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**Enterococcus hermanniensis** sp. nov., from modified-atmosphere-packaged broiler meat and canine tonsils

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Isolates 302, 334, 356, 377 and 379, detected in modified-atmosphere-packaged broiler meat, together with strains LMG 12317^T^ and LMG 13617, detected in dog tonsils, were analysed in a polyphasic taxonomy study, including numerical analysis of ribopatterns and whole-cell protein patterns, 16S rRNA gene sequence analysis, DNA–DNA hybridization and determination of some phenotypic properties. The results indicated that these isolates represent a novel species in the genus *Enterococcus*. The isolates showed classical phenotypic reactions for the genus *Enterococcus* with the exception of not possessing the Lancefield group D antigen. Isolates 334, LMG 12317^T^ and LMG 13617 showed the highest 16S rRNA gene sequence similarity (98.3–99.0%) to the *Enterococcus pallens* type strain. In the distance matrix tree based on 16S rRNA gene sequences, the three isolates were located in the *Enterococcus avium* group with *E. pallens* as their closest phylogenetic neighbour. Numerical analyses of whole-cell protein patterns and *HindIII/EcoRI* ribotypes placed all seven isolates together in a single cluster separated from the *E. avium* group reference strains. The DNA–DNA hybridization level between strains 334 and LMG 12317^T^ was 93.5%, confirming that they represent the same species. Low hybridization levels (12–30%) were, by contrast, obtained with the *E. pallens* and *Enterococcus raffinosus* type strains. The name *Enterococcus hermanniensis* sp. nov. is proposed, with strain LMG 12317^T^ (= CCUG 48100^T^) as the type strain.

Phylogenetically, the genus *Enterococcus* belongs to the clostridial branch of the Gram-positive bacteria. It was not officially recognized as a separate genus until 1984, when [*Streptococcus* *faecalis* and *Streptococcus* *faecium* were reclassified as *Enterococcus faecalis* and *Enterococcus faecium*, respectively (Schleifer & Kilpper-Balz, 1984). Since then, the number of enterococcal species described has increased, not only by the species transferred from the group D *Streptococcus*, but also by the description of several novel species. At the time of writing, over 20 species are classified as enterococci. Based on 16S rRNA gene sequence analyses, four phylogenetic groups (*E. faecium, Enterococcus avium, Enterococcus gallinarum* and *Enterococcus cecorum* species groups) have been described (Williams et al., 1991).

During a study of lactic acid bacteria (LAB) isolated from the spoilage population in modified-atmosphere-packaged (MAP), marinated, broiler legs, several unidentified LAB isolates were detected (Björkroth et al., 2004). Five isolates (302, 334, 356, 377 and 379) originating from fresh packages showed *HindIII* ribopatterns resembling the patterns of some known enterococci. The patterns of these five isolates were designated types UIⅣa and UIⅣb by Björkroth et al. (2004). When these isolates were initially studied by means of whole-cell protein analysis, they were found to possess similar patterns to two isolates (LMG 12317^T^ and LMG 13617) originating from canine tonsils. The present polyphasic taxonomic study, including numerical analysis of ribopatterns and whole-cell protein patterns, 16S rRNA gene analysis, DNA–DNA hybridization and examination of essential phenotypic properties, set out to evaluate whether these seven isolates represent a novel enterococcal species.
All isolates were routinely cultured at 30 °C either overnight in MRS broth (Difco) or for 3 days on MRS agar plates (Oxoid). The plates were incubated under an anaerobic CO₂ atmosphere [Anaerogen (Oxoid); 9–13 % CO₂ according to the manufacturer] at 30 °C. For PAGE of whole-cell proteins, isolates were grown for 24 h on MRS agar (Oxoid) at 24 °C in a microaerobic atmosphere (approximately 5 % O₂, 10 % CO₂, 85 % N₂). All isolates were maintained in MRS broth (Difco) at −70 °C.

