



**HAL**  
open science

**Noncontiguous finished genome sequence and description of *Mediterranea massiliensis* gen. nov., sp. nov., a new member of the Bacteroidaceae family isolated from human colon.**

I. I. Ngom, M. Mailhe, D. Ricaboni, V. Vitton, A. Benezech, S. Khelaifia, C. Michelle, F. Cadoret, N. Armstrong, A. Levasseur, et al.

► **To cite this version:**

I. I. Ngom, M. Mailhe, D. Ricaboni, V. Vitton, A. Benezech, et al.. Noncontiguous finished genome sequence and description of *Mediterranea massiliensis* gen. nov., sp. nov., a new member of the Bacteroidaceae family isolated from human colon.. *New Microbes and New Infections*, 2018, 21, pp.105-116. 10.1016/j.nmni.2017.11.009 . hal-01795914

**HAL Id: hal-01795914**

**<https://amu.hal.science/hal-01795914>**

Submitted on 1 Jun 2018

**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.

# Noncontiguous finished genome sequence and description of *Mediterranea massiliensis* gen. nov., sp. nov., a new member of the *Bacteroidaceae* family isolated from human colon

I. I. Ngom<sup>1</sup>, M. Mailhe<sup>1</sup>, D. Ricaboni<sup>1</sup>, V. Vitton<sup>2</sup>, A. Benezech<sup>2</sup>, S. Khelaifia<sup>1</sup>, C. Michelle<sup>1</sup>, F. Cadoret<sup>1</sup>, N. Armstrong<sup>1</sup>, A. Levasseur<sup>1</sup>, D. Raoult<sup>1</sup> and M. Million<sup>1</sup>

1) Aix-Marseille Université, URMITE, UM63, CNRS7278, IRD198, Inserm 1095, Institut Hospitalo-Universitaire Méditerranée-Infection, Faculté de médecine and 2) Service de Gastroentérologie, Hôpital Nord, Assistance Publique-Hôpitaux de Marseille, Marseille, France

## Abstract

Strain Marseille-P2645<sup>T</sup> was isolated in a colon sample from a Frenchwoman who underwent a colonoscopy. Bacterial cells were Gram negative, non-spore forming, mobile and strictly anaerobic. The genome of strain Marseille-P2645<sup>T</sup> is 3 950 441 bp long and contains 3374 protein-coding genes. The DNA G+C content is of 51.66 mol%. Strain Marseille-P2645<sup>T</sup> exhibited a 92.9% sequence similarity with *Bacteroides helcogenes* strain P36-108<sup>T</sup> (GenBank accession no. CP002352), the phylogenetically closest species with standing in nomenclature. Strain Marseille-P2645<sup>T</sup> (= CSUR P2645 = DSM 103034) is therefore a candidate as a type species of a new genus belonging to the *Bacteroidaceae* family, for which the name of *Mediterranea massiliensis* gen. nov., sp. nov., is proposed.

© 2017 The Author(s). Published by Elsevier Ltd.

**Keywords:** Colon, culturomics, genome, *Mediterranea massiliensis* gen. nov., sp. nov., taxonogenomics

**Original Submission:** 28 September 2017; **Revised Submission:** 17 November 2017; **Accepted:** 27 November 2017

**Article published online:** 5 December 2017

**Corresponding author:** M. Million, Aix Marseille Université, URMITE, Institut Hospitalier Universitaire Méditerranée-Infection, UM63, CNRS7278, IRD198, INSERM1095, Marseille, France  
E-mail: [matthieumillion@gmail.com](mailto:matthieumillion@gmail.com)

The first two authors contributed equally to this article, and both should be considered first author.

## Introduction

The concept of culturomics [1–3], developed in our laboratory since 2010, aims at deciphering the living microbial diversity in any milieu, notably microbes that live with humans. In contrast to metagenomics, it focuses on culture, and especially the characterization of new species become available to the scientific and medical community. Indeed, culture is the first step before experimental studies, multispecies probiotics or selection of strains for specific microbiotherapy.

The combination of endoscopic sampling and microbial culturomics allowed us to isolate a new bacterial genus from the colon lavage of a 58-year-old woman without medical history, who underwent a colonoscopy because of a positive screening test for a colorectal cancer. Strain Marseille-P2645<sup>T</sup> is the type strain of *Mediterranea massiliensis* gen. nov., sp. nov., the first species of the genus *Mediterranea*, a new member of the *Bacteroidaceae* family. To describe strain Marseille-P2645<sup>T</sup>, we report here the characterization of a new bacterial species using a new taxonomic strategy called taxonogenomics [4]. Taxonogenomics integrates proteomic information obtained by matrix-assisted desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) and genomic tests to describe new bacterial species [5,6]. This polyphasic approach overcomes limitations of conventional methods for new species description (genetic, phenotypic and chemotaxonomic characteristics for new species description) [7,8]. It combines phenotypic characteristics, analyses and comparison of the complete genome sequence. *Bacteroides helcogenes* strain P36-108<sup>T</sup> (GenBank accession no. CP002352) was the

phylogenetically closest species with standing in nomenclature [9]. Study of the phenotypic, phylogenetic and genomic characteristics of strain Marseille-P2645<sup>T</sup> revealed that *M. massiliensis* was sufficiently different from *Bacteroides helcogenes* type strain (P36-108<sup>T</sup>) to be classified as a new genus of bacteria of the *Bacteroides* family [10]. We previously reported the ribosomal 16S sequence and the MALDI-TOF MS spectrum [11]. Since the first report, a new strain was isolated confirming the new species. Here we present the complete description of strain Marseille-P2645<sup>T</sup> (= CSUR P2645 = DSM 103034), together with the description of the complete genomic sequencing and annotation.

## Materials and Methods

### Sample collection

Strain Marseille-P2645<sup>T</sup> was first isolated in April 2016 in a liquid colon sample from a 58-year-old woman without medical history, who underwent a colonoscopy because of a positive screening test for a colorectal cancer in the gastroenterology department of Hôpital Nord, Marseille, France. Signed informed consent was collected from the patient, and the study obtained approval from the ethics committee of the Institut Fédératif de Recherche IFR48 under number 2016-010.

### Strain isolation and identification by MALDI-TOF MS

After collection using sterilized devices, the colonic sample was immediately placed in an antioxidant-enriched liquid medium [12] and transported to our laboratory (Institut Hospitalo-Universitaire Méditerranée Infection, Marseille, France). Once in the laboratory, the sample was placed under a laminar flow cabinet before being diluted in phosphate-buffered saline and seeded on different solid and liquid culture media. The initial growth of strain Marseille-P2645<sup>T</sup> was achieved after 1 day at 37°C on 5% sheep's blood-enriched Columbia agar (bioMérieux, Marcy l'Etoile, France) in anaerobic atmosphere (anaeroGEN; Oxoid, Dardilly, France). After isolation on pure culture, the identification of all different bacterial colonies was performed using MALDI-TOF MS using a Microflex spectrometer (Bruker Daltonics, Bremen, Germany), as previously reported [13,14]. Each colony was deposited in duplicate on a MALDI-TOF MS target to be analysed. A matrix solution of 1.5 µL (saturated solution of cyano-4-hydroxycinnamic acid diluted in 50% acetonitrile and 2.5% trifluoroacetic acid, completed with high-performance liquid chromatography water) was deposited on each spot. After the reading of the plate, the obtained protein spectra were compared by MALDI Biotyper software with those of

the Bruker database (continuously updated with our recent data). When the resulting score was >2, the identification was made at the species level, while a score of <1.7 did not enable any identification.

### 16S rRNA sequencing and phylogeny

After 3 failed MALDI-TOF MS identifications, a standard 16S rRNA PCR was performed using universal primers pair fD1 and rP2 in a GeneAmp PCR System 2720 thermal cycler (Thermo Fisher Scientific, Waltham, MA, USA). The amplified DNA was revealed by electrophoresis on 1.5% agarose gel. Once validated, the PCR product was purified and sequenced using the Big Dye Terminator Sequencing Kit and the following internal primers: 536F, 536R, 800F, 800R, 1050F, 1050R, 357F and 357R, as previously described [1]. Sequences were corrected using the Codon Code Aligner software (<http://www.codoncode.com>), and then a BLAST search (Basic Local Alignment Search Tool) was performed against the GenBank nucleotide collection (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>). A strain was considered as a candidate novel genus if the percentage of 16S rRNA similarity with the closest species with standing in nomenclature was <95% [15]. We performed a phylogenetic analysis based on the 16S rRNA of our isolate to identify its phylogenetic affiliations. Sequences were aligned using Muscle 3.8.31 [16], and phylogenetic inferences were obtained using the approximately maximum-likelihood method within FastTree software [17]. Only bootstrap values of >95% are shown, and the numbers at the nodes are the computed local values [18].

