Reclassification of *Clostridium coccoides*, *Ruminococcus hansenii*, *Ruminococcus hydrogenotrophicus*, *Ruminococcus luti*, *Ruminococcus productus* and *Ruminococcus schinkii* as *Blautia coccoides* gen. nov., comb. nov., *Blautia hansenii* comb. nov., *Blautia hydrogenotrophica* comb. nov., *Blautia luti* comb. nov., *Blautia producta* comb. nov., *Blautia schinkii* comb. nov. and description of *Blautia wexlerae* sp. nov., isolated from human faeces

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Phenotypic and phylogenetic studies were performed on 15 isolates of an unidentified Gram-positive, anaerobic, non-sporulating coccobacillus-shaped bacterium isolated from human faeces. The novel organisms were catalase-negative, indole-negative and produced acetate and succinate as end products of metabolism. Comparative 16S rRNA gene sequencing demonstrated that the 15 isolates were highly related to each other and formed a hitherto unknown subline within the clostridial rRNA cluster XIVa. The novel isolates formed a robust phylogenetic group with a number of organisms which included *Clostridium coccoides*, *Ruminococcus luti*, *Ruminococcus obeum* and a number of other misclassified ruminococci. On the basis of these studies, a novel genus, *Blautia* gen. nov., is proposed. It is suggested that *Clostridium coccoides*, *Ruminococcus hansenii*, *Ruminococcus hydrogenotrophicus*, *Ruminococcus luti*, *Ruminococcus productus*, and *Ruminococcus schinkii* are transferred to this genus as *Blautia coccoides* gen. nov., comb. nov., *Blautia hansenii* comb. nov., *Blautia hydrogenotrophica* comb. nov., *Blautia luti* comb. nov., *Blautia producta* comb. nov. and *Blautia schinkii* comb. nov. One of the new isolates, the hitherto unknown coccus-shaped bacterial strain WAL 14507T (=ATCC BAA-1564T=DSM 19850T) is proposed as representing the type strain of a novel species, *Blautia wexlerae* sp. nov.

It is becoming increasingly clear that humans have a symbiotic relationship with their intestinal microbial community. This community enjoys a stable nutrient-rich environment with limited host immune responses, and in turn, it facilitates the normal functions of the body. Although this community has been studied using culture techniques, culture-independent investigations based on sequence analysis of rRNA genes suggest that 40 to 80% of...
the total 16S rRNA gene sequences retrieved represent as-yet uncultivated species (Suau et al., 1999). It is recognized that 16S rRNA gene sequencing used in conjunction with culturing techniques represents a powerful approach for discerning novel species diversity within the human gut and faeces (Barcenilla et al., 2000; Suau et al., 1999). In the present study, a combination of culture-based and molecular-based methodologies was used to facilitate the identification of 15 isolates of a hitherto unknown species within the Clostridium cocoides rRNA XIVa cluster. On the basis of an investigation using a polyphasic taxonomic, it is proposed that these strains be classified, alongside a number of misclassified ruminococci, in a novel genus.

