Cellulomonas chitinilytica sp. nov., a chitinolytic bacterium isolated from cattle-farm compost

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A bacterial strain, designated X.bu-b^T, with chitin-, xylan-, cellulose- and starch-degrading activities, was isolated from compost at a cattle farm near Daejeon, Republic of Korea. The strain comprised Gram-positive, aerobic or facultatively anaerobic, non-motile, rod-shaped bacteria. On the basis of an analysis of 16S rRNA gene sequences, the phylogenetic position of X.bu-b^T was within the genus *Cellulomonas*, and the strain exhibited relatively high sequence similarities with respect to *Cellulomonas biazotea* DSM 20112^T (98.1%), *C. cellasea* DSM 20118^T (98.1%), *C. fimi* DSM 20113^T (98.0%), *C. terrae* DB5^T (97.9%), *C. humilata* ATCC 25174^T (97.7%), *C. xylanilytica* XIL11^T (97.5%), *C. uda* DSM 20107^T (97.4%), *C. gelida* DSM 20111^T (97.3%), *C. iranensis* O^T (97.3%) and *C. flavigena* DSM 20109^T (97.0%). The phylogenetic distance from other *Cellulomonas* species with validly published names was greater than 3% (i.e. less than 97.0% sequence similarity). Chemotaxonomic data also supported the classification of strain X.bu-b^T within the genus *Cellulomonas*: L-ornithine was the cell-wall diamino acid, anteiso-C_{15:0} and anteiso-C_{17:0} were the major fatty acids, rhamnose, galactose, xylose and ribose were the cell-wall sugars, MK-9(H₄) was the predominant menaquinone and diphosphatidylglycerol and phosphatidylglycerol were present in the polar lipids. The G + C content of the genomic DNA was 73.6 mol%. DNA–DNA hybridization experiments showed that the values for DNA–DNA relatedness between strain X.bu-b^T and the phylogenetically closest neighbours were below 23%. On the basis of its phenotypic properties and phylogenetic distinctiveness, strain X.bu-b^T represents a novel species of the genus *Cellulomonas*, for which the name *Cellulomonas chitinilytica* sp. nov. is proposed. The type strain is X.bu-b^T (=KCTC 19133^T =DSM 17922^T).

Polysaccharide-degrading enzymes such as cellulase, chitinase and xylanase are widespread in nature. They can be found in every type of organism, including mammals, plants, algae, moulds, bacteria and phages (Terra & Ferreira, 1994; Bhat, 2000; Oshima *et al.*, 2002). For the production of polysaccharases, micro-organisms are usually the most convenient sources and can be obtained from various natural environments.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain X.bu-b^T is AB268586.

Results of 2D TLC showing the polar lipids of strain X.bu-b^T and tables listing selected characteristics and fatty acids of X.bu-b^T in comparison with those of related *Cellulomonas* species are available as supplementary material with the online version of this paper.

During the course of a study on the polysaccharide-degrading bacterial community, using a developed agar plate screening technique (Ten *et al.*, 2004), a large number of bacteria were isolated from compost at a cattle farm near Daejeon (Republic of Korea). Among those isolates was strain X.bu-b^T, which was able to break down chitin, cellulose, xylan and starch. On the basis of 16S rRNA gene sequence data, the strain was found to be a member of the genus *Cellulomonas*, which currently contains 14 species with validly published names (Bagnara *et al.*, 1985; Stackebrandt & Keddie, 1986; Funke *et al.*, 1995; Collins & Pascual, 2000; Elberson *et al.*, 2000; Rivas *et al.*, 2004; An *et al.*, 2005; Brown *et al.*, 2005; Jones *et al.*, 2005; Yi *et al.*, 2007). Further study of this strain, based on a polyphasic approach that included chemotaxonomic, physiological and DNA–DNA hybridization analyses, confirmed its

position as a representative of novel species within the genus *Cellulomonas*.

Strain X.bu-b^T was isolated from compost by using nutrient agar plates supplemented with insoluble coloured substrates, as described previously (Ten *et al.*, 2004). After isolation, strain X.bu-b^T was cultivated by being transferred onto R2A agar (Difco) every month. Stock cultures were preserved as suspensions in glycerol (20 %, v/v) at -70 °C. Biomass for chemotaxonomic studies was prepared by growing the strain in shake flasks containing R2A broth (Difco) at 150 r.p.m. for 3 days at 25 °C. Cultures were checked for purity, harvested by centrifugation and freeze-dried.

