Pantoea gaviniae sp. nov. and *Pantoea calida* sp. nov., isolated from infant formula and an infant formula production environment

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Five Gram-negative, facultatively anaerobic, non-spore-forming, coccoid rod-shaped bacterial isolates were obtained from infant formula and an infant formula production environment and were investigated by use of a polyphasic taxonomic study. Biochemical tests and partial *rpoB* gene sequence analysis of the five isolates revealed that they formed two distinct groups in the family *Enterobacteriaceae*, closely related to several species of the genera *Pantoea* and *Erwinia*, which indicated a phylogenetic position within the genus *Pantoea* or the genus *Erwinia*. Multilocus sequence analysis of concatenated partial *atpD*, *gyrB*, *infB* and *rpoB* gene sequences of two of the isolates suggested that they represented two novel species of the genus *Pantoea*, phylogenetically related most closely to *Pantoea septica*. The five isolates had general characteristics consistent with those of the genus *Pantoea*, and DNA–DNA hybridizations between two representatives and the type strains of their phylogenetically closest relatives based on comparative 16S rRNA gene sequence analysis showed that the isolates represented two novel genospecies. These two genospecies could be differentiated from each other based on fermentation of galacturonate, sorbitol and potassium 5-ketogluconate. They could be differentiated from phylogenetically related *Pantoea* species based on their ability to ferment lactose and to utilize β -gentiobiose and raffinose, their inability to ferment or utilize D-arabitol, and their inability to produce indole. On the basis of the results obtained, the five isolates are considered to represent two novel species of the genus *Pantoea*, for which the names *Pantoea gaviniae* sp. nov. (type strain A18/07^T = LMG 25382^T = DSM 22758^T) and *Pantoea calida* sp. nov. (type strain 1400/07^T = LMG 25383^T = DSM 22759^T) are proposed.

Over the past few years, the family *Enterobacteriaceae* has gained in importance for the food industry, especially for infant formula processing plants. During a recent study by us, 470 *Enterobacteriaceae* isolates from raw ingredients, environmental samples and products of an infant formula processing plant were investigated by biochemical tests

(API ID32E) and *rpoB* gene sequence analysis. This technique has proven to be useful for species identification and classification in the family *Enterobacteriaceae* (Mollet *et al.*, 1997; Drancourt *et al.*, 2001; Case *et al.*, 2007; Stephan *et al.*, 2007, 2008). Of these 470 isolates, 65 could not be identified to species level (Popp *et al.*, 2009). The present study deals with the further characterization of five of these isolates and shows that they represent two novel species of the genus *Pantoea*.

The five isolates were obtained from powdered infant formula (1400/07^T, A11/07, A18/07^T) and an infant formula production environment (484/07, 1378/07) by using the following approach. After enrichment of the samples by incubation for 24 h at 37 °C in buffered peptone water, 0.1 ml was transferred to 9 ml *Enterobacteriaceae*

Abbreviation: MLSA, multilocus sequence analysis.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA, *atpD*, *gyrB*, *infB* and *rpoB* gene sequences of isolates A18/07^T and 1400/07^T are GQ367483, GQ367482, GQ367485, GQ367481 and GQ367484, and GQ367478, GQ367477, GQ367480, GQ367476 and GQ367479, respectively.

A neighbour-joining dendrogram based on *rpoB* gene sequences is available with the online version of this paper.

enrichment broth (Becton Dickinson) and incubated for a further 24 h at 37 °C. The culture obtained was then plated on violet red bile glucose agar (Becton Dickinson), incubated for 24 h at 37 °C and the five isolates were recovered as typical red colonies.