### Phenotype characteristics

Different growth conditions were tested on a 5% sheep's blood-enriched Columbia agar (bioMérieux) for strain Marseille-P2645<sup>T</sup>. Five temperatures (room temperature, 28, 37, 45 and 55°C) and three atmospheres—anaerobic (anaeroGen Compact; Oxoid), microaerophilic (campyGen Compact; Oxoid) and aerobic (in a plastic pouch to maintain a humid atmosphere)—were evaluated. Tolerance of this strain to salt was tested using 5%, 7.5%, 10%, 15% and 20% of NaCl, and the pH tolerance (5, 5.5, 6, 6.5, 7, 7.5 and 8) was also tested. Individual cells of strain Marseille-P2645<sup>T</sup> were visualized using a Tecnai G20 electron microscope (FEI Company, Limeil-Brevannes, France). Gram staining was performed and observed using a photonic microscope Leica DM2500 (Leica, Wetzlar, Germany) with a 100× oil-immersion objective. Motility testing was performed by observation of a fresh colony between the blades and slats using a DM1000 photonic microscope (Leica) at 40×. To check the ability to sporulate, strain Marseille-P2645<sup>T</sup> was grown on 5% sheep's blood-

enriched Columbia agar (bioMérieux) for 2 days, and then a heat-shock test (20 minutes at 80°C) was performed.

### Biochemical characterization and antibiotic susceptibility

The commercially available API ZYM, API 50CH and API 20A strips (bioMérieux) were used for biochemical tests according to the manufacturer's instructions. Catalase (bioMérieux) and oxidase (Becton Dickinson, Le Pont de Claix, France) activities were also tested.

Cellular fatty acid methyl ester (FAME) analysis was performed by gas chromatography/mass spectrometry (GC/MS). Two samples were prepared with approximately 60 mg of bacterial biomass per tube collected from several culture plates. FAMES were prepared as described by Sasser [19]. GC/MS analyses were carried out as described by Dione et al. [20] in genome analysis and description of *Anaerobaculum massiliensis*. Briefly, FAMES were separated using an Elite 5-MS column and monitored by mass spectrometry (Clarus 500-SQ 8 S; Perkin Elmer, Courtaboeuf, France). Spectral database search was performed using MS Search 2.0 operated with the Standard Reference Database 1A (National Institute of Standards and Technology, Gaithersburg, MD, USA) and the FAMES mass spectral database (Wiley, Chichester, UK).

Sensitivity to antibiotics was determined using a disc diffusion method on Mueller-Hinton E agar (bioMérieux). The following antibiotics were tested using Sirscan discs (i2a, Montpellier, France): doxycycline, rifampicin, vancomycin, amoxicillin, ceftriaxone, penicillin, trimethoprim/sulfamethoxazole, imipenem, oxacillin, erythromycin, tobramycin, cefotaxime, amoxicillin/clavulanic acid, gentamicin, fosfomicin and metronidazole. Inhibition diameters were measured using the Scan1200 scanner (Interscience, Saint-Nom-La Bretèche, France).

### Genome sequencing and assembly

After pretreatment by a lysozyme incubation at 37°C for 2 hours, DNA of strain Marseille-P2645<sup>T</sup> was extracted on the EZ1 biorobot (Qiagen, Germantown, MD, USA) with a EZ1 DNA tissue kit. The elution volume was 50 µL. Genomic DNA was quantified by a Qubit assay with the high-sensitivity kit (Life Technologies, Carlsbad, CA, USA) to 80.7 ng/µL.

Genomic DNA of strain Marseille-P2645<sup>T</sup> was sequenced on the MiSeq Technology (Illumina, San Diego, CA, USA) with the mate-pair strategy. The genomic DNA was barcoded in order to be mixed with 11 other projects with the Nextera Mate Pair sample prep kit (Illumina). The mate-pair library was prepared with 1.5 µg of genomic DNA using the Nextera mate pair Illumina guide. The genomic DNA sample was simultaneously fragmented and tagged with a mate-pair junction

adapter. The pattern of the fragmentation was validated on an Agilent 2100 BioAnalyzer (Agilent Technologies, Santa Clara, CA, USA) with a DNA 7500 labchip. The DNA fragments ranged in size from 1.5 to 11 kb, with an optimal size at 8.44 kb. No size selection was performed, and 600 ng of tagged fragments were circularized. The circularized DNA was mechanically sheared to small fragments with an optimal at 916 bp on a Covaris device S2 in T6 tubes (Covaris, Woburn, MA, USA). The library profile was visualized on a High Sensitivity Bioanalyzer LabChip (Agilent Technologies), and the final concentration library was measured at 81.95 nmol/L. The libraries were normalized at 2 nM and pooled. After a denaturation step and dilution at 15 pM, the pool of libraries was loaded onto the reagent cartridge and then onto the instrument along with the flow cell. Automated cluster generation and sequencing run were performed in a single 39-hour run at a 2 × 151 bp read length.

Total information of 5.3 Gb was obtained from a 559K/mm<sup>2</sup> cluster density, with a cluster passing quality control filters of 96.3% (10 450 000 passed filter clusters). Within this run, the index representation for strain Marseille-P2645<sup>T</sup> was determined to be 10.02%. The 1 047 418 paired-end reads were filtered according to the read qualities.

### Genome annotation and comparisons

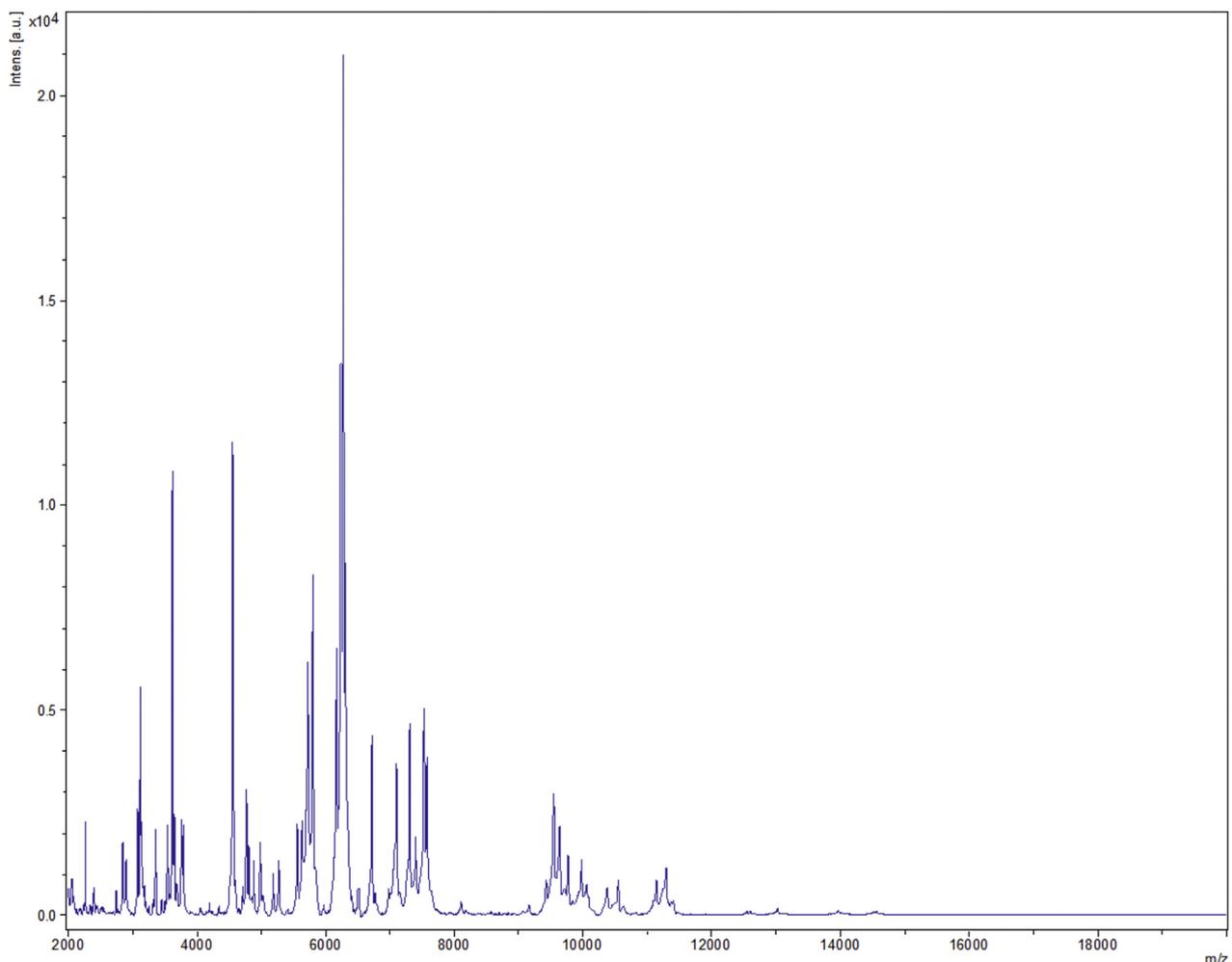
Prodigal was used for open reading frame (ORFs) prediction [21] with default parameters, but the predicted ORFs were excluded if they spanned a sequencing gap region (containing N). The predicted bacterial protein sequences were searched against the GenBank database [22] and the Clusters of Orthologous Groups database (COGs) using BLASTP (*E* value 1e-03, coverage 0.7 and identity percentage 30%). If no hit was found, a search was performed against the NR database using BLASTP with an *E* value of 1e-03, coverage of 0.7 and identity percentage of 30%. If the sequence lengths were smaller than 80 aa, we used an *E* value of 1e-05. Both tRNAs and rRNAs were predicted using the tRNAScan-SE [23] and RNAmmer [24] tools, respectively. Lipoprotein signal peptides and the number of transmembrane helices were predicted using SignalP [25] and TMHMM [26], respectively. ORFans were identified when their BLASTP *E* value was lower than 1e-03 for an alignment length greater than 80 aa. If alignment lengths were smaller than 80 aa, we used an *E* value of 1e-05. Such parameter thresholds have already been used in previous works to define ORFans. Artemis [27] and DNA Plotter [28] were used for data management and for visualization of genomic features, respectively. To estimate the mean level of nucleotide sequence similarity at the genome level between strain Marseille-P2645<sup>T</sup> and other bacteria, we used the average genomic identity of orthologous gene sequences (AGIOS) homemade software

