Monoglobus pectinilyticus gen. nov., sp. nov., a pectinolytic bacterium isolated from human faeces


**Abstract**

A novel anaerobic pectinolytic bacterium (strain 14\(^{T}\)) was isolated from human faeces. Phylogenetic analysis based on 16S rRNA gene sequences revealed that strain 14\(^{T}\) belonged to the family Ruminococcaceae, but was located separately from known clostridial clusters within the taxon. The closest cultured relative of strain 14\(^{T}\) was Acetivibrio cellulolyticus (89.7 % sequence similarity). Strain 14\(^{T}\) shared ~99 % sequence similarity with cloned 16S rRNA gene sequences from uncultured bacteria derived from the human gut. Cells were Gram-stain-positive, non-motile cocci approximately 0.6 µm in diameter. Strain 14\(^{T}\) fermented pectins from citrus peel, apple, and kiwifruit as well as carbohydrates that are constituents of pectins and hemicellulose, such as galacturonic acid, xylose, and arabinose. TEM images of strain 14\(^{T}\) cultured in association with plant tissues, suggested extracellular fibrolytic activity associated with the bacterial cells, forming zones of degradation in the pectin-rich regions of middle lamella. Phylogenetic and phenotypic analysis supported the differentiation of strain 14\(^{T}\) as a novel genus in the family Ruminococcaceae. The name Monoglobus pectinilyticus gen. nov., sp. nov. is proposed; the type strain is 14\(^{T}\) (JCM 31914\(^{T}\)=DSM 104782\(^{T}\)).

The polysaccharide components of plant cell walls are insoluble and resist degradation by human enzymes when consumed as part of the diet. However, dietary components that are indigestible to humans are fermented by the colonic microbiota. Degradation of plant polysaccharides in the colon requires the action of a diverse array of gut bacteria enriched with genes encoding fibrolytic enzymes that cleave specific glycosidic linkages [1]. Pectin is a major non-cellulosic component of plant cell wall polysaccharides, comprising approximately one third of the wall dry weight of dicotyledons and non-Poales monocotyledon plants, and 0.5–4 % of the fresh weight of edible plant materials [2, 3]. Current understanding of the microbial degradation of pectin in the human colon is limited to a narrow taxonomic spectrum of organisms, almost exclusively Bacteroides species [4]. As a result, our knowledge of the process of pectin degradation is largely derived from studying the sequestration system of Bacteroides species. The few human gut bacteria from the Firmicutes which were reported to ferment pectin include Faecalibacterium prausnitzii, Eubacterium eligens, and members of the Clostridium butyricum-Clostridium beijerinckii group [5, 6]. We report here the isolation of a novel Gram-stain-positive, mesophilic, and pectinolytic bacterium (strain 14\(^{T}\)) from human faeces. We propose to assign strain 14\(^{T}\) to a novel genus within the family Ruminococcaceae, namely Monoglobus pectinilyticus gen. nov., sp. nov.

Strain 14\(^{T}\) was isolated from faeces from a healthy 27-year-old female living in New Zealand who had not been prescribed antibiotics for 6 months prior to the sample collection. Unless specified otherwise, all media and additives in this study were prepared using strictly anaerobic techniques under O\(_2\)-free 100 % CO\(_2\) or N\(_2\) [7]. Any additions of components and inoculum into the sterilized media were carried out by inserting 100 % N\(_2\)-flushed syringes and needles through the butyl rubber stoppers or inside a UV-sterilized anaerobic chamber. Fresh stool was weighed and 5 g of stool was mixed with anaerobically prepared phosphate buffered saline (PBS) solution to make a 10 % faecal slurry. The faecal slurry was serially diluted (10-fold) until 10\(^9\)-fold dilution.
dilution was achieved, and 0.5 ml of 10^-7, 10^-8, and 10^-9 dilutions were used to inoculate the basal medium (10 ml per tube) containing 0.2 % (w/v) kiwifruit pectin. After 15 days of incubation at 37 °C with constant rotary shaking, a small volume of culture was spread over the surface of a roll-tube containing basal agar medium with 0.2 % (w/v) kiwifruit pectin and 1.5 % (w/v) glucose. Cells from 1 to 2 weeks old cultures were Gram-stained and observed under a light microscope to compare the consistency and strength of growth in the presence and absence of pectin. Strain 14^T was selected for characterization as it grew only when citrus pectin was present in the basal medium. Strain 14^T was routinely cultivated using mineral medium for biochemical characterization procedures.

