***Enterococcus haemoperoxidus* sp. nov. and *Enterococcus moraviensis* sp. nov., isolated from water**

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A polyphasic taxonomic approach was used to study atypical enterococci isolated from surface waters. All strains were characterized by physiological and biochemical tests as well as by genotyping. The results of biochemical tests and tRNA intergenic length polymorphism analysis (tDNA-PCR) divided all studied strains uniformly into two groups. Because these groups were clearly separated from all enterococcal species described to date, 16S rDNA sequence analysis, DNA base composition analysis and DNA–DNA hybridization of representative strains were done to elucidate the taxonomic position of the analysed groups. On the basis of the results obtained, the names *Enterococcus haemoperoxidus* (type strain CCM 4851^T = LMG 19487^T) and *Enterococcus moraviensis* (type strain CCM 4856^T = LMG 19486^T) are proposed for the two hitherto undescribed species. The type strains and reference cultures have been deposited in the Czech Collection of Microorganisms (CCM), Masaryk University, Brno, Czech Republic, and in the BCCM/LMG Culture Collection, Ghent University, Belgium.

Keywords: *Enterococcus haemoperoxidus* sp. nov., *Enterococcus moraviensis* sp. nov., taxonomy, identification, water

INTRODUCTION

Enterococci are Gram-positive cocci that are commonly isolated from human clinical specimens, some kinds of food and the environment. Recent interest in this bacterial genus has been encouraged by their increasing clinical significance and acquired antibiotic resistance (Facklam *et al.*, 1999; Jett *et al.*, 1994). Therefore, most investigations relate to strains and species isolated from clinical samples. Unfortunately, little exact taxonomic information is available about the strains and species of enterococci occurring in the environment. Enterococci can be isolated from soil, plants, insects and wild animals as well as from water samples. *Enterococcus faecalis*, *Enterococcus faecium*, *Enterococcus mundtii* and *Enterococcus casseliflavus* are found associated with plants (Devriese *et al.*, 1992). Soil is probably not the natural habitat of enterococci,

and their presence therein represents contamination from animals and plants (Deibel, 1964). The incidence of enterococci in waters is generally considered to be due to faecal contamination and these bacteria are monitored during microbiological quality testing of water. In particular, *E. faecalis*, *E. faecium*, *Enterococcus durans* and *Enterococcus hirae* are considered to be of faecal origin (Godfree *et al.*, 1997). However, enterococci of non-faecal origin may be also found in surface waters. Niemi *et al.* (1993) described *E. casseliflavus* as a typical species in forest industry wastewaters in Finland, and they isolated atypical enterococcal strains from pristine waters.

A series of atypical enterococci were isolated during an investigation into the occurrence of different enterococcal species in surface waters (Švec & Sedláček, 1999). All strains were characterized using morphological, physiological as well as biochemical tests, but their phenotypic characteristics did not correspond to those of known enterococcal species. Because of their unclear taxonomic position, analysis of tRNA intergenic length polymorphism (tDNA-PCR), 16S rDNA

The GenBank accession numbers for the 16S rRNA gene sequences of *E. moraviensis* CCM 4856^T and *E. haemoperoxidus* CCM 4851^T are AF286831 and AF286832, respectively.

sequencing, DNA base composition analysis and DNA–DNA hybridization were carried out. Our results showed that the enterococcal strains analysed represent two new species, for which the names *Enterococcus haemoperoxidus* sp. nov. and *Enterococcus moraviensis* sp. nov. are proposed.

METHODS

Bacterial strains. The strains analysed in this work were isolated from surface waters by membrane filtration and subsequent incubation of the filters on Slanetz–Bartley agar plates at the 37 °C during a routine analysis of water quality, as described previously (Švec & Sedláček, 1999). All strains were isolated from different sampling sites in the region of North Moravia in the Czech Republic (see Table 1).