Gram staining was done according to standard protocols. Preliminary characterization based on API ID32E analysis (bioMérieux) was performed according to the manufacturer's instructions. The results suggested that the five strains represented *Pantoea* spp. 1, *Pantoea* spp. 3 and *Serratia plymuthica*, but with low levels of confidence. In a next step, partial *rpoB* gene sequences were determined following the procedure described by Mollet *et al.* (1997). Comparison of partial *rpoB* gene sequences of the new isolates amongst each other suggested that they formed two distinct groups, with 1400/07^T, A11/07, 484/07 and 1378/07 showing 99–100 % similarity, and isolate A18/07^T showing 97 % similarity to the other four isolates. Additional phenotypic tests (API 20E and API 50CHE; bioMérieux) were then performed, and the same two groups could be delineated based on the fermentation of galacturonate, sorbitol and potassium 5-ketogluconate, and the utilization of citrate within 24 h (positive for isolates 1400/07^T, A11/07, 484/07 and 1378/07; negative for A18/07^T).

In the present study, the phylogenetic position of these isolates based on partial *rpoB* gene sequences was investigated, as a multilocus sequence analysis (MLSA) scheme for the genus *Pantoea* according to partial *atpD*, *gyrB*, *infB* and *rpoB* gene sequences was recently reported (Brady *et al.*, 2008). By using the software package BioNumerics (Applied Maths), the *rpoB* gene sequences of the new isolates were compared with those of reference strains of recognized *Pantoea* species and related taxa (Brady *et al.*, 2008) or a newly determined sequence (*Erwinia aphidicola* LMG 24877^T). Phylogenetic trees were reconstructed by using the neighbour-joining (Saitou & Nei, 1987; see Supplementary Fig. S1 in IJSEM Online), maximum-parsimony and maximum-likelihood (Felsenstein, 1985) methods. The robustness of the branches was evaluated by bootstrap resamplings of the data (Felsenstein, 1985; Supplementary Fig. S1). The maximum-parsimony and maximum-likelihood trees showed basically the same topology as the neighbour-joining tree (data not shown). The new *rpoB* gene sequence analysis revealed that the five isolates formed two groups closely related to several species of the genera *Pantoea* and *Erwinia*, which indicated a phylogenetic position in the genus *Pantoea* or the genus *Erwinia*.

To refine the taxonomic position of the isolates, two representatives (A18/07^T and 1400/07^T) were subjected to MLSA of concatenated partial *atpD*, *gyrB*, *infB* and *rpoB* gene sequences, as Brady *et al.* (2008) reported that a concatenated dataset tree based on these four gene sequences is preferred over trees based on single gene sequences for species identification in the genus *Pantoea*. In their concatenated dataset trees, *Pantoea* species were supported by higher bootstrap values. Total DNA for *atpD*, *gyrB* and *infB* gene

sequence analysis was prepared according to the protocol described by Niemann *et al.* (1997), and partial fragments of the *atpD*, *gyrB* and *infB* genes were amplified and sequenced following the protocol of Brady *et al.* (2008), except for the *gyrB* gene fragment of isolate 1400/07^T, which was sequenced using the following forward and reverse primers: *gyrB* 07-F, *gyrB* 05-R (5'-TCGGAAGAAACCAGTTTGTCTT-3') and *gyrB* 08-R. Sequence assembly was performed by using the program AutoAssembler (Applied Biosystems), and phylogenetic analysis was performed by using the software package BioNumerics. The partial *atpD*, *gyrB*, *infB* and *rpoB* gene sequences of the isolates were concatenated and aligned with concatenated partial *atpD*, *gyrB*, *infB* and *rpoB* gene sequences of reference strains of *Pantoea* species and related taxa (Brady *et al.*, 2008) or of *Erwinia aphidicola* LMG 24877^T. Phylogenetic trees were reconstructed by using the neighbour-joining (Saitou & Nei, 1987; Fig. 1) and maximum-parsimony (Felsenstein, 1985) methods, and the robustness of the branches was evaluated by bootstrap resamplings of the data (Felsenstein, 1985). The maximum-parsimony tree showed basically the same topology as the neighbour-joining tree and the maximum-likelihood tree by Brady *et al.* (2008) (data not shown). MLSA revealed that isolates A18/07^T and 1400/07^T represented two novel species of the genus *Pantoea*, phylogenetically closely related to *Pantoea septica* (Brady *et al.*, 2010). The two isolates were therefore characterized further.