The Gram reaction was determined using the non-staining method, as described by Buck (1982). Cell morphology was observed under a Nikon light microscope at ×1000, with cells grown for 3 days at 25 °C on R2A agar. Catalase and oxidase tests were performed as outlined by Cappuccino & Sherman (2002). For single-carbon-source assimilation studies, a defined liquid medium was used made up of a basal salt medium containing the following (g l⁻¹): 1.8 g K₂HPO₄, 1.08 g KH₂PO₄, 0.5 g NaNO₃, 0.5 g NH₄Cl, 0.1 g KCl, 0.1 g MgSO₄ and 0.05 g CaCl₂. A vitamin solution (Widdel & Bak, 1992), trace element solution SL-10 (Widdel *et al.*, 1983) and selenite/tungstate solution (Tschech & Pfennig, 1984) were added to this medium, and the pH was adjusted to 6.8. Aliquots (0.25 ml) of this liquid medium were added to the wells of a 96-well tray and then filter-sterilized carbon sources were added (0.1 %, w/v, in each case). Growth was examined visually, after incubation at 25 °C for 7 days. The negative-control well did not contain an added carbon source. The positive control well contained R2A broth. Some physiological characteristics were determined with API 20E, API 20NE and API 32GN galleries according to the instructions of the manufacturer (bioMérieux). Tests for anaerobic growth was performed in serum bottles containing R2A broth supplemented with thioglycolate (1 g l⁻¹) under a nitrogen atmosphere. Nitrate- and nitrite-reduction tests were performed in serum bottles containing R2A broth supplemented with KNO₃ (10 mM) and NaNO₂ (10 mM), respectively. The reduction of nitrate and nitrite was monitored by using an ion chromatograph (model 790 personal IC; Metrohm) equipped with a conductivity detector and an anion-exchange column (Metrosep Anion Supp 4; Metrohm). Tests for the degradation of DNA [DNase activity; using DNase agar (Scharlau) and flooding plates with 1 M HCl], casein, starch (Atlas, 1993), lipid (Kouker & Jaeger, 1987), chitin, xylan, cellulose and collagen (Ten *et al.*, 2004, 2005) were performed and evaluated after 7 days. Growth at different temperatures (0, 4, 15, 25, 30, 37 and 42 °C) and pH values (pH 5.0–10.0, in increments of 0.5 pH units) was assessed after incubation for up to 5 days. The effect of pH on growth was determined on R2A broth medium by using three different buffers (final concentration, 50 mM): acetate buffer (for pH 5.0–5.5), phosphate buffer (for pH 6.0–8.0) and Tris

buffer (for pH 8.5–10.0). Salt tolerance was tested on R2A medium supplemented with NaCl at 1–10 % (w/v) after incubation for up to 5 days. Growth on nutrient agar, trypticase soy agar (TSA; Difco) and MacConkey agar was also evaluated at 25 °C.

For the phylogenetic analysis of strain X.bu-b^T, DNA was extracted using a genomic DNA extraction kit (Core Biosystem), the 16S rRNA gene was amplified by using a PCR and then sequencing of the purified PCR product was carried out, as described by Kim *et al.* (2005). The complete 16S rRNA gene sequence was compiled using SeqMan software (DNASTAR). The 16S rRNA gene sequences of related taxa were obtained from the GenBank database. Multiple alignments were performed by using the CLUSTAL_X program (Thompson *et al.*, 1997). Gaps were edited in the BioEdit program (Hall, 1999). Evolutionary distances were calculated using Kimura's two-parameter model (Kimura, 1983). Phylogenetic trees were constructed by using the neighbour-joining (Saitou & Nei, 1987) and maximum-parsimony (Fitch, 1971) methods in the MEGA3 program (Kumar *et al.*, 2004), with bootstrap values based on 1000 replications (Felsenstein, 1985).