Basal medium contained (per litre) 2 g Difco peptone water; 2 g Bacto yeast extract; 0.5 g bile salts (Oxoid); 10 ml Mineral A stock solution (0.4 g K₂HPO₄ dissolved in 100 ml distilled water); 10 ml Mineral B stock solution (0.4 g KH₂PO₄; 0.1 g MgSO₄.7H₂O; 0.1 g CaCl₂.6H₂O; and 1.0 g NaCl dissolved in 100 ml distilled water); 2 ml Tween 80 (Fischer Scientific); 0.05 g haemin (Sigma); 10 µl vitamin K (Sigma); 0.5 g L-cysteine-HCl; 0.02 g resazurin; and 4.2 g NaHCO₃. The basal medium was prepared under O₂-free 100 % N₂. The mineral medium contained (per litre) 1.4 g KH₂PO₄; 0.6 g (NH₄)₂SO₄; 1.5 g KCl; 1 g yeast extract; 0.5 g L-cysteine-HCl; 0.02 g resazurin; and 4.2 g NaHCO₃. The mineral medium was prepared under 100 % CO₂. For both basal and mineral media, the required volumes of the medium were dispensed into Hungate tubes (10 ml) or serum vials (50 ml), and then sealed with caps and stoppers for autoclaving. Pectin substrates, 5 % (v/v) clarified rumen fluid, and 0.02 % (v/v) RPMI 1640 vitamins solution (Sigma-Aldrich; R7256) were added to both types of media immediately prior to inoculation. RPMI 1640 vitamins solution contained (per litre) 20 mg D-biotin; 0.3 g choline chloride; 0.1 g folic acid; 3.5 g myo-inositol; 0.1 g niacinamide; 0.1 g p-amino benzoic acid; 25 mg calcium d-pantothenate; 0.1 g pyridoxine HCl; 0.1 g thiamine HCl; 20 mg riboflavin; and 0.5 mg vitamin B12. Seasonal green kiwifruit (Hayward) harvested at maturity were used to sequentially extract (80 % ethanol, CDTA, and Na₂CO₃) pectic polysaccharides from the kiwifruit cell walls as described in Melton and Smith [8]. Freeze-dried samples of kiwifruit pectin fractions were sterilized by gamma-irradiation at 17 kGy (MSD Animal Health, Wellington, NZ). The monomeric sugar compositions of pectin extracts and the sample purity were assessed using high-performance anion-exchange chromatography coupled with pulsed electrochemical detection (HPAEC-PAD) chromatography and nuclear magnetic resonance (NMR) spectroscopy (Table S1, available in the online version of this article ) [9]. Cell morphology, motility, and the presence of capsular polysaccharides were investigated using transmission electron microscopy (TEM) and phase-contrast microscopy. The presence of endospores was tested after 4 weeks of incubation at 37 °C using the Schaeffer–Fulton staining method [10]. Gram-staining was performed using a conventional methodology [11].

In preparation for TEM, strain 14^T was grown at 37 °C for 96 h in mineral medium containing 0.5 % (w/v) d-fructose. To examine bacterial adhesion to complex substrates, thinly sliced kiwifruit or orange peel were incubated in exponentially growing cultures of strain 14^T, and were processed for TEM imaging upon sample collection at 72 h. Free bacterial cells and the cells bound to thin slices of kiwifruit or orange peel were fixed, stained, and prepared as ultra-thin sections for TEM. Samples were fixed in modified Karnovsky’s fixative (3 % glutaraldehyde (v/v) 2 % formaldehyde (w/v) in 0.1 M phosphate buffer (pH 7.2)) for 2 h at room temperature. The samples embedded in resin (Procura812, ProSciTech) were sliced into ultra-thin sections (100 nm) with a diamond knife (Diatome) using an Ultramicrotome (Leica Microsystems). Sections were stretched over a copper grid and stained with saturated uranyl acetate in 50 % (v/v) ethanol for 4 min. Grids were washed with 50 % (v/v) ethanol and MilliQ water, followed by a further staining in lead citrate for 4 min. Samples were viewed using an FEI Tecnai G2 Spirit BioTWIN TEM (FEI).

