Lactobacillus oligofermentans sp. nov. associated with spoilage of modified atmosphere packaged poultry products

Koort, Joanna
American Society for Microbiology (ASM)
2005


http://hdl.handle.net/1975/515

Downloaded from Helda, University of Helsinki institutional repository.
This is an electronic reprint of the original article.
This reprint may differ from the original in pagination and typographic detail.
Please cite the original version.
**Lactobacillus oligofermentans** sp. nov., Associated with Spoilage of Modified-Atmosphere-Packaged Poultry Products

Joanna Koort,\(^1\)* Anna Murros,\(^1\) Tom Coenye,\(^2\) Susanna Eerola,\(^3\) Peter Vandamme,\(^2\) Antti Sukura,\(^4\) and Johanna Björkroth\(^1\)

Department of Food and Environmental Hygiene, University of Helsinki, Helsinki, Finland,\(^1\) Laboratory of Microbiology, University of Ghent, Ghent, Belgium,\(^2\) National Veterinary and Food Research Institute, Helsinki, Finland,\(^3\) and Department of Basic Veterinary Sciences, University of Helsinki, Helsinki, Finland\(^4\)

* Corresponding author. Mailing address: Department of Food and Environmental Hygiene, Faculty of Veterinary Medicine, P.O. Box 66, FIN-00014 University of Helsinki, Helsinki, Finland, Phone: 358-9-19157119. E-mail: joanna.koort@helsinki.fi.

Received 11 October 2004/Accepted 21 February 2005

Unidentified lactic acid bacterium (LAB) isolates which had mainly been detected in spoiled, marinated, modified atmosphere packaged (MAP) broiler meat products during two previous studies, were identified and analyzed for their phenotypic properties and the capability to produce biogenic amines. To establish the taxonomic position of these isolates, 16S rRNA gene sequence analysis, numerical analysis of ribopatterns, and DNA-DNA hybridization experiments were done. Unexpectedly for a meat-spoilage-associated LAB, the strains utilized glucose very weakly. According to the API 50 CHL test, arabinose and xylose were the only carbohydrates strongly fermented. None of the six strains tested for production of histamine, tyramine, tryptamine, phenylethylamine, putrescine, and cadaverine were able to produce these main meat-associated biogenic amines in vitro. The polyphasic taxonomy approach showed that these strains represent a new *Lactobacillus* species. The six isolates sequenced for the 16S rRNA encoding genes shared the highest similarity (95.0 to 96.3%) with the sequence of the *Lactobacillus durianis* type strain. In the phylogenetic tree, these isolates formed a distinct cluster within the *Lactobacillus reuteri* group, which also includes *L. durianis*. Numerical analyses of HindIII-EcoRI ribotypes placed all isolates together in a cluster with seven subclusters well separated from the *L. reuteri* group reference strains. The DNA-DNA hybridization levels between *Lactobacillus* sp. nov. isolates varied from 67 to 96%, and low hybridization levels (3 to 15%) were obtained with the *L. durianis* type strain confirming that these isolates belong to the same species different from *L. durianis*. The name *Lactobacillus oligofermentans* sp. nov. is proposed, with strain LMG 22743\(^T\) (also known as DSM 15707\(^T\) or AMKR18\(^T\)) as the type strain.

In recent years, the consumption of broiler meat has been increasing in Finland. Marinated broiler meat cuts packaged under a modified atmosphere (MA) are favored especially by consumers. Marinating in this context means mixing the meat cuts with acidic (acetic or citric-acid-containing) emulsified water-oil sauces which contain glucose or sucrose, NaCl, rheology-improving additives (like xanthan gum or guar gum), antimicrobial agents (sorbate and/or benzoate), aroma and protein swell, proteins are decomposed by proteolytic enzyme action and the subsequent decarboxylation of amino acids leads to the production of CO\(_2\) and biogenic amines. Decrease in acidity has been attributed to the production of ammonia by the bacterial deamination of amino acids. To identify the spoilage organisms associated with this product, the 16 and 23S HindIII restriction fragment length polymorphism (RFLP) patterns (HindIII ribopatterns) of the isolates were compared to the corresponding patterns in the previously established LAB database (14) at the Department of Food and Environmental Hygiene, University of Helsinki, Helsinki, Finland. This database comprised about 2,400 isolates (nowadays, about 4,000) and type strains (about 200) of all relevant spoilage LAB in the genera of *Carnobacterium, Lactobacillus, Leuconostoc, Enterococcus,* and *Weissella* (2, 3, 4, 6, 14). The dominating organism was found to be a novel cocccoid LAB species for which the name *Leuconostoc gascomitatum* was proposed. A group of unidentified gram-positive, rod-shaped LAB was also detected in this study (6). The ribopatterns of these strains clustered together in the numerical analysis but remained apart from the typical meat spoilage LAB.