Phenotypic studies. Isolated strains were cultivated on Columbia agar with 5% sheep blood. Consequently, growth was checked and characterized on Slanetz–Bartley agar, kanamycin/aesculin/azide agar, BBL Enterococcosel agar, Edwards agar, aesculin/bile agar and skim milk medium. Growth in a 5% CO₂ atmosphere and in a normal atmosphere was compared on blood agar at 37 °C. Tests for growth at various temperatures as well as in 6.5% NaCl were performed in brain/heart infusion (BHI) broth and bacteria were cultivated for up to 5 d. Catalase tests were done by dispersing growth from Columbia agar with and without blood in 3% hydrogen peroxide. Motility was tested on semi-solid medium according to Facklam & Wilkinson (1981). Group D antigen was tested using a Streptococcal grouping kit (Oxoid). Amylase production was looked for on Columbia agar base containing 0.1% starch. Biochemical tests were performed using API galleries 20 STREP and 50 CH (bioMérieux) as well as the CRYSTAL Gram-positive ID kit (Becton Dickinson) according to the manufacturers' instructions.

DNA isolation. One loop of a bacterial culture grown

overnight on Columbia agar with 5% sheep blood was suspended in 20 µl lysis buffer (0.25% SDS, 0.05 M NaOH) and heated at 95 °C for 5 min. Subsequently, 180 µl sterile distilled water was added and the suspension was centrifuged at 13 000 r.p.m. for 5 min. The supernatant was used directly for tDNA-PCR as well as for 16S rDNA sequencing.

tRNA intergenic length polymorphism analysis (tDNA-PCR).

tDNA-PCR was done using the consensus primers T5A (5'-AGTCCGGTGCTCTAACCAACTGAG-3') and fluorescent-labelled T3B (5'-AGGTCGCGGGTTCGAATCC-3') described by Welsh & McClelland (1992). Capillary electrophoresis of PCR products was done on an ABI PRISM 310 Genetic Analyzer (Applied Biosystems) as described previously (Baele *et al.*, 2000). Cluster analysis of tDNA-PCR fingerprints was done using the UPGMA algorithm with the PHYLIP software (Felsenstein, 1989) and the dendrogram was visualized using the TREEVIEW program described by Page (1996).

16S rRNA sequence analysis. The 16S rRNA gene was amplified using the primers $\alpha\beta$ -NOT (5'-TCAAACCTAGG-ACCGAGTC-3') and ω_{MB} (5'-TACCTTGTTACTTCACCCCA-3') and the Taq Mastermix (Qiagen). The subsequent sequencing reactions were done using the BigDye Terminator sequencing kit (Applied Biosystems) and forward sequencing primers *Gamma, *PD, *O, *3, *R and reverse primers Gamma, PD and 3 described by Coenye *et al.* (1999). The sequences were determined on an ABI PRISM 310 Genetic Analyzer (Applied Biosystems). Cluster analysis was done using program GENEBASE (Applied Maths). Pairwise alignment homologies were calculated and a dendrogram was constructed using the neighbour-joining method with 100% open gap penalty and 0% unit gap penalty values.

DNA base composition. DNA was prepared as described elsewhere (Vancanneyt *et al.*, 2001). The enzymic degradation of DNA into nucleosides was done as described by Mesbah *et al.* (1989). The nucleotide mixture was then separated by HPLC using a Waters SymmetryShield C8

Table 1. Source and locality of isolation of the strains

Strain	Source and locality
<i>Enterococcus haemoperoxidus</i> sp. nov.	
25 (= CCM 4855)	River Olše, Třinec
60 (= CCM 4853), 152, 313,	Drinking water, Frýdek-Místek
504 (= CCM 4886), 616	
382	Drinking water, Čeladná
434	Spring Hájek, Frýdek-Místek
435, 457, 473	Drinking water, Třinec
440 ^T (= CCM 4851 ^T = LMG 19487 ^T)	Service water, Paskov
450 (= CCM 4854)	Swimming pool, Frýdek-Místek
466	Swimming pool, Třinec
501 (= CCM 4852)	Drinking water, Vítkovice
562	Drinking water, Lhotka
<i>Enterococcus moraviensis</i> sp. nov.	
206 (= CCM 4857)	Drinking water, Čeladná
330 ^T (= CCM 4856 ^T = LMG 19486 ^T)	Spring Hájek, Frýdek-Místek
430 (= CCM 4859), 494, 568 (= CCM 4885),	Drinking water, Frýdek-Místek
570 (= CCM 4858)	
531 (= CCM 4860)	Drinking water, Fryčovice

Fig. 1. Dendrogram based on tDNA-PCR fingerprint patterns demonstrating the relatedness between *E. haemoperoxidus* sp. nov., *E. moraviensis* sp. nov. and other enterococcal species. Numbers of strains analysed are indicated in parentheses.

column thermostatted at 37 °C. The solvent was 0.02 M $\text{NH}_4\text{H}_2\text{PO}_4$ (pH 4.0) with 1.5% acetonitrile. Non-methylated lambda phage DNA (Sigma) was used as the calibration reference.