The culture viability of strain 14^T was monitored over five successive transfers on 0.5 % (w/v) substrates. Generation times were determined by measuring the daily changes in optical density at 595 nm using a FLUOstar Optima Microplate Reader (MBG Labtech). Growth experiments were performed in triplicate, using mineral medium. The substrates tested (from Sigma unless otherwise stated) were pectin from citrus peel (esterification ≥6.4 %), pectin from apple pomace (esterification ≥75 %), starch from wheat, arabinan from sugar beet (Megazyme), xylan from oat spelt, galactan from ex gum arabic (Sigma–Aldrich), β-glucan from barley, arabinoxylan from wheat (Megazyme), oligo-fructose-enriched inulin from chicory (Orafti Synergy1), Whatman filter papers (number 1), Avicel PH-101 (~50 µm particle size; Fluka Analytical), Sigmacell cellulose (Type 101), glucose, mannitol, lactose, sucrose, maltose, salicin, xylene, arabinose, cellobiose, mannose, sorbitol, rhamnose, galacturonic acid, raffinose, galactose, fructose, galactitol, glycerol, and fucose.

Cultures grown in mineral medium containing 0.5 % (w/v) citrus pectin were incubated at ranges of temperatures (25–45 °C at 5 °C intervals) and pH (5.0–9.0 at intervals of 0.5 pH units at 37). The pH of the medium was adjusted using HCl and NaOH. Optical density at 595 nm was measured daily using a Spectronic 20 spectrophotometer (Bausch and Lomb) until stationary phase was reached. Oxygen sensitivity was determined by testing culture viability under aerobic and microaerophilic (2–4 % O₂) conditions.
Genomic DNA was extracted using a phenol–chloroform method followed by ethanol precipitation [12]. The G+C content of DNA was determined as part of whole-genome sequencing using an Illumina Hiseq 2500 (Macro-gen). PCR amplification of the 16S rRNA gene of strain 14T was achieved using universal primers 8F (5'-AGAGTTTGA TCCTGGCTCAG-3') and 1510R (5'-GGTTACCTTG TTACGACTT-3') [13]. The following PCR cycling conditions were used: initial heat polymerase activation at 95°C for 15 min, 35 cycles of 95°C for 30 s (denaturation), 56°C for 30 s (annealing), 72°C for 90 s (extension), final extension at 72°C for 10 min, and products were stored at 4°C until further use. PCR was performed using an Applied Biosystems GeneAmp PCR System 9700. PCR products were purified using QIAquick PCR Purification Kit (QIAGEN) according to the manufacturer’s instructions. Sequencing was carried out using BigDye Terminator version 3.1 Cycle Sequencing Kit on ABI3730 capillary instrumentation (Applied Biosystems). Multiple sequence alignments were performed on CLUSTALW (default parameters) using MEGA7 software [14]. A phylogenetic tree was reconstructed using a neighbour-joining method [15]. Bootstrap values were calculated using 2000 resamplings to evaluate the support of tree topology. Reference 16S rRNA gene sequences from type strains and cloned 16S rRNA gene sequences from uncultured bacteria were obtained from the

![Fig. 1. Micrographs of strain 14T.](image)

(a) TEM micrograph of strain 14T grown in mineral medium plus 0.5% (w/v) fructose. (b, c) TEM micrographs of strain 14T showing attachment to the middle lamella of kiwifruit (b) and orange peel (c). Liquid culture-grown cells bound to thin slices of kiwifruit or orange peel were collected after 72 h of incubation at 37. (d) Cells of strain 14T in proximity to the plant cell wall of orange peel. ML, middle lamella; PCW, plant cell wall.
GenBank database. Only near full-length 16S rRNA sequences (1350–1500 bp) were used for comparisons in this study. The 16S rRNA gene sequence from *Lutispora thermophila* strain EBR46T (GenBank accession number NR_041236) was used as an outgroup.

Production of gas (CO$_2$ and H$_2$) was examined by gas chromatography (Aerograph 660, Varian Associates) fitted with a Porapak Q80/100 mesh column and a thermal conductivity detector operated at 100 °C. The column was operated at room temperature using N$_2$ as a carrier gas at 12 cm$^3$ min$^{-1}$. Concentrations of organic acids were quantified using the method of Richardson [16], as modified by Parkar et al. [17]. Fermentation products were measured in cultures grown on citrus pectin for at least 5 days.

Cellular fatty acid contents were determined by gas chromatography by the Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (DSMZ, Braunschweig, Germany). Using the media and reagents indicated, strain 14$^T$ was tested for catalase (H$_2$O$_2$, Sigma), cytochrome oxidase (TMPD, Aldrich), casein hydrolysis (Skim milk agar), aesculin hydrolysis (BBL Bile Aesculin Agar), gelatinase (nutrient gelatin), indole production (Kovac’s reagent), lipase/lecithinase (BBL Baird Parker Agar Base), and urease (BBL Urea Agar Base).

