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

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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.

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

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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'Etoile, 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.

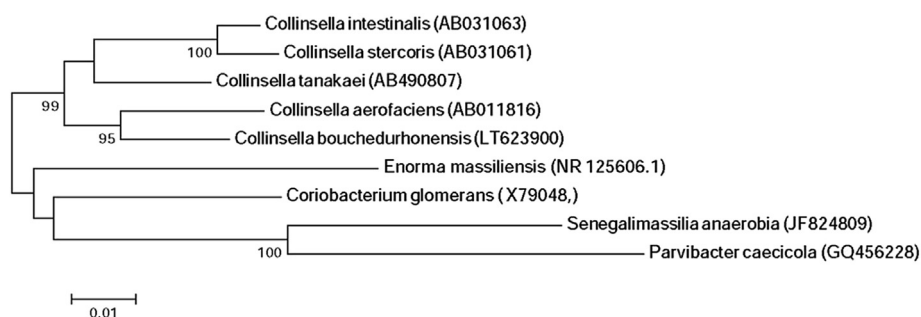


FIG. 1. Phylogenetic tree showing branching of “*Collinsella bouchesdurhonensis*” strain Marseille-P3296 among other phylogenetically close neighbours. Sequence alignment was performed by CLUSTALW tool; then MEGA software was used for phylogenetic tree generation by neighbour-joining method. Five hundred 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.

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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.