[29]. This software combines the Proteinortho software for detecting orthologous proteins between genomes compared two by two [30], then retrieves the corresponding genes and determines the mean percentage of nucleotide sequence identity among orthologous ORFs using the Needleman-Wunsch global alignment algorithm. The genome of strain Marseille-P2645<sup>T</sup> was compared with other *Bacteroidetes*: *Bacteroides fragilis* strain NCTC 9343, *Bacteroides fingoldii* strain DSM 17565, *Bacteroides thetaiotaomicron* strain VPI 8452, *Bacteroides coprocola* DSM 17136, *Bacteroides plebeius* DSM 17135, *Bacteroides vulgatus* ATCC 8482, *Bacteroides massiliensis* DSM 17679, *Bacteroides fluxus* YIT 12057 and *Bacteroides rodentium* JCM 16496. Annotation and comparison processes were performed by the multiagent software system DAGOBAN [31], which includes Figenix [32] libraries that provided pipeline analysis. We also performed genome-to-genome distance calculator (GGDC) analysis using the GGDC Web server, as previously reported [33,34].

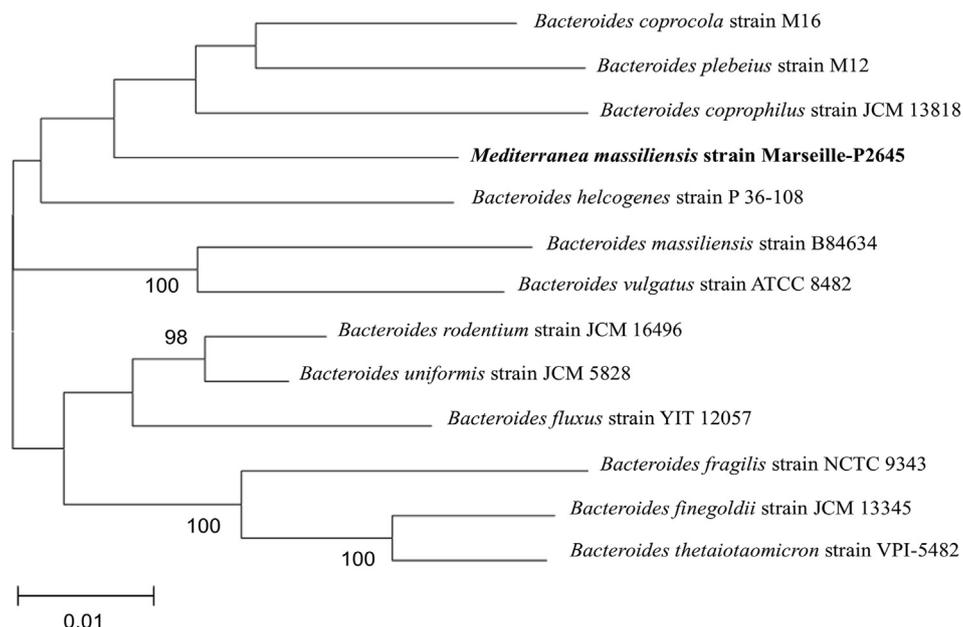
## Results

### Phylogenetic analysis

Strain Marseille-P2645<sup>T</sup> was first isolated after a 1-day anaerobic incubation period of cultivation of the sample seeded on Colombia agar with 5% sheep's blood. MALDI-TOF MS spectrum of P2645<sup>T</sup> (Fig. 1) did not match anything in our database or in Brucker's database. Phylogenetic analysis based on the 16S rRNA showed that strain Marseille-P2645<sup>T</sup> exhibited a 92.9% sequence similarity [10] with *Bacteroides helcogenes* strain P36-108<sup>T</sup> (GenBank accession no. CP002352), the phylogenetically closest species with standing in nomenclature (Fig. 2) [9]. *Bacteroides coprophilus* strain CB42T (AB260026) [35] was also a close validated species of strain Marseille-P2645<sup>T</sup>; this strain is a Gram-negative anaerobic bacterium isolated from human faeces in 2007. Because of a 16S rRNA gene sequence divergence of >5% from its phylogenetically closest species with standing in



**FIG. 1.** Reference mass spectrum from *Mediterranea massiliensis* strain Marseille-P2645.



**FIG. 2.** Phylogenetic tree highlighting phylogenetic position of *Mediterranea massiliensis* strain Marseille-P2645<sup>T</sup> relative to other phylogenetically close members of family *Bacteroidaceae*. Sequences were aligned using CLUSTALWV, and phylogenetic inferences were obtained using maximum likelihood method within MEGA7 software. Numbers at nodes are percentages of bootstrap values obtained by repeating analysis 500 times to generate majority consensus tree. Only bootstraps scores  $\geq 95\%$  were retained. Scale bar indicates 1% nucleotide sequence divergence.

nomenclature, we propose that strain Marseille-P2645<sup>T</sup> be a member of a novel genus in the family of *Bacteroidaceae* in the phylum of *Bacteroidetes*, for which we propose the name *Mediterranea* gen. nov. The 16S rRNA of strain Marseille-P2645<sup>T</sup> was deposited in GenBank under accession number LT558847.3 (Table 1). A gel view was performed in order to observe spectra differences between *M. massiliensis* and other close bacteria (Fig. 3).