The 16S rRNA genes of isolates A18/07^T and 1400/07^T were amplified and sequenced as described by Franz *et al.* (2006), by using the primers listed by Coenye *et al.* (1999). Almost-complete 16S rRNA gene sequences comprising 1494 nt (A18/07^T) and 1495 nt (1400/07^T) were obtained, and compared with almost-complete 16S rRNA gene sequences of reference strains of species of the genus *Pantoea* and related taxa (Brady *et al.*, 2008) or of newly determined sequences (i.e. *Erwinia aphidicola* LMG 24877^T and *Erwinia toletana* LMG 24162^T). Pairwise similarities were calculated with the BioNumerics software package by using an open gap penalty of 100 % and a unit gap penalty of 0 %. A phylogenetic tree was reconstructed by using the neighbour-joining method (Saitou & Nei, 1987), and the robustness of the branches was evaluated by bootstrap resamplings of the data (Felsenstein, 1985; Fig. 2). Isolates A18/07^T and 1400/07^T showed highest levels of 16S rRNA gene sequence similarity with *Pantoea deleyi* LMG 24200^T (98.0 and 97.9 %, respectively), *Pantoea conspicua* LMG 24534 (97.9 and 98.0 %), *Pantoea brenneri* LMG 5343 (97.8 and 97.9 %), *Pantoea cypripedii* ICMP 1591^T (97.8 and 97.7 %), *Erwinia toletana* LMG 24162^T (97.8 and 98.0 %), *Erwinia tasmaniensis* Et1/99^T (97.7 % each), *P. septica* LMG 5345 (97.7 and 97.5 %), *Pantoea* MLSA group G LMG 24248 (97.7 % each), *Pantoea vagans* LMG 24199^T (97.7 and 97.9 %), *Pantoea agglomerans* NCTC 9381^T (97.6 and 97.8 %), *Pantoea eucalypti* LMG 24197^T (97.6 % each), *Pantoea anthophila* LMG 2558^T (97.5 and 97.7 %), *Pantoea ananatis* ATCC 33244^T (97.5 and 97.4 %), *Pantoea dispersa* LMG 2603^T (97.4 and 97.8 %), *Erwinia aphidicola* LMG

Fig. 1. Neighbour-joining dendrogram based on concatenated partial *atpD*, *gyrB*, *infB* and *rpoB* gene sequences of strains 1400/07^T and A18/07^T and related taxa within the family *Enterobacteriaceae*. The reference strains of MLSA groups reported by Brady *et al.* (2008) are indicated with a superscript R. Numbers at nodes are bootstrap values (percentages of 500 replicates). Bar, 0.1 substitutions per nucleotide position.

Fig. 2. Neighbour-joining dendrogram based on 16S rRNA gene sequences showing the phylogenetic relationships between strains 1400/07^T and A18/07^T and related taxa within the family *Enterobacteriaceae*. The reference strains of MLSA groups reported by Brady *et al.* (2008) are indicated with a superscript R. Numbers at nodes are bootstrap values (percentages of 1000 replicates). Bar, 0.01 substitutions per nucleotide position.

24877^T (97.4 % each), *Erwinia persicina* LMG 11254^T (97.2 and 97.3 %), *Enterobacter cowanii* CIP 107300^T (97.1 and 97.4 %), *Pantoea eucrina* LMG 2781 (97.1 and 97.0 %) and *Pantoea stewartii* subsp. *stewartii* LMG 2715^T (97.0 and 97.2 %). The level of 16S rRNA gene sequence similarity between isolates 1400/07^T and A18/07^T was 99.6 %. Levels of 16S rRNA gene sequence similarity were below the range of 98.7–99 % recommended for delimiting species (Stackebrandt & Ebers, 2006), suggesting again that the isolates represented novel species within the family *Enterobacteriaceae*.

As the branches representing the different genera of the *Enterobacteriaceae* are not monophyletic and are not supported by high bootstrap values, and as highest levels of similarity with the new isolates are found with reference strains of different genera, it can be concluded that for the *Enterobacteriaceae*, the similarity values obtained reflect a high level of homoplasy in the 16S rRNA gene sequences.