Fifteen isolates were recovered from stool specimens from control children and children with late onset autism at the Rush Children’s Hospital, Chicago, USA (Finegold et al., 2002). The strains were characterized biochemically by using a combination of conventional tests as described previously in the Wadsworth and VPI anaerobic bacteriology manuals (Holdeman et al., 1977; Jousimies-Somer et al., 2002) and the API ZYM and Rapid ID32A systems (bioMérieux) according to the manufacturer’s instructions. All biochemical tests were performed in duplicate. Carbohydrate fermentation tests were conducted using pre-reduced, anaerobically sterilized (PRAS) peptone-yeast-carbohydrate broth tubes (Anaerobe Systems). The strains were grown in peptone-yeast (PY) broth and peptone-yeast-glucose (PYG) broth (Anaerobe Systems) for metabolic end product (short-chain volatile and non-volatile fatty acids) analysis by GLC (Jousimies-Somer et al., 2002). Long-chain cellular fatty acids were analysed as previously described (Wexler et al., 1996). The 16S rRNA genes were amplified by PCR using universal primers 8Ua (positions 8–28, Escherichia coli numbering) and 1485B (positions 1485–1507) as described previously (Brosius et al., 1978). The amplified product was purified by using QIAamp PCR purification kit (Qiagen, Inc.) and directly sequenced with an ABI 3100 Avant genetic system (Applied QIAamp PCR purification kit (Qiagen, Inc.) and directly sequenced with an ABI 3100 Avant genetic system (Applied Biosystems). The closest known relatives of the new isolates, their 16S rRNA genes were amplified by PCR and sequenced. The 15 isolates were highly related to each other following subculture in an atmosphere of 2% or 6% O2. All of the isolates were negative for lecinthinase, lipase, catalase and indole. They were capable of hydrolysing aesculin, but not gelatin. All of the isolates utilized arabinose, glucose, mannose, ribose, xylose, but not glycogen as substrates when grown in PRAS carbohydrate broths. The utilization of amygdalin, cellobiose, fructose, lactose, maltose, mannitol, melezitose, melibiose, raffinose, rhamnose, salicin, sorbitol, sucrose and trehalose was variable. Analysis of end products by GLC from peptone-yeast-glucose broth revealed acetate and succinate as the major end products of metabolism. The long-chain cellular fatty acids of the isolates were of the straight-chain saturated and monounsatuated types, with C16:0 (major component), C14:0, and C16:0 dimethyl acetal fatty acids predominating. Using the API ZYM and Rapid ID32A systems, all 15 isolates produced a similar profile. Positive reactions were obtained for α-galactosidase, β-galactosidase, α-glucosidase, β-glucosidase and α-fucosidase by both systems. With the Rapid ID32A system, α-arabinosidase activity showed as positive and acid phosphatase was detected by the API ZYM system. No activity was detected for N-acetyl-β-glucosaminidase, alkaline phosphatase, α-chymotrypsin, cystine arylamidase, β-glucuronidase, lipase (C14), leucine arylamidase, α-mannosidase, trypsin or valine arylamidase. Urease results were variable when tested by the Rapid ID32A system and esterase (C4), esterase lipase (C8), and naphthol-AS-BI-phosphohydrolase were variable as tested by the API ZYM system. The isolates were sensitive to vancomycin (5 μg) and kanamycin (1000 μg), but resistant to colistin (10 μg) identification discs.