Cells of strain 14$^T$ were cocci (approximately 0.6 µm in diameter) most often found as single cells or in pairs. A relatively thick Gram-stain-positive type bacterial cell wall structure (50–60 nm) was present (Fig. 1a). Strain 14$^T$ was not encapsulated and did not form extracellular coat materials on the cell surface. Cells lacked flagella and were confirmed to be non-motile by phase-contrast microscopic examination. Endospore formation was not detected from nutrient-deprived cells after 4 weeks of incubation at 37 °C. Strain 14$^T$ grew poorly on the roll-tubes and on agar surfaces, forming a small number of colonies which were too small in size to allow an accurate morphological description. Strain 14$^T$ was strictly anaerobic and exposure to aerobic or microaerophilic conditions prevented its growth. A temperature range of 30–40 °C and the acidity range of pH 6.5–8.0 provided optimal growth conditions. Even under optimal conditions, strain 14$^T$ had a doubling time of 40 h and a log phase of 72 h until reaching stationary phase. Maximum optical density (OD$_{595}$) ranged from 0.2 to 0.3. The addition of rumen fluid and vitamin solution was required to maintain growth during multiple successive transfers.

Although the penetration of structurally intact plant cell walls did not occur after 72 h of incubation, strain 14$^T$ formed zones of degradation in the pectin-rich regions (middle lamella) overlaying the plant cell walls (Fig. 1b, c). Some bacterial cells appeared to degrade fibrous material in proximity to undamaged plant cell walls (Fig. 1d). Most cells were positioned at a slight distance (~50 nm) from the sites of attachment, possibly indicating diffusion of degradative enzymes from bacterial cells. Extremely thin fibres from the middle lamella and the plant cell wall appeared to be anchored to the surface of the bacterial cell wall. Adhesion of bacterial cells at damaged or cut surfaces of the plant cell walls was occasionally observed, indicating strain 14$^T$ may also be capable of degrading pectin materials present within the plant cell wall.

![Fig. 2. Neighbour-joining phylogenetic tree reconstructed based on 16S rRNA gene sequences to infer the phylogenetic relationship of strain 14$^T$ to members of *Clostridium* clusters III and IV. Bootstrap test (2000 replicates) results are shown as percentage values next to the branches. *Lutispora thermophila* strain EBR46T was used as an outgroup](image-url)
The neighbour-joining tree of 16S rRNA gene sequences grouped strain 14\textsuperscript{T} within the family Ruminococcaceae (Fig. 2). Strain 14\textsuperscript{T} shared the highest 16S rRNA gene sequence similarities with the members of Clostridium cluster III, Acetivibrio cellulolyticus NRC 2248\textsuperscript{T} (89.7%), Clostridium clariflavum DSM 19732\textsuperscript{T} (89.3%), Clostridium thermocellum ATCC 27405\textsuperscript{T} (88.8%), and Clostridium aldrichii DSM 6159\textsuperscript{T} (89.1%). These members of Clostridium cluster III are celluloletic Gram-stain-positive rods isolated from non-gut anaerobic environments, such as anaerobic sewage and agricultural waste fermenters [18–21]. Of the strains isolated from the human gut, Ruminococcus bromii ATCC 27255 (85.4%) and Ruminococcus champanellensis 18P13 (84.5%) were the closest relatives of strain 14\textsuperscript{T}. Overall, these sequence similarity values to cultured bacteria were considerably below the threshold values used for species (≥97%) and genus (≥95%) delineations [22]. The closest GenBank relatives of strain 14\textsuperscript{T} were 16S rRNA gene sequences of uncultured bacterial species derived from human gut communities, with 16S rRNA gene sequence similarity of ~99% (GenBank accession numbers DQ326608, DQ327275, DQ327290, DQ799841, DQ804302, FJ363849 and GQ493741). It was noted that the phylogenetic divergence of strain 14\textsuperscript{T} occurred outside Clostridium clusters III and IV, forming a distinct lineage of descent within the family Ruminococcaceae. A similar tree topology was obtained based on maximum parsimony analysis, whereas maximum likelihood analysis positioned strain 14\textsuperscript{T} in a lineage clearly separated from the neighbouring clostridial groups (Figs S1–S3). The DNA G+C content of strain 14\textsuperscript{T} was 37.21%, which was close to the G+C ranges for A. cellulolyticus NRC 2248\textsuperscript{T} (38%), C. thermocellum YS (39%), C. clariflavum DSM 19732\textsuperscript{T} (36.9%), and C. stercorarium DSM 8532\textsuperscript{T} (39%) [19–21, 23]. DNA G+C content of strain 14\textsuperscript{T} was lower compared to Ruminococcus flavefaciens C94\textsuperscript{T} (39–44%), Ruminococcus albus ATCC 27210\textsuperscript{T}.

