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TAXONOMIC DESCRIPTION
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Dysosmobacter welbionis gen. nov., sp. nov., isolated from human faeces and emended description of the genus *Oscillibacter*

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Abstract

A strictly anaerobic, Gram-stain-negative, non-spore-forming, non-motile, non-pigmented bacterium, strain J115^T, was isolated from human faeces. Cells of strain J115^T were straight rods, generally 1.8–3.0 µm, but could be up to 18 µm long. Growth occurred below 2 % (w/v) NaCl and 2 % (v/v) bile. Strain J115^T produced acid from *myo*-inositol but not from D-glucose, D-ribose or D-xylose. Butyric acid was the major end-product from *myo*-inositol. The genomic DNA G+C content was 58.92 mol%. Phylogenetic analysis based on 16S rRNA gene sequencing indicated that the closest cultivated neighbours of strain J115^T were *Oscillibacter ruminantium* GH1^T (95.4 % similarity) and *Oscillibacter valericigenes* Sjm18-20^T (94.1 %). Strain J115^T was also related to the not-yet-cultured bacterium *Oscillospira guilliermondii* (92–93 % similarity). Coherently with the 16S rRNA gene sequence results, the ANI scores don't have units of strain J115^T to *O. ruminantium* GH1^T and *O. valericigenes* Sjm18-20^T were 73.37 and 73.24, respectively, while *in silico* estimations of DNA–DNA hybridization were both 20.4 %, with confidence intervals of 18.2–22.9 % and 18.2–22.8 %, respectively. The major fatty acids were iso-$C_{15:0}$ (24.2 %), $C_{18:0}$ DMA (18.4 %), anteiso-$C_{15:0}$ (15.2 %) and $C_{16:0}$ DMA (7.6 %). No respiratory quinone was detected. Based on phenotypic features and phylogenetic position, it is proposed that this isolate represents a novel species in a new genus, *Dysosmobacter welbionis* gen. nov., sp. nov. The type strain of *Dysosmobacter welbionis* is J115^T (DSM 106889^T=LMG 30601^T).

Clostridial cluster IV is a phenotypically heterogeneous group that includes motile as well as non-motile species, sporulating as well as non-sporulating bacteria, and Gram-stain-positive, negative or variable species. The majority of them are anaerobic rods isolated from or at least encountered in the digestive tract of diverse representatives of the Animalia kingdom, for example corbicula clams with *Oscillibacter valericigenes* [1], cattle with *Oscillibacter ruminantium* [2], wood-feeding termite with *Sporobacter termitidis* [3], cat with *Agathobaculum desmolans* [4, 5] and human with *Clostridium leptum* [6], *Faecalibacterium prausnitzii* [7] or *Papillibacter cinnamivorans* [8]. Several of them, *F. prausnitzii* and *Butyricicoccus pullicaecorum* in particular, are major butyrate producers in the gastrointestinal tract and have demonstrated health-promoting properties [9, 10]. Others are suspected to have beneficial properties due to their regular association with health-related parameters in cultivation-independent studies. This is the case of *Oscillospira guilliermondii*, which is positively associated with leanness and negatively associated with inflammatory bowel disease and liver disease [11]. The absence of cultivable strains representative of those taxa hinders a better understanding of the physiology of those bacteria and the demonstration of their causal impact on human health.

In this study, strain J115 ^{T} was isolated from a faecal sample from a healthy 25 year old female (*Homo sapiens*) in July 2017. The faecal sample was collected on the campus of Université catholique de Louvain, Brussels, Belgium (50° 51′ 4.5″ N 4° 27′ 20″ E). The isolation of strain J115^T was part of the Walloon Excellence in Life Sciences and

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Keywords: Clostridial cluster IV; human intestinal microbiota; human faeces; *Ruminococcaceae*; *Oscillospiraceae*.
Abbreviations: ANI, average nucleotide identity; DDH, DNA–DNA hybridization; HSP, high-scoring segment pair; YCFA, yeast extract–casein hydrolysate–fatty acids.
The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of *D. welbionis* strain J115^T is MG963288. The whole genome sequence of *D. welbionis* strain J115^T has been deposited into GenBank/EMBL/DDBJ under accession number CP034413.
One supplementary table and two supplementary figures are available with the online version of this article.