DNA-DNA hybridization. Whole genomic DNA of representative strains isolated according to Vancanneyt *et al.* (2001) was hybridized in microdilution wells with photobiotin-labelled probe DNAs as described by Ezaki *et al.* (1989). The enzymic reaction intensity was measured using HTS7000 Bio Assay Reader (Perkin Elmer). The hybridization temperature was 32 °C. The hybridization temperature was calculated from the G+C content with the formula of De Ley (1970) and corrected for the presence of 50% formamide in the hybridization mixture (McConaughy *et al.*, 1969).

RESULTS AND DISCUSSION

Genotypic studies

tDNA-PCR separated all strains investigated into two unique clusters and showed genetic homogeneity of the strains within each group (Fig. 1). Moreover, the tDNA-PCR fingerprint patterns clearly separated both groups from all enterococcal species included in the

database of Department of Bacteriology, Faculty of Veterinary Medicine, University of Ghent, Belgium, described by Baele *et al.* (2000). Typical tDNA spacer fragment lengths were 74.7, 257 and 331.3 bp for the first group (*E. haemoperoxidus* sp. nov.) and 74, 258 and 332.2 bp for the second group (*E. moraviensis* sp. nov.). Although there were only small differences in the fragment lengths between these two groups, Baele *et al.* (2000) have shown that some enterococcal species can be differentiated by only 1 bp (*E. faecium*–*E. durans*) or 2 bp (*Enterococcus avium*–*Enterococcus malodoratus*) differences in length.

This molecular method has been used successfully for species typing of streptococci (De Gheldre *et al.*, 1999; McClelland *et al.*, 1992), acinetobacters (Ehrenstein *et al.*, 1996), staphylococci (Maes *et al.*, 1997; Welsh & McClelland, 1992) and listerias (Vaneechoutte *et al.*, 1998) and it appears to be reliable for the rapid identification of enterococci as well as for the detection and study of new enterococcal species.

The 16S rRNA sequences of representative strains from each group were determined and compared

Fig. 2. Distance matrix tree based on 16S rRNA gene sequence comparisons showing the phylogenetic relationships of *E. haemoperoxidus* sp. nov., *E. moraviensis* sp. nov. and all generally recognized *Enterococcus* species described to date. *Vagococcus fluvialis* (X54258) was used as the outgroup. Bootstrap percentages are indicated at the branching points of the dendrogram.

Table 2. DNA–DNA homology values of *E. haemoperoxidus* sp. nov., *E. moraviensis* sp. nov. and the phylogenetically closest species, *E. faecalis*

Strain	G + C content (mol %)	DNA relatedness (%):				
		1	2	3	4	5
1. <i>E. haemoperoxidus</i> CCM 4851 ^T	35.3	100				
2. <i>E. haemoperoxidus</i> CCM 4886	35.5	98	100			
3. <i>E. moraviensis</i> CCM 4856 ^T	36.3	48	43	100		
4. <i>E. moraviensis</i> CCM 4885	35.6	46	37	91	100	
5. <i>E. faecalis</i> LMG 7937 ^T	37.7	17	19	16	16	100

(Fig. 2). The data showed that these two groups are highly related: 99.7% 16S rRNA sequence similarity was found between strain 330^T, representative of the one group, and strain 440^T, representing the other group. The phylogenetically closest species is *E. faecalis*. The 16S rDNA sequence similarity of *E. faecalis* NCIMB 775^T to strains 330^T and 440^T was 97.4%. The interspecies 16S rRNA homologies between enterococcal species are mostly high and exceed the generally accepted value of 97% for species differentiation. They may be as high as 99.8%, as is the case with *E. casseliflavus*–*Enterococcus gallinarum*, or 99.7%, for *E. durans*–*E. faecium* (Williams *et al.*, 1991). However, the percentages of DNA–DNA hybridization of these species are low and clearly indicate their species identity.