To determine the phylogenetic affinities of the novel isolates, their 16S rRNA genes were amplified by PCR and sequenced. The 15 isolates were highly related to each other with 99.5–100% 16S rRNA gene sequence similarity. Sequence searches of GenBank and Ribosomal Database Project libraries revealed that the isolates were members of the phylum Firmicutes. It was evident from tree analysis that the novel isolates represented a previously unknown lineage within the clostridial rRNA cluster XIVa subgroup and, in particular, shared a close relationship with Ruminococcus luti and Ruminococcus obeum. Pairwise comparison revealed approximately 5.0% sequence divergence between the novel isolates and the type strains of the closest recognized species, R. luti and R. obeum, based on the almost full-length 16S rRNA gene sequences (=1400 nt). A phylogenetic tree, constructed by the maximum-parsimony method, depicting the phylogenetic affinity of the novel bacterium as exemplified by strain WAL 14507T is shown in Fig. 1. Strain WAL 14507T formed a distinct lineage within a small subcluster of species which included several recognized ruminococcal species (Ruminococcus hansenii, Ruminococcus hydrogenotrophicus, R. luti, R. obeum, Ruminococcus productus, Ruminococcus schinkii) and Clostridium cocoides. The major branching orders were confirmed by using the
maximum-likelihood method (see Supplementary Fig. S1 in IJSEM Online). Although there is no precise correlation between the 16S rRNA gene sequence divergence value and species delineation, it is generally recognized that similarity values of 97% or less are significant (Stackebrandt & Goebel, 1994). However, Stackebrandt & Ebers (2006) have recently made the recommendation that this value should be increased to 98.7–99% without sacrificing the quality and precision of a species description and as an aid to taxonomists. This followed observations that with a threshold value of 98.5% gene sequence similarity, the corresponding DNA–DNA reassociation values were always lower than 70%, the accepted value for a species. It is apparent that the 16S rRNA gene, although a powerful tool in phylogenetic reconstructions, has limitations in discriminating recent speciation events. This is reflected in an increasing number of species now being described within the literature with very high rRNA gene sequence similarities to their nearest relatives. For example, Clostridium carboxidivorans displayed 99.7% and 99.8% to Clostridium scatologenes and Clostridium drakei, respectively (Liou et al., 2005), with DNA–DNA reassociation values demonstrating that all three strains represent distinct species. When such high 16S rRNA gene sequence similarity values are used for describing novel species, they must always be accompanied by appropriate phenotypic observations that can be used to distinguish the novel taxa. Support for the distinctiveness of the novel bacterium isolated from human faeces is provided by the phenotypic characterization. Although 16S rRNA gene sequence analysis showed the closest phylogenetic relatives to the novel bacteria are R. luti and R. obeum, strain WAL 14507T could be distinguished easily from R. luti and R. obeum by several features. In contrast to R. luti, the novel strain did not produce β-N-acetylglucosaminidase, alkaline phosphatase or α-mannosidase. Similarly, strain WAL 14507T could be differentiated from R. obeum by the production of acetate and succinate as major fermentation products, but not ethanol and also by its ability to strongly hydrolyse aesculin and produce significant amounts of α-arabinosidase and α-fucosidase. The characteristics that distinguish the novel
strains from their most closely related species are summarized in Table 1.

In several studies, a number of uncultured bacteria represented by sequences derived from faecal 16S rRNA gene clone libraries were found to be closely related to R. obeum (Suau et al., 1999; Zoetendal et al., 1998). Zoetendal et al. (2002) followed up on these studies using a combination of fluorescent in situ hybridization and flow cytometry. Several probes, one of which was designated Urobe63, were specific for these R. obeum-like sequences. Their data showed that approximately 16% of the total community belonged to the cluster XIVa (C. coccoides group) and of this 2.5% belonged to R. obeum-like organisms, although this value varied between 1 and 6% for different individuals. A comparison of the nucleotide sequence of the Urobe63 probe and the 16S rRNA gene sequence of our novel organism showed that the probe sequence was present within the 16S rRNA genes of the novel bacterium. Furthermore, two of the sequences that were used by Zoetendal et al. (2002) to validate and test the probes were found to be 98–99% related to our novel organism and it is highly likely that these sequences correspond to strains of this hitherto unknown bacterium. Therefore it can be reasonably assumed that some proportion of the organisms enumerated by the Urobe63 probe represented our novel organism and this suggests that the novel bacterium (and other closely related R. obeum-like strains) comprises a significant fraction of the faecal community.

A number of studies have shown that the genus Ruminococcus is not monophyletic and is phylogenetically heterogeneous (Rainey & Janssen, 1995; Willems & Collins, 1995; Rieu-Lesme et al., 1996). The type species, Ruminococcus flavefaciens, is a member of a cluster designated clostridial rRNA cluster IV (Collins et al., 1994) and this cluster is also referred to as the Clostridium leptum group of organisms. Ruminococcus albus, Ruminococcus callidus and Ruminococcus bromii are also members of this suprageneric cluster, although the latter species is somewhat removed from the former species. Phylogenetically, the remainder of the ruminococci are members of the rRNA cluster XIVa (Collins et al., 1994) and therefore should not be considered true phylogenetic members of the genus Ruminococcus sensu stricto. This grouping is often referred to as the Clostridium coccoides group, although this label is misleading due to this large supra-generic cluster embracing taxa that bear a plethora of generic names. Currently the grouping embraces almost 20 genera such as Acetitomaculum, Anaerostipes, Bryantella, Butyribrio, Catonella, Clostridium, Coprococcus, Dorea, Eubacterium, Hespella, Johnsonella, Lachnospira, Lachnobacterium, Pseudobutyribrio, Roseburia, Ruminococcus, Shuttleworthia, Sporobacterium and Syntrophococcus and many misclassified clostridial species. It is now recognized that members of this cluster are in need of extensive taxonomic revision with Collins et al. (1994) proposing to retain the true clostridia in cluster I which bears Clostridium butyricum as the type species.

