

“*Lachnoclostridium touaregense*,” a new bacterial species isolated from the human gut microbiota

M. Tidjani Alou, S. Khelaifia, B. La Scola and N. Cassir

Aix-Marseille Univ, URMITE, UM63, CNRS7278, IRD198, Inserm 1095, Institut Hospitalo-Universitaire Méditerranée-Infection, Faculté de médecine, Marseille, France

Abstract

We report the main characteristics of “*Lachnoclostridium touaregense*” strain Marseille-P2415^T (= CSUR P2415 = DSM 102219), a new bacterial species isolated from the gut microbiota of a healthy young girl from Niger.

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Corresponding author: N. Cassir, Aix-Marseille Univ, URMITE, UM63, CNRS7278, IRD198, Inserm 1095, Institut Hospitalo-Universitaire Méditerranée-Infection, Faculté de médecine, 27 Boulevard Jean Moulin, 13385, Marseille Cedex 05, France
E-mail: cassirmadim@gmail.com

Using the culturomics approach [1,2], strain Marseille-P2415^T was isolated in January 2016 from the stool sample of a 44-month-old healthy girl from Niger. Her weight-for-height z score was -0.65. This study was validated by the ethics committee of the Institut Fédératif de Recherche IFR48, and oral consent was obtained from the parents. We isolated strain Marseille-P2415^T through 30-day preincubation in anaerobic Colombia-like broth supplemented with sheep's blood and seeding on 5% sheep's blood-enriched Colombia agar (bioMérieux, Marcy L'Etoile, France) in anaerobic atmosphere. Strain Marseille-P2415^T forms on this medium a translucent biofilm formed by Gram-positive rods.

Cells have a mean diameter of 0.54 µm and a mean length of 3.35 µm. Oxidase and catalase activities were absent. Protein spectra were obtained for strain Marseille-P2415^T using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) on a Microflex spectrometer (Bruker Daltonics, Bremen, Germany) [3,4]. Because these spectra did not match any species in our database, 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 sequence obtained had a 97.9% similarity with the 16S rRNA gene of *Lachnoclostridium saccharolyticum* strain WMI (GenBank accession no. NR_102852.1), the closest species with a validly published name (Fig. 1). According to the 16S rRNA gene sequence similarity for species delineation of prokaryotes [6,7], we propose that strain AT5^T is representative of a new species within the recently described *Lachnoclostridium* genus [8], for which we propose the name *Lachnoclostridium touaregense* (twa.reg'ense, N.L. *touaregense*, “of Touareg,” because the stool sample was isolated from a young Touareg girl from Niger).

MALDI-TOF MS spectrum

The MALDI-TOF MS spectrum of “*Lachnoclostridium touaregense*” 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 LT161895.

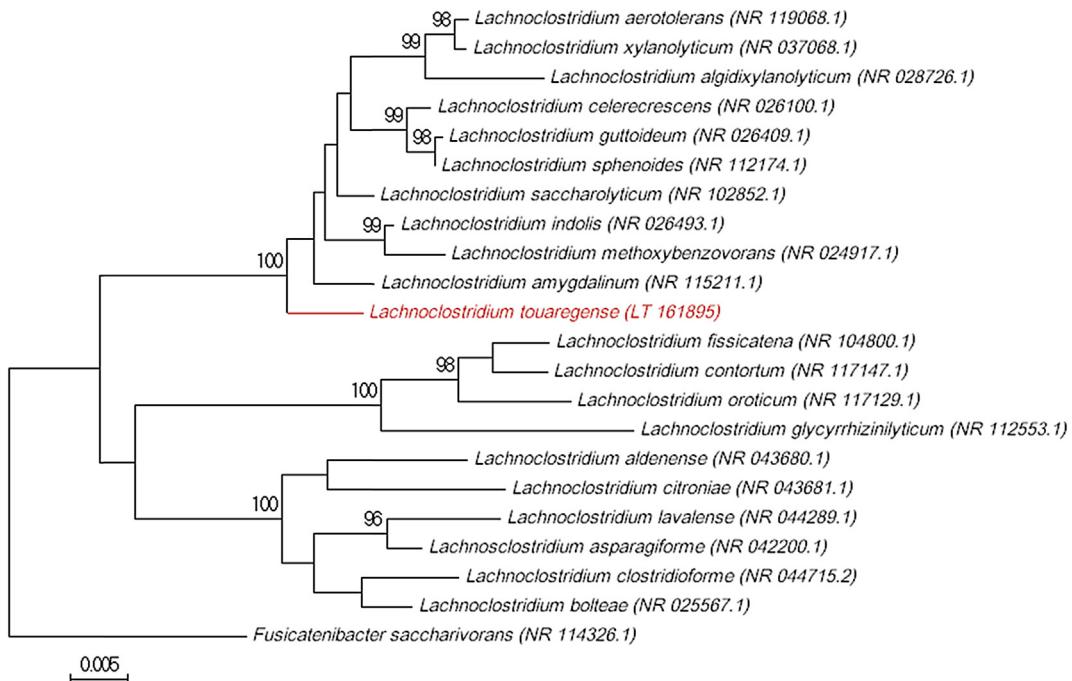


FIG. 1. Phylogenetic tree showing position of *Lachnoclostridium touaregense* sp. nov. strain Marseille-P2415^T relative to other phylogenetically close neighbors. Sequences were aligned using CLUSTALW, and phylogenetic inferences obtained using maximum-likelihood method within MEGA software. Numbers at nodes are percentages of bootstrap values (>95%) obtained by repeating analysis 500 times to generate majority consensus tree. *Fusicatenibacter saccharivorans* was used as outgroup. Scale bar indicates 5% nucleotide sequence divergence.

Deposit in a culture collection

Strain Marseille-P2415^T was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under number P2415 and in the Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (DSMZ) under number DSM 102219.

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Conflict of Interest

None declared.

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