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# '*Metaprevotella massiliensis*' gen. nov., sp. nov., isolated from human ileum

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## Abstract

We report here the main characteristics of '*Metaprevotella massiliensis*' strain Marseille-P-3114<sup>T</sup> (CSURP3114) that was isolated from a human ileum sample.

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**Keywords:** Culturomics, human gut, *Metaprevotella massiliensis*, microbiota, taxonogenomics

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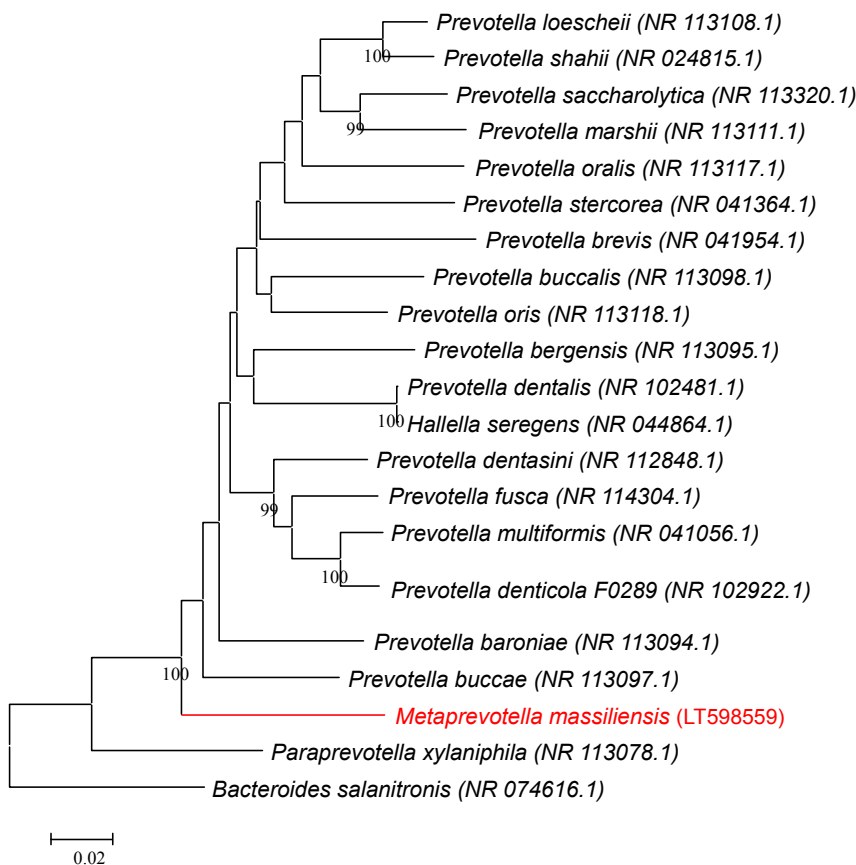
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In 2016, as a part of culturomics study [1] targeted at the study of the modifications of the human microbiome along the whole gastrointestinal tract, we isolated from the ileum of a 25-year-old patient with Crohn disease a bacterial strain that escaped identification by our systematic matrix-assisted desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) screening on a Microflex spectrometer (Bruker Daltonics, Bremen, Germany) [2]. The patient provided signed informed consent, and the study was validated by the ethics committee of the Institut Fédératif de Recherche IFR48 under number 09-022.

Strain Marseille P-3114<sup>T</sup> growth was obtained on 5% sheep's blood–enriched Columbia agar medium (bioMérieux, Marcy l'Etoile, France) in an anaerobic atmosphere (anaeroGEN, Oxoid, Dardilly, France) after a 30-day enrichment of the fresh ileal sample in an anaerobic haemoculture bottle (Becton Dickinson, Pont de Claix, France) added with 5 mL of sterile sheep's blood (bioMérieux) and 5 mL of 0.2 µm filtered (Thermo Fisher Scientific, Villebon-sur-Yvette, France) rumen at 37°C.

After 96 hours' anaerobic incubation on 5% sheep's blood–enriched agar (bioMérieux) at 37°C, colonies were circular, convex with entire edges and translucent. Mean diameter was 0.5 to 2 mm. After 3 weeks' incubation under the same conditions, dark pigment production was observed. Bacterial cells were Gram-negative rods 0.3 to 0.5 µm wide by 1 to 2 µm long. Strain Marseille-P-3114<sup>T</sup> tested catalase and oxidase negative. Different temperatures (20, 28, 37, 45 and 55°C) and atmospheres (anaerobic, microaerophilic and aerobic conditions) were tested on 5% sheep's blood–enriched Columbia agar (bioMérieux). Growth was achieved only under anaerobic atmosphere at 37°C. Sporulation test (20 minutes at 80°C) was negative.