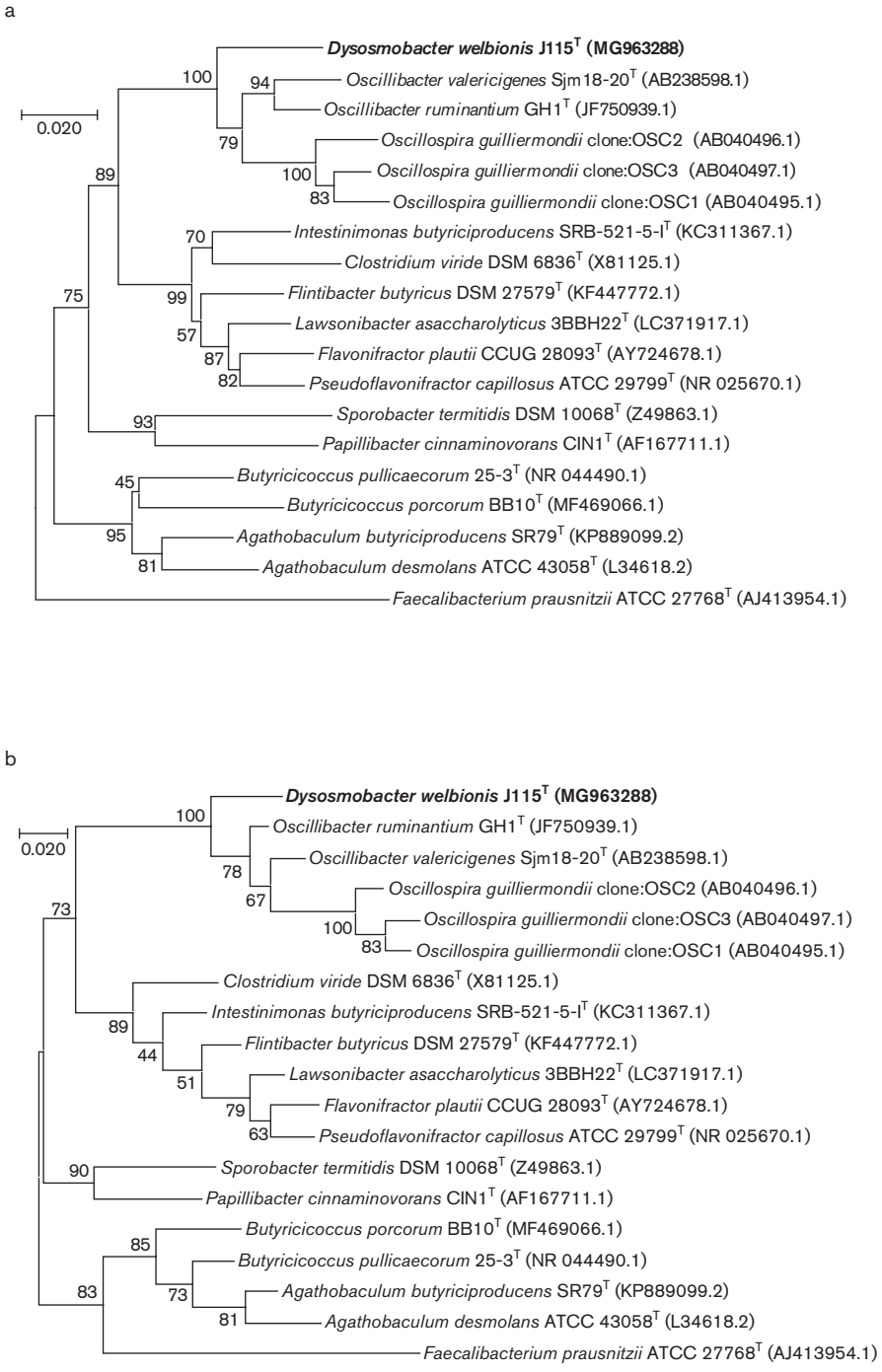

Fig. 1. Phylogenetic trees based on 16S rRNA gene sequences, showing the connections between strain J115^T, the two *Oscillibacter* species, *Oscillospira guilliermondii* clones and some related taxa. GenBank accession numbers are shown in parentheses. Bootstrap values based on 1000 replicates are indicated on branch points. Bars, 0.02 substitutions per nucleotide position. (a) Neighbour-joining phylogenetic tree, (b) maximum-likelihood phylogenetic tree.

