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Gorillibacterium timonense sp. nov., isolated from an obese patient

Sokhna Ndongo^{1,3} · Mamadou Beye^{1,3} · Noémie Labas^{1,3} · Fabrizio Di Pinto^{1,3} · Magali Richez^{1,3} · Jean-Christophe Lagier^{1,3} · Pierre-Edouard Fournier^{2,3} · Didier Raoult^{1,3} · Fadi Bittar^{1,3} 

Abstract

A Gram-negative and facultative anaerobic bacterium, designated strain SN4^T, was isolated from the stool sample of an obese Amazonian patient. The new isolate was characterized by the taxonogenomics approach. The strain SN4^T was beige-colored, circular and not haemolytic. Cells are rod shaped and motile with several flagella. Strain SN4^T grows optimally at pH 7 and can survive in the presence of a saline concentration of up to 75 g/l NaCl. The 16S ribosomal RNA gene sequence analysis of the novel strain SN4^T showed 95.28% similarity in nucleotide sequence with *Gorillibacterium massiliense* G5^T, the phylogenetically closest neighbor and the type species of this genus. Anteiso-C_{15:0}, iso-C_{15:0} and C_{16:0} were found as the major components in the cellular fatty acid analysis of this isolate. The genomic draft of strain SN4^T is 5,263,742 bp long with 53.33% of G+C content. The differences in physiological, biochemical characteristics and phylogenetic and genomic data make it possible to clearly distinguish the strain SN4^T from *G. massiliense* G5^T. Based on the taxonogenomic description and the phenotypic and biochemical characteristics of this bacterium presented in this article, we propose the SN4^T strain (= CSUR P2011 = DSM 100,698) as a new species, *Gorillibacterium timonense* sp. nov.

Keywords *Gorillibacterium timonense* · Genome · Taxonogenomics · Human gut microbiota

Introduction

The development of metagenomics has allowed, over the last 10 years, a better exploration of the intestinal microbiota and has demonstrated the relationship between altered gut microflora and several diseases such as obesity, inflammatory bowel disease and irritable bowel syndrome (Salazar et al. 2014). However, the composition of human gut microbiota and its relationship to the host, particularly with respect to

human health and disease, provides several challenges for microbiologists (Lagier et al. 2012b). Indeed, 1 g of a human stool sample contains between 10¹¹ and 10¹² bacteria (Raoult and Henrissat 2014), but only about 2000 different bacterial species are actually isolated from human microbiota. In this respect, and given the insufficient attention previously paid to culture methods, our laboratory has developed culturomics (Lagier et al. 2012a) to improve the isolation of bacteria from the human gut. Since the application of this technique in 2012, many novel genera and species have been isolated from the human gut. Moreover, for the description of these new bacteria, complete genome sequencing, matrix-assisted laser-desorption/ionization time-of-flight (MALDI-TOF) spectrum analysis of cellular proteins, cellular fatty acid methyl ester (FAME) analysis (Sasser 2006) and more traditional methods for phenotypic characterization have recently been developed (Ramasamy et al. 2014). This strategy, named taxonogenomics, has proven useful in describing new bacterial taxa (Ramasamy et al. 2014).

Among these new taxa, *Gorillibacterium timonense* strain SN4 (= CSUR P2011 = DSM 100,698) is a new member of the genus *Gorillibacterium* first described by Keita et al. (Keita et al. 2014). The genus *Gorillibacterium* belongs to

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the family *Paenibacillaceae* and the strain SN4 is the second species of this genus following the isolation of *G. massiliense* from the fecal flora of a gorilla.

We present here the isolation, a summary classification, phenotypic characteristics, as well as a description of the complete genome sequencing and annotation of the SN4 strain of *G. timonense*.

