

## NEW SPECIES

# *Christensenella timonensis*, a new bacterial species isolated from the human gut

S. Ndongo<sup>1</sup>, G. Dubourg<sup>1</sup>, S. Khelaifia<sup>1</sup>, P.-E. Fournier<sup>1</sup> and D. Raoult<sup>1,2</sup>

<sup>1</sup> Aix Marseille Université, URMITE, UM63, CNRS 7278, IRD 198, INSERM 1095, Institut Hospitalo-Universitaire Méditerranée-Infection, Faculté de médecine, Marseille, France and <sup>2</sup> Special Infectious Agents Unit, King Fahd Medical Research Center, King Abdulaziz University, Jeddah, Saudi Arabia

## Abstract

We propose a new species, *Christensenella timonensis*, strain Marseille-P2437<sup>T</sup> (CSUR P2437<sup>T</sup>), which was isolated from gut microbiota of a 66-year-old patient as a part of culturomics study. *C. timonensis* represents the second species isolated within the *Christensenella* genus.

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**Keywords:** *Christensenella timonensis*, culturomics, emerging bacterium, gut microbiota, taxonomy

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**Corresponding author:** D. Raoult, URMITE, CNRS (UMR 7278), IRD (198), INSERM (U1095), AMU (UM63), Faculté de Médecine, Aix-Marseille Université, 27 Boulevard Jean Moulin, 13385 Marseille Cedex 5, France  
**E-mail:** [didier.raoult@gmail.com](mailto:didier.raoult@gmail.com)

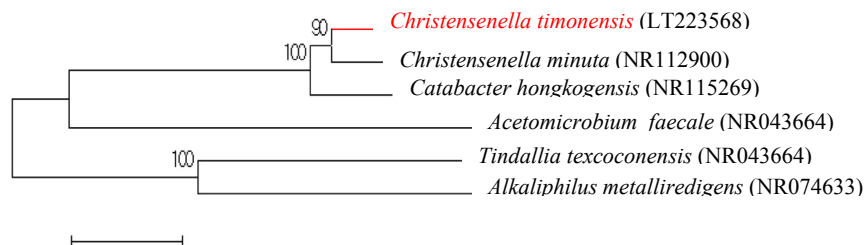
In January 2016, we isolated a bacterial strain that could not be identified by our systematic matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) screening on a Microflex spectrometer (Bruker Daltonics, Leipzig, Germany) [1] as part of study of the human microbiome by culturomics [2]. The strain came from the stool sample of a 66-year-old diabetic patient hospitalized in November 2015 at the Timone Hospital in Marseilles, France, for a malignant blood disease. This study had been previously approved by the local ethics committee of the IFR48 (Marseille, France) under agreement 09-022.

After receiving signed informed consent, the stool specimen was preincubated in anaerobic conditions at 37°C in a culture bottle containing a blood-enriched Columbia agar liquid medium (bioMérieux, Marcy l'Etoile, France). After 7 days of preincubation, the sample was seeded on 5% sheep's blood agar (bioMérieux), and the initial growth was obtained after 4 days

under anaerobic generated by AnaeroGen (bioMérieux). The colonies are beige and about 0.1 to 0.2 mm in diameter. Cells are Gram-negative bacilli (0.3–0.5 × 1.2–1.5 µm), strictly anaerobic, nonmotile and non-spore forming. The strain Marseille-P2437 presents no catalase and oxidase activities. The 16S rRNA gene of the strain Marseille-P2437 was sequenced using fDI-rP2 primers (Eurogentec, Angers, France) as previously described [3], and the obtained amplicon showed a similarity of 97.4% with *Christensenella minuta* strain YIT 12065 (GenBank accession no. NR112900), the phylogenetically closest species with standing in nomenclature (Fig. 1), which classifies it as a member within the genus *Christensenella* in the Firmicutes phylum [4]. To date, *Christensenella minuta* is the only species published and validated name within the *Christensenella* genus, and was also isolated from human faeces.

The 16S rRNA gene sequencing of strain Marseille-P2437 (DSM 102800) yielded divergence of more 1.3% with its phylogenetically closest species with a validly published name standing in nomenclature [5]. On the basis of these results, strain Marseille-P2437 (DSM 102800) is proposed as a novel species of the genus *Christensenella*, namely *Christensenella timonensis* sp. nov. (ti.mo.nen'sis. L. masc. adj., timonensis, pertaining to Timone, named after Hôpital de la Timone, the hospital in Marseilles, France, where the type strain was isolated).

**FIG. 1.** Phylogenetic tree showing position of *Christensenella timonensis* strain Marseille-P2437<sup>T</sup> relative to other phylogenetically close members of family Christensenellaceae. GenBank accession numbers are indicated in parentheses. 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 values greater than 95% are displayed. Scale bar indicates 2% nucleotide sequence divergence.



## MALDI-TOF MS spectrum

The MALDI-TOF MS spectrum of *C. timonensis* is available at <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 LT223568.

## Deposit in a culture collection

Strain Marseille-P2437<sup>T</sup> was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR) under number P2437.

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## Conflict of Interest

None declared.

## References

- [1] 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.
- [2] 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.
- [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] Morotomi M, Nagai F, Watanabe Y. Description of *Christensenella minuta* gen. nov., sp. nov., isolated from human faeces, which forms a distinct branch in the order Clostridiales, and proposal of Christensenellaceae fam. nov. *Int J Syst Evol Microbiol* 2012;62:144–9.
- [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.