DNA for all analyses was isolated as described by Björkroth & Korkeala (1996). HindIII and EcoRI enzymes were used for digestion of DNA as specified by the manufacturer (New England Biolabs). Restriction endonuclease analysis was performed as described by Björkroth & Korkeala (1996) and Southern blotting was via a vacuum device (Vacugene; Pharmacia). The rRNA gene probe for ribotyping was labelled by reverse transcription [AMV-RT (Promega) and Dig labelling kit (Roche Molecular Biochemicals)] as described by Blumberg et al. (1991). Membranes were hybridized at 58 °C overnight and detection of the digoxigenin label was performed as recommended by Roche Molecular Biochemicals. Scanned (Hewlett Packard Scan Jet 4c/T) ribopatterns were analysed using the BIONUMERICS 3.0 software package. The similarity between all pairs was expressed by the Dice coefficient correlation and UPGMA clustering was used for the construction of dendrograms.

Preparation of cellular protein extracts and PAGE was performed as described by Pot et al. (1994). Whole-cell protein profiles were scanned using an LKB 2202 UltraScan laser densitometer. Densitometric analysis, normalization and interpolation of the protein profiles and numerical analysis using the Pearson product moment correlation coefficient were performed using the GELCOMPAR 4.2 software package (Applied Maths). The isolates investigated formed a homogeneous group clearly separated from reference strains of their closest phylogenetic neighbours (see below) (results from the numerical analysis of whole-cell protein patterns are available as Supplementary Fig. B in IJSEM Online).

The nearly complete 16S rRNA gene was amplified by PCR with a universal primer pair F8–27 (5’-AGAGTTTGATCCTGGCTGAG-3’) and R1541–1522 (5’-AAGGAGGTATCCAGCCGCA-3’). Sequencing of the purified (QIAquick PCR purification kit; Qiagen) PCR product was performed by Sanger’s dideoxynucleotide chain-termination method using two long [primers F19–38 (5’-CTGGCTCAGGAYGAACGCTG-3’) and R1541–1522] and two shorter reactions [primers P926 (5’-AACCTCAAAGGAATTGACGG-3’) and R519 (5’-GTATTACC CGCGCTGCTG-3’)]. Samples obtained by combining the unweighted pattern information of both EcoRI and HindIII ribotypes into one numerical analysis is available as Supplementary Fig. A in IJSEM Online. In all RFLP analyses, the seven isolates formed tight and distinct clusters with sequence similarity values ranging from 94·1 to 100 %, whereas the similarity values between the patterns of these isolates and the reference strains located in the most adjacent clusters ranged from 56·2 to 69·4 %.

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were run in a Global IR² sequencing device with E-SEQ 1.1 software (LiCor) according to the manufacturer’s instructions. The consensus sequences of these isolates and representative strains belonging to the same phylogenetic group [retrieved from GenBank (http://www.ncbi.nlm.nih.gov), using BLASTN 2.2.6; Altschul et al., 1997] were aligned and a phylogenetic tree (Fig. 2) was constructed from the global alignment by the neighbour-joining algorithm using BIONUMERICS 3.0 software package (Applied Maths). In the BLAST analyses, isolates LMG 12317¹, LMG 13617 and 334 showed the highest 16S rRNA gene sequence similarities to 16S rRNA gene sequences of strains classified as Enterococcus pallens (98-3, 99-0, 98-9 %, respectively), Enterococcus pseudoavium (97-7, 98-4 and 98-2 %, respectively) and E. avium (97-7, 98-1 and 98-1 %, respectively). In the distance matrix tree based on 16S rRNA gene sequences (Fig 2), the three isolates were located in the E. avium group with E. pallens as their closest phylogenetic neighbour.

For determination of the G+C content, DNA was enzymically degraded into nucleosides as described by Mesbah et al. (1989). The nucleoside mixture was then separated by HPLC using a Waters SymmetryShield C8 column thermostatted at 37 °C. The solvent was 0-02 M NH₄H₂PO₄ with 1-5 % acetonitrile. Non-methylated lambda phage DNA (Sigma) was used as the calibration reference. DNA–DNA hybridizations were performed with photobiotin-labelled probes in microplate wells as described by Ezaki et al. (1989), using an HTS7000 Bio Assay Reader (Perkin-Elmer) for the fluorescence measurements. The hybridization temperature was 35 °C in 50 % formamide. The G+C content of DNA of isolates LMG 12317 and 334 was 37-1 and 36-6 mol %, respectively. The level of DNA–DNA relatedness between isolates 334 and LMG 12317 was 93-5 %, whereas the levels between isolate LMG 12317 and E. pallens or Enterococcus raffinosus type strains were only 11-5 and 23-7 %, respectively. Each value given is the mean of at least two hybridization experiments.

