# 'Olsenella congonensis' sp.nov., identified in human stool sample

#### M. Bilen<sup>1,2</sup>, F. Cadoret<sup>1</sup>, G. Dubourg<sup>1</sup>, Z. Daoud<sup>2</sup>, P. E. Fournier<sup>1</sup> and D. Raoult<sup>1</sup>

1) Aix-Marseille Université, URMITE, UM63, CNRS7278, IRD198, Inserm 1095, Institut Hospitalo-Universitaire Méditerranée-Infection, Faculté de médecine, Marseille, France and 2) Clinical Microbiology Laboratory, Saint George University Hospital, Faculty of Health Sciences, University of Balamand, Beirut, Lebanon

#### Abstract

We report the main characteristics of 'Olsenella congonensis' strain Marseille-P3359<sup>T</sup> (CSUR P3359), which was isolated from the stool sample of a healthy 47-year-old pygmy female.

© 2017 Published by Elsevier Ltd on behalf of European Society of Clinical Microbiology and Infectious Diseases.

Keywords: Culturomics, Emerging bacteria, Gut microbiota, Human microbiota, 'Olsenella congonensis' Original Submission: 28 April 2017; Revised Submission: 18 May 2017; Accepted: 29 May 2017 Article published online: 3 June 2017

**Corresponding author:** D. Raoult, Aix-Marseille Université, URMITE, UM63, CNRS7278, IRD198, Inserm 1095, Institut Hospitalo-Universitaire Méditerranée-Infection, Faculté de médecine, 27 Boulevard Jean Moulin, 13385, Marseille cedex 05, France **E-mail: didier.raoult@gmail.com** 

The approval of the ethics committee of the Institut Fédératif de Recherche was obtained under the number 09-022 before sample collection from Congo and project start up. Samples collection and analysis were performed with the aim of describing the human gut microbiota using the culturomics approach [1].

As a first step, stool sample (I g) was diluted with I mL of phosphate buffered saline then incubated in an anaerobic culture bottle, supplemented with 5% filtered rumen and 5% sheep blood, at 37°C for a 30-day follow up. At day 15 a 'Olsenella congonensis' colony was purely isolated on 5% blood-enriched Columbia agar (bioMérieux, Marcy l'Etoile, France). The first method used for the identification of Strain Marseille-P3359 was matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) using a Microflex spectrometer (Bruker Daltonics, Leipzig, Germany) [2]. However, identification failed and 16S rRNA gene sequencing was performed, as previously reported, for further analysis using a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France) with fD1-rP2 primers (Eurogentec, Seraing, Belgium) [3]. Strain Marseille-P3359 exhibited a 95% sequence identity with Olsenella scatoligenes, the phylogenetically closest species with standing nomenclature (Fig. 1). Hence, it can be classified as a new species within the genus Olsenella [4]. When comparing the I6S rRNA gene sequences of the different closely related species of Olsenella, we found a range of similarity between 93% and 97%. Hence, we propose that strain Marseille-P3359 is a new species of the genus Olsenella.

# Description of the new species 'Olsenella congonensis'

Colonies of the strain Marseille-P3359<sup>T</sup> were smooth with a mean diameter of 0.8-1 mm. Bacterial cells were Grampositive bacilli, catalase and oxidase negative with a mean length of 1.08 µm. We propose the discovery of the new species 'Olsenella congonensis' (co.ng.on.en'sis. N.L. masc. adj. congonensis to refer to Congo, from where the stool's donor came). Strain Marseille-P3359<sup>T</sup> is the type strain of the new species 'Olsenella congonensis'.

# MALDI-TOF MS spectrum accession number

The MALDI-TOF MS spectrum of '0. *congonensis*' is available online (http://www.mediterranee-infection.com/article.php?lare f=256&titre=urms-database).

New Microbe and New Infect 2017; 19: 132-133

<sup>© 2017</sup> Published by Elsevier Ltd on behalf of European Society of Clinical Microbiology and Infectious Diseases This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/) http://dx.doi.org/10.1016/j.nmni.2017.05.013



0.01

FIG. I. Phylogenetic tree showing the branching of 'Olsenella congonensis' strain Marseille-P3359 among the other phylogenetically close neighbours. CLUSTALW and MEGA software were used for alignment and phylogenetic tree generation, respectively. The neighbour joining method was adapted with 500 bootstraps and only scores of at least 90% were kept on the nodes. The scale bar indicates a 1% nucleotide sequence divergence.

### Nucleotide sequence accession number

The 16S rRNA gene sequence was deposited in GenBank under Accession number LT797539.

# Deposit in a culture collection

Strain Marseille-P3359 was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under number P3359.

# **Conflicts of interest**

None to declare.

**Funding sources** 

This work was funded by Mediterrannée Infection Foundation.

#### References

- Lagier J-C, 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 J-C, 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, 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] Sakamoto M, Benno Y. Reclassification of Bacteroides distasonis, Bacteroides goldsteinii and Bacteroides merdae as Parabacteroides distasonis gen. nov., comb. nov., Parabacteroides goldsteinii comb. nov. and Parabacteroides merdae comb. nov. Int J Syst Evol Microbiol 2006;56: 1599-605.