\begin{table}[h]
\centering
\begin{tabular}{|l|c|c|c|c|c|c|l|c|}
\hline
\textbf{Characteristic} & \multicolumn{8}{|c|}{\textbf{Isolation source}} \\
\hline & \multicolumn{3}{|c|}{\textbf{Human faeces}} & \multicolumn{2}{|c|}{\textbf{Sludge}} & \multicolumn{2}{|c|}{\textbf{Wood fermenter}} & \multicolumn{2}{|c|}{\textbf{Human faeces}} \\
\hline
\textbf{Morphology} & \textbf{Cocci} & \textbf{Rod} & \textbf{Rod} & \textbf{Rod} & \textbf{Rod} & \textbf{Rod} & \textbf{Rod} & \textbf{Cocci} & \textbf{Cocci} \\
\hline
\textbf{Gram strain} & + & Variable & + & + & + & + & + & + & + \\
\hline
\textbf{Cell size (\textmu m)} & & & & & & & & & \\
\hline
\textbf{Length/diameter} & 0.6–0.7 & 2.0–5.0 & 4.0–10 & 2.5–5.0 & 2.0–4.0 & 3.0–5.0 & 0.7–1.1 & 0.9–1.3 \\
\hline
\textbf{Width} & – & 0.4–0.5 & 0.5–0.8 & 0.5–0.7 & 0.3–0.4 & 0.5–1 & – & – \\
\hline
\hline
\textbf{Utilization of} & & & & & & & & & \\
\hline
\textbf{Cellubios} & – & + & + & + & + & – & + & + \\
\textbf{Cellulose} & – & + & + & + & + & – & + & + \\
\hline
\textbf{Fructose} & + & – & – & + & – & – & + & + \\
\hline
\hline
\textbf{DNA G+C content (mol%)} & 37.2 & 36.9 & 35.5 & 39 & 39 & 40 & 41.4 & 53.1 \\
\hline
\end{tabular}
\caption{Differential phenotypic characteristics between strain 14\textsuperscript{T} and related species of Clostridium clusters III and IV.}
\end{table}

* A, acetate; F, formate; L, lactate; E, ethanol; P, propionate; B, butyrate; S, succinate.
(42.6–45.8 %), R. champanellensis 18P13T (53.05 %), and R. bromii ATCC 27255T (41.05 %) [24, 25]. Strain 14T was able to utilize D-galacturonic acid, D-xylene, L-arabinose, D-fructose, and pectin from citrus peel, apple, and kiwifruit (Table 1). With the exception of D-fructose, strain 14T utilized a narrow spectrum of substrates which were either pectin or monosaccharides of pectin and hemi-cellulose (arabinose, xylose and galacturonic acid). Pectin-associated polysaccharides such as galactan and arabinan were unable to support the growth of strain 14T. The end products of citrus and apple pectin fermentation were acetate, formate, H2, and CO2, with lactate also being produced in a smaller quantity.

The major fatty acids of strain 14T were C18:1ω9c (21.7 %), C16:0 (19.2 %), ante-C18:1ω6 (12.0 %), iso-C15:0 (11.8 %), anteiso-C15:0 (11.8 %), anteiso-C17:0 (8.5 %), and C18:1ω9c (5.3 %). The cellular fatty acid profile of strain 14T was unusual in that Cl8:1ω9c, an 18C-straight monounsaturated fatty acid, seldom occurs as a major cellular fatty acid in its close relatives. Previous findings showed predominantly 15C- or 16C-rich fatty acid profiles for C. thermocellum, C. clariflavum, C. stercorarium, R. flavefaciens, R. albus, and R. champanellensis [21, 24, 26, 27]. 18C-fatty acids were either absent or produced as minor fatty acids in these organisms. Although 18C-fatty acids made up 39 % of the total fatty acid in strain 14T, 15C-, 16C-, and 17C-fatty acids were also present in significant amounts. Strain 14T tested positive for catalase, and negative for casein hydrolysis, aesculin hydrolysis, gelatinase, indole production, lipase/lecithinase, cytochrome oxidase, and urease.