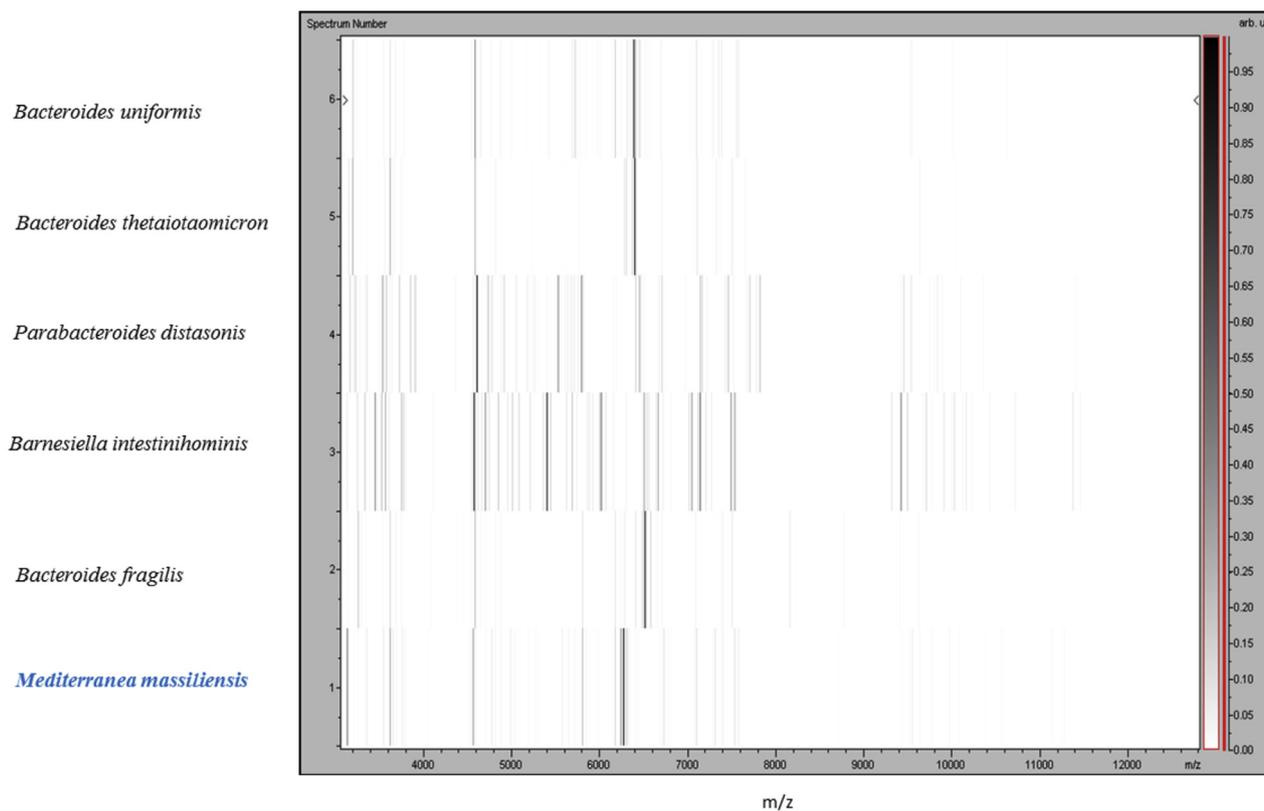
**Phenotypic and biochemical characterizations**

The optimum growth of Strain Marseille-P2645<sup>T</sup> was obtained after 1 day of culture at 37°C in anaerobic conditions (anaer-oGEN, Oxoid). Colonies grown on 5% sheep’s blood–enriched Columbia agar medium were translucent and slightly haemolytic, with a diameter of 0.5 mm. Bacterial cells were Gram-negative bacilli (Fig. 4a), 1 µm in length and 0.6 µm in

diameter (Fig. 4b). This strain is non–spore-forming, peritrichous and motile. Catalase and oxidase reactions were negative. Marseille-P2645<sup>T</sup> was able to grow at 28°C and 45°C. It is strictly anaerobic and unable to grow under micro-aerophilic or aerobic conditions. The range of salinity used shows that strain Marseille-P2645<sup>T</sup> does not tolerate salt. Strain Marseille-P2645<sup>T</sup> survives from pH 5 to 8 with an optimal pH at 7. Classification and general features are summarized in Table 2. Using API ZYM (bioMérieux), positive reactions were obtained for alkaline phosphatase, acid phosphatase, α-galactosidase, β-galactosidase, α-glucosidase, β-glucosidase, α-fucosidase and N-acetyl β-glucosaminidase, but negative reactions for α-mannosidase, α-chymotrypsin, trypsin and lipase-C14. In the API 20A (bioMérieux), the strain showed gelatin production but no indole or esculin production (ferric citrate). Using API 50CH system, positive reactions were obtained for D-glucose,

**TABLE I.** Percentage of 16S rRNA similarities between strain Marseille-P2645<sup>T</sup> and *Bacteroides* genus

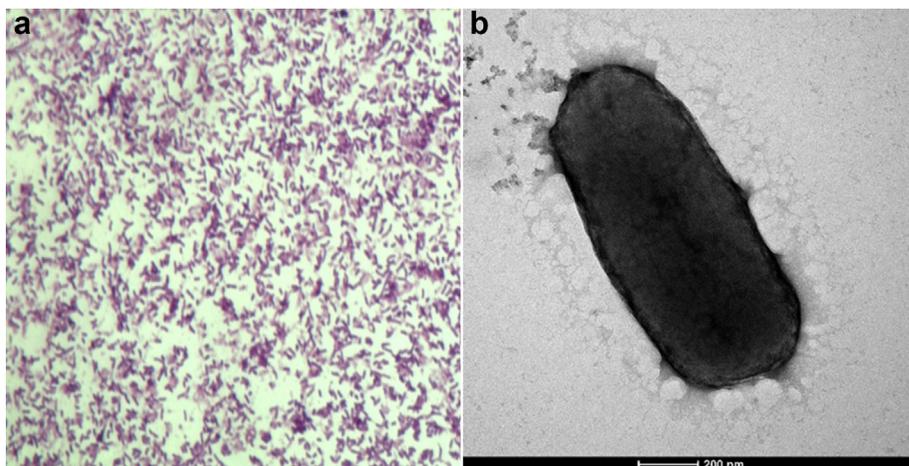
	<i>Mediterranea massiliensis</i>	<i>Bacteroides helcogenes</i>	<i>Bacteroides coprophilus</i>	<i>Bacteroides plebeius</i>	<i>Bacteroides coprocola</i>	<i>Bacteroides massiliensis</i>
<i>M. massiliensis</i>	100	94.90	94.11	92.68	93.00	91.63
<i>B. helcogenes</i>		100	93.39	92.98	92.97	93.12
<i>B. coprophilus</i>			100	93.86	93.05	92.38
<i>B. plebeius</i>				100	94.55	93.34
<i>B. coprocola</i>					100	92.58
<i>B. massiliensis</i>						100



**FIG. 3.** Gel view comparing *Mediterranea massiliensis* strain Marseille-P2645<sup>T</sup> to other members of family *Bacteroidaceae*. Gel view displays raw spectra of loaded spectrum files arranged in pseudo-gel-like look. x-axis records *m/z* value. Left y-axis displays running spectrum number originating from subsequent spectra loading. Peak intensity is expressed as greyscale. Colour bar and right axis indicate intensity of each matrix-assisted desorption ionization–time of flight mass spectrometry peak and peak intensity in arbitrary units.

mannose, starch and potassium 5-ketogluconate, whereas negative reactions were observed for L-arabinose, D-ribose, D-fructose, D-maltose, D-lactose and other constituents. Phenotypic characteristics were compared to other members of the genus *Bacteroides* (Table 3). Among the tested antibiotics, cells

were susceptible to amoxicillin, rifampicin, imipenem, metro-nidazole and amoxicillin/clavulanic acid, but resistant to van-comycin, cefotaxime, gentamicin, penicillin, clindamycin, oxacillin, tobramycin, fosfomycin, ceftriaxone, doxycycline, erythromycin and trimethoprim/sulfamethoxazole. Analysis of



**FIG. 4.** (a) Gram staining of *Mediterranea massiliensis* strain Marseille-P2645<sup>T</sup>. (b) Transmission electron microscopy of *M. massiliensis* strain Marseille-P2645<sup>T</sup> with Tecnai G20 electron microscope. Scale bar = 200 nm.

**TABLE 2. Classification and general features of *Mediterranea massiliensis* strain Marseille-P2645<sup>T</sup>**

Property	Term
Current classification	Domain: Bacteria Phylum: <i>Bacteroidetes</i> Class: <i>Bacteroidia</i> Order: <i>Bacteroidales</i> Family: <i>Bacteroidaceae</i> Genus: <i>Mediterranea</i> Species: <i>Mediterranea massiliensis</i> Type: Strain Marseille-P2645 <sup>T</sup>
Gram stain	Negative
Cell shape	Rod
Motility	Motile
Sporulation	No sporulating
Temperature range	28–45°C
Optimum temperature	37°C
pH range: optimum	7
Salinity	0g/L
Oxygen requirement	Anaerobic
Carbone source	Unknown
Habitat	Colon
Biotic relationship	Free-living
Pathogenicity	Unknown

the total cellular fatty acid composition of *Mediterranea massiliensis* demonstrated that the fatty acids detected are mainly saturated. The major fatty acids found for this strain were 15:0 iso (42%) and 15:0 anteiso (20%). Several specific 3-hydroxy fatty acids were observed: 17:0 3-OH iso, 16:0 3-OH and 15:0 3-OH iso (Table 4).

