

'*Colibacter massiliensis*' gen. nov., sp. nov., a new bacterial species isolated from human left colon

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Abstract

We present here the main characteristics of the strain Marseille-P2911 (= CSUR P2911 = DSMZ 103304), a bacterial species isolated from the left colon liquid sample of a 60-year-old man.

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Culturomics is a new approach to study the human microbiome, especially the gut microbiota, in addition to the metagenomics approach [1]. Using various culture conditions, culturomics allows isolation of new bacterial species. By applying this method to staggered samples from the digestive tract, we isolated the strain Marseille-P2911 from the left colon liquid sample of a 60-year-old man who underwent a colonoscopy for an aetiological investigation of iron-deficiency anaemia. The patient provided signed informed consent, and the study was approved by the ethics committee of the Institut Fédératif de Recherche IFR48 under number 2016-010.

In March 2016, strain Marseille-P2911 was first isolated after a 3-day preincubation in an anaerobic blood culture bottle (VersaTREK REDOX 2, Thermo Scientific, Villebon sur Yvette, France) supplemented with 5 mL of a 0.2 µm filtered rumen. This enriched liquid medium was then inoculated on Columbia agar enriched with 5% sheep's blood (COS, bio-Mérieux, Marcy l'Etoile, France), followed by an incubation at 37°C in an anaerobic atmosphere (AnaeroGen Compact, Oxoid, Thermo Scientific, Dardilly, France). After 2 days of growth, translucent microcolonies with a diameter of 0.1 mm

were observed. Cells were Gram-positive diplococci with a length varying from 1000 to 1400 nm and a width varying from 400 to 600 nm. Strain Marseille-P2911 did not exhibit catalase or oxidase activities.

Routine identification by matrix-assisted desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) (Microflex; Bruker Daltonics, Bremen, Germany) [2] was not able to identify strain Marseille-P2911, so the 16S rRNA gene was sequenced using fD1-rP2 primers as previously described [3] using a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France). Strain Marseille-P2911 exhibited a 93.9% sequence identity with *Megasphaera cerevisiae* type strain ATCC 43254^T (accession no. L37040), the phylogenetically closest species with standing in nomenclature [4] (Fig. 1), which was isolated for the first time in 1985 from spoiled bottled beer [5].

Because of a 16S rRNA gene sequence similarity of <95% [6] with its phylogenetically closest species with standing in nomenclature [7], we suggest the creation of a new genus named '*Colibacter*' gen. nov. (Co.li.bac'ter, N.L. masc. n. colon, the organ from which the strain was first isolated). '*Colibacter massiliensis*' gen. nov., sp. nov. (mas.si.li.en'sis; L. fem. adj. *massiliensis*, for Massilia, the Roman name of Marseille, the place where the strain was first isolated), is classified as a member of the *Veillonellaceae* family and the *Firmicutes* phylum. Strain Marseille-P2911^T is the type strain of the new species '*Colibacter massiliensis*' gen. nov., sp. nov.

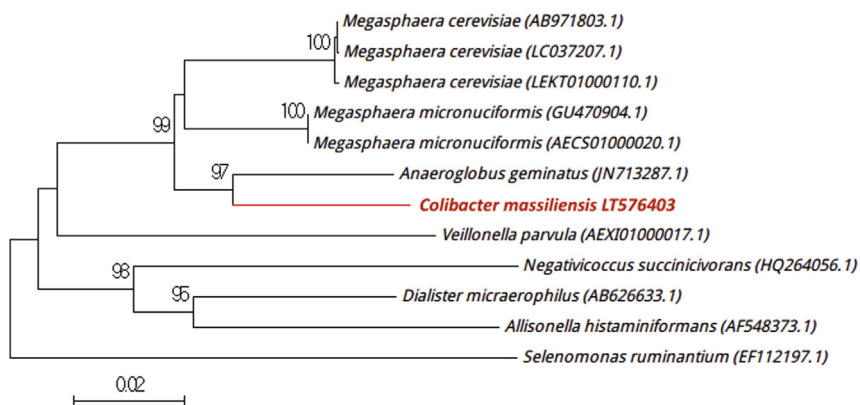


FIG. 1. Phylogenetic tree showing position of ‘*Colibacter massiliensis*’ strain Marseille-P2911^T relative to other phylogenetically close neighbours. Sequences were aligned using Muscle v3.8.31 with default parameters, and phylogenetic inferences were obtained using neighbour-joining method with 1000 bootstrap replicates within MEGA6 software. Only bootstrap values >95% are shown. Scale bar represents 2% nucleotide sequence divergence.

MALDI-TOF MS spectrum

The MALDI-TOF MS spectrum of ‘*Colibacter massiliensis*’ strain Marseille-P2911^T 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 LT576403.

Deposit in a culture collection

Strain Marseille-P2911^T was deposited in the Collection de Souches de l’Unité des Rickettsies (CSUR, WDCM 875) under the number P2911 and in the Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ) under the number DSM 103304.

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Conflict of Interest

None declared.

References

- [1] Lagier JC, Khelaifia S, Tidjani Alou M, Ndongo S, Dione N, Hugon P, et al. Culture of previously uncultured members of the human gut microbiota by culturomics. *Nat Microbiol* 2016 [In press].
- [2] 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.
- [3] Drancourt M, Bollet C, Carlouz 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] 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(Pt 2):346–51.
- [5] Engelmann U, Weiss N. *Megasphaera cerevisiae* sp. nov.: a new Gram-negative obligately anaerobic coccus isolated from spoiled beer. *Syst Appl Microbiol* 1985;6:287–90.
- [6] Huson DH, Auch AF, Qi J, Schuster SC. MEGAN analysis of metagenomic data. *Genome Res* 2007;17:377–86.
- [7] Stackebrandt E, Frederiksen W, Garrity GM, Grimont PAD, Kämpfer P, Maiden MCJ, et al. Report of the Ad Hoc Committee for the Re-evaluation of the Species Definition in Bacteriology. *Int J Syst Evol Microbiol* 2002;52(Pt 3):1043–7.