DNA–DNA hybridizations were performed between isolates A18/07^T and 1400/07^T and the type strains of their phylogenetically closest relatives based on comparative 16S

rRNA gene sequence analysis. DNA for DNA–DNA hybridizations was prepared according to the method of Wilson (1987), with minor modifications (Cleenwerck *et al.*, 2002), and hybridizations were carried out at 45 °C by using a modification (Goris *et al.*, 1998; Cleenwerck *et al.*, 2002) of the microplate method described by Ezaki *et al.* (1989). Levels of DNA–DNA relatedness reported are the means ($\pm$ SD) of a minimum of seven hybridizations. Reciprocal reactions (i.e. A $\times$ B and B $\times$ A) were performed and the variation between them was within the limits of this method (Goris *et al.*, 1998). The level of DNA–DNA relatedness between isolates 1400/07^T and A18/07^T was 59 $\pm$ 4 %. Levels of less than 25 % were found between isolate 1400/07^T and selected reference strains: *P. deleyi* LMG 24200^T (14 $\pm$ 5 %), *P. conspicua* LMG 24534^T (15 $\pm$ 1 %), *P. brenneri* LMG 5343^T (15 $\pm$ 6 %), *P. cypridii* LMG 2657^T (14 $\pm$ 5 %), *Erwinia toletana* LMG 24162^T (16 $\pm$ 14 %), *Erwinia tasmaniensis* LMG 25318^T (15 $\pm$ 4 %), *P. septica* LMG 5345^T (23 $\pm$ 4 %), *P. vagans* LMG 24199^T (15 $\pm$ 4 %), *P. agglomerans* LMG 1286^T (18 $\pm$ 1 %), *P. eucalypti* LMG 24197^T (14 $\pm$ 3 %), *P. ananatis* LMG 2665^T (14 $\pm$ 0 %), *P. dispersa* LMG 2603^T (18 $\pm$ 13 %), *P. eucrinea* LMG 2781^T (15 $\pm$ 7 %) and *P. stewartii* subsp. *stewartii* LMG 2715^T (8 $\pm$ 6 %). These values are below the 70 % generally accepted for species delineation (Wayne *et al.*, 1987), demonstrating that the two isolates represented two novel genospecies.

The DNA G+C content of isolates A18/07^T and 1400/07^T was determined from DNA prepared in the frame of the DNA–DNA hybridization experiments, according to the HPLC method described by Mesbah *et al.* (1989). The values (means of three independent analyses of the same DNA sample) for A18/07^T and 1400/07^T were 58.4 and 57.4 mol%, respectively. These values are consistent with the DNA G+C contents of other members of the genus *Pantoea* (Gavini *et al.*, 1989; Mergaert *et al.*, 1993; Brady *et al.*, 2009, 2010).

The phenotypic characteristics of the five new isolates were compared with those of strains of the genus *Pantoea* by using various biochemical tests (API ID32E, API 20E, API 50CHE and Biotype 100 with Biotype Medium 1; bioMérieux) performed according to the manufacturer's instructions. The phenotypic characteristics of the five isolates were in accordance with the emended description of the genus *Pantoea* (Brady *et al.*, 2010); however, the new isolates could be differentiated from phylogenetically related *Pantoea* species by their ability to ferment lactose and utilize β -gentiobiose and raffinose, their inability to ferment and utilize D-arabitol, and their inability to produce indole (Table 1). The two genospecies themselves could be differentiated, as previously mentioned, based on fermentation of galacturonate, sorbitol and potassium 5-ketogluconate (Table 1). Details of the physiological and

Table 1. Differential phenotypic characteristics between *Pantoea gaviniae* sp. nov. and *Pantoea calida* sp. nov. and species of the genus *Pantoea*