Biotechnology project (WELBIO) (http://welbio.org/cms/c_5039/en/about-welbio). One of the goals of the project is to identify new beneficial microbes isolated from the human gut. The 16S rRNA gene sequence of this particular isolate indicated that strain J115^T belonged to the family *Ruminococcaceae* and had 16S rRNA gene sequence similarity to species with standing in nomenclature below the threshold value currently recommended to determine the affiliation of

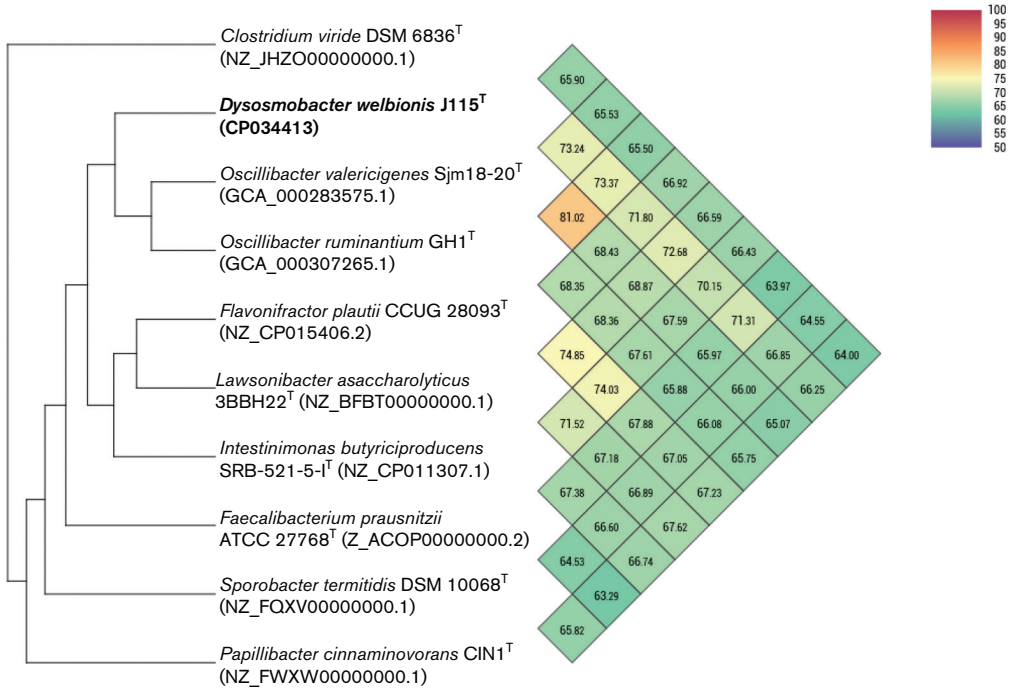

Fig. 2. UPGMA phylogenetic tree of the average nucleotide identity scores based on the whole genomes, showing the connections between strain J115^T, the two *Oscillibacter* species and some related taxa. GenBank accession numbers of the complete genomes used are shown in parentheses.

bacterial isolates to an existing species. Thus, we proceeded to phylogenetic and biochemical characterization of the strain. Based on the results presented here, we propose that this isolate should be classified as representing novel species of a new genus.

The faecal sample was kept in a sealed container with an O_2 -absorbing and CO_2-generating agent (Genbox Anaer, bioMérieux) and isolation was performed less than 2 hours after collection. The samples were transferred into an anaerobic chamber (Coy) containing 100 % N_2 as gas atmosphere and immediately diluted 1/10 in modified YCFA (yeast extract–casein hydrolysate–fatty acids) [7] enriched in antioxidants (Table S1, available in the online version of this article) [12]. The faecal suspension was then transferred in tubes hermetically sealed with butyl rubber under an atmosphere of 20 % CO_2–80 % N_2. Then, single-cell cultivation was performed using the extinction dilution technique, i.e. we diluted and aliquoted the faecal suspension in 300 vials such that a single vial received on average one cell [13]. Positive cultures after 48 h to 7 days at 37 °C were spread onto solid modified YCFA and incubated 72 h to 7 days at the same temperature in anaerobic jars (Merck) with an O_2-absorbing and CO_2-generating agent (Genbox Anaer, bioMérieux). Single colonies were picked and transferred to fresh medium and the process was repeated until the cultures were deemed pure. Among the cultures obtained, one strain, designated J115^T, was considered for further study.