**Genome properties**

The genome of strain Marseille-P2645<sup>T</sup> is 3 950 441 bp long with 51.66 mol% G+C content (Fig. 5). It is composed of 25

scaffolds (composed of 34 contigs). Of the 3439 predicted genes, 3374 were protein-coding genes and 65 were RNA genes (three genes are 5S rRNA, one gene is 16S rRNA, one gene is 23S rRNA and 60 genes are tRNA genes). A total of 2772 genes (82.16%) were assigned a putative function (by COGs or by NR BLAST), and 92 genes were identified as ORFans (2.73%). The remaining genes were annotated as hypothetical proteins (449 genes, 13.31%). Genome statistics are summarized in Table 5, and the distribution of the genes into COGs functional categories is presented in Table 6.

**Genome comparison**

The draft genome sequence of strain Marseille-P2645<sup>T</sup> (3.95 Mb) is smaller than the *Bacteroides* genome analysed, and particularly that of *Bacteroides finegoldii* (4.89Mb), *Bacteroides vulgatus* (5.16), *Bacteroides rodentium* (4.88), *Bacteroides plebeius* (4.42), *Bacteroides fragilis* (5.24), *Bacteroides fluxus* (4.33), *Bacteroides thetaiotaomicron* (6.29), *Bacteroides coprocola* (4.30) and *Bacteroides massiliensis* (4.64). The G+C content of *Mediterranea massiliensis* (51.66%) is much higher (widely >1%) than that of *Bacteroides finegoldii* (42.93%), *Bacteroides vulgatus* (42.2%), *Bacteroides plebeius* (44.31%), *Bacteroides fragilis* (43.11%), *Bacteroides thetaiotaomicron* (42.86%), *Bacteroides massiliensis* (42.69%), *Bacteroides rodentium* (47.05%), *Bacteroides coprocola* (41.87%) and *Bacteroides fluxus* (45.57%). The gene content of *Mediterranea massiliensis* (3374 genes) is smaller than that of *Bacteroides finegoldii* (4485), *Bacteroides vulgatus* (4065), *Bacteroides plebeius* (3933), *Bacteroides fragilis* (4236), *Bacteroides*

**TABLE 3. Differential characteristics of *Mediterranea massiliensis* strain Marseille-P2645 compared to other close bacteria of family *Bacteroidaceae***

Property	<i>Mediterranea massiliensis</i>	<i>Bacteroides finegoldii</i>	<i>Bacteroides vulgatus</i>	<i>Bacteroides plebeius</i>	<i>Bacteroides fragilis</i>	<i>Bacteroides thetaiotaomicron</i>	<i>Bacteroides massiliensis</i>	<i>Bacteroides rodentium</i>	<i>Bacteroides coprocola</i>	<i>Bacteroides fluxus</i>
Cell diameter (µm)	0.6	1–2	0.5–0.8	0.8	1.3	0.7–2	0.8–1.4	0.5–2	0.8	1.0–1.4
Oxygen requirement	Anaerobic	Anaerobic	Anaerobic	Anaerobic	Anaerobic	Anaerobic	Anaerobic	Anaerobic	Anaerobic	Anaerobic
Shape	Bacilli	Bacilli	Bacilli	Bacilli	Bacilli	Bacilli	Bacilli	Bacilli	Bacilli	Bacilli
Gram stain	–	–	–	–	–	–	–	–	–	–
Motility	+	–	–	–	–	–	–	–	–	–
Indole	–	–	–	–	–	+	–	–	–	+
Production of:										
Alkaline phosphatase	+	+	+	NA	NA	+	NA	NA	NA	+
Catalase	–	NA	–	NA	+	+	–	NA	NA	NA
Oxidase	–	NA	NA	NA	+	NA	NA	NA	NA	NA
Nitrate reductase	NA	–	–	NA	NA	+	NA	NA	NA	–
Urease	–	–	NA	NA	NA	–	NA	NA	NA	–
β-Galactosidase	+	+	–	NA	+	+	NA	NA	NA	+
N-acetyl glucosamine	–	+	NA	NA	+	+	NA	NA	NA	NA
Acid from:										
L-Arabinose	–	+	+	+	–	+	–	+	–	+
Ribose	–	NA	+	NA	–	NA	–	NA	NA	NA
Mannose	+	+	+	NA	+	+	NA	NA	NA	+
Mannitol	–	–	–	NA	–	–	NA	NA	NA	+
Sucrose	NA	+	+	NA	+	+	NA	NA	NA	+
D-Glucose	+	+	+	NA	+	+	NA	NA	NA	+
D-Fructose	–	NA	+	NA	+	+	NA	NA	NA	+
D-Maltose	–	+	+	NA	+	+	NA	NA	NA	+
D-Lactose	–	+	+	NA	+	+	NA	NA	NA	+
G+C content (%)	51.66	42.93	42.2	44.31	43.11	42.86	42.69	47.05	41.87	45.57
Habitat	Human colon	Human gut	Human gut	Human gut	Human gut	Human gut	Human gut	Human gut	Human gut	Human gut

+, positive result; –, negative result; NA, data not available.

**TABLE 4.** Total cellular fatty acid composition of *Mediterranea massiliensis* strain Marseille-P2645<sup>T</sup>

Fatty acid	Name	Mean relative % <sup>a</sup>
15:0 iso	13-methyl-Tetradecanoic acid	41.7 ± 0.9
15:0 anteiso	12-methyl-Tetradecanoic acid	19.7 ± 0.2
16:00	Hexadecanoic acid	6.7 ± 0.3
14:00	Tetradecanoic acid	6.0 ± 0.4
18:1n9	9-Octadecenoic acid	5.8 ± 0.3
18:2n6	9,12-Octadecadienoic acid	4.5 ± 0.3
17:0 3-OH iso	3-hydroxy-15-methyl-Hexadecanoic acid	4.1 ± 0.1
16:0 3-OH	3-hydroxy-Hexadecanoic acid	3.8 ± 0.1
15:00	Pentadecanoic acid	1.9 ± 0.1
18:00	Octadecanoic acid	1.5 ± 0.1
13:0 iso	11-methyl-Dodecanoic acid	1.4 ± 0.1
5:0 anteiso	2-methyl-Butanoic acid	1.0 ± 0.1
17:0 iso	15-methyl-Hexadecanoic acid	TR
14:0 iso	12-methyl-Tridecanoic acid	TR
18:1n6	12-Octadecenoic acid	TR
15:0 3-OH iso	3-hydroxy-13-methyl-Tetradecanoic acid	TR
20:4n6	5, 8, 11,14-Eicosatetraenoic acid	TR
17:00	Heptadecanoic acid	TR
17:0 anteiso	14-methyl-Hexadecanoic acid	TR
13:0 anteiso	10-methyl-Dodecanoic acid	TR
13:00	Tridecanoic acid	TR
16:0 iso	14-methyl-Pentadecanoic acid	TR
16:1n7	9-Hexadecenoic acid	TR

TR, trace amounts < 1%.  
<sup>a</sup>Mean peak area percentage.

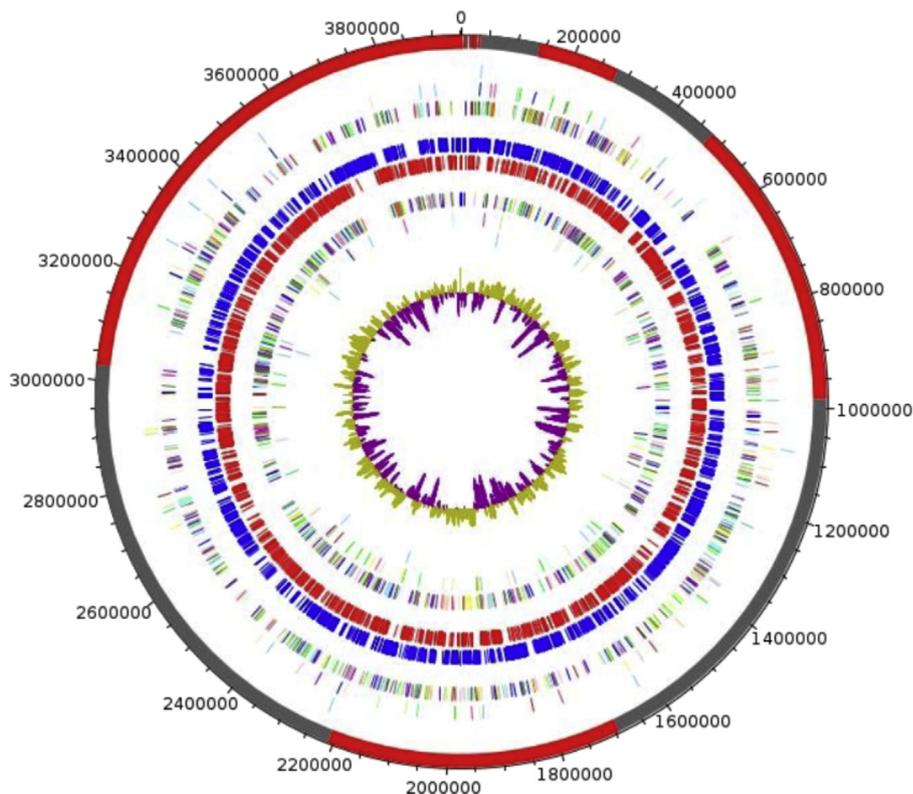
*thetaitaomicron* (4825), *Bacteroides massiliensis* (3935), *Bacteroides rodentium* (4993), *Bacteroides coprocola* (4291) and *Bacteroides fluxus* (3921). Distribution of functional classes of predicted genes according to the clusters of orthologous