Taxa: 1, *P. gaviniae* sp. nov. (n=1); 2, *P. calida* sp. nov. (n=4); 3, *P. brenneri*; 4, *P. conspicua*; 5, *P. septica*; 6, *P. eucrinea*; 7, *P. cypridii*; 8, *P. vagans*; 9, *P. eucalypti*; 10, *P. deleyi*; 11, *P. anthophila*; 12, *P. agglomerans*; 13, *P. dispersa*; 14, *P. ananatis*; 15, *P. stewartii* subsp. *stewartii*; 16, *P. stewartii* subsp. *indologenes*. For taxa 3–7, indole production and fermentation data are from the present study and carbon source utilization data are from Brady *et al.* (2010); data for taxa 8–11 from Brady *et al.* (2009); data for taxa 12 and 13 from Gavini *et al.* (1989); data for taxa 14–16 from Mergaert *et al.* (1993). Fermentation data (API 50CHE) were recorded after 48 h. Data for carbon source utilization tests (Biotype 100) were recorded after 4 days. –, 0–10 % positive; (–), 10–20 % positive; v, 20–80 % positive; (+), 80–90 % positive; ++, 90–100 % positive; ND, no data available.

Characteristic	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
Indole production	–	–	–	–	–	–	–	–	–	–	–	–	–	+	–	+
Fermentation of:																
Potassium 2-ketogluconate	+	+	+	+	+	+	+	ND	ND	ND	ND	ND	ND	(–)	–	(–)
D-Arabitol	–	–	–	+	+	+	–	ND	ND	+	+	ND	ND	+	–	+
Lactose	+	+	–	+	–	–	+	+	+	ND	ND	(–)	–	+	–	+
β -Gentiobiose	+	+	+	+	–	–	–	ND	ND	+	ND	ND	ND	v	–	v
Potassium 5-ketogluconate	–	+	–	–	–	+	+	ND	ND	ND	ND	ND	ND	v	–	v
Melibiose	+	+	–	–	–	–	+	ND	ND	ND	ND	–	–	(+)	+	+
D-Sorbitol	–	+	–	–	–	–	–	ND	ND	ND	ND	–	–	(+)	–	–
Potassium gluconate	+	+	–	+	+	+	+	ND	ND	ND	ND	ND	ND	ND	ND	ND
Carbon source utilization																
β -Gentiobiose	+	+	–	+	ND	ND	+	+	–	+	–	–	+	ND	ND	ND
4-Aminobutyrate	–	–	ND	ND	ND	ND	ND	ND	ND	ND	ND	+	+	ND	ND	ND
Raffinose	+	+	ND	–	ND	–	–	–	–	–	–	ND	–	ND	ND	ND
α -Ketoglutarate	+	+	ND	ND	ND	ND	ND	–	–	–	–	ND	ND	ND	ND	ND
D-Arabitol	–	–	ND	+	ND	+	+	ND	ND	+	ND	ND	+	ND	ND	ND
L-Tartrate	–	–	ND	+	ND	–	ND	+	+	+	–	ND	+	ND	ND	ND

biochemical characteristics of the novel species are given in the descriptions below.

The results of this polyphasic taxonomic study support the recognition of two novel species of the genus *Pantoea*, for which the names *Pantoea gaviniae* sp. nov. and *Pantoea calida* sp. nov. are proposed.

Description of *Pantoea gaviniae* sp. nov.

Pantoea gaviniae (ga.vi.ni'a.e. N.L. fem. gen. n. *gaviniae* of Gavini, in honour of Françoise Gavini, a French microbiologist who first described the genus *Pantoea*).