Purified cell walls were obtained according to the modified method of Schleifer & Kandler (1972), as follows: 2 g wet cell material was suspended in 0.05 M phosphate buffer (pH 7.2) and sonicated three times for 10 min in iced water. After centrifugation at 4000 g for 20 min, the supernatant was transferred to a new tube, which was then centrifuged at 40 000 g for 25 min. After precipitated debris had been obtained, a 4 % SDS solution (6 ml) was added and the resuspended material was transferred to a glass tube and maintained at 100 °C for 40 min until it became colourless. It was then centrifuged at 40 000 g for 25 min at room temperature and washed three times with water. Hydrolysis of the purified cell walls was carried out by using 6 M HCl at 100 °C for 16 h. Amino acids and peptides in the cell-wall hydrolysates were analysed by using two-dimensional TLC on cellulose plates with the solvent systems described by Schleifer & Kandler (1972). Cell-wall sugars were analysed as described by Stanek & Roberts (1974). Menaquinones were extracted from cells grown on R2A broth and then analysed as described by Komagata & Suzuki (1987), using reversed-phase HPLC. Cellular fatty acids were analysed from bacteria grown on TSA for 2 days at 25 °C. The cellular fatty acids were saponified, methylated, extracted and identified by using the Microbial Identification software package (Sasser, 1990). Polar lipids were extracted and examined by using two-dimensional TLC (Minnikin *et al.*, 1984).

The G+C content of the chromosomal DNA was determined, as described by Mesbah *et al.* (1989), using reversed-phase HPLC. DNA–DNA hybridization was performed fluorometrically by using the method of Ezaki *et al.* (1989), with photobiotin-labelled DNA probes (Sigma) and micro-dilution wells (Greiner). Five hybridization replications were

performed for each sample: the highest and lowest values obtained for each sample were excluded and the means of the remaining three values are quoted as DNA hybridization values.

Cells of strain X.bu-b^T were found to be Gram-positive, non-motile, straight rods, 0.4–0.6 µm in diameter and 1.5–2.2 µm long. Colonies on R2A agar were circular, convex, entire, smooth and yellowish within 3 days at 25 °C. The strain showed a positive result for catalase activity but was negative for oxidase activity, it was aerobic or facultatively anaerobic, it could reduce nitrate to nitrite and it could hydrolyse chitin, xylan, CM-cellulose and starch. The strain grew at 4–30 °C but not at 0 or 37 °C; the optimum temperature was 25 °C. Growth was observed at pH 5.0–8.5, the optimum pH being 7.0–7.5. Strain X.bu-b^T has a phenotypic profile that distinguishes it from representatives of all species of the genus *Cellulomonas* with validly published names (Table 1). Moreover, strain X.bu-b^T could be easily differentiated from its phylogenetically closest relatives, *Cellulomonas biazotea* and *Cellulomonas fimi*, using tests for the utilization of substrates as sole carbon sources (see Supplementary Table S1, available in IJSEM Online). In particular, in contrast to both of the above-mentioned species, strain X.bu-b^T was able to assimilate D-mannitol, gluconate, phenyl acetate and malonate but did not utilize L-rhamnose or lactate.

The peptidoglycan composition of strain X.bu-b^T corresponded to type A4β: it contained L-ornithine-D-glutamic acid, which is the composition reported for most members of the genus *Cellulomonas* and has been emphasized as an important feature for delineation at the genus level within the *Actinobacteria* (Stackebrandt & Schumann, 2000). The cell-wall sugars of strain X.bu-b^T were rhamnose, galactose, xylose and ribose. The cellular fatty acid profiles of strain X.bu-b^T and its closest neighbours are shown in Supplementary Table S2. The major fatty acids of strain X.bu-b^T were anteiso-C_{15:0} (61.3 %) and anteiso-C_{17:0} (15.9 %). The fatty acid profile was similar to those of *Cellulomonas* species analysed previously, although there were differences in the proportions of some fatty acids, perhaps because of differences in cultivation conditions (Funke *et al.*, 1995; An *et al.*, 2005). The polar lipids detected were diphosphatidylglycerol, phosphatidylglycerol, an unidentified lipid, two unidentified phospholipids and three unidentified phosphoglycolipids (Supplementary Fig. S1). The predominant isoprenoid quinone in strain X.bu-b^T was a tetrahydrogenated menaquinone with nine isoprene units [MK-9(H₄)], which is the major lipoquinone found in members of the family *Cellulomonadaceae*.

