

”Collinsella bouchesdurhonensis” sp. nov., identified in human stool sample

M. Bilen, F. Cadoret, Z. Daoud, Pierre-Edouard Fournier, Didier Raoult

► **To cite this version:**

M. Bilen, F. Cadoret, Z. Daoud, Pierre-Edouard Fournier, Didier Raoult. ”Collinsella bouchesdurhonensis” sp. nov., identified in human stool sample. *New Microbes and New Infections*, Wiley Online Library 2017, 17, pp.39–40. 10.1016/j.nmni.2016.11.004 . hal-01795974

HAL Id: hal-01795974

<https://hal-amu.archives-ouvertes.fr/hal-01795974>

Submitted on 27 Mar 2019

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.



“*Collinsella bouchesdurhonensis*” sp. nov., identified in human stool sample

M. Bilen¹, F. Cadoret¹, Z. Daoud², P.-E. Fournier¹ and D. Raoult¹

¹ Aix-Marseille Université, URMITE, UM63, CNRS7278, IRD198, Inserm 1095, Institut Hospitalo-Universitaire Méditerranée-Infection, Faculté de médecine, Marseille, France and ² Clinical Microbiology Department, Faculty of Medicine and Medical Sciences, University of Balamand, Amioun, Lebanon

Abstract

We report the main characteristics of “*Collinsella bouchesdurhonensis*” strain Marseille-P3296, which was isolated from a stool sample of a healthy 50-year-old pygmy (Baka) woman.

© 2016 The Authors. Published by Elsevier Ltd on behalf of European Society of Clinical Microbiology and Infectious Diseases.

Keywords: “*Collinsella bouchesdurhonensis*”, culturomics, emerging bacteria, gut microbiota, human microbiota

Original Submission: 20 October 2016; **Revised Submission:** 3 November 2016; **Accepted:** 9 November 2016

Article published online: 15 November 2016

Corresponding author: D. Raoult, Aix-Marseille Université, 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: didier.raoult@gmail.com

We obtained approval for the study from the ethics committee of the Institut Fédératif de Recherches 48 (no. 09-022) before we initiated the project. Samples were collected in Congo for analysis as part of the project describing the human microbiome by culturomics [1].

First, a stool sample from a 50-year-old pygmy (Baka) woman was diluted with 1 mL phosphate-buffered saline and incubated in a blood culture bottle containing an extra 5 mL of filtered rumen and sheep’s blood. The culture bottle was incubated at 37°C for 30 days under anaerobic conditions. At day 10, a “*Collinsella bouchesdurhonensis*” colony was isolated on 5% sheep’s blood–enriched Columbia agar (bioMérieux, Marcy l’Étoile, France). Strain Marseille-P3296 identification by matrix-assisted desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) using a Microflex spectrometer (Bruker Daltonics, Leipzig, Germany) failed [2]. Then, 16S rRNA gene sequencing was performed for further analysis using a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France) with fDI-rP2 primers (Eurogentec, Seraing, Belgium) as previously described [3]. Strain Marseille-P3296 exhibited a 96.19% sequence identity with *Collinsella aerofaciens* type strain JCM

10188 (AB 011816), the phylogenetically closest species with standing in nomenclature (Fig. 1). Thus, strain Marseille-P3296 can be classified as a new species within *Collinsella* genus [4].

Because the 16S rRNA gene sequence of strain Marseille-P3296 diverges by more than 1.3% from the 16S rRNA gene sequence of its phylogenetically closest species with standing in nomenclature [5], we suggest the discovery of the new species “*Collinsella bouchesdurhonensis*” (*bou.ches.du.rho.nen’sis*, N.L. fem. adj. *bouchesdurhonensis*, pertaining to Bouches du Rhône, the name of the French territory where strain Marseille-P3296 was isolated). Strain Marseille-P3296 is the type strain of the new species “*Collinsella bouchesdurhonensis*.” Colonies were smooth with a mean diameter of 0.1 to 0.5 mm. Bacterial cells were Gram-positive bacilli, were catalase and oxidase negative and had a mean diameter of 2.6 µm.

MALDI-TOF MS spectrum accession number

The MALDI-TOF MS spectrum of “*C. bouchesdurhonensis*” 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 LT623900.

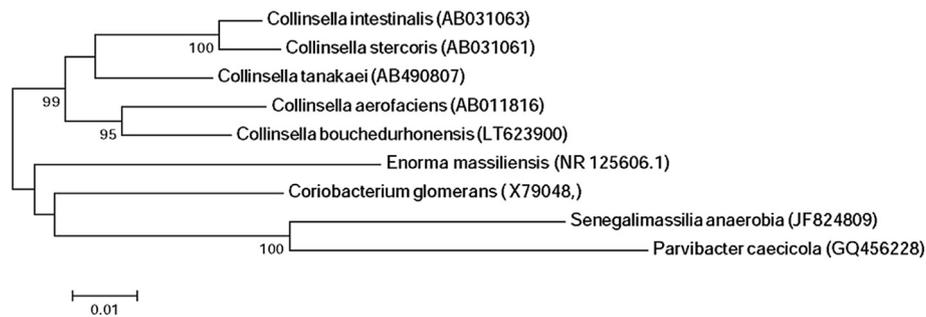


FIG. 1. Phylogenetic tree showing branching of “*Collinsella bouchedurhonensis*” strain Marseille-P3296 among other phylogenetically close neighbours. Sequence alignment was performed by CLUSTALW tool; then MEGA software was used for phylogenetic tree generation by neighbour-joining method. Five hundred bootstraps were performed; scores of at least 90% are shown on nodes. Scale bar indicates 2% nucleotide sequence divergence.

Deposit in a culture collection

Strain Marseille-P3296 was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under number P3296.

Acknowledgement

This study was funded by the Fondation Méditerranée Infection.

Conflict of Interest

None declared.

References

- [1] 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.
- [2] 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.
- [3] 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.
- [4] Sakamoto M, Benno Y. Reclassification of *Bacteroides distasonis*, *Bacteroides goldsteinii* and *Bacteroides merdae* as *Parabacteroides distasonis* gen. nov., comb. nov., *Parabacteroides goldsteinii* comb. nov. and *Parabacteroides merdae* comb. nov. *Int J Syst Evol Microbiol* 2006;56:1599–605.
- [5] 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.