O. ruminantium JCM 18333^T (=GH1^T=KCTC 15176=NBRC 108824) was obtained from the Japan Collection of Microorganisms (JCM) while *O. valericigenes* DSM 18026^T (Sjm18-20^T=NBRC 101213) was obtained from the Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ). Forty-eight hour old cultures in modified YCFA medium at 37 °C were used for routine incubation, growth tests and biochemical analyses. The strains were stored at −80 °C in 20 % glycerol.

An almost-complete (1428 bp) 16S rRNA sequence of strain J115^T was obtained using the universal primers 8F (5′-AGAGTTTGATCCTGGCTCAG-3′) and 1492R (5′-GGTTACCTTGTTACGACTT-3′) [NCBI accession number MG963288] [14]. 16S rRNA sequences of the closest previously identified relatives of strain J115^T were determined and retrieved using EzBioCloud's Identify service [15] and the GenBank database.

Multiple alignment of the sequences was performed using MUSCLE [16]. Distances were computed using the maximum composite likelihood method and [17] the phylogenetic trees were reconstructed by the using neighbour-joining and maximum-likelihood methods [18, 19] in MEGA 7.0 [20] after gaps and unknown bases were eliminated. The trees were reconstructed with 1000 bootstrap replications. Strain J115^T falls within cluster IV of the low G+C content clostridial bacteria branch (Fig. 1) [21]. Strain J115^T was related to *O. ruminantium* JCM 18333^T (95.4 % similarity)

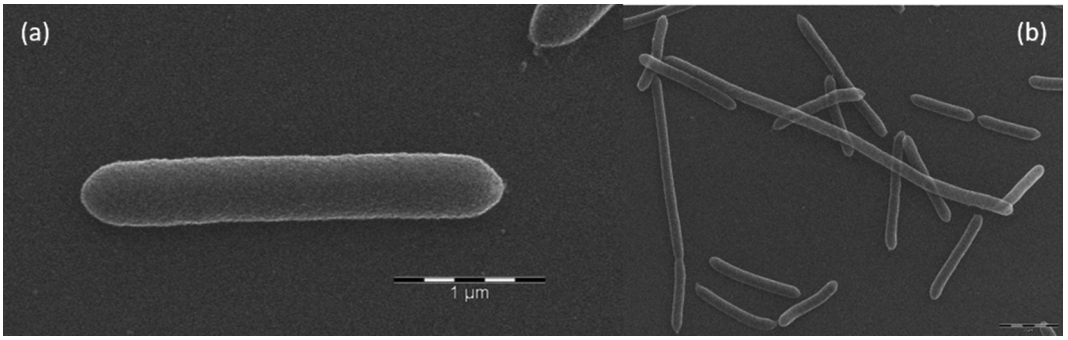

Fig. 3. Scanning electron micrographs of cells of strain J115^T in late exponential phase. (a) ×50 000 magnification; bar, 1 µm. (b) ×10 000 magnification; bar, 2 µm.

and *O. valericigenes* DSM 18026^T (94.1 %) [1, 2]. Strain J115^T was also located near the *O. guilliermondii* clade. Phylogenetically, strain J115^T formed a monophyletic separate branch that was located as a sister clade to the *Oscillibacter–Oscillospira* clade supported by a 100 % bootstrap value in both the neighbour-joining and maximum-likelihood trees (Fig. 1).

For whole-genome sequencing, high molecular weight DNA was extracted using Qiagen DNeasy UltraClean Microbial kit. Long-reads were obtained using PacBio technology at the Eurofins GATC company. Assembly was performed using the hierarchical genome-assembly process as previously described [22] and produced a 3 576 111 bp complete genome in one contig (NCBI accession number CP034413), whose depth of coverage was 242×. Genome analysis using the ContEst16S algorithm indicated that the genome of strain J115^T was not contaminated [23]. The sequences of three 16S rRNA gene copies were retrieved and compared to the 16S rRNA gene sequence obtained by PCR and Sanger sequencing. The three copies were strictly identical to the sequence obtained by PCR.