Similarly, the DNA–DNA hybridization results (Table 2) obtained with two strains selected from each of the groups studied here and the type strain of the phylogenetically closest species *E. faecalis* confirmed

the species identity of the analysed enterococcal groups, as revealed by tDNA-PCR and 16S rRNA sequencing. These DNA–DNA homology values clearly differentiated the strains from *E. faecalis* LMG 7937^T and revealed high similarities of the two strains selected from each group (values higher than 90%). Moreover, the DNA–DNA homology values between strains of these two groups (37–48%) confirmed the phylogenetic similarity of these species shown by 16S rRNA gene analysis.

On the basis of these results, we propose to add two new species, *Enterococcus haemoperoxidus* sp. nov. and *Enterococcus moraviensis* sp. nov., to the genus *Enterococcus*.

Phenotype studies

All strains grew well on Columbia agar supplemented with 5% sheep blood at 37 °C under aerobic as well as anaerobic conditions. They formed circular and

smooth colonies with entire margins. Colonies reached about 1 mm in diameter after 24 h of cultivation and their growth continued at room temperature up to 3–4 mm. No haemolysis was observed on sheep-blood agar. Growth was enhanced slightly by cultivation in a 5% CO₂ atmosphere and was more abundant at 37 °C in comparison with 30 or 25 °C. Growth occurred at 10 °C but was strongly inhibited at 42 °C. Uniform turbidity was produced in BHI broth culture at 37 °C and all strains were able to grow when the NaCl content was increased to 6.5%. No change of skim milk medium was detected.

All strains grew on kanamycin/aesculin/azide agar, BBL Enterococcosel agar, Edwards agar and aesculin/bile agar and were aesculin-positive on all these media. Colonies formed on Slanetz–Bartley agar were small and dark-red with a metallic sheen. They were very similar to colonies of *E. faecalis*, but smaller.

In complete agreement with the genotypic examinations described above, the biochemical test results divided all strains into two groups and separated them clearly from all described enterococcal species. Although the new species are phylogenetically as well as phenotypically close to *E. faecalis*, they can be differentiated using a few biochemical tests. Both new species are sorbitol-negative and methyl α -D-glucoside-positive, while *E. faecalis* generally gives opposite results for these two tests. Moreover, *E. haemoperoxidus* is not able to acidify D-tagatose and *E. moraviensis* is L-arabinose-positive and arginine dihydrolase-negative. Surprisingly, 16 strains (all strains of the proposed *E. haemoperoxidus* sp. nov.) were clearly and strongly positive in the catalase test when cultivated on blood medium but negative when grown on blood-free medium. Lactic acid bacteria (including enterococci) are generally unable to synthesize haem groups (Gibson *et al.*, 2000; Whittenbury, 1978; Deibel & Evans, 1960; Smith, 1954). The destruction of peroxide by some enterococcal strains was detected when cultivated on blood-containing medium under aerobic conditions. Seeley & VanDemark (1951) described the formation of peroxidase in *Streptococcus faecalis* (now *E. faecalis*) B33 A. The enzyme was formed adaptively (after anaerobic growth, when exposed to air) and differed from classical peroxidase in that it lacked haemin. Deibel (1964) did not detect iron-porphyrin compounds either chemically or spectrophotometrically in catalase-positive *S. faecalis*. Although *S. faecalis* lacks cytochrome pigments, it is able to respire and flavin co-enzymes occupy a central role in aerobic hydrogen transport (Deibel, 1964). Smith (1954) detected flavoprotein compounds, rather than cytochromes, in *S. faecalis*. Finally, Miller *et al.* (1990) described the flavin-containing NADH peroxidases of *S. faecalis* ATCC 9790 and found greater diversity of these enzymes among the group D streptococci. Although catalase or pseudocatalase production has been described previously in many streptococcus- and enterococcus-like strains (Rurangirwa *et al.*, 2000; Murray, 1990;

Whittenbury, 1978; Deibel, 1964), this is probably the first case of a clearly positive catalase reaction detected in a homogeneous group of enterococcal strains. This simple test could be useful for the differentiation of *E. haemoperoxidus* from other enterococcal species. However, of course, it will be necessary to test more isolates in order to evaluate the catalase test as an identification test for this species.

The two new species can be clearly differentiated from each other by testing for acidification of D-tagatose and L-arabinose as well as by the arginine dihydrolase reaction. The tests most useful for the identification and differentiation of the proposed new species from all enterococci and enterococcal species groups are listed in Table 3.

