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## '*Traorella massiliensis*' gen. nov., sp. nov., a new bacterial species isolated from the left colon of a 76-year-old woman

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### Abstract

We present here the summary of main characteristics of '*Traorella massiliensis*' strain Marseille-P3110<sup>T</sup>, which was isolated from a left colon liquid sample of a 76-year-old woman.

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**Keywords:** Culturomics, gut microbiota, new species, taxonogenomics, *Traorella massiliensis*

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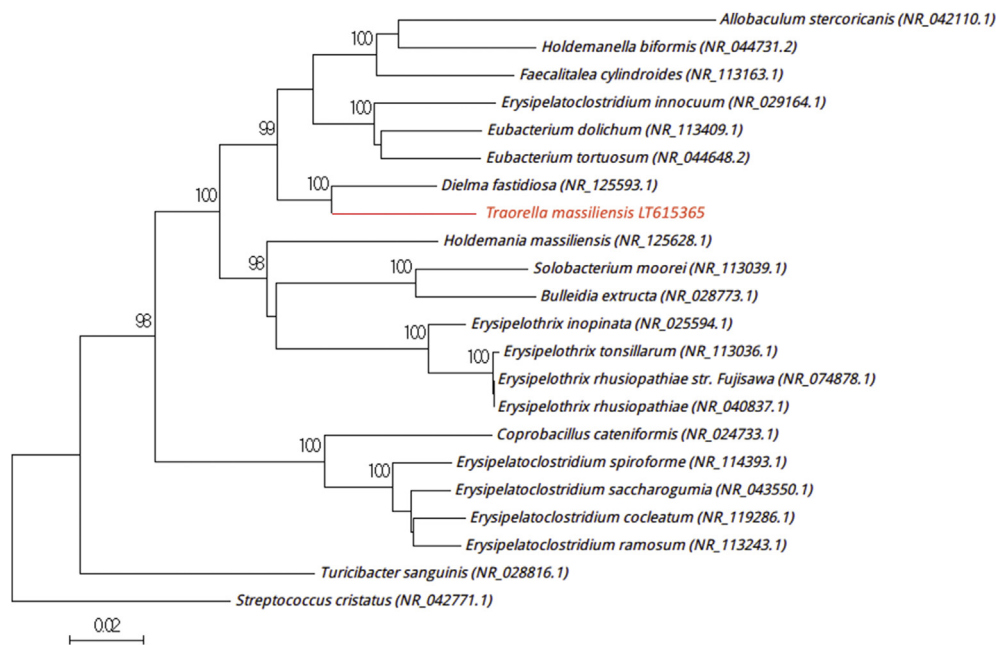
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In May 2016, using the culturomics approach [1] on stored samples from the digestive tract, we isolated the strain Marseille-P3110<sup>T</sup> from the left colon liquid sample of a 76-year-old woman who underwent colonoscopy for a history of colonic polyp. The patient provided signed informed consent, and the ethics committee of the Institut Fédératif de Recherche IFR48 approved the study under number 2016-010.

The sample was directly inoculated on Columbia agar enriched with 5% of sheep's blood (COS; bioMérieux, Marcy l'Etoile, France), and strain Marseille-P3110<sup>T</sup> was obtained after a 3-day incubation at 37°C in an anaerobic atmosphere (anaeroGen Compact; Oxoid, Thermo Scientific, Dardilly, France). Colonies were white, convex and circular with a diameter of 0.8 mm. Cells were Gram-negative bacilli with a mean diameter of 0.3 µm and a length varying from 2.0 to 3.6 µm. Strain Marseille-P3110<sup>T</sup> was motile and non-endspore forming. This strain exhibited neither catalase nor oxidase activities.

The 16S rRNA gene was sequenced using fD1-rP2 primers as previously described [2] with a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France) because of the impossibility of identifying strain Marseille-P3110<sup>T</sup> by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) (Microflex LT; Bruker Daltonics, Bremen, Germany) [3]. Strain Marseille-P3110<sup>T</sup> exhibited a 93.2% sequence similarity [4] with *Dielma fastidiosa* type strain JCI3<sup>T</sup> (GenBank accession no. JF824807), the phylogenetically closest species with standing in nomenclature (Fig. 1), which was isolated from the stool of a healthy Senegalese patient for the first time in 2013 [5]. This taxonomic name has been effectively published but not validly published under the rules of the International Code of Nomenclature of Bacteria.

Because of a 16S rRNA sequence similarity of <95% between strain Marseille-P3110<sup>T</sup> and its phylogenetically closest species with standing in nomenclature [6], we propose the creation of a new genus '*Traorella*' gen. nov. (tra.o.rel'la, N.L. masc. n. *Traorella*, in honor of a Senegalese scientist, Sory Ibrahima Traore, a pioneer of culturomics). '*Traorella massiliensis*' gen. nov., sp. nov. (mas.si.li.en'sis, L. masc. adj. *massiliensis*, 'Massilia,' the Roman name of Marseille), is part of the *Erysipelotrichaceae* family and the *Firmicutes* phylum. Strain Marseille-P3110 is the type strain of the new species *Traorella massiliensis* gen. nov., sp. nov.



**FIG. 1.** Phylogenetic tree showing position of *Traorella massiliensis* strain Marseille-P3110<sup>T</sup> relative to other phylogenetically close neighbours. Sequences were aligned using Muscle 3.8.31 with default parameters, and phylogenetic inferences were obtained using neighbour-joining method with 1000 bootstrap replicates within MEGA6 software. Only bootstrap values of >95% are shown. Scale bar represents 2% nucleotide sequence divergence.

## MALDI-TOF MS spectrum

The MALDI-TOF MS spectrum of *Traorella massiliensis* strain Marseille-P3110<sup>T</sup> is available online (<http://www.mediterranean-infection.com/article.php?laref=256&titre=urms-database>).

## Nucleotide sequence accession number

The 16S rRNA gene sequence of *Traorella massiliensis* strain Marseille-P3110<sup>T</sup> was deposited in GenBank under accession number LT615365.

## Deposit in a culture collection

*Traorella massiliensis* strain Marseille-P3110<sup>T</sup> was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under the number P3110 and in the Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ) under number DSM 103514.

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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;1:203.
- [2] 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.
- [3] 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.
- [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] Ramasamy D, Lagier JC, Nguyen TT, Raoult D, Fournier PE. Non-contiguous finished genome sequence and description of *Dielma fastidiosa* gen. nov., sp. nov., a new member of the Family *Erysipelotrichaceae*. *Stand Genomic Sci* 2013;8:336–51.
- [6] Huson DH, Auch AF, Qi J, Schuster SC. MEGAN analysis of metagenomic data. *Genome Res* 2007;17:377–86.