Multilocus sequence analysis (MLSA) was performed to obtain a higher resolution of the phylogenetic relationships between strain J115^T and neighbour taxa belonging to the *Ruminococcaceae* family. The sequences of 12 protein-coding genes (*sigE*, *purM*, *ass*, *lysC*, *phoH*, *crh*, *groEL*, *thdF*, *infB*, *recA*, *rpoD* and *gyrB*) were retrieved from the complete genomes of all type strains except for *Oscillispira guillermondii* and *Flintibacter butyricus* whose complete genomes are not available. Similarly to the 16S rRNA gene analysis, the concatenated sequences were aligned using MUSCLE and phylogenetic trees were reconstructed by using the neighbour-joining and maximum likelihood methods with 1000 bootstrap replications (Fig. S1). As found previously, J115^T formed a monophyletic separate branch that was located as a sister clade to the *Oscillibacter* clade supported by a 100 % bootstrap value in both trees.

Average nucleotide identity (ANI) scores between strain J115^T and available reference strain genomes were calculated using OAT standalone 0.93.1 software [24]. The ANI scores were represented as a heatmap and used to reconstruct a dendrogram with the unweighted pair group method with arithmetic mean (UPGMA) (Fig. 2). As found in the 16S rRNA gene sequencing and MLSA, the closest taxa to strain J115^T were *O. ruminantium* JCM 18333^T and *O. valericigenes* DSM 18026^T with ANI scores of 73.37 and 73.24, respectively. To complement this analysis based on ANI, we calculated intergenome distance using the Genome-to-Genome Distance Calculator 2.1 provided by DSMZ [25, 26]. The settings used were BLAST+ as a local alignment tool and formula 2, that is to say the sum of all identities found in high-scoring segment pairs (HSPs) divided by overall HSP length. Intergenome distances were then used to determine the probability to have a DNA–DNA hybridization (DDH) equal or above 70 % and to generate a heatmap along with an UPGMA tree using OAT standalone 0.93.1 software (Fig. S2). The UPGMA tree based on intergenome distances had a quite different topology from the previously obtained trees. Indeed, the closest species with standing in nomenclature according to intergenome distance was *F. prausnitzii* ATCC 27768^T with an intergenome distance of 0.1342, which corresponds to a probability of DDH equal or above 70 % of 0.19 % and an *in silico* DDH value of 31.5 % with a confidence interval of 29.1–34.0 %. Despite the divergences in the 16S rRNA gene sequencing, MLSA and ANI results, the *in silico* DDH results clearly indicated that strain J115^T belongs to the family *Ruminococcaceae* in Clostridial cluster IV and differs significantly from the closest taxa with Standing in Nomenclature.

Scanning electron microscopy of cultures showed that cells were straight rods, occurred singly and measured mainly 0.5–0.6×1.8–3.0 µm, but rods of up to 18 µm long were regularly observed during the exponential and early stationary phases, that is to say after 48 h of culture when inoculated at 1 % v/v (Fig. 3). Colonies of strain J115^T colonies on solid modified YCFA after 72 h of incubation at 37 °C in anaerobic atmosphere were punctiform, cream, translucent, circular, entire, slightly convex and smooth. Strain J115^T was negative for motility when stab-inoculated into semi-solid

Table 1. Characteristics of *Dysosmobacter welbionis* J115^T, *Oscillibacter valericigenes* DSM 18026^T and *Oscillibacter ruminantium*

Strains: 1, *Dysosmobacter welbionis* J115^T; 2, *O. valericigenes* DSM 18026^T; 3, *O. ruminantium* JCM 18333^T. Source of isolation and G+C content of reference strains were obtained from [1 and [2. All other data were generated in the present study

Characteristic	1	2	3
Source of isolation	Human gut	Alimentary canal of Japanese corbicula clams	Rumen of Korean native cattle
Motility	Non-motile	Motile	Motile
G+C content by HPLC (mol%)	59.3	52.7	54.6
G+C content based on genome data (mol%)	58.9	53.2	55.0
Bile concentration range for growth (%)	0–2	0–1	0–2
NaCl concentration range for growth (%)	0–1.4	0–3.5	0–2.5
Production of acid from:			
myo-Inositol	+	−	−
D-Xylose	−	+	+
D-Arabinose	−	−	+
D-Ribose	−	−	+
D-Glucose	−	+	+
D-Melezitol	−	−	+
Tagatose	−	+	−
Enzymatic activity of aesculinase	+	−	+

modified YCFA (0.5 % agar) and anaerobically incubated at 37 °C for 72 h. The ability to tolerate bile and NaCl was tested in liquid modified YCFA containing increasing concentration of bovine bile (Sigma; 1 % w/v dehydrated bile corresponding to 10 % w/v fresh bile) or NaCl (VWR). Growth of the strain occurred on medium containing below 2 % bile or 2 % NaCl but not on medium containing 2.25 % or above bile or NaCl. *O. ruminantium* JCM 18333^T had an identical tolerance to bile while *O. valericigenes* DSM 18026^T could grow in medium containing only 0–1% bile.