Materials and methods

Sample information and strain isolation

A stool sample was collected from an obese Amazonian man (45 years old; Manaus, Brazil) during a culturomics project exploring the human intestinal microbiota. An informed consent was obtained from the patient and the procedures were approved by the local ethics committee of the Institut Fédératif de Recherche 48 (Marseille, France) under the agreement number 09-022. The stool sample was conserved at -80°C at La Timone Hospital in Marseille until being investigated. Strain SN4^T was isolated in 2015 by cultivation on Columbia agar supplemented with 5% sheep blood (BioMérieux, Marcy l'Etoile, France) in microaerophilic atmosphere generated by CampyGen (Oxoid, Dardilly, France) after 48 h at 37°C . Briefly, 1 g of aliquot of the thawed stool was suspended in phosphate-buffered saline. 1 ml of this suspension was diluted several times to the tenth. 50 μl of each dilution was spread in Columbia agar plates and then incubated at 37°C for 48 h under microaerophilic conditions. Isolated colonies were purified by individual subculture in the same type of culture medium in which they were first isolated.

Strain identification by MALDI-TOF mass spectrometry (MS) and phylogenetic analysis

MALDI-TOF MS analysis of proteins was performed for the identification of bacteria following the same protocol previously described (Lagier et al. 2012c). The generated spectra were then compared to the Bruker database, which is supplemented by spectra of new strains found by various cultural projects, including four *Gorillibacterium massiliense* G5^T spectra. The identification and discrimination of the analyzed strain depend on the score obtained by comparison with the BioTyper database spectra: a score > 2 with a validated species enabled the identification at the species level; and a score < 1.7 did not enable any identification. Following a failed identification of our strain by MALDI-TOF MS, sequencing of the 16S ribosomal RNA gene was achieved as previously described (Drancourt et al. 2000). The 16S rRNA nucleotide sequence obtained was aligned and analyzed using the CodonCode Aligner software (<https://www.codoncode.com/>).

The BLAST nucleotide was then searched in the National Center for Biotechnology Information (NCBI) online database (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>). CLUSTAL W was used for sequences alignment of the different species and MEGA 7 (Molecular Evolutionary Genetics Analysis) software was used to construct the phylogenetic tree.

Phenotypic, biochemical and chemotaxonomic analyses

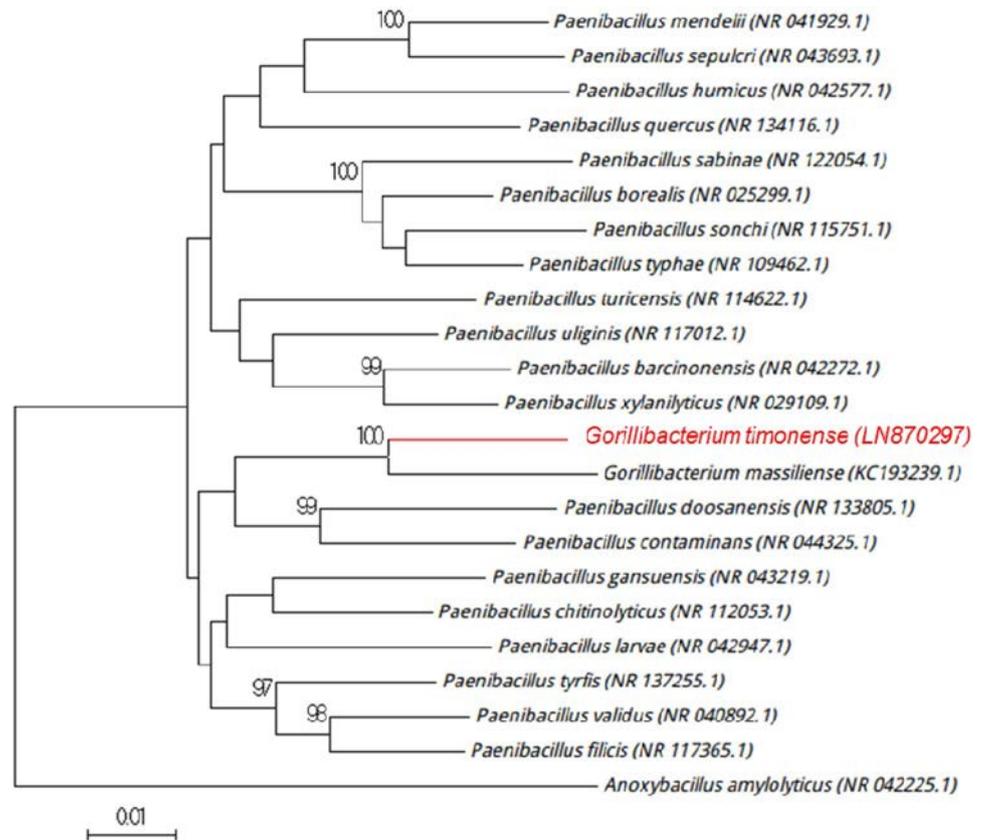
Different growth temperatures (28°C , 37°C , 45°C , 55°C) were assessed for strain SN4^T by cultivating it on 5% sheep's blood-enriched Columbia agar (bioMérieux) under anaerobic and microaerophilic conditions using AnaeroGenTM and CampyGenTM, respectively (bioMérieux, ThermoFisher scientific). Growth was also tested aerobically with or without 5% CO_2 . The salinity tolerance for strain SN4^T was tested using 0, 5, 25 and 50% NaCl concentrations and four pH values for growth were tested: 6, 6.5, 7 and 8.5. Gram staining and motility were observed from fresh colonies between blades and slats using a DM1000 photonic microscope (Leica Microsystems, Nanterre, France) with a $40\times$ objective lens.