Phylogenetic analysis employing a number of software programs (neighbour-joining, maximum-likelihood and parsimony) using only matched nucleotides demonstrated that the novel faecal organism formed a robust group with a number of misclassified ruminococci (R. hansenii, R. hydrogenotrophicus, R. luti, R. obeum, R. productus, R. schinkii) together with C. coccoides (Fig. 1). It is pertinent to point out that C. coccoides, the only species isolated from animal sources (mice), produces endospores unlike all other species in this clade. It may be argued that this organism should not be included in any new genus that contains these Ruminococcus species. However, C. coccoides and R. productus share a very high 16S rRNA gene sequence similarity (99.7%) and an examination of the literature demonstrates that the biochemical profiles, products of glucose metabolism and DNA G + C content of these two organisms are almost identical (Kaneuchi et al., 1976; Ezaki et al., 1994). Although some internal structure is present (see Table 2 and Fig. 1), with C. coccoides, R. hansenii, and R. productus forming a somewhat separate subcluster, the biochemical, morphological and phylogenetic characteristics of these organisms are consistent with generic unity. From a practical standpoint, taxonomy should be a practical subject embracing groups of organisms with unifying features. The proliferation of taxa based solely on a few traits should be resisted. In this diverse group of organisms (cluster XIVa), an accurate identification relies to a great extent upon molecular genetic techniques such as 16S rRNA gene sequence comparisons. Once the sole domain of specialized research facilities, these high throughput methodologies are becoming increasingly automated, reducing costs and making them routinely accessible. The availability of these methods facilitates more rapid and accurate identification of hitherto unknown or misclassified taxa. In addition to the above-mentioned taxa, the species Ruminococcus

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**Table 1. Some distinguishing characteristics of Blautia wexlerae sp. nov. and its closest relatives**

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hydrolysis of aesculin</td>
<td>+</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Enzyme activities:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>β-N-acetylglucosaminidase</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Alkaline phosphatase</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>α-Arabinosidase</td>
<td>+</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>α-Fucosidase</td>
<td>+</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>α-Mannosidase</td>
<td>+</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Major end products of glucose</td>
<td>A, S, A, S, H₂</td>
<td>A, E</td>
<td></td>
</tr>
<tr>
<td>metabolism</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

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_Blautia wexlerae_ gen. nov., sp. nov.
Table 2. Biochemical characteristics that can be used to distinguish species of the genus *Blautia* and *Ruminococcus obeum*

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>End products of metabolism</strong></td>
<td>A</td>
<td>S</td>
<td>A</td>
<td>S</td>
<td>A</td>
<td>L</td>
<td>A</td>
</tr>
<tr>
<td><strong>Fermentation of:</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Aesculin</td>
<td>+</td>
<td>+</td>
<td>ND</td>
<td>D</td>
<td>D</td>
<td>+</td>
<td>ND</td>
</tr>
<tr>
<td>Arabinose</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Cellobiose</td>
<td>D</td>
<td>+</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Glucose</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Lactose</td>
<td>D</td>
<td>ND</td>
<td>ND</td>
<td>+</td>
<td>ND</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Maltose</td>
<td>D</td>
<td>ND</td>
<td>ND</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Mannitol</td>
<td>D</td>
<td>W</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>ND</td>
</tr>
<tr>
<td>Mannose</td>
<td>+</td>
<td>+</td>
<td>D</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Raffinose</td>
<td>D</td>
<td>ND</td>
<td>ND</td>
<td>+</td>
<td>ND</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Sucrose</td>
<td>D</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Xylose</td>
<td>+</td>
<td>+</td>
<td>ND</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
</tbody>
</table>