Cells are Gram-negative rods that are facultatively anaerobic and motile. Cells are 1.0 µm wide by 2.0–3.0 µm long and occur singly or in pairs. After 24 h of aerobic incubation at 37 °C on trypticase soy agar (TSA) medium, colonies are non-pigmented and convex. Oxidase-negative and catalase-positive. Colonies grow well at 10 °C but poorly at 7 °C (within 3 days). They grow poorly at 41.5 °C and no growth occurs at 44 °C. Positive for β-glucosidase, β-galactosidase, α-galactosidase, aesculin hydrolysis and the Voges–Proskauer Test, but negative for ornithine decarboxylase, arginine dihydrolase, lysine decarboxylase, urease, lipase, β-glucuronidase, *N*-acetyl-β-glucosaminidase, α-glucosidase, α-maltosidase, *L*-aspartic acid arylamidase, tryptophan deaminase and gelatinase, and indole and H₂S production. Acid is produced under anaerobic conditions from the following compounds within 48 h: glycerol, *L*-arabinose, *D*-ribose, *D*-xylose, *D*-galactose, *D*-glucose, *D*-fructose, *D*-mannose, *L*-rhamnose, inositol, *D*-mannitol, *N*-acetylglucosamine, arbutin, salicin, cellobiose, maltose, lactose, melibiose, sucrose, trehalose, raffinose, β-gentiobiose, potassium gluconate and potassium 2-ketogluconate. No acid is produced from erythritol, *D*-arabinose, *L*-xylose, adonitol, methyl β-*D*-xylopyranoside, *L*-sorbose, dulcitol, *D*-sorbitol, methyl α-*D*-mannopyranoside, methyl α-*D*-glucopyranoside, amygdalin, inulin, melezitose, starch, glycogen, xylitol, turanose, *D*-lyxose, *D*-tagatose, *D*-fucose, *L*-fucose, *D*-arabitol, *L*-arabitol, potassium 5-ketogluconate or galacturonate. Positive for utilization of α-*D*-glucose, β-*D*-fructose, *D*-galactose, trehalose, *D*-mannose, α-melibiose, sucrose, raffinose, maltotriose, maltose, α-lactose, lactulose, 1-0-methyl β-galactopyranoside, 1-0-methyl α-galactopyranoside, cellobiose, β-gentiobiose, 1-0-methyl β-*D*-glucopyranoside, aesculin, *D*-ribose, *L*-arabinose, *D*-xylose, α-*L*-rhamnose, glycerol, *myo*-inositol, *D*-mannitol, *D*-sorbitol, *D*-saccharate, mucate, *L*-malate, *cis*-aconitate, *trans*-aconitate, citrate, *D*-glucuronate, *D*-galacturonate, 2-keto-*D*-gluconate, 5-keto-*D*-gluconate, *N*-acetyl-*D*-glucosamine, *D*-gluconate, *DL*-lactate, succinate, fumarate, *DL*-glycerate, *D*-glucosamine, *L*-aspartate, *L*-glutamate, *L*-proline, *D*-alanine, *L*-alanine, *L*-serine and α-ketoglutarate within 4 days. The following compounds are not utilized as sole carbon sources within 4 days: *L*-sorbose, palatinose, α-*L*-fucose, melezitose, *D*-arabitol, *L*-arabitol, xylitol, dulcitol, *D*-tagatose, maltitol, turanose, adonitol, hydroxyquinoline-β-glucuronide, *D*-lyxose, *i*-erythritol, 1-0-methyl α-*D*-glucopyranoside, 3-0-methyl

D-glucopyranoside, *L*-tartrate, *D*-tartrate, *meso*-tartrate, *D*-malate, tricarballoylate, *L*-tryptophan, phenylacetate, protocatechuate, *p*-hydroxybenzoate, quinate, gentisate, *m*-hydroxybenzoate, benzoate, 3-phenylpropionate, *m*-coumarate, trigonelline, betaine, putrescine, 4-aminobutyrate, histamine, caprate, caprylate, *L*-histidine, glutarate, 5-aminovaleate, ethanolamine, tryptamine, itaconate, 3-hydroxybutyrate, malonate, propionate and *L*-tyrosine. The DNA G + C content of the type strain is 58.4 mol%.

The type strain, A18/07^T (=LMG 25382^T =DSM 22758^T), was isolated from powdered infant formula.

Description of *Pantoea calida* sp. nov.

Pantoea calida (ca.li'da. L. fem. adj. *calida* warm, hot, reflecting its ability to grow at 44 °C).