Gram-staining results on cultures in exponential and stationary growing phases were negative while the KOH test (3 %, w/v) result was positive [27]. No spore formation was observed in transmission or scanning electron microscopy at exponential and stationary growing phase. No spores could be observed after malachite green staining and no growth occurred after heating at 75 °C during 30 min. No catalase was detected using the 3 % w/v H_2O_2 test for strain J115 ^{T} and the strain grew only in strict anaerobic conditions. A comparison of the morphological, biochemical and physiological properties can be found in Table 1.

We used the rapid ID 32A anaerobe identification kit (bioMérieux) according to the manufacturer's instruction and the API 20A anaerobe test kit and the API 50CH carbohydrates kit (bioMérieux) with modified YCFA without a carbon source. Results were observed after 4 h with the API 32A anaerobe test kit and after 72 h for the API 20A anaerobe and the API 50CH carbohydrates kits. Tests were performed three times on three separate cultures.

Rapid ID 32A and API 20A kits showed that strain J115^T and *O. ruminantium* JCM 18333^T were positive for aesculinase activity, which was not the case of *O. valericigenes* DSM 18026^T. The enzymatic activities of strain J115^T and the two *Oscillibacter* species were positive for arginine dihydrolase and glutamic acid decarboxylase, but negative for the other tests of Rapid ID 32A kit. Acid production by fermentation from 49 carbon sources was tested using the API 50CH kit and strain J115^T could be differentiated from both *Oscillibacter* species by its ability to ferment *myo*-inositol and its inability to ferment D-glucose and D-xylose (Table 1). In addition to D-glucose and D-xylose, *O. valericigenes* DSM 18026^T produced acid from tagatose and *O. ruminantium* JCM 18333^T produced acid from D-arabinose and D-melezitol.

Oscillibater species are known to produce butyrate from their fermentable carbon sources [1, 2]. After 72 h of cultivation in modified YCFA containing 1 % (w/v) *myo*-inositol, butyrate, propionate and valerate represented 60, 20.6 and 19.4 % of the amount of produced short-chain fatty acids, respectively.

Cellular fatty acids of strain J115^T, *O. valericigenes* DSM 18026^T and *O. ruminantium* JCM 18333^T were analysed by the Identification Service of the DSMZ, Braunschweig, Germany from 30 mg freeze-dried cells by saponification, methylation and extraction using minor modifications of the method of Miller [28] and Kuykendall *et al.* [29]. The major cellular fatty acids of strain J115^T were iso-$C_{15:0}$, $C_{18:0}$ DMA, anteiso-$C_{15:0}$ and $C_{16:0}$ DMA (24.2, 18.4, 15.2 and 7.6 %, respectively) (Table 2). Iso-$C_{15:0}$ and $C_{16:0}$ DMA are also major cellular fatty acids of *O. valericigenes* DSM 18026^T and *O. ruminantium* JCM 18333^T, however the quantities differed quite substantially as iso-$C_{15:0}$ represented only 9.8 and 8.9 % of the cellular fatty acids while $C_{16:0}$ DMA represented 25.2 and 19.9 % of the cellular fatty acids in the two *Oscillibacter* species. In contrast to

Table 2. Cellular fatty acids compositions of *Dysosmobacter welbionis* strain J115^T, *Oscillibacter ruminantium* JCM 18333^T and *Oscillibacter valericigenes* DSM 18026^T after 48h of culture in modified YCFA medium

Strains : 1, *Dysosmobacter welbionis* J115^T ; 2, *O. valericigenes* DSM 18026^T; 3, *O. ruminantium* JCM 18333^T. TR, trace amount (<1 %) ; –, not detected. All data have been generated in the present study.