Spore formation was determined by a heat shock (80°C for 20 min) and then subcultured on 5% sheep blood-enriched Columbia agar medium (bioMérieux). The SN4^T strain was analyzed by electron microscopy using Formvar-coated grids placed on a 40 μl drop of bacterial suspension and incubated at 37°C for 30 min, followed by a 10 s incubation with ammonium molybdate. The grids were then dried on blotting paper and observed using a transmission electron microscope Tecnai G20 (FEI Company, Limeil-Brévannes, France) at an operating voltage of 60 kV.

Biochemical characteristics of strain SN4^T and strain G5^T (*Gorillibacterium massiliense*) were obtained using the API ZYM strips, API 50CH and API 20NE performed according to the manufacturer's instructions (bioMérieux). Catalase and oxidase activities were determined using a BD BBL DrySlide (Becton, Dickinson, New Jersey, USA) according to the manufacturer's instructions. The antimicrobial activity test was performed by the disk diffusion method (Le Page et al. 2015) using 16 antibiotics including Ceftriaxone, Ciprofloxacin, Clindamycin, Colistin, Doxycycline, Erythromycin, Gentamycin, Oxacillin, Rifampicin, Penicillin, Teicoplanin, Trimethoprim-sulfamethoxazole, Vancomycin, Imipenem, Fosfomicin and Metronidazole. The discs used were purchased from i2a (Montpellier, France) and strain SN4^T was cultivated on Mueller–Hinton agar in a Petri dish (bioMérieux, Marcy-l'Etoile, France).

Cellular fatty acid methyl ester (FAME) analyses of this isolate and of *G. massiliense* strain G5^T were performed by gas chromatography/mass spectrometry (GC/MS) as

Fig. 1 Phylogenetic tree highlighting the position of *Gorillibacterium timonense* strain SN4^T relative to the type species of the genus *Gorillibacterium* (*G. massiliense* strain G5^T) and some other members of the family *Paenibacillaceae*. GenBank accession numbers are indicated in parentheses. Sequences were aligned using CLUSTALW, and phylogenetic inferences obtained using the maximum-likelihood method within the MEGA 6 software. Numbers at the nodes are bootstrap values obtained by repeating the analysis 1000 times to generate a majority consensus tree. The scale bar indicates a 1% nucleotide sequence divergence



previously described by Dione et al. (Dione et al. 2016). Briefly, strain SN4^T and strain G5^T were cultured on 5% sheep's blood-enriched Columbia agar (bioMérieux) under aerobic condition for 24 h at 37 °C. Approximately 100 mg of bacterial biomass of each strain was collected from four different agar plates. Fatty acid methyl esters were then prepared as described by Sasser (2006), were separated using an Elite 5-MS column and were 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 (NIST, Gaithersburg, USA) and the FAME mass spectral database (Wiley, Chichester, UK).

