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# “*Libanicoccus massiliensis*” gen. nov., sp. nov., a new bacterium isolated from a stool sample from a pygmy woman

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## Abstract

This study supports the main characteristics of a new genus “*Libanicoccus massiliensis*” strain Marseille-P3237 (CSURP3237); a new member of the order *Coriobacteriaceae* that was isolated from a stool sample from a healthy 35-year-old pygmy woman.

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**Keywords:** Culturomics, emerging bacteria, gut microbiota, human microbiota, *Libanicoccus massiliensis*

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Samples were collected in Congo in 2015 as part of the analysis project of human microbiome by culturomics [1]. This study was approved by the ethics committee of the Institut Federatif de Recherche IFR48 (Marseille, France) under number 09-022. Samples were diluted with phosphate-buffered saline and inoculated in a blood culture media supplemented with 5 mL blood and rumen at 37°C under anaerobic conditions. After 5 days of growth, *Libanicoccus massiliensis* was isolated on 5% sheep’s blood–enriched Columbia agar (bioMérieux, Marcy l’Etoile, France). Colonies were rough, with a mean diameter of 0.8 to 1.2 mm. Strain Marseille-P3237 cells are cocci, Gram negative, catalase and oxidase negative with an average diameter of 1.06 µm. This strain 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, Bremen, Germany) [2]. Thus, 16S rRNA gene sequencing was performed using fDI-rP2 primers as previously described (Eurogentec, Seraing, Belgium) by a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France) [3].

*L. massiliensis* exhibited a 93.05% sequence identity with *Olsenella uli* strain DSM7084 (NR\_074414), the phylogenetically closest species published with standing in nomenclature (Fig. 1). Thus, strain Marseille-P3237 exhibits a 16S rRNA sequence divergence of >5% with its phylogenetically closest species with a validly published name with standing in nomenclature [4]. We propose the creation of a new genus, “*Libanicoccus*” (Li.ba.ni.coc’cus, N.L. masc.gen.n., *Libanicoccus* to refer to the Lebanese nationality for of the person who cultivated strain Marseille-P3237). Marseille-P3237 is the type strain of the new species “*Libanicoccus massiliensis*” gen. nov., sp. nov. (mas.i.li.en’sis, L. gen. masc. n., *massiliensis* pertaining to Massilia, the ancient name of the city of Marseille, where this bacterium was discovered). The sample was isolated from a stool sample from a healthy 35-year-old pygmy woman.

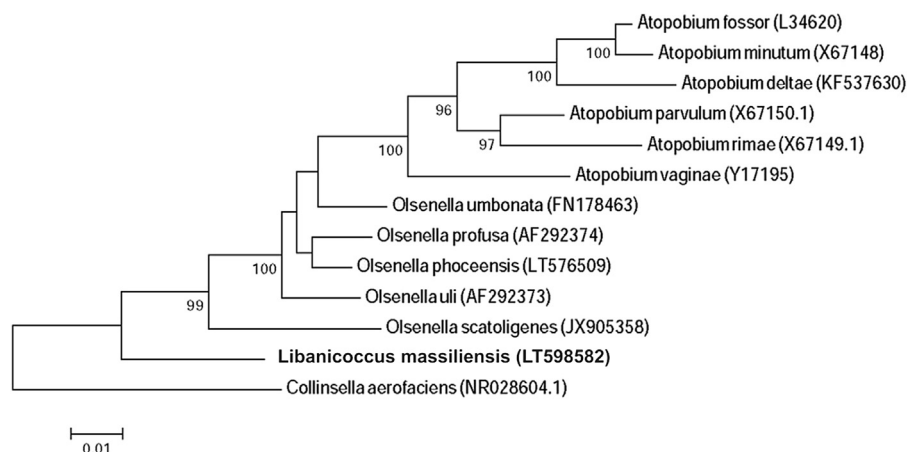
## MALDI-TOF MS spectrum accession number

The MALDI-TOF MS spectrum of *L. massiliensis* is available online (<http://www.mediterranee-infection.com/article.php?leref=256&titre=urms-database>).

## Nucleotide sequence accession number

The 16s rRNA gene sequence was deposited in GenBank under accession number LT598582.1.

**FIG. 1.** Phylogenetic tree showing position of *Libanicoccus massiliensis* strain Marseille-P3237 between phylogenetically closest species. CLUSTALW was used for sequences alignment, and phylogenetic inferences were generated by MEGA software by maximum likelihood method. Bootstrap values obtained after 500 repeats are shown on nodes. Bootstrap scores of at least 90% were kept. Scale bar indicates 2% nucleotide sequence divergence.



## Deposit in a culture collection

Strain Marseille-P3237 was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under number P3237.

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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, Carlizot 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;64:346–51.