



'Clostridium massiliodielmoense', a new species isolated from the human gut microbiota

Maryam Tidjani Alou, Cheikh Sokhna, Fadi Bittar, Saber Khelaifia,
Pierre-Edouard Fournier, Didier Raoult

► To cite this version:

Maryam Tidjani Alou, Cheikh Sokhna, Fadi Bittar, Saber Khelaifia, Pierre-Edouard Fournier, et al.. 'Clostridium massiliodielmoense', a new species isolated from the human gut microbiota. *New Microbes and New Infections*, 2016, 13, pp.27 - 28. 10.1016/j_nmni.2016.05.014 . hal-01478544

HAL Id: hal-01478544

<https://amu.hal.science/hal-01478544v1>

Submitted on 26 Aug 2024

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution - NonCommercial - NoDerivatives 4.0 International License

'*Clostridium massiliodielmoense*', a new species isolated from the human gut microbiota

Maryam Tidjani Alou ^{1,2,3}, Cheikh Sokhna ², Fadi Bittar ^{1,2,3}, Saber Khelaifia ^{1,2,3}, Pierre-Edouard Fournier ^{1,2,3} and Didier Raoult ^{1,2,3,4}

1) Aix-Marseille Université, URMITE, UM63, CNRS7278, IRD198, Inserm 1095, Institut Hospitalo-Universitaire Méditerranée-Infection, Faculté de médecine, 2) Unité de Recherche sur les Maladies Infectieuses et Tropicales Emergentes IRD 198, CNRS 7278, Aix-Marseille Université, Marseille, France, 3) Campus Commun UCAD-IRD of Hann, Dakar, Senegal and 4) Special Infectious Agents Unit, King Fahd Medical Research Centre, King Abdulaziz University, Jeddah, Saudi Arabia

Abstract

Herein, we report the main characteristics of '*Clostridium massiliodielmoense*' strain mt26 (= CSUR P2255), representative of a new species isolated from the gastrointestinal tract of a healthy 28-month-old Senegalese boy.

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

Keywords: '*Clostridium massiliodielmoense*', culturomics, gut microbiota, taxono-genomics

Original Submission: 11 May 2016; **Revised Submission:** 20 May 2016; **Accepted:** 23 May 2016

Article published online: 2 June 2016

Corresponding author: P.-E. Fournier, Unité de Recherche sur les Maladies Infectieuses et Tropicales Emergentes, UM 63, CNRS7278, IRD198, Inserm1095, Aix-Marseille Université, Marseille, France
E-mail: pierre-edouard.fournier@univ-amu.fr

The culturomics approach is the method of choice to explore as exhaustively as possible the viable population of a microbial ecosystem [1,2]. We used culturomics to study the stool sample of a healthy 28-month-old Senegalese boy with a weight-for-height z-score of -0.99. Oral informed consent was given by the boy's parents and the study was approved by the ethics committee of the Institut Federatif de Recherche IFR48 under number 09-022. Primo-culture of strain mt26 was performed after a 7-day pre-incubation of the stool filtered on a 5-μm filter in an anaerobic blood-culture bottle supplemented with 5% sterile sheep blood. Subculture was performed on 5% sheep blood-enriched Columbia agar (bioMérieux, Marcy-l'Etoile, France) at 37°C in anaerobic atmosphere. Strain mt26 formed a translucent biofilm covering the Petri dish. Cells were Gram-positive, rod-shaped and had mean diameter and length of 0.54 and 2.11 μm, respectively. Strain mt26 exhibited catalase and oxidase

activities. Our routine identification method, matrix-assisted laser desorption-ionization time-of-flight mass spectrometry (MALDI-TOF-MS) using a Microflex spectrometer (Bruker Daltonics, Bremen, Germany) [3,4], failed to identify strain mt26 at the species level. Following 16S rRNA gene amplification and sequencing using the fD1-rP2 primers, as previously described [5], and using a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France), strain mt26 was 98.4% similar to *Clostridium novyi* strain ATCC 17861 [6] (GenBank Accession number AB045606), the phylogenetically closest species with a validly published name (Fig. 1). *Clostridium novyi* strains have previously been isolated in soil, marine sediments and in animal and human wounds, and sometimes grow forming a biofilm covering the plate [7]. As the 16S rRNA gene similarity level was lower than the 98.65% threshold to define a new species [8,9], we propose the creation of a new species within the genus *Clostridium* that we named '*Clostridium massiliodielmoense*' (mas.si.li.o.di.el.mo.en'se, L. neutr. adj., a combination of *massilio*, of Massilia, the Roman name of Marseille, where strain mt26 was isolated, and *dielmoense*, of Dielmo, the Senegalese village where the boy from whom the strain was cultivated lived). Strain mt26^T is the type strain of '*C. massiliodielmoense*' sp. nov.