Genomic DNA preparation, genome sequencing and assembly

Genomic DNA (gDNA) from strain SN4^T was extracted using the EZ1 biorobot (Qiagen, Courtaboeuf, France) with EZ1 DNA tissue kit as previously described (Abou Abdallah et al. 2017). gDNA was sequenced on the MiSeq sequencer (Illumina Inc, San Diego, CA, USA) with the mate pair sequencing strategy as previously described (Abou Abdallah et al. 2017). The genome's assembly was performed as previously described (Abou Abdallah et al. 2017) using a pipeline

which made it possible to create an assembly with different softwares [Velvet (Zerbino and Birney 2008), Spades (Bankovich et al. 2012) and Soap Denovo (Luo et al. 2012)], on trimmed [MiSeq and Trimmomatic software (Bolger et al. 2014)] or untrimmed data (only MiSeq software).

GapCloser (Luo et al. 2012) was used to reduce gaps for each of the assemblies performed. Then contamination with Phage Phix was identified (blastn against Phage Phix174 DNA sequence) and eliminated. In the end, scaffolds with a size of less than 800 bp were removed and scaffolds with a depth value of less than 25% of the average depth were identified as possible contaminants and removed.

Genome annotation and comparison

Open Reading Frames (ORFs), ORFans, tRNA genes, ribosomal RNAs and other nucleotide contents have been identified using the tools and settings as was previously described by Abou Abdallah et al. (2019).

Comparative genomic analysis was realized between the genome of strain SN4^T and the genome of *G. massiliense* strain G5^T (CBQR00000000). Two parameters were used to evaluate the genomic similarity between the two studied *Gorillibacterium* strains: digital DNA–DNA hybridization (dDDH) that exhibits a high correlation with DDH (Auch et al. 2010; Meier-Kolthoff et al. 2013a) and OrthoAni

Table 1 Differential characteristics of *Gorillibacterium timonense* strain SN4^T with *Gorillibacterium massiliense* strain G5^T

Properties	<i>Gorillibacterium timonense</i> strain SN4 ^T	<i>Gorillibacterium massiliense</i> strain G5 ^T
Motility	+	–
Endospore formation	+	–
Catalase	–	+
Esterase	+	–
Esterase lipase	+	–
L-Arginine	–	+
Urease	–	+
β-Galactosidase	+	–
D-Glucose	–	+
L-Arabinose	–	+
D-Mannose	–	+
N-Acetyl-glucosamine	–	+
D-Maltose	–	+
D-Ribose	+	–
D-Fructose	–	+
D-Galactose	+	–
Amygdalin	+	–
Salicin	–	+
Inulin	–	+
Xylitol	–	+
D-Xylose	–	+

+ = positive; – = negative

which is a software for calculating average nucleotide identity (ANI) (Lee et al. 2016).

Strain and sequence deposition

Strain SN4^T has been deposited in two microbial culture collections: the German collection of microorganisms (Deutsche Sammlung von Mikroorganismen und Zellkulturen, DSMZ), under the accession number DSM 100,698, and the French culture collection (Collection de Souches de l'Unité des Rickettsies, CSUR), under the accession number CSUR P2011. The 16S rRNA gene and genome sequences are deposited in EMBL-EBI under the accession numbers LN870297 and CYUM00000000, respectively. The Digital Protologue database (<https://imedea.uib-csic.es/dprotologue>) e) taxon number for strain SN4T is TA00778.