Comparative 16S rRNA gene sequence analysis for strain X.bu-b^T (1460 bp) showed that it is phylogenetically affiliated to species of the genus *Cellulomonas*. In the phylogenetic tree based on the neighbour-joining algorithm (Fig. 1), strain X.bu-b^T occupies a distinct phylogenetic position within the genus *Cellulomonas*. The almost-complete 16S rRNA gene sequence of strain

X.bu-b^T exhibited relatively high levels of similarity with respect to *C. biazotea* DSM 20112^T (98.1 %), *Cellulomonas cellasea* DSM 20118^T (98.1 %), *C. fimi* DSM 20113^T (98.0 %), *Cellulomonas terrae* DB5^T (97.9 %), *Cellulomonas humilata* ATCC 25174^T (97.7 %), *Cellulomonas xylanilytica* XIL11^T (97.5 %), *Cellulomonas uda* DSM 20107^T (97.4 %), *Cellulomonas gelida* DSM 20111^T (97.3 %), *Cellulomonas iranensis* O^T (97.3 %), *Cellulomonas flavigena* DSM 20109^T (97.0 %), *Cellulomonas persica* I^T (96.8 %) and *Cellulomonas denverensis* ATCC BAA-788^T (96.7 %). The phylogenetic distances, based on 16S rRNA gene sequence similarity, from any other species within the family *Cellulomonadaceae* with validly published names, including *Cellulomonas hominis* ATCC 51964^T and *Cellulomonas bogoriensis* DSM 16987^T, were above 3.7 %. The generally recommended and accepted criteria for delineating bacterial species state that strains with a DNA–DNA relatedness below 70 % (as measured from hybridization) or with a 16S rRNA gene sequence dissimilarity above 3 % are considered to belong to separate species (Wayne *et al.*, 1987; Stackebrandt & Goebel, 1994; Stackebrandt *et al.*, 2002). In view of this definition, the above-mentioned data indicate that strain X.bu-b^T can be considered to represent a novel species of the genus *Cellulomonas*. For further verification of the taxonomic position of strain X.bu-b^T, DNA–DNA hybridization was performed with the members of the genus *Cellulomonas* most closely related to it. Strain X.bu-b^T exhibited relatively low levels of DNA–DNA relatedness values with respect to *C. fimi* KCTC 9143^T (23 %), *C. biazotea* KCTC 1370^T (18 %), *C. terrae* KCTC 19081^T (12 %), *C. cellasea* KCTC 3410^T (15 %), *C. humilata* JCM 11945^T (11 %), *C. uda* KCTC 1441^T (10 %), *C. xylanilytica* LMG 21723^T (10 %), *C. iranensis* KCTC 9983^T (8 %), *C. gelida* KCTC 3231^T (8 %), *C. persica* KCTC 9984^T (10 %), *C. flavigena* KCTC 9104^T (7 %) and *C. denverensis* DSM 15764^T (7 %), indicating that it is not related to them at the species level (Wayne *et al.*, 1987). The DNA G + C content of the strain was found to be 73.6 mol%, a value that falls within the range reported for members of the genus *Cellulomonas*.

The results obtained from the phenotypic and phylogenetic characterizations indicated that strain X.bu-b^T belongs to the genus *Cellulomonas*. The phylogenetic distinctiveness, DNA–DNA hybridization results and the presence of some differential phenotypic features (Table 1 and Supplementary Table S1) serve to confirm that strain X.bu-b^T represents a species that is distinct from recognized *Cellulomonas* species. Therefore, on the basis of the data presented, strain X.bu-b^T should be classified within the genus *Cellulomonas* as a novel species, for which the name *Cellulomonas chitinilytica* sp. nov. is proposed.

Description of *Cellulomonas chitinilytica* sp. nov.

Cellulomonas chitinilytica (chi.ti.ni.ly'ti.ca. N.L. n. *chitinum* chitin; Gr. adj. *lutikos* able to loosen, able to dissolve; N.L. adj. *lytica* dissolving; N.L. fem. adj. *chitinilytica* decomposing chitin).

Table 1. Comparison of selected characteristics of strain X.bu-b^T with those of its nearest phylogenetic neighbours in the genus *Cellulomonas*

Strains: 1, X.bu-b^T; 2, *C. biazotea* DSM 20112^T; 3, *C. fimi* DSM 20113^T; 4, *C. cellasea* DSM 20118^T; 5, *C. terrae* KCTC 19081^T; 6, *C. humilata* ATCC 25174^T; 7, *C. xylanilytica* LMG 21723^T; 8, *C. uda* DSM 20107^T; 9, *C. gelida* DSM 20111^T; 10, *C. iranensis* ATCC 700643^T; 11, *C. flavigena* DSM 20109^T; 12, *C. persica* ATCC 700642^T; 13, *C. denverensis* ATCC BAA-788^T. Data for reference strains were taken from Stackebrandt & Kandler (1979), Bagnara *et al.* (1985), Stackebrandt & Keddle (1986), Funke *et al.* (1995), Collins & Pascual (2000), Elberson *et al.* (2000), Rivas *et al.* (2004), An *et al.* (2005), Brown *et al.* (2005) and Jones *et al.* (2005) unless indicated. D-Glu, D-Glutamic acid; L-Orn, L-ornithine; Fuc, fucose; Gal, galactose; Glc, glucose; GlcN, glucosamine; Man, mannose; Rib, ribose; Rha, rhamnose; 6dTal, 6-deoxytalose; Xyl, xylose; ai, anteiso-branched; i, iso-branched. +, Positive; –, negative; w, weakly positive; ND, no data available.

