

NEW SPECIES

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

T. Amadou, M. Hosny, B. La Scola and N. Cassir

Unité de Recherche sur les Maladies Infectieuses et Tropicales Emergentes (URMITE), UM63 CNRS 7278 IRD 198 INSERM U1095, IHU Méditerranée Infection, Pôle des Maladies Infectieuses, Assistance Publique-Hôpitaux de Marseille, Faculté de Médecine, Marseille, France

Abstract

We report the main characteristics of “*Lachnoclostridium bouchesdurhonense*” strain AT5^T (=CSUR P2181), a new bacterial species isolated from the gut microbiota of an obese patient from Marseille.

© 2016 The Author(s). Published by Elsevier Ltd on behalf of European Society of Clinical Microbiology and Infectious Diseases.

Keywords: Culturomics, gut microbiota, “*Lachnoclostridium bouchesdurhonense*”, obese, taxonogenomics

Original Submission: 24 June 2016; **Revised Submission:** 29 June 2016; **Accepted:** 29 June 2016

Article published online: 5 July 2016

Corresponding author: N. Cassir, Unité de Recherche sur les Maladies Infectieuses et Tropicales Emergentes (URMITE), UM63 CNRS 7278 IRD 198 INSERM U1095, IHU Méditerranée Infection, Pôle des Maladies Infectieuses, Assistance Publique-Hôpitaux de Marseille, Faculté de Médecine, 27 Bd Jean 9 Moulin, 13005 Marseille, France
E-mail: cassirnadim@gmail.com

In order to describe the bacterial flora of the gastrointestinal tract, a stool sample was collected from a 38-year-old obese patient from France. The patient, who provided informed oral consent, had a body mass index of 33 kg/m². The study was approved by the ethics committee of the Institut Fédératif de Recherche 48, Marseille. The stool was cultivated using the culturomics approach [1,2]. The culture of strain AT5^T was achieved on 5% sheep’s blood–enriched Columbia agar (bio-Mérieux, Marcy l’Etoile, France). The colonies obtained were small, circular and smooth, with a mean diameter of 0.5 mm. Bacterial cells were Gram negative and rod shaped. Strain AT5^T did not exhibit catalase and oxidase activities.

Colonies were not identified by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) using a Microflex spectrometer (Bruker Daltonics, Bremen, Germany) [3,4]. Therefore, we sequenced the 16S rRNA gene of strain AT5^T using the fD1-rP2 primers as

previously described [5] and a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France). The obtained sequence was 94.79% similar to the 16S rRNA gene sequence of *Lachnoclostridium boltea* strain 16351 (GenBank accession number NR_025567) (Figure 1) [6]. According to the 16S rRNA gene sequence similarity for species demarcation of prokaryotes [7,8], we propose that strain AT5^T is representative of a new species within the recently described *Lachnoclostridium* genus [9] for which we propose the name “*Lachnoclostridium bouchesdurhonense*” sp. nov. (bouch.du.rhon.ense, L. fem. adj. *bouchedurhonense*, for Bouches-du-Rhône, the department where the city of Marseille is located, where strain AT5^T was isolated).

MALDI-TOF MS spectrum

The MALDI-TOF MS spectrum of “*Lachnoclostridium bouchesdurhonense*” is available online (<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 LN881614.