Fatty acid	1	2	3
Saturated straight-chain:			
$C_{12:0}$	TR	1.2	5.3
$C_{14:0}$	2.4	14.7	11.5
$C_{15:0}$	TR	1.7	TR
$C_{16:0}$	TR	8.7	14.3
$C_{18:0}$	TR	TR	1.7
Unsaturated straight-chain:			
$C_{18:2\,\omega6,9c}$	TR	TR	TR
Dimethylacetal (DMA):			
$C_{14:0}$ DMA	TR	6.5	4.5
anteiso-$C_{15:0}$ DMA	1.0	TR	TR
$C_{16:0}$ DMA	7.6	25.2	19.9
$C_{17:0}$ DMA	2.2	TR	TR
$C_{18:0}$ DMA	18.4	TR	TR
Saturated branched-chain:			
iso-$C_{13:0}$	TR	1.3	11.8
iso-$C_{14:0}$	1.5	TR	TR
iso-$C_{15:0}$	24.2	9.8	8.3
iso-$C_{16:0}$	TR	–	–
anteiso-$C_{13:0}$	TR	TR	1.2
anteiso-$C_{15:0}$	15.2	3.0	3.0
iso-$C_{17:0}$	TR	–	–
anteiso-$C_{17:0}$	TR	–	–
Summed features:*			
1	TR	1.0	TR
3	TR	TR	TR
5	TR	TR	1.9

*Summed features represent groups of two or three fatty acids that could not be separated using the MIDI Sherlock system. Summed feature 1 contains $C_{13:1}\,\omega1c$ and/or $C_{14:0}$ ALDE. Summed feature 3 contains one or more of an unknown fatty acid of ECL 13.570 and/or iso-$C_{15:0}$ ALDE. Summed feature 5 contains $C_{15:0}$ DMA and/or $C_{14:0}$ 3-OH.

strain J115^T, $C_{18:0}$ DMA and anteiso-$C_{15:0}$ are not major cellular fatty acids of *O. valericigenes* DSM 18026^T and *O. ruminantium* JCM 18333^T as they represent less than 3 % of the cellular fatty acids. Conversely, the saturated straight fatty acids $C_{14:0}$ and $C_{16:0}$ are major cellular fatty acids of *O. valericigenes* DSM 18026^T and *O. ruminantium* JCM 18333^T but are detected only in trace amounts in strain J115^T. In addition, $C_{14:0}$ DMA is detected in appreciable amounts in *O. valericigenes* DSM 18026^T and *O. ruminantium* JCM 18333^T(6.2 and 4.5 %, respectively) but represents only a trace amount of the cellular fatty acids of strain J115^T.

Respiratory lipoquinones and diaminopimelic acid of strain J115^T were analysed by the Identification Service of the DSMZ, Braunschweig, Germany. Briefly, quinones were extracted from 100 mg freeze-dried cells using methanol: hexane, followed by phase separation into hexane according to Tindall's method [30, 31]. As for *Oscillibacter* species, no quinone was detected in strain J115^T. Whole-cell hydrolysates were examined by thin-layer chromatography on cellulose plates using the solvent system of Rhuland *et al.* [32]. Strain J115^T contained *meso*-2,6-diaminopimelic acid as the diagnostic diamino acid of the cell-wall peptidoglycan.

Cells of strain J115^T were straight rods, normally 1.8–3.0 µm and often formed elongated rods. Strain J115^T was strictly anaerobic and had no respiratory quinone. These properties are similar to those of *Oscillibacter* species [1, 2]. However, strain J115^T had no flagella, was non-motile and had a different cellular fatty acid composition. Phylogenetically, strain J115^T formed a separate branch to the clade *Oscillibacter–Oscillospira*. These two subclades are already accommodated as two separate genera. On the basis of its phylogenetic position along with the biochemical and physiological properties described above, strain J115^T differs

significantly from the nearest cultivated genus members, namely *Oscillibacter ruminantium* and *Oscillibacter valericigenes*. Consequently, we propose that strain J115^T represents a novel species of a new genus, for which the name *Dysosmobacter welbionis* gen. nov., sp. nov. is proposed.

EMENDED DESCRIPTION OF THE GENUS *OSCILLIBACTER* IINO *ET AL.* 2007

The description is as given by Iino *et al.* 2007 with the following modifications. Positive for glutamic acid decarboxylase and arginine dihydrolase. Negative for alkaline phosphatase, α-galactosidase, β-galactosidase, α-glucosidase, β-glucosidase, α-arabinosidase, β-glucuronidase, *N*-acetylglucosaminidase, α-fucosidase, arginine arylamidase, proline arylamidase, leucyl-glycine arylamidase, phenylalanine arylamidase, pyroglutamic acid arylamidase, tyrosine arylamidase, alanine arylamidase, glycine arylamydase, histidine arylamidase and serine arylamidase. Indole is not produced from tryptophane. Gelatin is not digested.