Characteristic	1	2	3	4	5	6	7	8	9	10	11	12	13	
Motility	–	+	+	–	–	–	–	–	+	+	–	+	+	
Morphology	Rods	Rods	Rods	Rods	Rods	Rods, coccoid, diphtheroid	Rods, coccoid	Rods	Rods	Rods	Rods	Rods	Rods	
Mycelium	–	–	–	–	ND	+	–	–	–	–	–	–	–	
Colony colour	Yellow	Yellow–white	Yellow–white	Yellow	Yellow	White	Yellow	White	Yellow–white	Yellow–white	Yellow	Yellow–white	Pale yellow	
Nitrate reduction	+	+	–*	+	+	–	+	+	+	+	+	+	+	
Peptidoglycan	L-Orn–D-Glu	L-Orn–D-Glu	L-Orn–D-Glu	L-Orn–D-Glu	L-Orn–D-Glu	L-Orn–D-Glu	L-Orn–D-Glu	L-Orn–D-Glu	L-Orn–D-Glu	L-Orn–D-Glu	L-Orn–D-Asp	L-Orn–D-Asp	L-Orn–D-Asp	ND
Cell-wall sugars	Gal, Rib, Xyl, Rha	GlcN, Rha, 6dTal, Gal	GlcN, Rha, Fuc	Rha, Man, 6dTal	Rha, Gal, Glc	Rha, Glc, Fuc	Man, Rha, Fuc	GlcN, Glc	GlcN, Glc	GlcN, Glc	GlcN, Rha, Glc, Man	GlcN, Rha, Rib, Man	GlcN, Rha, Glc, Man	Man, Rha, Rib
Utilization of:														
Acetate	+	+	+	–	–	–	–	+	+	+	+	+	+	ND
Gluconate	+	–	–	–	–	+	–	–	–	–	+	–	–	ND
D-Lactose	+	+	+	–	+	+	+	+	+	–	+	–	–	ND
Lactate	–	+	+	+	–	–	–	–	–	–	–	–	–	ND
D-Mannose	+	+	+	+	+	+	+	+	+	+	+	+	+	ND
D-Mannitol	+	–	–	+	–	+	–	ND	ND	ND	ND	ND	ND	ND
Raffinose	+	+	–	–	ND	ND	ND	–	–	–	–	–	–	ND
L-Rhamnose	–	+	+	–	W	+	+	–	–	+	–	–	ND	ND
D-Ribose	–	–	+	–	–	ND	–	–	–	–	+	–	–	ND
Fermentation of:														
D-Glucose	–	+	+	+	+	+	+	+	+	ND	+	ND	+	+
L-Rhamnose	–	+	+	–	ND	+	+	–	–	ND	–	ND	+	+
Sucrose	–	+	+	+	+	+	+	+	+	ND	+	ND	+	+
D-Mannitol	–	–	–	+	ND	+	ND	–	–	ND	–	ND	–	–
Enzyme activity														
Catalase	+	+	+	+	–	–	+	+	+	ND	+	ND	+	+
DNase	–	–	ND	–	+	ND	ND	+	+	+	–	+	+	ND
Cellulase	W	+	+	+	+	ND	+	+	+	+	+	+	+	ND
Gelatin hydrolysis	+	+	+	–	ND	W	W	+	+	W	+	W	–	–
Urease	–	–	–	–	–	–	–	–	–	+	–	+	–	–

Table 1. cont.

