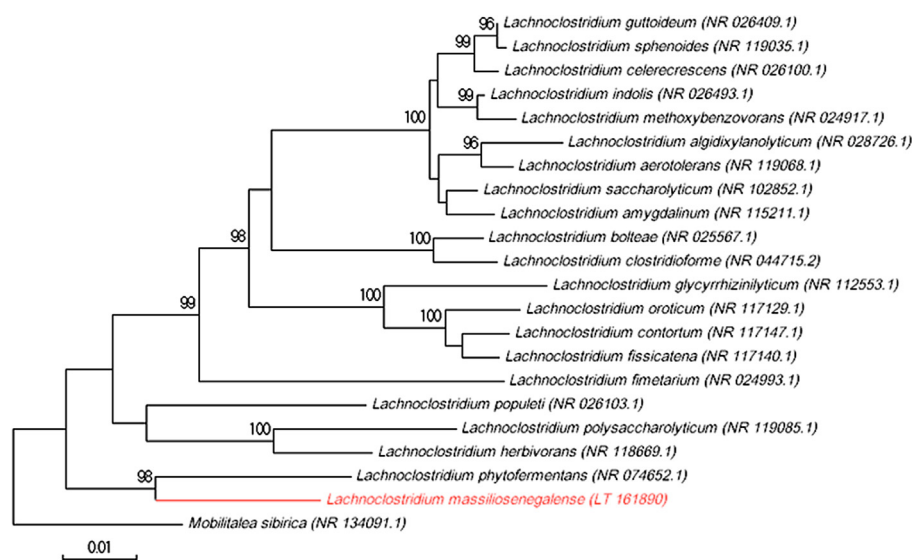
described [5] using a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France). The resulting sequence showed a 95.1% similarity with the 16S rRNA gene of *Lachnoclostridium phytofermentans* strain ISDg (GenBank Accession number NR\_074652.1), the phylogenetically closest species (Fig. 1) [6]. According to the 16S rRNA gene sequence similarity for species delineation of prokaryotes [7,8], strain mt23<sup>T</sup> is representative of a new species within the recently described *Lachnoclostridium* genus. We then propose the name of '*Lachnoclostridium massilosenegalense*' (mas.si.li.o.se.ne.gal.en'sis. L. gen. masc. n. *massilosenegalense* contraction of the Latin name of Marseille where strain mt23<sup>T</sup> was isolated and Senegal where the stool sample was collected) for which strain mt23 is the type strain.

**MALDI-TOF-MS spectrum.** The MALDI-TOF-MS spectrum of '*L. massilosenegalense*' is available at <http://www.mediterranee-infection.com/article.php?laref=256&titre=urms-database>.

**Nucleotide sequence accession number.** The 16S rRNA gene sequence was deposited in GenBank under Accession number LT161890.

**Deposit in a culture collection.** Strain mt23<sup>T</sup> was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under number P299 and in the Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (DSMZ) under number DSM 102084.

**FIG. 1.** Phylogenetic tree showing the position of '*Lachnoclostridium massilosenegalense*' sp. nov. strain mt23<sup>T</sup> relative to other phylogenetically close neighbours. Sequences were aligned using CLUSTALW, and phylogenetic inferences were obtained using the maximum-likelihood method within the MEGA software. Numbers at the nodes are percentages of bootstrap values (>95%) obtained by repeating the analysis 500 times to generate a majority consensus tree. *Mobilitea sibirica* was used as an outgroup. The scale bar indicates a 1% nucleotide sequence divergence.



## Conflict of interest

None to declare.

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