*Blautia* wexlerae and *Ruminococcus torques* are also present in the XIVa suprageneric cluster although these species are phylogenetically removed from the cluster which contains *C. coccoides*, *R. hansenii*, *R. hydrogenotrophus*, *R. luti*, *R. obeum*, *R. productus*, *R. shinkii* and the novel faecal isolate. It is not the purpose of this article to reclassify all misclassified ruminococci. We believe that the most appropriate time to reclassify these remaining three species will be when additional novel strains are isolated and can be assigned along with these species to form the nuclei of new genera.

Therefore, based on morphological, phenotypic and phylogenetic considerations, we believe that *C. coccoides* and a number of misclassified *ruminococcus* merit classification in a novel genus for which we propose the name *Blautia* gen. nov. The novel cocccobacillus-shaped organisms isolated from human faeces are proposed as a distinct species within this genus as *Blautia wexlerae* sp. nov. *R. obeum* is clearly a member of the genus *Blautia*, as currently defined. The rules of the Bacteriological Code currently require that the type strains of all new species and subspecies (including new combinations) be deposited in two different collections in two different countries. The type strain of *R. obeum* is currently only deposited in the ATCC and a second independent deposit, as required by the Code, has not been possible (requests to the ATCC were made to enable this but could not be accommodated satisfactorily). Consequently, the transfer of this species to the genus *Blautia* cannot be made because the resulting species name would not conform to the Rules of the Code governing the valid publication of species names and deposit of type material (Rules 27 and 30) and consequently would not be considered to be validly published.

**Description of *Blautia* gen. nov.**

*Blautia* (Blau’ti.a. N.L. fem. n. *Blautia* in honour of Michael Blaut, a German microbiologist, in recognition of his many contributions to human gastrointestinal microbiology).

Gram-positive staining, non-motile. Coccolid or oval-shaped, pointed ends are often observed. Spores are not normally observed, but may be produced by some strains. Chemo-organotrophic and obligately anaerobic having a fermentative type of catabolism. Some species use H2/CO2 as major energy sources. The major end products of glucose metabolism are acetate, ethanol, hydrogen, lactate and succinate. The G+C content of the DNA is 37–47 mol%. Isolated from animal and human faeces. The type species of the genus is *Blautia coccoides* (Kaneuchi, Benno & Mitsuoka, 1976).

**Description of *Blautia coccoides* comb. nov.**

*Blautia coccoides* (cocc.co’i.des. Gr. n. coccus a berry; Gr. n. eidos shape; N.L. adj. coccoides berry shaped).


The description of *Blautia coccoides* is identical to that proposed for *C. coccoides* (Kaneuchi *et al.*, 1976). The type strain is ATCC 29236T (=DSM 935T=JCM 1395T=NCTC 11035T).

**Description of *Blautia hansenii* comb. nov.**

*Blautia hansenii* (han.sen’i.i. N.L. gen. n. *hansenii* of Hansen, in honour of P. Arne Hansen, a Danish–American bacteriologist).


The description of *Blautia hansenii* is identical to that proposed for *Ruminococcus hansenii* (Holdeman & Moore, 1974). The type strain is ATCC 27752T (=CIP 104219T=DSM 20583T=JCM 14655).

**Description of *Blautia hydrogenotrophica* comb. nov.**

*Blautia hydrogenotrophica* (hy.dro.gen.o.tro’phi.ca. N.L. n. hydrogenum hydrogen; Gr. adj. trophikos nursing, tending
or feeding; N.L. fem. adj. *hydrogenotrophica* (sic) feeding on hydrogen).


