



HAL
open science

”Eggerthella timonensis” gen. nov. isolated from a human stool sample

M. Bilen, F. Cadoret, Z. Daoud, Pierre-Edouard Fournier, Didier Raoult

► To cite this version:

M. Bilen, F. Cadoret, Z. Daoud, Pierre-Edouard Fournier, Didier Raoult. ”Eggerthella timonensis” gen. nov. isolated from a human stool sample. *New Microbes and New Infections*, 2017, 17, pp.41–42. 10.1016/j.nmni.2016.11.001 . hal-01795980

HAL Id: hal-01795980

<https://amu.hal.science/hal-01795980>

Submitted on 9 Jul 2024

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L’archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d’enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution - NonCommercial - NoDerivatives 4.0 International License

“*Eggerthella timonensis*” gen. nov. isolated from a human stool sample

M. Bilen¹, F. Cadoret¹, Z. Daoud², P.-E. Fournier¹ and D. Raoult¹

1) Aix-Marseille Université, URMITE, UM63, CNRS7278, IRD198, Inserm 1095, Institut Hospitalo-Universitaire Méditerranée-Infection, Faculté de médecine, Marseille, France and 2) Clinical Microbiology Department, Faculty of Medicine and Medical Sciences, University of Balamand, Amioun, Lebanon

Abstract

We report the main characteristics of “*Eggerthella timonensis*” strain Marseille-P3135 which was isolated from a stool sample of a healthy 8-year-old pygmy (Baka) girl.

© 2016 The Authors. Published by Elsevier Ltd on behalf of European Society of Clinical Microbiology and Infectious Diseases.

Keywords: Culturomics, *Eggerthella timonensis*, emerging bacteria, gut microbiota, human microbiota

Original Submission: 17 October 2016; **Revised Submission:** 3 November 2016; **Accepted:** 9 November 2016

Article published online: 15 November 2016

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

Ahead of the initiation of the study, ethical approval (09-022) was obtained from Institut Fédératif de Recherche IFR48. Samples were collected from Congo and stored at 4°C. “*Eggerthella timonensis*” strain Marseille-P3135 was isolated from a stool sample of a healthy 8-year-old pygmy (Baka) girl as part of the study aiming to describe the human gut microbiota using culturomics as a technique [1].

Samples were diluted with phosphate-buffered saline and incubated for 30 days in a blood culture bottle with 5 mL of sheep’s blood under anaerobic conditions at 37°C. Strain Marseille-P3135 was isolated after 10 days on 5% sheep’s blood–enriched Columbia agar (bioMérieux, Marcy l’Étoile, France). We failed to identify this bacteria using matrix-assisted desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) screening on a Microflex spectrometer (Bruker Daltonics, Bremen, Germany) [2].

The colonies of strain Marseille-P3135 were smooth with a mean diameter of 0.5 mm. Bacterial cells were Gram and catalase positive, oxidase negative and rod shaped with a diameter of 0.7 to 1.6 µm. The 16S rRNA gene sequencing was performed on 3130-XL sequencer (Applied Biosciences, Saint Aubin, France) using fD1-rP2 primer (Eurogentec, Seraing,

Belgium) as previously described [3]. Strain Marseille-P3135 exhibited a 97.62% sequence identity with *Eggerthella sinensis* strain HKU14 (NR_042840.1), the phylogenetically closest species with standing in nomenclature (Fig. 1). Thus, strain Marseille-P3135 can be classified as a member of the genus *Eggerthella* within the family *Coriobacteriaceae* and under the *Actinobacteria* phylum [4].

Because the 16S rRNA gene sequence of Marseille-P3135 and *E. sinensis* strain HKU14 diverge by more than 1.3% [5], we discovered a new species “*Eggerthella timonensis*” (ti.m-o.nen’sis, N.L. masc. adj. *timonensis*, pertaining to Timone, the name of the main university hospital in Marseille, France, where strain Marseille-P3135 was isolated). Strain Marseille-P3135 is the type strain of the new species “*Eggerthella timonensis*.”

MALDI-TOF MS spectrum

The MALDI-TOF MS spectrum of “*Eggerthella timonensis*” 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 LT598568.

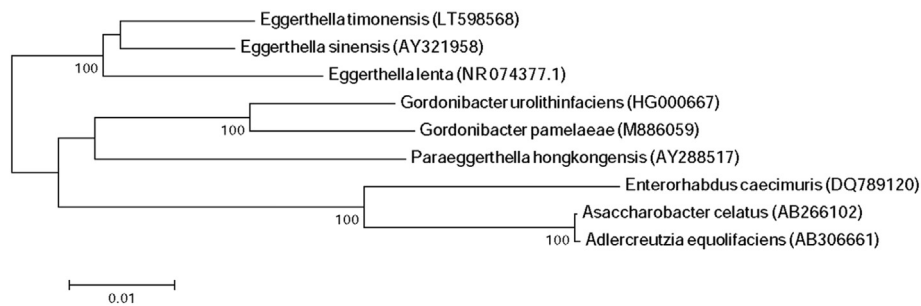


FIG. 1. Phylogenetic tree representing position of “*Eggerthella timonensis*” strain Marseille-P3135 among its neighbours. Sequences of strains utilized in this tree were aligned using CLUSTALW. Additionally, by means of MEGA software, and using maximum-likelihood method, phylogenetic inferences were obtained. Bootstrapping values obtained after 500 repeats are shown on nodes. Note that only bootstrap scores of at least 90% were kept. Scale bar indicates 2% nucleotide sequence divergence.

Deposit in a culture collection

Strain Marseille-P3135 was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under number P3135.

Acknowledgement

This study was funded by the Fondation Méditerranée Infection.

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, 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] Lau SKP, Woo PCY, Woo GKS, Fung AMY, Wong MKM, Chan KM, et al. *Eggerthella hongkongensis* sp. nov. and *Eggerthella sinensis* sp. nov., two novel *Eggerthella* species, account for half of the cases of *Eggerthella* bacteremia. *Diagn Microbiol Infect Dis* 2004;49:255–63.
- [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.