Description of *Enterococcus haemoperoxidus* sp. nov.

Enterococcus haemoperoxidus (hae.mo.per.o'xi.dus. G. n. *haema* blood; *per* G. prefix intensification; *oxys* G. adj. sour; N. L. adj. *haemoperoxidus* blood peroxide, derived from the ability of the species to decompose hydrogen peroxide into oxygen and water when cultivated on blood-agar media).

Cells are Gram-positive, ovoid cocci, occurring in pairs, short chains or small groups. They are elongated in the direction of the chains. Non-motile. A slightly yellowish pigment may be produced; this pigment is most readily visible when growth is collected from plates within inoculation loops. A positive catalase reaction is clearly evident when cultivated on blood agar, but cells grown on blood-free medium are catalase-negative. Weakly positive in the amylase test. Streptococcal group D antigen-positive. Growth characteristics and physiological traits are as described above. Acid is produced from glycerol, ribose, galactose, D-glucose, D-fructose, D-mannose, methyl α -D-glucoside, N-acetylglucosamine, amygdalin, arbutin, salicin, cellobiose, maltose, lactose, sucrose, trehalose, melezitose, β -gentiobiose and maltotriose. Most strains produce acid from starch. Acid is not produced from erythritol, D- or L-arabinose, D- or L-xylose, adonitol, methyl β -xyloside, L-sorbose, rhamnose, dulcitol, inositol, sorbitol, methyl α -D-mannoside, melibiose, inulin, D-raffinose, xylitol, D-lyxose, D-tagatose, D- or L-fucose, D- or L-arabitol, gluconate, 2-ketogluconate or 5-ketogluconate. Most strains do not produce acid from glycogen and D-turanose. Mannitol acidification is variable. Positive in tests for acetoin, hippurate, aesculin, pyrrolidonyl arylamidase, leucine arylamidase and arginine dihydrolase; negative for β -glucuronidase, β -galactosidase, alkaline phosphatase and urease. Most strains are α -galactosidase-negative. Positive enzymic hydrolysis of 4-methylumbelliferyl (4MU) β -D-glucoside, L-pyrogutamic acid 7-amido-4-methyl coumarin (AMC), L-tryptophan, 4MU N-acetyl β -D-glucosaminide, *p*-nitrophenyl β -D-cellobioside and *p*-nitrophenyl α -D-maltoside; mostly positive for L-phenylalanine AMC, 4MU α -D-glucoside, proline and leucine *p*-nitroanilide and *o*-

Table 3. Biochemical tests useful for the differentiation of *E. haemoperoxidus* sp. nov. and *E. moraviensis* sp. nov. from other enterococci

Taxa are identified as: 1, *E. haemoperoxidus*; 2, *E. moraviensis*; 3, *E. faecalis*; 4, the *E. faecium* group (*E. faecium*, *E. durans*, *E. hirae*, *E. mundtii*); 5, the *E. avium* group (*E. avium*, *Enterococcus pseudoavium*, *E. malodoratus*, *Enterococcus raffinosus*); 6, the *E. gallinarum* group (*E. gallinarum*, *E. casseliflavus*); 7, the *Enterococcus cecorum* group (*E. cecorum*, *Enterococcus columbae*); 8, *Enterococcus sulfureus*; 9, *Enterococcus saccharolyticus*; 10, *Enterococcus dispar*; 11, *Enterococcus asini*. Data for *E. asini* were derived from de Vaux *et al.* (1998) and for the other species as well as species groups from Devriese & Pot (1995) except the test results of D-tagatose for *E. faecalis* (Schleifer & Kilpper-Bälz, 1984) and melibiose for *E. sulfureus* (Martinez-Murcia & Collins, 1991). Characteristics are scored as: +, positive; D, variable; D+, usually positive; D-, usually negative; -, negative.

