

“*Intestinimonas massiliensis*” sp. nov, a new bacterium isolated from human gut

G. Durand^{1,3}, P. Afouda¹, D. Raoult^{1,2,3} and G. Dubourg^{1,3}

1) Unité de Recherche sur les Maladies Infectieuses et Tropicales Emergentes, UM 63, CNRS 7278, IRD 198, Inserm 1095, Institut Hospitalo-Universitaire Méditerranée-Infection, Faculté de médecine, Aix-Marseille Université, 2) Institut Hospitalo-Universitaire (IHU) Méditerranée Infection, Assistance Publique-Hôpitaux de Marseille and 3) Pôle des Maladies Infectieuses et Tropicales Clinique et Biologique, Fédération de Bactériologie-Hygiène-Virologie, University Hospital Centre Timone, Marseille, France

Abstract

Here we report the main features of the proposed new bacterial species “*Intestinimonas massiliensis*” sp. nov. The type strain GD2^T (CSUR = PI930) was isolated from the gut microbiota of a healthy patient using a culturomics approach combined with taxonogenomics. © 2016 The Authors. Published by Elsevier Ltd on behalf of European Society of Clinical Microbiology and Infectious Diseases.

Keywords: Anaerobe, culturomics, gut microbiota, “*Intestinimonas massiliensis*” sp. nov., taxonogenomics

Original Submission: 21 September 2016; **Accepted:** 28 September 2016

Article published online: 3 October 2016

Corresponding author: G. Dubourg, URMITE UM63, CNRS7278, IRD198, INSERM1095, Faculté de Médecine, Aix-Marseille Université, 27 boulevard Jean Moulin, 13385 Marseille cedex 5, France
E-mail: greg.dubourg@gmail.com

As a part of our study of the human microbiome by culturomics [1], we isolated in the stool of a healthy 28-year-old French donor the Gram-negative rod and strictly anaerobe strain GD2^T. The written consent of the donor was obtained, and the study was validated by the ethics committee of the Federative Research Institute IFR48 under number 09-022. The stool was stored at -20°C for 10 days, then inoculated on agar enriched with sheep’s blood (5%) and rumen fluid (5%) previously filter sterilized through a 0.2 µm pore filter (Thermo Fisher Scientific, Villebon sur Yvette, France). The plates were then incubated under anaerobic condition into an anaerobic cabinet for 72 hours. The subculture of colonies using the same protocol allowed the isolation of the GD2^T strain. The strain GD2^T could not be identified by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) screening (score <1.7) using a Microflex spectrometer (Bruker Daltonics, Bremen, Germany) [1–3].

Colonies appeared white and regular with a mean diameter of 1 to 2 mm on blood agar–enriched Colombia. “*Intestinimonas massiliensis*” is a nonmotile, Gram-negative rod with a mean diameter of 0.5 µm and 1.8 µm in length, without spore-forming activity. Catalase and oxidase were also negative. The 16S rRNA gene was completely sequenced as previously described [4]. It shared 94.4% sequence identity with *Intestinimonas butyriciproducens* DSM 26588^T (NR_118554). The bacterium was therefore putatively classified as a new species belonging to the *Intestinimonas* genus.

Because of the 16S identity percentage was lower than 98.65% to the species closest with a validly published name standing in nomenclature [5], we propose the new strain “*Intestinimonas massiliensis*” GD2^T (mas.il.i.en’sis, L. gen. masc. n. *massiliensis*, “of Massilia,” the Latin name for Marseille, where the strain GD2^T was first isolated) belonging to the genus *Intestinimonas* (Fig. 1).

MALDI-TOF MS spectrum accession number

The MALDI-TOF MS spectrum of “*Intestinimonas massiliensis*” is available at <http://mediterranee-infection.com/article.php?laref=256&titre=urms-database>.

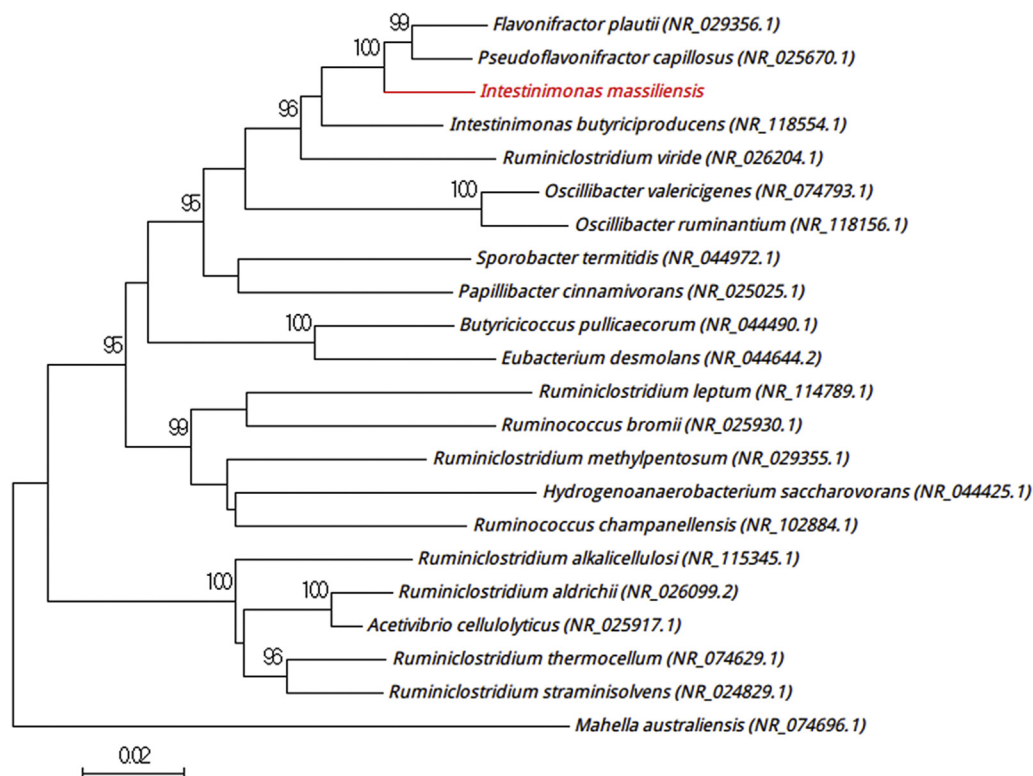


FIG. 1. Phylogenetic tree based on 16S rRNA gene sequence showing position of “*Intestinimonas massiliensis*” sp. nov., strain GD2^T with other close relative species among *Firmicutes* phylum. European Molecular Biology Laboratory (EMBL) database accession numbers are indicated in parentheses. Sequences were aligned using CLUSTALW, and phylogenetic inferences were obtained with Kimura two-parameter model using neighbour-joining method with 1000 bootstrap replicates within MEGA6 software. Scale bar represents 1% nucleotide sequence divergence.

Nucleotide sequence accession number

The 16S rRNA gene sequence was deposited in GenBank under accession number LN866996.

Deposit in a culture collection

Strain GD2^T was deposited in the collection de Souches de l'Unités des Rickettsies (CSUR, WDCM 875) under number P1930.

Acknowledgement

This study was funded by the Fondation Méditerranée Infection.

Conflict of Interest

None declared.

References

- [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] Lagier JC, Armougom F, Million M, Hugon P, Pagnier I, Robert C, et al. Microbial culturomics: paradigm shift in the human gut microbiome study. *Clin Microbiol Infect* 2012;18:1185–93.
- [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] 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.
- [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(Pt 2):346–51.