Characteristic	1	2	3	4	5	6	7	8	9	10	11	12	13
Predominant fatty acids	ai-C _{15:0} ai-C _{17:0}	ai-C _{15:0} i-C _{15:0} C _{16:0}	ai-C _{15:0} C _{16:0} ai-C _{17:0}	ai-C _{15:0} C _{16:0} C _{17:0}	ai-C _{15:0} i-C _{15:0} C _{16:0}	ai-C _{15:0} ai-C _{17:0} C _{16:0}	ai-C _{15:0} C _{16:0} C _{18:0}	ai-C _{15:0} C _{16:0} C _{15:0}	ai-C _{15:0} C _{16:0} C _{15:0}	ND	ai-C _{15:0} C _{16:0} C _{14:0}	ND	ai-C _{15:0} i-C _{15:0} C _{14:0} C _{16:0} 68.5
DNA G+C content (mol%)†	73.6	71.5–75.6	71.3–72.0	75.0	73.9	73.0	73.0	72.0–76.3	72.4–74.4	ND	72.7–74.8	ND	

*Determined in this study.
†Ranges are values for all known strains reported by Stackebrandt & Kiedde (1986). Single values are for the type strains listed.

Fig. 1. Neighbour-joining phylogenetic tree, based on 16S rRNA gene sequences, showing the relationships between strain X.bu-b^T and members of the genus *Cellulomonas*. Bootstrap percentages (based on 1000 replications) greater than 50 % are shown at branch points. Filled circles indicate that the corresponding nodes were also recovered in the tree generated with the maximum-parsimony algorithm (not shown). The tree was rooted by using *Sanguibacter suarezii* ST26^T as an outgroup. Bar, 0.005 substitutions per nucleotide position.

Cells are Gram-positive, aerobic or facultatively anaerobic, non-motile and rod-shaped. Colonies on R2A agar are circular, convex, entire, smooth and yellowish within 3 days at 25 °C. Grows between 4 and 30 °C, the optimum temperature being 25 °C. The pH range for growth is pH 5.0–8.5, with an optimum between pH 6.9 and 7.5. NaCl is not required for growth; 2 % (w/v) NaCl is tolerated. Catalase-positive and oxidase-negative. Growth occurs on nutrient agar and TSA, but not on MacConkey agar. Nitrate is reduced to nitrite aerobically but not anaerobically. Hydrolyses chitin, xylan, CM-cellulose (weakly) and starch, but not casein, collagen or DNA. The following substrates are utilized for growth: D-galactose, D-arabinose, L-arabinose, D-fructose, D-glucose, D-mannose, L-xylose, D-xylose, D-lyxose, maltose, trehalose, raffinose, D-lactose, melibiose, cellobiose, sucrose, gluconate, acetate, formate, phenyl acetate, malonate, pyruvate, dulcitol, methanol, glycerol, xylitol, D-sorbitol, D-mannitol, D-adonitol, amygdalin, glycogen, N-acetyl-D-glucosamine, salicin, L-cysteine and L-glutamate. The following substrates are not utilized for growth: L-rhamnose, L-fucose, D-ribose, L-sorbose, ethanol, inositol, dextran, inulin, citrate, lactate, DL-3-hydroxybutyrate, valerate, fumarate, malate, succinate, itaconate, propionate, caprate, glutarate, adipate, suberate, benzoate, maleate, oxalate, 3-hydroxybenzoate, 4-hydroxybenzoate, tartrate, 2-ketogluconate, 5-ketogluconate, L-alanine, L-arginine, L-aspartate, L-asparagine, L-glutamine, glycine, L-isoleucine, L-histidine, L-lysine, L-proline, L-serine, L-threonine, L-leucine, L-methionine, L-valine, L-phenylalanine, L-tryptophan and L-tyrosine. In API 20E tests, β -galactosidase and the Voges–Proskauer reaction give weakly positive results, gelatin hydrolysis give

a positive result and arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, tryptophan deaminase, urease, hydrogen sulphide and indole production produce negative results. Acid is produced weakly from L-arabinose, but acid is not produced from D-glucose, L-rhamnose, D-mannitol, inositol, D-sorbitol, amygdalin, sucrose or melibiose. The predominant isoprenoid quinone is MK-9(H₄). Phosphatidylglycerol, diphosphatidylglycerol and unidentified phospholipids and phosphoglycerolipids are the major polar lipids. The major fatty acids are anteiso-C_{15:0} (61.3 %), anteiso-C_{17:0} (15.9 %) and iso-C_{17:0} (5.4 %). The G + C content of the genomic DNA of the type strain is 73.6 mol%. The peptidoglycan contains L-Orn-D-Glu (type A4β). The cell-wall sugars are galactose, ribose, xylose and rhamnose.

The type strain, X.bu-b^T (=KCTC 19133^T =DSM 17922^T), was isolated from compost at a cattle farm near Daejeon, Republic of Korea.

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