Results and discussion

Strain identification and phylogenetic analyses

Strain SN4^T was first isolated in 2015 by the cultivation of a stool sample from an obese Amazonian patient on 5% sheep

Table 2 Cellular fatty acids composition for *Gorillibacterium timonense* strain SN4^T and for *Gorillibacterium massiliense* strain G5^T

Fatty acids	IUPAC name	<i>G. timonense</i> strain SN4 ^{Ta}	<i>G. massiliense</i> strain G5 ^{Ta}
15:0 anteiso	12-Methyl-tetradecanoic acid	38.0 ± 2.3	66.7 ± 0.9
15:0 iso	13-Methyl-tetradecanoic acid	24.0 ± 1.5	4.9 ± 0.1
16:00	Hexadecanoic acid	16.9 ± 1.4	11.9 ± 0.7
18:1n9	9-Octadecenoic acid	5.0 ± 0.8	TR
14:00	Tetradecanoic acid	4.2 ± 0.5	1.2 ± 0.1
18:00	Octadecanoic acid	2.7 ± 0.1	TR
14:0 iso	12-Methyl-tridecanoic acid	2.0 ± 0.1	TR
16:0 iso	14-Methyl-pentadecanoic acid	1.7 ± 0.2	5.3 ± 0.2
15:00	Pentadecanoic acid	TR	1.4 ± 0.1
13:0 anteiso	10-Methyl-dodecanoic acid	TR	NF
17:0 anteiso	14-Methyl-hexadecanoic acid	TR	4.9 ± 0.1
18:2n6	9,12-Octadecadienoic acid	TR	TR
17:0 iso	15-Methyl-hexadecanoic acid	TR	TR
18:1n6	12-Octadecenoic acid	TR	TR
16:1n7	9-Hexadecenoic acid	TR	TR
17:00	Heptadecanoic acid	TR	NF
5:0 anteiso	2-Methyl-butanoic acid	TR	NF
12:00	Dodecanoic acid	TR	NF
13:0 iso	11-Methyl-dodecanoic acid	TR	TR

TR trace amounts < 1%, NF not found

^aMean relative % ± SD

blood agar under microaerophilic conditions. The spectrum generated from clean strain SN4^T (Supplementary Fig. 1), following MALDI-TOF MS analysis, displayed an identification score of 1.3, which suggested that the spectrum was unknown in our database, indicating that the strain could be a new species. The 16S ribosomal RNA gene sequence of strain SN4^T (GenBank accession number LN870297) showed 95.3% similarity with the nucleotide sequence of *Gorillibacterium massiliense* G5^T (GenBank accession number NR_146838) (Fig. 1). The second closest species was a member of *Paenibacillus* genus (*Paenibacillus turicensis* strain MOL722, 93.13%). This value of similarity was lower than the 98.7% 16S rRNA gene sequence threshold recommended by Stackebrandt and Ebers to delineate a new species (Stackebrandt and Ebers 2006) and without the need for carrying out DDH according to the recommendation of Meier-Kolthoff et al. for *Firmicutes*, with a maximum error

Table 3 Nucleotide content and gene count levels of the genome of *G. timonense* strain SN4^T

Attribute	Genome (total)	
	Value	Total (%) ^a
Size (bp)	5,263,742	100
G+C content (%)	2,807,257	53.33
Coding region (bp)	4,561,907	86.66
Total genes	4778	100
RNA genes	68	1.42
Protein-coding genes	4712	100
Genes with function prediction	3261	69.23
Genes assigned to COGs	2797	59.38
Genes with peptide signals	613	13.01
Genes with transmembrane helices	1105	23.46
Genes associated to toxin/antitoxin	134	2.84
ORFn genes	301	6.39
Genes associated with PKS or NRPS	9	0.19

^aThe total is based on either the size of the genome in base pairs or the total number of protein-coding genes in the annotated genome