All isolates were Gram stained and tested for catalase. For size and precise morphology determinations in a transmission electron microscope, cells were suspended in physiological NaCl, negatively stained with 1 % phosphotungstic acid and examined using a JEOI JEM 100 electron microscope. A transmission electron micrograph of cells of strain LMG 12317 is available as Supplementary Fig. C in IJSEM Online. Growth at different temperatures (4, 37 and 45 °C) or in the presence of NaCl, 6 and 10 % w/v) was tested in MRS broth (Difco) incubated until growth was observed or otherwise at least for 21 days. Lancefield antigen D was tested using the Streptococcal grouping kit (Oxoid). Isolates were tested for their carbohydrate fermentation profiles by API 50 CHL (bioMérieux) and for biochemical activities by API STREP identification systems (bioMérieux) according to the manufacturer’s instructions. Production of ammonia from arginine was tested in broth containing 0.5 % arginine, 0.5 % peptone, 0-3 % yeast extract, 0-1 % glucose and 0-016 % brom cresol purple. Formation of typical colonies for enterococci was tested on bile-esculin (Gibco) and Slanetz-Bartley (Oxoid) agar. Haemolyses were tested on blood agar. Each test was carried out at least twice. Phenotypic tests mainly resulted in typical reactions for enterococci as listed by Devriese et al. (1993) and Devriese & Pot (1995). There were some exceptions; all isolates were negative for Lancefield D, none grew at 45 °C, and isolates 302, 377 and 379 did not grow in the presence of 6-5 % NaCl. Detailed results are given in the species description below. Table 1 shows characteristics useful in differentiating Enterococcus hermanniensis sp. nov. from other species in the E. avium group.

On the basis of this polyphasic study, it is evident that isolates 302, 334, 356, 377, 379, LMG 12317 and LMG 13617 belong to a novel Enterococcus species within the E. avium group, for which we propose the name Enterococcus hermanniensis sp. nov. To date, E. hermanniensis has been isolated from MAP, fresh broiler leg packages and canine

![Fig. 2. Phylogenetic tree based on similarities of almost entire 16S rRNA gene sequences (at least 1400 bp) of Enterococcus hermanniensis sp. nov. and its phylogenetic neighbours. Bootstrap probability values from 500 trees resampled are given at the branch points.](http://ijs.sgmjournals.org)
Characteristics that differentiate Enterococcus hermanniensis sp. nov. from the other species of the E. avium group

Table 1. Characteristics that differentiate Enterococcus hermanniensis sp. nov. from the other species of the E. avium group

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
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<th>5</th>
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<td>Acid production from:</td>
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Semi-spherical cocci growing in pairs (Supplementary Strains are Gram-positive, catalase-negative, spherical to Helsinki, Finland. E. hermanniensis adj. canines tonsils (Devriese et al., 1991). It is also possible that Enterococcus, acid is produced from arbutin, cellobiose, D-fructose, D-glucose, maltose, D-mannose, N-acetylglucosamine, ribose and salicin but not from erythritol, L-xyllose, glycerogen or fucose. Unlike most of the other enterococci, no acid is produced from lactose, galactose and amygdalin, although there may sometimes be a weak positive reaction with the latter two. All strains produce acid from mannitol. Acid production from D-arabitol, β-gentiobiose and trehalose may be weak or delayed. No acid production from adonitol, starch, L-arabinose, L-arabitol, dulcitol, ketogluconate, gluconate, glycerol, inositol, inulin, lyxose, melezitose, melibiose, methyl β-xyloside, D-raffinose, sucrose, sorbitol, L-sorbose, tagatose, D-turanose, xylitol or D-xylose is detected. Acid production from rhamnose and D-arabinose is weak or absent. The G+C content of DNA is 36–67 mol%.

The type strain is LMG 12317T (= CCUG 48100T), which was isolated from dog tonsils. Strains LMG 13617 and 334 (=LMG 21990) have also been deposited in the Belgian Co-ordinated Collections of Microorganisms (BCCM/LMG).

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