Cells are Gram-negative coccoid rods that are facultatively anaerobic and motile. Cells are 1.0 µm wide by 1.5–2.0 µm long and occur singly or in pairs. After 24 h of aerobic incubation at 37 °C on TSA medium, colonies are non-pigmented and convex. Oxidase-negative and catalase-positive. Colonies grow poorly at 10 °C (within 3 days) but well at 44 °C. Positive for β-glucosidase, β-galactosidase, aesculin hydrolysis and the Voges–Proskauer test, but negative for ornithine decarboxylase, arginine dihydrolase, lysine decarboxylase, urease, lipase, β-glucuronidase, α-maltosidase, *L*-aspartic acid arylamidase, tryptophan deaminase and gelatinase, and indole and H₂S production. Acid is produced under anaerobic conditions from the following compounds within 48 h: glycerol, *L*-arabinose, *D*-ribose, *D*-xylose, *D*-galactose, *D*-glucose, *D*-fructose, *D*-mannose, *L*-rhamnose, inositol, *D*-mannitol, *D*-sorbitol, *N*-acetylglucosamine, arbutin, salicin, cellobiose, maltose, lactose, melibiose, trehalose, β-gentiobiose, potassium gluconate, potassium 2-ketogluconate, potassium 5-ketogluconate and galacturonate. No acid is produced from erythritol, *D*-arabinose, *L*-xylose, adonitol, methyl β-*D*-xylopyranoside, *L*-sorbose, dulcitol, methyl α-*D*-mannopyranoside, methyl α-*D*-glucopyranoside, amygdalin, inulin, melezitose, starch, glycogen, xylitol, turanose, *D*-lyxose, *D*-tagatose, *D*-fucose, *L*-fucose, *D*-arabitol or *L*-arabitol. Positive for utilization of α-*D*-glucose, β-*D*-fructose, *D*-galactose, trehalose, *D*-mannose, α-melibiose, sucrose, raffinose, maltotriose, maltose, α-lactose, lactulose, 1-0-methyl β-galactopyranoside, cellobiose, β-gentiobiose, 1-0-methyl β-*D*-glucopyranoside, aesculin, *D*-ribose, *L*-arabinose, α-*L*-rhamnose, glycerol, *myo*-inositol, *D*-mannitol, *D*-sorbitol, *D*-saccharate, mucate, *L*-malate, *cis*-aconitate, *trans*-aconitate, citrate, *D*-glucuronate, *D*-galacturonate, 2-keto-*D*-gluconate, 5-keto-*D*-gluconate, *N*-acetyl-*D*-glucosamine, *D*-gluconate, *DL*-lactate, succinate, fumarate, *DL*-glycerate, *D*-glucosamine, *L*-aspartate, *L*-glutamate, *L*-proline, *D*-alanine, *L*-alanine, *L*-serine and α-ketoglutarate within 4 days. The following compounds are not utilized as sole carbon sources within 4 days: *L*-sorbose, 1-0-methyl α-galactopyranoside, palatinose, α-*L*-fucose, melezitose, *D*-arabitol, *L*-arabitol, xylitol, dulcitol, *D*-tagatose, maltitol, turanose, adonitol, hydroxyquinoline-β-glucuronide, *D*-lyxose,

i-erythritol, 1-0-methyl α -D-glucopyranoside, 3-0-methyl D-glucopyranoside, L-tartrate, D-tartrate, meso-tartrate, D-malate, tricarballylate, L-tryptophan, phenylacetate, protocatechuate, *p*-hydroxybenzoate, quinate, gentisate, *m*-hydroxybenzoate, benzoate, 3-phenylpropionate, *m*-coumarate, trigonelline, betaine, putrescine, 4-aminobutyrate, histamine, caprate, caprylate, L-histidine, glutarate, 5-aminovalerate, ethanolamine, tryptamine, itaconate, 3-hydroxybutyrate, malonate, propionate and L-tyrosine. The DNA G+C content of the type strain is 57.4 mol%.

The type strain, 1400/07^T (=LMG 25383^T =DSM 22759^T), was isolated from powdered infant formula. A11/07, 484/07 and 1378/07 are additional strains of the species.

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