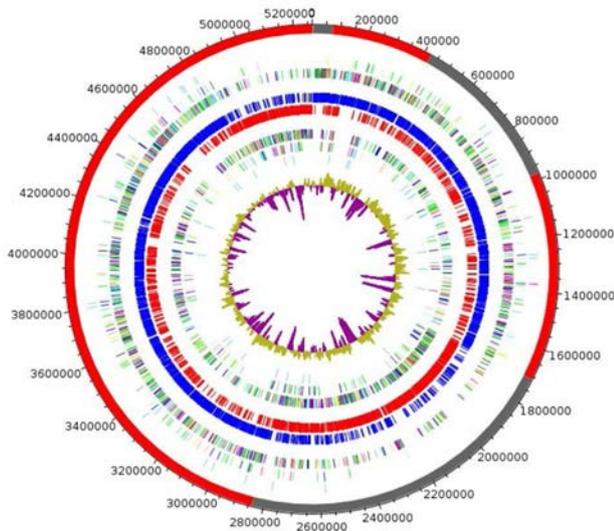


Fig. 2 Graphical circular map of the genome of *Gorillibacterium timonense* strain SN4^T. From outside to the center: contigs (red/grey), COG category of genes on the forward strand (three circles), genes on forward strand (blue circle), genes on the reverse strand (red circle), COG category on the reverse strand (three circles), GC content

probability of 0.01% (Meier-Kolthoff et al. 2013b). Based on these results, strain SN4^T was thus classified as a putative new species of the genus *Gorillibacterium* and named *Gorillibacterium timonense*. The reference spectrum was then added to our database (Supplementary Fig. 1) (<https://www.mediterranee-infection.com/article.php?larub=280&titre=urms-database>) and the gel view highlighted

the differences with *G. massiliense* G5^T, the first member of the genus *Gorillibacterium* (Supplementary Fig. 2).

Phenotypic, biochemical and chemotaxonomic analyses

Although strain SN4^T was first isolated under microaerophilic condition, it grows better under aerobic condition on 5% sheep's blood-enriched Columbia agar at 37 °C after 24 h. Bacterial growth, morphology, antimicrobial susceptibility testing and biochemical characteristics for strain SN4^T are detailed in the description of the species, Supplementary Table 1, Supplementary Fig. 3).

The main phenotypic and biochemical differences of strain SN4^T compared with *G. massiliense* strain G5^T are presented in Table 1. Analysis of cellular FAMES shows that the most abundant fatty acids are unsaturated: 12-methyl-tetradecanoic acid (38%), 13-methyl-tetradecanoic acid (24%) and hexadecanoic acid (17%) (Table 2). Almost half of the described fatty acids are branched (iso or anteiso). Cellular fatty acid profile of strain SN4^T compared to this of *G. massiliense* strain G5^T is presented in Table 2.

Genome properties

The genome is 5,263,742 bp long with 53.33% of G+C content (Table 3, Fig. 2). It is composed of seven scaffolds (composed of nine contigs). Of the 4,778 predicted genes, 4,710 were protein-coding genes and 68 were RNAs (5 genes are 5S rRNA, 1 gene is 16S rRNA, 1 gene is 23S rRNA, 61 genes are tRNA genes). A total of 3,261 genes (69.24%) were assigned as putative function (by cogs or by NR BLAST) (Supplementary Table 2). 301 genes were identified as ORFans (6.39%) and 964 genes were annotated as hypothetical proteins (20.47%).

Genome comparison

The draft genome sequence of strain SN4^T is smaller than that of *Gorillibacterium massiliense* strain G5^T (5.26 MB vs 5.55 MB, respectively). The G+C content of strain SN4^T is higher than that of *G. massiliense* strain G5^T (53.33% vs 50.39%, respectively). The gene content of strain SN4^T is lower than that of *G. massiliense* strain G5^T (4,778 vs 5,151, respectively). A similar distribution of genes into COG categories was observed between the 2 compared genomes (Fig. 3). dDDH estimation of strain SN4^T against *G. massiliense* strain G5^T is 20.8% [18.5–23.2%]. This value is very low and below the 70% threshold used for species delineation in the classification of prokaryotes. The ANI value between the genome of