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-P-3114<sup>T</sup> exhibited a 89.39% sequence identity with *Prevotella buccae* strain ATCC 33574<sup>T</sup> (GenBank accession no. L16477), the phylogenetically closest species with standing in nomenclature (Fig. 1), which putatively classified strain Marseille-P-3114<sup>T</sup> as a member of a new genus within the family *Prevotellaceae* in the phylum *Bacteroidetes*. The Family *Prevotellaceae* was proposed by Krieg in 2012 and was validated the same year [4]; it actually comprises four genera with validly published names: *Prevotella*, *Alloprevotella*, *Hallella* and *Paraprevotella* [5]. The genus *Prevotella* was created in 1990 to accommodate those *Bacteroides* that were only moderately



**FIG. 1.** Phylogenetic tree showing position of 'Metaprevotella massiliensis' strain Marseille-P-3114<sup>T</sup> relative to other phylogenetically close neighbours. Sequences were aligned using CLUSTALW, and phylogenetic inferences were obtained using maximum-likelihood method within MEGA software. Numbers at nodes are percentages of bootstrap values obtained by repeating analysis 500 times to generate majority consensus tree. Only bootstrap scores of at least 95 were retained. *Bacteroides salanitronis* DSM 18170 was used as outgroup.

saccharolytic and were not able to properly grow in bile-enriched medium [6], and today it contains 49 species with a standing in nomenclature. Species belonging to this genus are Gram-negative, anaerobic, non-spore-forming, nonmotile rods, and their common habitats are mammals, although one species has been retrieved from environmental source (*Prevotella oryzae*, isolated from rice field soil) [7]. They are generally considered to be a commensal species, but under particular circumstances, they are able to induce a wide range of diseases such as bacteraemia, disseminated abscesses, meningitis and endocarditis [8].

On the basis of the 16S rRNA sequence divergence of strain Marseille-P3114<sup>T</sup> with the phylogenetically closest species with standing in nomenclature [9], we propose here the creation of the new genus *Metaprevotella* (Me.ta.pre.vo.tel'la, Gr. adv. *meta*, 'besides'; N.L. 'beyond'; N.L. fem. n. *Prevotella*, a bacterial generic name; N.L. fem. n. *Metaprevotella* 'organism related to the genus *Prevotella* but different') for which the strain Marseille-P-3114<sup>T</sup> (= CSURP3114 = DSM 103534) is the type strain. Strain Marseille-P3114<sup>T</sup> is the type strain of *Metaprevotella massiliensis* gen.

nov., sp. nov. (mas.si.li.en'is, L. fem. adj. *massiliensis*, for Massilia, the Roman name of Marseille).

The MALDI-TOF MS spectrum of 'Metaprevotella massiliensis' strain Marseille-P3114<sup>T</sup> 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 LT598559.

### Deposit in a culture collection

Strain Marseille-P3114<sup>T</sup> was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under number P3114 and in the Deutsche Sammlung von Mikroorganismen und Zellkulturen under number DSM103534.

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## Conflict of Interest

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None declared.

## References

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- [1] Lagier JC, Hugon P, Khelaifia 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, 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] List of new names and new combinations previously effectively, but not validly, published. *Int J Syst Evol Microbiol* 2012;62:1–4.
- [5] Rosenberg E. The Family *Prevotellaceae*. In: Rosenberg E, DeLong EF, Lory S, Stackebrandt E, Thompson F, editors. *The prokaryotes*. Berlin: Springer; 2014. p. 825–7.
- [6] Shah HN, Collins DM. *Prevotella*, a new genus to include *Bacteroides melaninogenicus* and related species formerly classified in the genus *Bacteroides*. *Int J Syst Bacteriol* 1990;40:205–8.
- [7] Sakamoto M, Ohkuma M. Reclassification of *Xylanibacter oryzae* Ueki et al. 2006 as *Prevotella oryzae* comb. nov., with an emended description of the genus *Prevotella*. *Int J Syst Evol Microbiol* 2012; 2012;62:2637–42.
- [8] Glazunova OO, Launay T, Raoult D, Roux V. *Prevotella timonensis* sp. nov., isolated from a human breast abscess. *Int J Syst Evol Microbiol* 2007;57:883–6.
- [9] Huson DH, Auch AF, Qi J, Schuster SC. MEGAN analysis of meta-genomic data. *Genome Res* 2007;17:377–86.