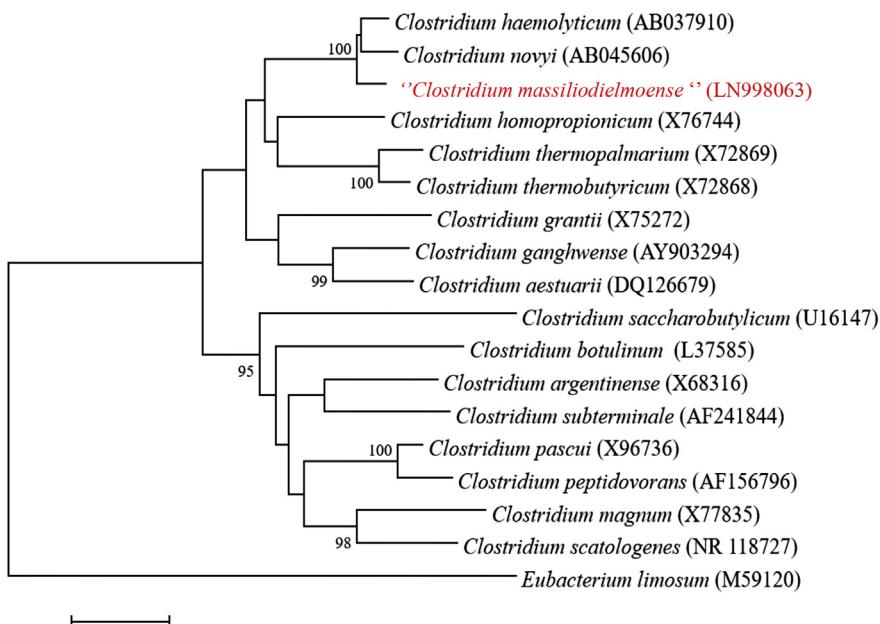


FIG. 1. Phylogenetic tree showing the position of '*Clostridium massilioidelmoense*' strain mt26^T relative to phylogenetically close species with standing in nomenclature. Sequences were aligned using CLUSTALW, and phylogenetic inferences were obtained using the maximum-likelihood method within the MEGA software. Numbers at the nodes are percentages of bootstrap values obtained by repeating the analysis 500 times to generate a majority consensus tree. Only bootstraps values >95% were displayed. *Eubacterium limosum* was used as an outgroup. The scale bar indicates a 2% nucleotide sequence.

MALDI-TOF-MS Spectrum

The MALDI-TOF-MS spectrum of '*C. massilioidelmoens*' 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 LN998063.

Deposit in a Culture Collection

Strain mt26^T was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under number P2255.

Conflicts of Interest

The authors certify that they have no conflict of interest in relation to this research.

Funding

This work was funded by Méditerranée-Infection Foundation.

References

- [1] Lagier J-C, 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 J-C, Hugon P, Khelaifia S, Fournier P-E, 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 P-E, 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 J-C, 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] Sasaki Y, Takikawa N, Kojima A, Norimatsu M, Suzuki S, Tamura Y. Phylogenetic positions of *Clostridium novyi* and *Clostridium haemolyticum* based on 16S rDNA sequences. *Int J Syst Evol Microbiol* 2001;51:901–4.
- [7] Whitman WB, editor. *Systematic Bacteriology*. New York, NY: Springer New York; 2009.
- [8] Stackebrandt E, Ebers J. Taxonomic parameters revisited: tarnished gold standards. *Microbiol Today* 2006;33:152.
- [9] Kim M, Oh H-S, Park S-C, 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.