**TABLE 5.** Nucleotide content and gene count level of genome of strain Marseille-P2645<sup>T</sup>

Attribute	Genome (total)	
	Value	% of total <sup>a</sup>
Size (bp)	3 950 441	100
No. of GC	2 039 331	51.66
Coding region	3 499 039	88.57
Total genes	3439	100
RNA genes	65	1.890084386
Protein-coding genes	3374	100
Genes with function prediction	2772	82.16
Genes assigned to COGs	1601	47.45
Genes with peptides signal	835	24.75
Genes with Pfam-A domains	2999	87
Genes with transmembrane helices	646	19.1464138
Genes associated to PKS or NRPS	9	0.27
Genes associated to virulence	588	17.43
Proteins associated to ORFans	92	2.726733923

COGs, Clusters of Orthologous Groups database; NRPS, nonribosomal peptide synthase; ORF, open reading frame; PKS, polyketide synthase.  
<sup>a</sup>Total is based on either size of genome in base pairs or total number of protein-coding genes in annotated genome.

groups of proteins between *M. massiliensis* and other members of the genus of *Bacteroides* was reported (Fig. 6). In addition, strain Marseille-P2645<sup>T</sup> shared 4485, 4065, 3933, 4236, 4825, 3935, 4993, 4291 and 3921 orthologous genes with *Bacteroides finegoldii* strain DSM 17565, *Bacteroides vulgatus* strain ATCC 8482, *Bacteroides plebeius* strain DSM 17135, *Bacteroides fragilis* strain NCTC 9343, *Bacteroides thetaiotaomicron* strain VPI 5482,

**FIG. 5.** Graphical circular map of genome. From outside to centre: contigs (red/grey), COGs category of genes on forward strand (three circles), genes on forward strand (blue circle), genes on reverse strand (red circle), COGs category on reverse strand (three circles), GC content. COGs, Clusters of Orthologous Groups database.

**TABLE 6.** Number of genes associated with 25 general COGs functional categories of strain Marseille-P2645<sup>T</sup>.

Code	Value	% of total <sup>a</sup>	Description
J	178	5.275637	Translation
A	0	0	RNA processing and modification
K	90	2.667457	Transcription
L	124	3.6751633	Replication, recombination and repair
B	0	0	Chromatin structure and dynamics
D	25	0.7409603	Cell cycle control, mitosis and meiosis
Y	0	0	Nuclear structure
V	75	2.2228808	Defense mechanisms
T	72	2.1339657	Signal transduction mechanisms
M	150	4.4457617	Cell wall/membrane biogenesis
N	11	0.32602254	Cell motility
Z	0	0	Cytoskeleton
W	0	0	Extracellular structures
U	32	0.9484292	Intracellular trafficking and secretion
O	66	1.9561353	Posttranslational modification, protein turnover, chaperones
X	33	0.97806764	Mobilome: prophages, transposons
C	97	2.8749259	Energy production and conversion
G	146	4.327208	Carbohydrate transport and metabolism
E	122	3.6158864	Amino acid transport and metabolism
F	63	1.86722	Nucleotide transport and metabolism
H	94	2.7860107	Coenzyme transport and metabolism
I	58	1.719028	Lipid transport and metabolism
P	102	3.023118	Inorganic ion transport and metabolism
Q	19	0.56312984	Secondary metabolites biosynthesis, transport and catabolism
R	141	4.179016	General function prediction only
S	61	1.8079432	Function unknown
—	1773	52.548904	Not in COGs

COGs, Clusters of Orthologous Groups database.  
<sup>a</sup>Total is based on total number of protein-coding genes in annotated genome.

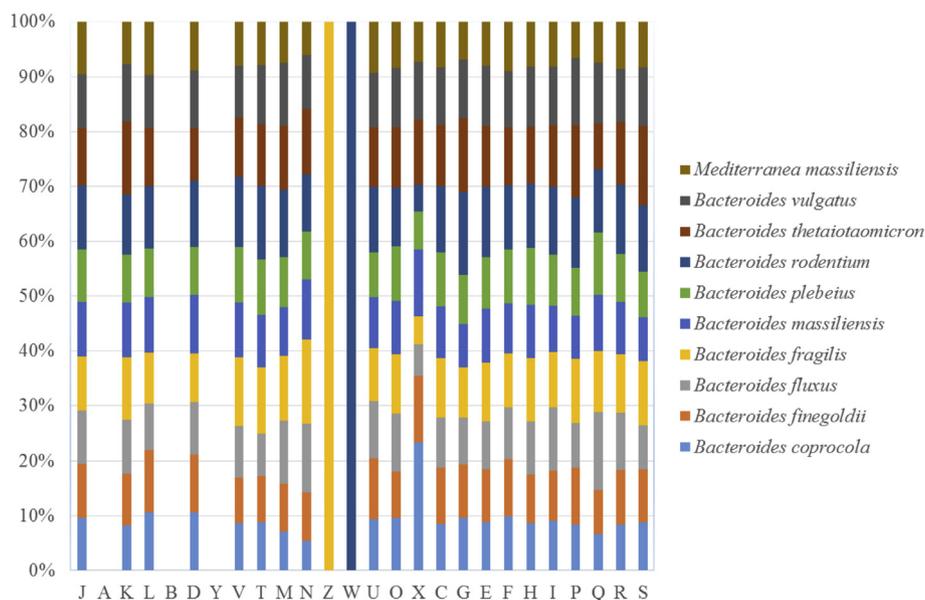
*Bacteroides massiliensis* strain B84634, *Bacteroides rodentium* strain JCM 16496, *Bacteroides coprocola* strain DSM 17136 and *Bacteroides fluxus* strain YIT 12057. The average nucleotide sequence identity ranged from 58.89% to 66.13% between strain Marseille-P2645<sup>T</sup>, as well as the nine other members of

the family *Bacteroidaceae* (Table 7). Results from pairwise comparison obtained for the analysis of the digital DNA-DNA hybridization (dDDH) using GGDC software are reported in Table 8. The probability of error when saying that this strain is a new species (DDH >70%) compared to nine other member of the genus *Bacteroides* was 0.02% (GGDC2.1 formula 2; DSMZ, <http://ggdc.dsmz.de/distcalc2.php>). When comparing strain Marseille-P2645<sup>T</sup> with other strains, dDDH values ranged from 21.60% ± 4.7 for *Bacteroides fluxus* strain YIT 12057 to 28.10% ± 4.9 for *Bacteroides coprocola* strain M16 (DSM 17136).

**Taxonomical and nomenclatural proposals**

*Description of Mediterranea gen. nov.* The genus name is *Mediterranea* (me.di.ter.ra.nea', N.L. fem. n., from *mediterraneum*, the Latin name of the Mediterranean Sea), as this strain was first isolated in Marseille, on the banks of the Mediterranean sea. This is a Gram-negative, non-spore forming, nonmotile and preferentially anaerobic bacilli. Cells do not show catalase or oxydase activity. On the basis of 16S rRNA gene sequence analysis, *Mediterranea* is a member of the family *Bacteroidaceae*. Its type species is *Mediterranea massiliensis* strain Marseille-P2645<sup>T</sup>.

*Description of Mediterranea massiliensis gen. nov., sp. nov.* *Mediterranea massiliensis* gen. nov., sp. nov. (mas.si.li.en.'sis, L. fem. adj., from *massiliensis*, 'of Massilia,' the Latin name for Marseille, where the strain was first cultivated) is classified as a member of the family *Bacteroidaceae* in the phylum *Bacteroidetes*. It is a Gram-negative and motile bacillus whose cells measure 1 µm in



**FIG. 6.** Distribution of functional classes of predicted genes according to clusters of orthologous groups of proteins of *Mediterranea Massiliensis* strain Marseille-P2645.

