Taxonomic Note

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Description of strain FC3T as the neotype strain of Actinobaculum massiliense

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Actinobaculum massiliense (Euzéby, 2006) was isolated from the urine of an elderly woman in 2001. Unfortunately, the strain deposited as the type strain was, by error, an Actinobaculum schaali strain (Yassin et al., 2015). In 2015, we isolated a new strain of A. massiliense, FC3, from the urine of a 12-year-old patient with acute cystitis. We herein present the characteristics of strain FC3 (=CSUR P1982=DSM 100580) and formally propose it as the neotype strain of A. massiliense.

Greub & Raoult (2002) reported the isolation of a novel Actinobaculum species that they proposed as Actinobaculum massiliiae sp. nov. from the urine of an 81-year-old woman with chronic cystitis. The type strain exhibited a 16S rRNA gene sequence similarity of 95% with Actinobaculum suis and 92–93% with Actinobaculum schaali (Greub & Raoult, 2002). The type strain of A. massiliiae was deposited in the Collection de l’Institut Pasteur (CIP), Paris, France, under reference CIP 107404T (=CCUG 47753=DSM 19118T) (Greub & Raoult, 2002). Later, the name A. massiliiae was corrected to A. massiliense (Euzéby, 2006). Unfortunately, as highlighted by Yassin et al. (2015), the strain deposited under reference CIP 107404 at the CIP, and then transferred to the CCUG and DSMZ collections, was by mistake an A. schaali strain, and the original A. massiliense type strain was lost.

On 15 April 2015, we isolated a new strain of A. massiliense, FC3, from the urine of a 12-year-old patient suffering from acute cystitis. This strain exhibited a 16S rRNA gene sequence similarity of 99.93% with A. massiliense CIP 107404T (GenBank accession number AF487679) and of 92.75% with A. schaali CCUG 27420T (Y12329). The 16S rRNA gene sequence of strain FC3 was deposited in GenBank under reference LN870313. Strain FC3 was deposited in the Collection de Souches de l’Unité des Rickettsies (WDCM 875) under reference CSUR P1982, and in the Deutsche Sammlung von Mikroorganismen und Zellkulturen under number DSM 100580. The genome sequence from A. massiliense strain FC3 was deposited in GenBank under accession numbers CYUL01000001–CYUL01000005. The purpose of this note is to formally propose strain FC3 as the neotype strain of A. massiliense.

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A. massiliense strain FC3 cells were Gram-stain-positive cocci (few exhibited branching), non-motile, non-acid-fast, non-spore-forming, and catalase- and oxidase-negative. Strain FC3 grew optimally under anaerobic and microaerophilic conditions on 5% sheep blood-enriched Columbia agar (bioMérieux) at 37°C but slower in an aerobic atmosphere enriched with 5% CO2 (after 5–7 days of incubation). In anaerobic and microaerophilic atmospheres, colonies were pale grey, had a diameter of 0.5–1.5 mm after 72 h of incubation and exhibited α-haemolysis.

Using matrix-assisted laser desorption and ionization-time-of-flight mass spectrometry (Microflex; Bruker Daltonics) as previously described (Seng et al., 2009), strain FC3 was identified as representing A. massiliense (score values >2.3). Using API 20A, API Coryne, API 50CH and API ZYM strips (BioMérieux), strain FC3 produced acid from glucose, maltose, xylose and ribose, but not from trehalose, mannose, mannitol, sorbitol, starch or raffinose. Negative reactions were observed for aesculin and gelatin hydrolysis, and nitrate reduction. Leucine arylamidase, α-glucosidase and β-glucuronidase activities were detected. Slight activities were observed for pyrazinamidase and alkaline phosphatase, urase, α-galactosidase or N-acetyl-β-glucosaminidase activities were detected.

Cellular fatty acid methyl ester analysis was performed by GC-MS (Sasser et al., 2005; Dione et al., 2016). The major fatty acid detected for strain FC3 was hexadecanoic acid (42.9%) followed by 9-octadecenoic acid (21.5%), 9,12-octadecadienoic acid (17.3%) and octadecadienoic acid (9.3%). Strain CIP 107404T had exhibited a similar profile: hexadecanoic acid (41.5%), 9-octadecenoic acid (24.2%) and octadecadienoic acid (8.7%) (Greub & Raoult, 2002).
Antibiotic susceptibility testing revealed that strain FC3 was susceptible to amoxicillin, amoxicillin/clavulanic acid, ceftaxime, ceftriaxone, imipenem, trimethoprim/sulfamethoxazole, erythromycin, doxycycline, vancomycin, fosfomycin and rifampicin, but resistant to gentamicin, ciprofloxacin and colistin.

Strains FC3 and CIP 107404\textsuperscript{1} exhibited similar properties except for trehalose and raffinose acidification, and pyrazinamidase, \(\beta\)-glucuronidase, \(\beta\)-galactosidase and leucine arylamidase production (Greub & Raoult, 2002).

As described previously, strain FC3 exhibited a genome size of 2 065 184 bp with a G+C content of 60.17 mol\%. It contained 1772 protein-coding genes and 60 RNAs. A total of 1295 genes (73.08 \%) were assigned a putative function (Beye et al., 2016).

Based on this description, we propose strain FC3\textsuperscript{T} (=CSUR P1982\textsuperscript{T}=DSM 100580\textsuperscript{T}) as the neotype strain of \textit{A. massiliense}.

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**References**