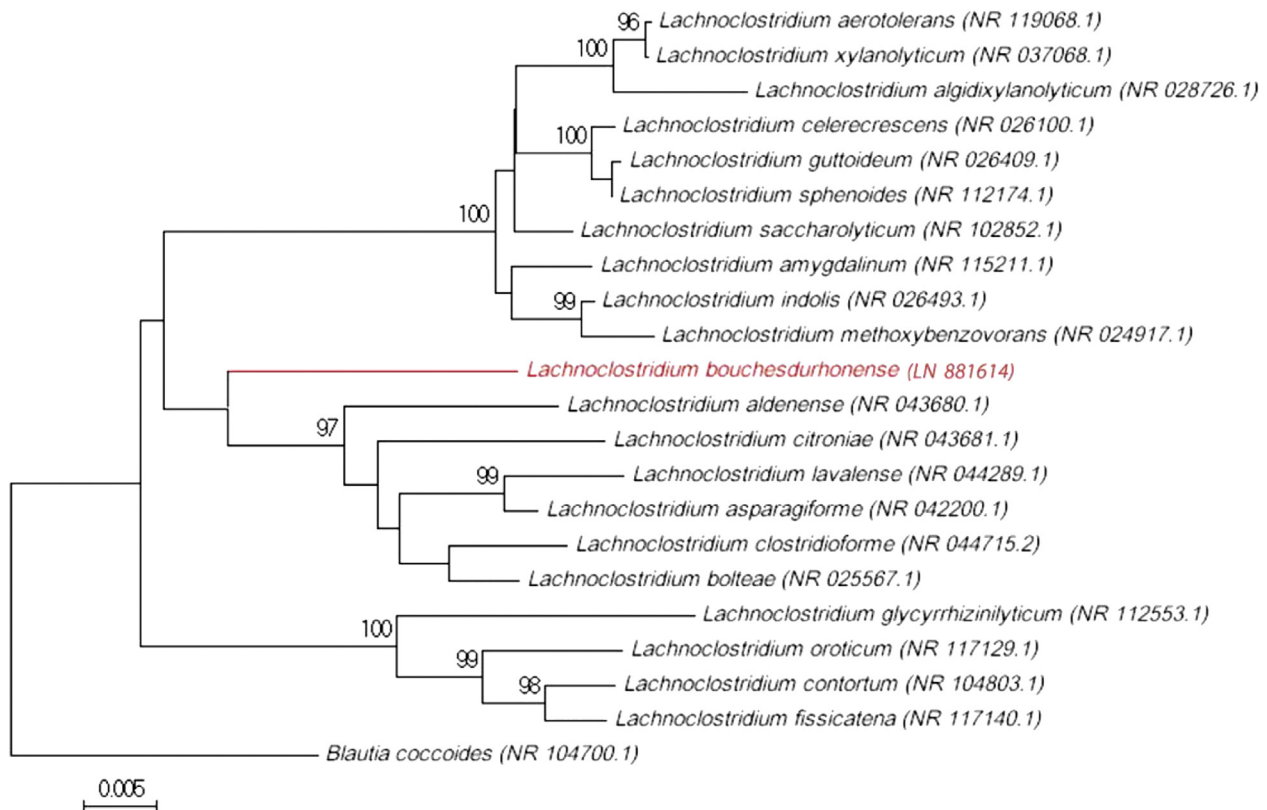


FIG. 1. Phylogenetic tree showing position of “*Lachnoclostridium bouchesdurhonense*” strain AT5^T relative to other phylogenetically close species with validly published name. Sequences were aligned using CLUSTALW, and phylogenetic inferences were obtained using maximum-likelihood method within MEGA software. Numbers at nodes are percentages of bootstrap values (>95%) obtained by repeating analysis 500 times to generate majority consensus tree. *Blautia coccoides* was used as outgroup. Scale bar indicates 5% nucleotide sequence divergence.

Deposit in a culture collection

Strain AT5^T was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR) under number P2181.

Acknowledgement

This study was funded by the Fondation Méditerranée Infection.

Conflict of Interest

None declared.

References

- [1] Lagier JC, Armougom F, Million M, Hugon P, Pagnier I, Robert C, et al. Microbial culturomics: paradigm shift in the human gut microbiome study. *Clin Microbiol Infect* 2012;18:1185–93.
- [2] Lagier JC, Hugon P, Khelaifa S, Fournier PE, La Scola B, Raoult D. The rebirth of culture in microbiology through the example of culturomics to study human gut microbiota. *Clin Microbiol Rev* 2015;28:237–64.
- [3] Seng P, Drancourt M, Gouriet F, La Scola B, Fournier PE, Rolain JM, et al. Ongoing revolution in bacteriology: routine identification of bacteria by matrix-assisted laser desorption ionization time-of-flight mass spectrometry. *Clin Infect Dis* 2009;49:543–51.
- [4] Seng P, Abat C, Rolain JM, Colson P, Lagier JC, Gouriet F, et al. Identification of rare pathogenic bacteria in a clinical microbiology laboratory: impact of matrix-assisted laser desorption ionization–time of flight mass spectrometry. *J Clin Microbiol* 2013;51:2182–94.
- [5] Drancourt M, Bollet C, Carlioz A, Martelin R, Gayral JP, Raoult D. 16S ribosomal DNA sequence analysis of a large collection of environmental and clinical unidentifiable bacterial isolates. *J Clin Microbiol* 2000;38:3623–30.
- [6] Moore WEC, Johnson JL, Holdeman LV. Emendation of *Bacteroidaceae* and *Butyrivibrio* and descriptions of *Desulfomonas* gen. nov. and ten new species in the genera *Desulfomonas*, *Butyrivibrio*, *Eubacterium*, *Clostridium*, and *Ruminococcus*. *Int J Syst Evol Microbiol* 1976;26:238–52.
- [7] Stackebrandt E, Ebers J. Taxonomic parameters revisited: tarnished gold standards. *Microbiol Today* 2006;33:152.
- [8] Kim M, Oh HS, Park SC, Chun J. Towards a taxonomic coherence between average nucleotide identity and 16S rRNA gene sequence similarity for species demarcation of prokaryotes. *Int J Syst Evol Microbiol* 2014;64:346–51.
- [9] Yutin N, Galperin MY. A genomic update on clostridial phylogeny: gram-negative spore formers and other misplaced clostridia. *Environ Microbiol* 2013;15:2631–41.