Strain 14T differed from its phylogenetic relatives of the Clostridium cluster III, in terms of spore formation, motility, optimum temperature range for growth, cellular fatty acid composition, and substrate utilization. Unlike its cellulolytic relatives, strain 14T could utilize galacturonic acid as a sole carbon source, which is an unusual trait for human colonic bacteria with the exception of Bacteroides spp. [28].

Despite sharing some phenotypic similarities with Ruminococcus species, strain 14T was phylogenetically separate from Clostridium cluster IV. Based on TEM images, the tendency of strain 14T to associate with plant cell wall material, and the aggregation of fibrous materials on bacterial cell surfaces suggest the presence of an extracellular substrate adhesion machinery. On the basis of the phenotypic and phylogenetic data obtained in this study, a novel genus of the family Ruminococcaceae, represented by the type species Monoglobus pectinilyticus gen. nov., sp. nov. is proposed.

**DESCRIPTION OF MONoglobus PECTINILYTICUS SP. NOV.**

Monoglobus pectinilyticus [pec.ti.ni.ly’ti.cus. N.L. neut. n. pectinum pectin; N.L. adj. lyticus (from Gr. adj. lytikos) able to loosen, able to dissolve; N.L. masc. adj. pectinilyticus, pectin-dissolving].

Cells are non-motile Gram-stain-positive cocci (≈0.6 µm), with Gram-stain-positive cell wall ultra-structures. Cells do not form endospores. Strictly anaerobic. Cytochrome oxidase-negative and catalase-positive. Ferments pectin, galacturonic acid, arabinose, xylose, and fructose. Fermentation end-products are acetate, formate, lactate, H2, and CO2. Grows at 25–40 °C (optimum 30–40 °C) and at pH 6.0–8.5 (optimum 6.5–8.0). Rumen fluid and vitamin supplement are required for growth. Indole-, urease-, and lipase/lecithinase-negative. Does not hydrolyse casein, aesculin, and gelatin. Grows with pectin, galacturonic acid, xylose, arabinose, and fructose. Does not grow using cellulbiose, fucose, galactitol, lactose, glycerol, lactose, maltoose, mannose, raffinose, rhamnose, salicin, sorbitol, sucrose, arabinan from sugar beet, galactan from ex gum arabic, arabinoylan from wheat, xylan from oat spelt, oligofructose-enriched inulin from chicory, cellulose, Whatman filter paper, starch from wheat, and β-glucan from barley. The major fatty acids are listed in the genus description above.

The type strain, 14T (=DSM 104782T=[CM 31914T]) was isolated from faeces of a healthy individual at The New Zealand Institute for Plant and Food Research Limited, Palmerston North, New Zealand. The DNA G+C content of the type strain is 37.21 %.

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**Conflicts of interest**

The authors declare that there are no conflicts of interest.

**References**


A member of the phylum *Firmicutes* comprising of low G+C, Gram-stain-positive bacteria. Cells are non-motile Gram-stain-positive cocci growing either as a single cell or in pairs. Relatively thick cell wall structure. Obligatory anaerobic and catalase-positive. Pectinolytic in pure culture. Major fatty acids are C18:1ω9c, C16:0, a sum of C18:2ω6, 9c/ante-C18:0, iso-C15:0, anteiso-C15:0, anteiso-C17:0 and C18:0. The type species is *Monoglobus pectinilyticus*. 

**DESCRIPTION OF MONoglobus GEN. NOV.**

Monoglobus (Mo.no.glo’bus. Gr. adj. monos, single, solitary; L. masc. n. globus, a ball, sphere; N.L. masc. n. Monoglobus single sphere).

A member of the phylum *Firmicutes* comprising of low G+C, Gram-stain-positive bacteria. Cells are non-motile Gram-stain-positive cocci growing either as a single cell or in pairs. Relatively thick cell wall structure. Obligatory anaerobic and catalase-positive. Pectinolytic in pure culture. Major fatty acids are C18:1ω9c, C16:0, a sum of C18:2ω6, 9c/ante-C18:0, iso-C15:0, anteiso-C15:0, anteiso-C17:0 and C18:0. The type species is *Monoglobus pectinilyticus*. 

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