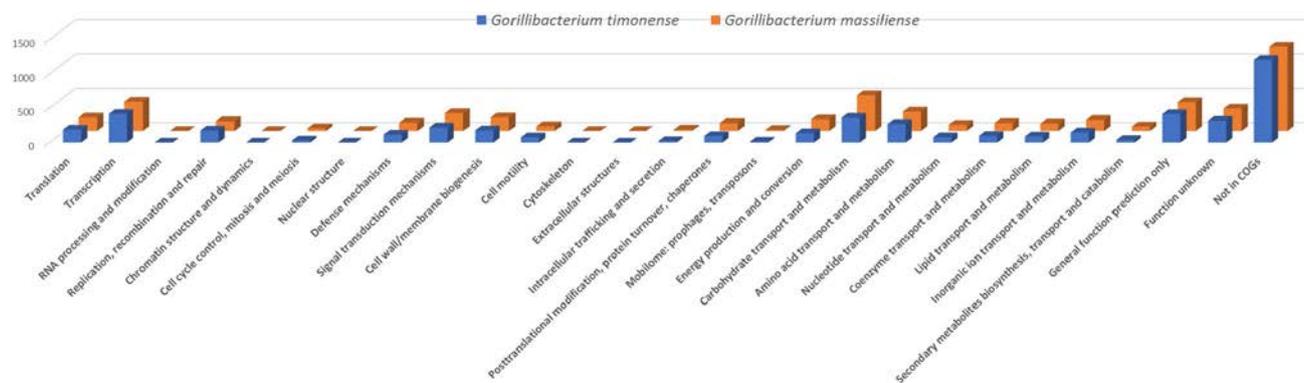


Fig. 3 Distribution of functional classes of predicted genes according to the clusters of orthologous groups of proteins of *Gorillibacterium timonense* strain SN4^T and *Gorillibacterium massiliense* strain G5^T

strain SN4^T and the genome of *G. massiliense* strain G5^T is 70.24%. This value is also below the 96% ANI cutoff for species circumscription (Ciufu et al. 2018), confirming again the status of strain SN4^T as a new species.

Taxonomomic conclusion

The phylogenetic and genomic distances between strain SN4^T and the only type species of the genus *Gorillibacterium* together with the combination of unique phenotypic characteristics indicate that strain SN4^T represents a novel species of the genus *Gorillibacterium*, for which the name *Gorillibacterium timonense* sp. nov. is formally proposed. This bacterial strain has been isolated from the fecal flora of an obese Amazonian patient.

Description of *Gorillibacterium timonense* sp. nov.

Gorillibacterium timonense (ti.mo.nen'se NL adj neut, *timonense* of Timone, the main hospital of Marseille where strain SN4^T was first cultivated).

A facultative anaerobic, mesophilic and Gram-negative bacterium. Cells are rod shaped with a mean diameter of 0.6 µm and a length of 1.8–2.5 µm. Catalase and oxidase negative. Colonies are circular, beige, smooth and not haemolytic on 5% sheep blood-enriched Columbia agar. Optimal growth occurs at 37 °C with 0–75 g/l of NaCl and at pH 7–8.5. Using API 20NE system, a positive reaction was obtained for esculin hydrolysis and β-galactosidase. Using API ZYM, positive reactions were observed for esterase, esterase lipase, naphthol-AS-BI-phosphohydrolase, α-galactosidase and β-galactosidase. Using API 50 CH strip, strain SN4^T showed positive reactions for the fermentation of L-arabinose, D-xylose, methyl-β D-xylopyranoside, D-galactose, D-glucose, D-fructose, D-mannose, methyl-αD-glucopyranoside, N-acetylglucosamine, amygdalin,

esculin, D-cellobiose, D-maltose, D-lactose, D-melibiose, D-saccharose, D-trehalose, D-raffinose, starch, glycogen, gentiobiose and D-turanose. Cells are susceptible to ceftriaxone, ciprofloxacin, clindamycin, colistin, doxycycline, erythromycin, gentamicin, oxacillin, rifampicin, penicillin, teicoplanin, trimethoprim–sulfamethoxazole, vancomycin and imipenem, but resistant to fosfomycin and metronidazole. 12-methyl-tetradecanoic acid (38%), 13-methyl-tetradecanoic acid (24%) and hexadecanoic acid (17%) are the major components of the cellular fatty acid profile of strain SN4^T. The G+C content of the genome is 53.33%. The type strain is *Gorillibacterium timonense* strain SN4^T (= CSUR P2011 = DSM 100,698) and was isolated from a stool sample of an obese Amazonian man (45 years old; Manaus, Brazil).

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