**TABLE 7.** Number of orthologous proteins shared between genomes (upper right), average percentage similarity of nucleotides corresponding to orthologous protein shared between genomes (lower left), and number of proteins per genome (in bold)

	<i>Bacteroides massiliensis</i>	<i>Mediterranea massiliensis</i>	<i>Bacteroides coprocola</i>	<i>Bacteroides vulgatus</i>	<i>Bacteroides fluxus</i>	<i>Bacteroides rodentium</i>	<i>Bacteroides finegoldii</i>	<i>Bacteroides plebeius</i>	<i>Bacteroides thetaiotaomicron</i>	<i>Bacteroides fragilis</i>
<i>B. massiliensis</i>	<b>3935</b>	1623	1627	1866	1744	1429	1738	1711	1787	1795
<i>Mediterranea massiliensis</i>	57.96%	<b>3374</b>	1543	1554	1665	1399	1603	1630	1633	1594
<i>B. coprocola</i>	61.03%	58.89%	<b>4291</b>	1589	1583	1324	1662	1767	1635	1562
<i>B. vulgatus</i>	70.47%	57.83%	61.28%	<b>4065</b>	1708	1482	1737	1697	1912	1821
<i>B. fluxus</i>	60.98%	62.46%	60.63%	60.44%	<b>3921</b>	1546	1756	1659	1822	1814
<i>B. rodentium</i>	58.71%	74.68%	59.73%	59.03%	65.13%	<b>4993</b>	1451	1386	1591	1531
<i>B. finegoldii</i>	60.29%	60.03%	60.04%	59.18%	60.21%	60.75%	<b>4485</b>	1674	1978	1779
<i>B. plebeius</i>	61.51%	59.80%	63.84%	61.40%	58.94%	59.89%	59.99%	<b>3933</b>	1721	1643
<i>B. thetaiotaomicron</i>	61.30%	58.97%	58.95%	61.11%	58.49%	59.64%	66.51%	59.37%	<b>4825</b>	2014
<i>B. fragilis</i>	61.21%	58.10%	58.62%	61.12%	60.41%	59.26%	62.81%	59.18%	66.13%	<b>4236</b>

**TABLE 8.** Pairwise comparison of *Mediterranea massiliensis* strain Marseille-P2645<sup>T</sup> with other species of *Bacteroides* genus using GGDC formula 2 (DDH estimates based on identities/HSP length)<sup>a</sup>

	<i>Mediterranea massiliensis</i>	<i>Bacteroides coprocola</i>	<i>Bacteroides finegoldii</i>	<i>Bacteroides fluxus</i>	<i>Bacteroides fragilis</i>	<i>Bacteroides massiliensis</i>	<i>Bacteroides plebeius</i>	<i>Bacteroides rodentium</i>	<i>Bacteroides thetaiotaomicron</i>	<i>Bacteroides vulgatus</i>
<i>M. massiliensis</i>	100% ± 00	28.10% ± 4.9	27.40% ± 4.8	21.60% ± 4.7	22.30% ± 4.8	27.40% ± 4.8	22.90% ± 4.7	23.10% ± 4.8	22.20% ± 4.8	24.70% ± 4.8
<i>B. coprocola</i>		100% ± 00	34.30% ± 5	21.70% ± 4.7	23.70% ± 4.7	25.50% ± 4.8	22.10% ± 4.7	29.30% ± 4.9	22.60% ± 4.7	22.40% ± 4.7
<i>B. finegoldii</i>			100% ± 00	20.50% ± 4.6	21.10% ± 4.7	24.90% ± 4.8	25.90% ± 4.8	22.20% ± 4.7	25.70% ± 4.8	24.20% ± 4.8
<i>B. fluxus</i>				100% ± 00	22.00% ± 4.7	23.50% ± 4.8	29.10% ± 4.9	24.70% ± 4.8	20.60% ± 4.6	21.60% ± 4.7
<i>B. fragilis</i>					100% ± 00	20.20% ± 4.6	23.30% ± 4.8	21.90% ± 4.7	21.70% ± 4.7	22.30% ± 4.7
<i>B. massiliensis</i>						100% ± 00	23.40% ± 4.5	26.20% ± 4.8	26.70% ± 4.8	25.70% ± 4.8
<i>B. plebeius</i>							100% ± 00	27.40% ± 4.8	25.80% ± 4.8	21.20% ± 4.7
<i>B. rodentium</i>								100% ± 00	21.50% ± 4.7	26.70% ± 4.8
<i>B. thetaiotaomicron</i>									100% ± 00	26.40% ± 4.9
<i>B. vulgatus</i>										100% ± 00

DDH, DNA-DNA hybridization; GGDC, Genome-to-Genome Distance Calculator; HSP, high-scoring segment pairs.

<sup>a</sup>Confidence intervals indicate inherent uncertainty in estimating DDH values from intergenomic distances based on models derived from empirical test data sets (which are always limited in size). These results are in accordance with 16S rRNA and phylogenomic analyses as well as GGDC results.

length and 0.6 µm in diameter. Optimal growth conditions are obtained at 37°C, and it is strictly anaerobic. Colonies were translucent and slightly haemolytic, with a diameter of 0.5 mm after growth on 5% sheep's blood-enriched agar. Using API ZYM, strain Marseille-P2645<sup>T</sup> exhibited alkaline phosphatase, acid phosphatase, α-galactosidase, β-galactosidase, α-glucosidase, β-glucosidase α-fucosidase and *N*-acetyl β-glucosaminidase activities. Using API 20A (bioMérieux), *Mediterranea massiliensis* exhibited gelatin production but no indole or esculin activity. Strain Marseille-P2645<sup>T</sup> exhibits D-glucose, mannose, starch and potassium 5-ketogluconate activities and does not metabolize L-arabinose, ribose, mannitol, D-fructose, D-maltose and D-lactose assay. The bacterium is susceptible to amoxicillin, rifampicin, imipenem, metronidazole and amoxicillin/clavulanic acid. Predominant cellular fatty acids are 13-methyl-tetradecanoic acid (15:0 iso), 12-methyl-tetradecanoic acid (15:0 ante-iso), hexadecanoic acid (16:00), tetradecanoic acid (14:00), 9-octadecenoic acid (18:1n9), 9,12-octadecadienoic acid (18:2n6), 3-hydroxy-15-methyl-hexadecanoic acid (17:0 3-OH iso) and 3-hydroxy-hexadecanoic acid (16:0 3-OH). The genome of *Mediterranea massiliensis* strain Marseille-P2645<sup>T</sup> is 3 950 441 bp long with 51.66% G+C content. The genome and

16S rRNA sequences from strain Marseille-P2645<sup>T</sup> were deposited in GenBank under accession numbers FQSB00000000 and LT558847, respectively. The type strain Marseille-P2645<sup>T</sup> was deposited in CSUR and DSMZ collections under numbers CSUR P2645 and DSM 103034, and was cultivated from the colon lavage of a 58-year-old woman without medical history, who underwent a colonoscopy because of a positive screening test for a colorectal cancer.

## Discussion

Currently, the development of -omics technologies has provided an overview of the complexity of microbial communities living outside and inside our organism. These considerable technologic advances have led to an exponential progression in the knowledge of the human gut microbiota. However, we have recently developed a methodology for the dynamic description of new bacteria, including new species and genera of the digestive flora, using the original approach of culturomics to explore microbial diversity of clinical and environmental samples. We report here the isolation and culture of a new

bacterial genus from the colon lavage of a 58-year-old patient from Marseille, France. The isolation of this bacterium was confirmed by its deposit in two different collections: DSMZ (Deutsche Sammlung von Mikroorganismen und Zellkulturen) and the CSUR (Collection de Souches de l'Unité des Rickettsies). Thus, the use of an antioxidant-enriched transport medium before being seeded on a solid medium composed of 5% Columbia agar enriched with sheep's blood has allowed the isolation a new genus of bacteria called *Mediterranea* with the species *massiliensis*.