EMENDED DESCRIPTION OF *OSCILLIBACTER VALERICIGENES* IINO *ET AL.* 2007

The description is as given by Iino *et al.* 2007 with the following modifications. Aesculin is not hydrolysed. The bile concentration range allowing growth is 0–1 %. Acid is produced from tagatose. Acid is not produced from D/L-arabinose and D-ribose.

EMENDED DESCRIPTION OF *OSCILLIBACTER RUMINANTIUM* LEE *ET AL.* 2013

The description is as given by Lee *et al.* 2013 with the following modifications. Aesculin is hydrolysed. The bile concentration range allowing growth is 0–2 %. Acid is produced from D-arabinose and D-melezitol.

DESCRIPTION OF *DYSOSMOBACTER* GEN. NOV.

Dysosmobacter (Dys.os.mo.bac′ter. Gr. masc. adj. *dysosmos* bad smelling; N.L. masc. n. *bacter* a rod; N.L. masc. n. *Dysosmobacter* a bad-smelling rod).

Cells are obligatory anaerobic, non-pigmented, non-spore-forming, non-motile, Gram-stain-negative. Cells form straight rods mainly 1.8–3.0 µm but often form elongated rods whatever the growing phase. No respiratory menaquinones are produced. The diagnostic diamino acid in the cell wall is *meso*-2,6-diaminopimelic acid. The genus is a member of the family *Ruminococcaceae*. The type species is *Dysosmobacter welbionis*.

DESCRIPTION OF *DYSOSMOBACTER WELBIONIS* SP. NOV.

Dysosmobacter welbionis (wel.bi.o′nis. N.L. gen. n. *welbionis* of WELBIO, the Walloon Excellence in Life and BIOtechnology project).

Exhibits the following characteristics in addition to those in the genus description. Colonies on solid modified YCFA after 72 h of incubation at 37 °C under anaerobic conditions are punctiform, cream, translucent, circular, entire, slightly convex and smooth. Growth is inhibited by the presence of 2 % bile or 2 % NaCl. Major cellular fatty acids are saturated branched-chain fatty acids and DMAs. Aesculin is hydrolysed. Indole is not produced. Nitrate is not reduced. Gelatin is not digested. Urease is not produced. Catalase is not produced. Positive for arginine dihydrolase and glutamic acid decarboxylase. Negative for alkaline phosphatase, α-galactosidase, β-galactosidase, α-glucosidase, β-glucosidase, α-arabinosidase, β-glucuronidase, *N*-acetylglucosaminidase, α-fucosidase, arginine arylamidase, proline arylamidase, leucyl-glycine arylamidase, phenylalanine arylamidase, pyroglutamic acid arylamidase, tyrosine arylamidase, alanine arylamidase, glycine arylamydase, histidine arylamidase and serine arylamidase. Acid is produced from *myo*-inositol but not from D-adonytol, amygdaline, D/L-arabinose, D/L-arabitol, arbutin, cellobiose, dulcitol, erythritol, D-fructose, D/L-fucose, D-galactose, gentibiose, D-glucose, glycerol, glycogen, inulin, lactose, lyxose, maltose, D-mannitol, D-mannose, D-melezitol, D-melibiose, methyl α-D-glucopyranoside, methyl α-D-mannopyranoside, methyl β-D-xylanopyranoside, *N*-acetylglucosamine, raffinose, L-rhamnose, D-ribose, sucrose, salicin, D-sorbitol, L-sorbose, starch, tagatose, trehalose, turanose, xylitol and D/L-xylose. The major fermentation end-product from *myo*-inositol is butyric acid. The DNA G+C content of the type strain is 58.92 mol%. The major DMA fatty acid is $C_{18:0}$ DMA and major saturated branched-chain fatty acids are iso-$C_{15:0}$ and anteiso-$C_{15:0}$.

Type strain, J115^T (=DSM 106889^T=LMG 30601^T) was isolated from human faeces. The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of *D. welbionis* strain J115^T is MG963288. The whole genome sequence of *D. welbionis* strain J115^T has been deposited into GenBank/EMBL/DDBJ under accession number CP034413.

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Conflicts of interest
The authors declare that there are no conflicts of interest.

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