Characteristic	1	2	3	4	5	6	7	8	9	10	11
Acidification of:											
Sorbitol	—	—	D+	D—	+	D—	D	—	+	—	—
Methyl α -D-glucoside	+	+	—	—	D	+	D	+	+	+	—
D-Tagatose	—	+	+	D	D+	D	D	—	—	+	—
L-Arabinose	—	+	—	D	D	+	D	—	—	—	—
Melibiose	—	—	—	D	D	+	+	+	+	D	—
Melezitose	+	+	D+	—	D	D—	D	+	+	—	—
Raffinose	—	D—	—	D	D	D	+	+	+	+	—
Inulin	—	—	—	D—	—	D	+	—	+	—	—
2-Ketogluconate	—	—	D	—	+	—	D	+	+	+	—
Arginine dihydrolase	+	—	+	+	—	+	—	—	—	+	—

nitrophenyl β -D-galactoside. Negative for hydrolysis of L-valine, 4MU phosphate, 4MU β -D-glucuronide and L-isoleucine. Variable enzymic hydrolysis of *p*-nitrophenyl β -D-glucoside and *p*-nitrophenyl phosphate.

The type strain, 440^T (= CCM 4851^T = LMG 19487^T), was isolated from service (non-potable) water and its characteristics agree with the species description above. Tests that are variable for *E. haemoperoxidus* strains give the following results for strain 440^T: positive acidification of starch; negative for mannitol, glycogen and D-turanose. Weakly positive for α -galactosidase. Positive for enzymic hydrolysis of 4MU α -D-glucoside, L-phenylalanine AMC, proline and leucine *p*-nitroanilide, *o*-nitrophenyl β -D-galactoside, *p*-nitrophenyl β -D-glucoside and *p*-nitrophenyl phosphate. The strain is not pigmented. The G + C content of strain 440^T is 35.3 mol %.

Description of *Enterococcus moraviensis* sp. nov.

Enterococcus moraviensis (mo.ra.vi.en'sis. N. L. adj. *moraviensis* pertaining to Moravia, the region in the Czech Republic from which the strains originate).

Gram-positive, ovoid cells occurring in pairs, short chains or in small groups, elongated in the direction of chains. Non-pigmented, non-motile, catalase-negative and group D antigen-positive. Weak amylase production on Columbia agar. Other physiological features as well as growth characteristics are as described above. Acid is produced from glycerol, L-arabinose, ribose, galactose, D-glucose, D-fructose, D-

mannose, mannitol, methyl α -D-glucoside, *N*-acetylglucosamine, amygdalin, arbutin, salicin, cellobiose, maltose, lactose, sucrose, trehalose, melezitose, β -gentiobiose, D-turanose, D-tagatose and maltotriose. Most strains produce acid from inositol. Acid is not produced from erythritol, D-arabinose, D- or L-xylose, adonitol, methyl β -xyloside, rhamnose, dulcitol, sorbitol, methyl α -D-mannoside, melibiose, inulin, xylitol, D-lyxose, D- or L-fucose, D- or L-arabitol, gluconate, 2-ketogluconate or 5-ketogluconate. Most strains do not produce acid from L-sorbose, D-raffinose or glycogen. Acid production from starch is variable. Positive for acetoin, hippurate, aesculin and leucine arylamidase; mostly positive for β -galactosidase. Negative for β -glucuronidase, alkaline phosphatase, arginine dihydrolase and urease; mostly negative for α -galactosidase. Variable for pyrrolidonyl arylamidase. Positive for enzymic hydrolysis of 4MU β -D-glucoside, 4MU α -D-glucoside, L-tryptophan, 4MU *N*-acetyl β -D-glucosaminide, *p*-nitrophenyl β -D-cellobioside and *p*-nitrophenyl α -D-maltoside; mostly positive for hydrolysis of L-pyroglutamic acid AMC and *o*-nitrophenyl β -D-galactoside. Negative for enzymic hydrolysis of L-valine, 4MU phosphate, 4MU β -D-glucuronide and L-isoleucine. Variable for hydrolysis of L-phenylalanine AMC, *p*-nitrophenyl β -D-glucoside, proline and leucine *p*-nitroanilide and *p*-nitrophenyl phosphate.

The type strain, 330^T (= CCM 4856^T = LMG 19486^T), was isolated from spring water. It is positive in tests for inositol, starch, L-pyroglutamic acid AMC, *o*-nitrophenyl β -D-galactoside, proline and leucine *p*-nitroanilide and β -galactosidase; negative for L-sor-

bose, D-raffinose, glycogen, pyrrolidonyl arylamidase, L-phenylalanine AMC, *p*-nitrophenyl β -D-glucoside, *p*-nitrophenyl phosphate and α -galactosidase. All other characteristics are in agreement with the species description. The G+C content of strain 330^T is 36.3 mol %.

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