The description of *Blautia hydrogenotrophica* is identical to that proposed for *Ruminococcus hydrogenotrophicus* by Bernalier et al., 1996. The type strain is DSM 10507^T^ (=JCM 14656^T^).

**Description of Blautia luti comb. nov.**

*Blautia luti* (lu.ti. L. gen. n. luti of mud).


The description of *Blautia luti* is identical to that proposed for *Ruminococcus luti* Simmering et al., 2002. The type strain is DSM 14534^T^ (=CCUG 45635^T^).

**Description of Blautia producta comb. nov.**


The description of *Blautia producta* is identical to that proposed for *Ruminococcus productus* (Ezaki et al., 1994). The type strain is ATCC 27340^T^ (=CCUG 9990^T^=CCUG 10976^T^=DSM 2950^T^=JCM 1471^T^).

**Description of Blautia schinkii comb. nov.**

*Blautia schinkii* (schink’i.i. N.L. gen. n. *schinkii* of Schink, named after Bernard Schink).


The description of *Blautia schinkii* is identical to that proposed for *Ruminococcus schinkii* Rieu-Lesme et al., 1996. The type strain is CIP 105464^T^ (=CCUG 53897^T^=DSM 10518^T^).

**Description of Blautia wexlerae sp. nov.**

*Blautia wexlerae* (wex’ler.ae. N.L. fem. gen. n. *wexlerae* of Wexler, in honour of the American microbiologist Hannah M. Wexler, who has contributed significantly to our knowledge of anaerobic bacteria, particularly with regard to antimicrobial susceptibility testing and studies of mechanisms of antimicrobial resistance).

Cells are Gram-positive, non-spore-forming coccobacilli that are 1.0–1.5 × 1–3 μm in size. Strictly anaerobic. After 48 h of incubation at 37 °C under N2 and CO2 (80 : 20, v/v) gas phase, colonies on *Brucella* blood agar plates are 1–2 mm in diameter, grey with a white centre, umberonate and opaque with entire edges. Grows well anaerobically, but no growth occurs in an atmosphere of 2% or 6% O2. Isolates are negative in tests for lecithinase, lipase, catalase and indole, but are positive for urease. Aesculin is hydrolysed, but gelatin is not. Arabinose, glucose, mannose, ribose, and xylose are utilized as substrates when grown in PRAS carbohydrate broths, but glyconen is not utilized. Reactions for amygdalin, cellulbiose, fructose, lactose, maltose, mannitol, melezitose, melibiose, raffinose, rhamnose, salicin, sorbitol, sucrose and trehalose are variable. End products of metabolism from peptone-yeast-glucose broth are acetate and succinate. Long-chain cellular fatty acids are of the straight-chain saturated and monounsaturated types, with C16 : 0 (major component), and C14 : 0, C16 : 0 dimethyl acetal acids predominating. Using the API ZYM and Rapid ID32A systems, all isolates produce a similar profile. Positive reactions are obtained for α-galactosidase, β-galactosidase, α-glucosidase, β-glucosidase and α-fucosidase by both systems. With the Rapid ID32A system, α-arabinosidase is positive and acid phosphatase is detected by the API ZYM system. No activity was detected for N-acetyl-β-glucosaminidase, alkaline phosphatase, α-chymotrypsin, cystine arylamidase, β-glucuronidase, lipase (C14), leucine arylamidase, α-mannosidase, trypsin or valine arylamidase. Urease results are variable by the Rapid ID32A system. Esterase (C4), esterase lipase (C8) and naphthol-AS-BI-phosphohydrolase are variable using the API ZYM system. The isolates are sensitive to vancomycin (5 μg) and kanamycin (1000 μg), but resistant to colistin (10 μg) identification discs.

The type strain, WAL 14507^T^ (=ATCC BAA-1564^T^=DSM 19850^T^), was isolated from human faeces.

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**References**