Phylogenetically, *Mediterranea massiliensis* is close to bacteria of the genus *Bacteroides*, which are Gram-negative and anaerobic bacilli colonizing mainly the intestinal flora. Here, *Bacteroides helcogenes* is the phylogenetically closest species of strain Marseille-P2645<sup>T</sup>. As for *Bacteroides*, *Mediterranea massiliensis* does not form spores. The main differences with closest neighbours are the motility (positive for *M. Massiliensis* but negative for *Bacteroides* species) and sequence divergence of 16S rRNA gene (>5%) compared to *Bacteroides helcogenes* P36-108<sup>T</sup>, the type strain of the closest phylogenetic neighbour and difference in G+C content (51.66% for strain Marseille-P2645<sup>T</sup> vs. 41% to 47% for compared *Bacteroides* species). These differences confirm the classification of *Mediterranea massiliensis* as a distinct species. Furthermore, the values of the AGIOS and dDDH of *Mediterranea massiliensis* compared to all other known species confirm its new genus and species status.

## Conclusion

Microbial culturomics continue to significantly expand the repertoire of isolated bacteria in the digestive tract. Application of culturomics to the duodenum, ileum and colon would improve the understanding of microbiota involvement in human health and diseases. Thus, our study may contribute to a better knowledge of the associated human microorganisms, and could help to better understand physiologic functioning in health and disease. On the basis of phenotypic, genomic and phylogenetic analyses, we formally propose the creation of *Mediterranea massiliensis* gen. nov., sp. nov., represented by the strain Marseille-P2645<sup>T</sup> (= CSUR P2645 = DSM 103034).

## Acknowledgements

The authors thank the Xegen Company ([www.xegen.fr/](http://www.xegen.fr/)) for automating the genomic annotation process. This study was funded by the Fondation Méditerranée Infection.

## Conflict of interest

None declared.

## References

- [1] 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.
- [2] 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.
- [3] Lagier JC, Khelaifia S, Alou MT, Ndongo S, Dione N, Hugon P, et al. Culture of previously uncultured members of the human gut microbiota by culturomics. *Nat Microbiol* 2016;1:16203.
- [4] Fournier PE, Lagier JC, Dubourg G, Raoult D. From culturomics to taxonomogenomics: a need to change the taxonomy of prokaryotes in clinical microbiology. *Anaerobe* 2015;36:73–8.
- [5] Sentausa E, Fournier PE. Advantages and limitations of genomics in prokaryotic taxonomy. *Clin Microbiol Infect* 2013;19:790–5.
- [6] Pagani I, Liolios K, Jansson J, Chen IMA, Smirnova T, Nosrat B, et al. The Genomes OnLine Database (GOLD) v.4: status of genomic and metagenomic projects and their associated metadata. *Nucleic Acids Res* 2012;40:D571–9.
- [7] Vandamme P, Pot B, Gillis M, de Vos P, Kersters K, Swings J. Polyphasic taxonomy, a consensus approach to bacterial systematics. *Microbiol Rev* 1996;60:407–38.
- [8] Stackebrandt E. Taxonomic parameters revisited: tarnished gold standards. *Microbiol Today* 2006;6:152–5.
- [9] Benno Y, Watabe J, Mitsuoka T. *Bacteroides pyogenes* sp. nov., *Bacteroides suis* sp. nov., and *Bacteroides helcogenes* sp. nov., new species from abscesses and feces of pigs. *Syst Appl Microbiol* 1983;4:396–407.
- [10] 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.
- [11] Mailhe M, Ricaboni D, Benezech A, Saber K, Fournier PE, Raoult D. '*Mediterranea massiliensis*' gen. nov., sp. nov., a new human-associated bacterium isolated from the right and left colon lavage of a 58-year-old patient. *New Microbe New Infect* 2016;13:54–5.
- [12] La Scola B, Khelaifia S, Lagier JC, Raoult D. Aerobic culture of anaerobic bacteria using antioxidants: a preliminary report. *Eur J Clin Microbiol Infect Dis* 2014;33:1781–3.
- [13] Seng P, Drancourt M, Gouriet F, La Scola B, Fournier PE, Rolain JM, et al. Ongoing revolution in bacteriology: routine identification of bacteria by matrix-assisted laser desorption ionization time-of-flight mass spectrometry. *Clin Infect Dis* 2009;49:543–51.
- [14] Seng P, Rolain JM, Fournier PE, La Scola B, Drancourt M, Raoult D. MALDI-TOF–mass spectrometry applications in clinical microbiology. *Future Microbiol* 2010;5:1733–54.
- [15] Sankar SA, Lagier JC, Pontarotti P, Raoult D, Fournier PE. The human gut microbiome, a taxonomic conundrum. *Syst Appl Microbiol* 2015;38:276–86.
- [16] Edgar RC. MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res* 2004;32:1792–7.
- [17] Price MN, Dehal PS, Arkin AP. FastTree 2—approximately maximum-likelihood trees for large alignments. *PLoS One* 2010;5, e9490.
- [18] Shimodaira H, Hasegawa M. Multiple comparisons of log-likelihoods with applications to phylogenetic inference. *Mol Biol Evol* 1999;16:1114–6.

- [19] Sasser M. Bacterial identification by gas chromatographic analysis of fatty acids methyl esters (GC-FAME). Newark, NY: Microbial ID; 2006.
- [20] Dione N, Sankar SA, Lagier JC, Khelaifia S, Michele C, Armstrong N, et al. Genome sequence and description of *Anaerostipes massiliensis* sp. nov. *New Microbe New Infect* 2016;10:66–76.
- [21] Hyatt D, Chen GL, Locascio PF, Land ML, Larimer FW, Hauser LJ. Prodigal: prokaryotic gene recognition and translation initiation site identification. *BMC Bioinform* 2010;11:119.
- [22] Benson DA, Cavanaugh M, Clark K, Karsch-Mizrachi I, Lipman DJ, Ostell J, et al. GenBank. *Nucleic Acids Res* 2017;45:D37–42.
- [23] Lowe TM, Eddy SR. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. *Nucleic Acids Res* 1997;25:955–64.
- [24] Lagesen K, Hallin P, Rødland EA, Stærfeldt HH, Rognes T, Ussery DW. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. *Nucleic Acids Res* 2007;35:3100–8.
- [25] Dyrlov Bendtsen J, Nielsen H, von Heijne G, Brunak S. Improved prediction of signal peptides: SignalP 3.0. *J Mol Biol* 2004;340:783–95.
- [26] Krogh A, Larsson B, von Heijne G, Sonnhammer EL. Predicting transmembrane protein topology with a hidden markov model: application to complete genomes. *J Mol Biol* 2001;305:567–80.
- [27] Rutherford K, Parkhill J, Crook J, Horsnell T, Rice P, Rajandream MA, et al. Artemis: sequence visualization and annotation. *Bioinformatics* 2000;16:944–5.
- [28] Carver T, Thomson N, Bleasby A, Berriman M, Parkhill J. DNAPlotter: circular and linear interactive genome visualization. *Bioinformatics* 2009;25:119–20.
- [29] Ramasamy D, Mishra AK, Lagier JC, Padhmanabhan R, Rossi M, Sentausa E, et al. A polyphasic strategy incorporating genomic data for the taxonomic description of novel bacterial species. *Int J Syst Evol Microbiol* 2014;64:384–91.
- [30] Lechner M, Findeiß S, Steiner L, Marz M, Stadler PF, Prohaska SJ. Proteinortho: detection of (co-)orthologs in large-scale analysis. *BMC Bioinform* 2011;12:124.
- [31] Gouret P, Paganini J, Dainat J, Louati D, Darbo E, Pontarotti P, et al. Integration of evolutionary biology concepts for functional annotation and automation of complex research in evolution: the multi-agent software system DAGOBAN. In: Pontarotti P, editor. *Evolutionary biology—concepts, biodiversity, macroevolution and genome evolution*. Berlin: Springer-Verlag; 2011. p. 71–87.
- [32] Gouret P, Vitiello V, Balandraud N, Gilles A, Pontarotti P, Danchin EG. FIGENIX: intelligent automation of genomic annotation: expertise integration in a new software platform. *BMC Bioinform* 2005;6:198.
- [33] Meier-Kolthoff JP, Auch AF, Klenk HP, Göker M. Genome sequence-based species delimitation with confidence intervals and improved distance functions. *BMC Bioinform* 2013;14:60.
- [34] Auch AF, von Jan M, Klenk HP, Göker M. Digital DNA-DNA hybridization for microbial species delineation by means of genome-to-genome sequence comparison. *Stand Genomic Sci* 2010;2:117.
- [35] Hayashi H, Shibata K, Bakir MA, Sakamoto M, Tomita S, Benno Y. *Bacteroides coprophilus* sp. nov., isolated from human faeces. *Int J Syst Evol Microbiol* 2007;57:1323–6.