Later, in three independent studies of other MAP broiler products, several new isolates resembled the initial 12 isolates by their ribotypes. Thirty-seven isolates were found during an...
TABLE 1. Sources and references of the isolates and their division between the six ribogroups

<table>
<thead>
<tr>
<th>HindIII ribogroup</th>
<th>Producer</th>
<th>No. of strains</th>
<th>Product type</th>
<th>Reference, if exists (group*)</th>
</tr>
</thead>
<tbody>
<tr>
<td>I A</td>
<td>2</td>
<td>Broiler leg, marinated</td>
<td>6 (unknown)</td>
<td></td>
</tr>
<tr>
<td>Ia B</td>
<td>9</td>
<td>Broiler leg, tomato marinated</td>
<td>6 (unknown)</td>
<td></td>
</tr>
<tr>
<td>Ib B</td>
<td>7</td>
<td>Broiler leg, marinated</td>
<td>5 (UVIIIb)</td>
<td></td>
</tr>
<tr>
<td>II B</td>
<td>8</td>
<td>Broiler leg, marinated</td>
<td>5 (UVIIIa)</td>
<td></td>
</tr>
<tr>
<td>III A</td>
<td>4</td>
<td>Broiler leg, three marinated and one nonmarinated</td>
<td>6 (unknown)</td>
<td></td>
</tr>
<tr>
<td>IV C</td>
<td>1</td>
<td>Broiler meat strips, marinated</td>
<td>6 (unknown)</td>
<td></td>
</tr>
<tr>
<td>V B</td>
<td>6</td>
<td>Five filet strips and one breast filet, both marinated</td>
<td>6 (unknown)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>Minced meat</td>
<td>6 (unknown)</td>
<td></td>
</tr>
</tbody>
</table>

* Name of the corresponding group in the reference.

investigation of initial (three isolates) and spoilage (34 isolates) bacterial populations in marinated MAP broiler legs (5). One isolate had been detected in a study of bacterial population of marinated MAP broiler meat strips analyzed on sell-by day (21). Eighteen isolates have recently been found in marinated (five isolates) and nonmarinated (13 isolates) MAP broiler products (legs, meat strips, breast filet, or minced meat) also analyzed at the end of shelf life (unpublished data). These studies involved products manufactured by three completely distinct large-scale plants purchasing the broiler chickens from contract farmers supplying to only one manufacturer.

Due to the continuous detection in spoiled or late-shelf-life products, this study was carried out to clarify the taxonomic status of these unidentified isolates and to evaluate if they form biogenic amines from the typical meat-associated amino acids. A polyphasic approach, including numerical analysis of ribopatterns (16 and 23S rRNA gene RFLP patterns), 16S rRNA gene sequence analysis, DNA-DNA hybridization, and examination of phenotypic properties, was used for species description, and the formation of histamine, tyramine, tryptamine, phenylethylamine, putrescine, and cadaverine was measured by a high-performance liquid chromatography (HPLC) technique.

MATERIALS AND METHODS

Bacterial strains, the use of strains in different phases of the study, and culturing of these strains. Sixty-seven isolates with similar HindIII ribopatterns were detected in the earlier studies. In the preliminary numerical analyses, these isolates were divided into six different groups (I, Ia, Ib, III, IV, and V) according to their HindIII ribopatterns. Table 1 shows the source and reference (if existing) of the isolates and their division between the six ribogroups. To the present study, four to six isolates were selected randomly from each ribogroup unless the group contained only two isolates (I and III).

The HindIII ribotyping of the selected 26 isolates was repeated, and they were also subjected to EcoRI ribotyping. Sets of 6 to 11 isolates, representing each of the HindIII-deficient clusters (Fig. 1), were selected for further studies. Pheno-

typical testing was carried out using 11 isolates (1-1, 5-14, 406, 423, 518, 533, 557, AMKR18, AMKR26, AMKR32, MARL13) with the exception of determination of lactic acid configuration, which was studied using six isolates (5-14, 423, 557, AMKR18, AMKR26, MARL13). The HPLC analysis of biogenic amine forming capacity was carried out using six isolates and GenBank entries of type strains belonging to the Lactobacillus reuteri group (Fig. 2). For the DNA-DNA hybridization experiments, eight isolates (Table 2) and the Lactobacillus durians type strain LMG 19193 were selected on the basis of the results obtained in the BLAST search of 16S rRNA gene sequences.

All isolates were routinely cultured at 25°C either overnight in MRS broth (Difco, BD Diagnostic Systems, Sparks, MD) or for 5 days on MRS agar plates (Oxoid, Hampshire, United Kingdom). The plates were incubated under an anaerobic CO2 atmosphere (9 to 15% CO2 according to the manufacturer; Anaerogen, Oxoid). All isolates were maintained in MRS broth (Difco) at −70°C.

DNA isolation and 16S rRNA gene sequence analysis. DNA for all DNA-based analyses was isolated as previously described by Björkroth et al. (2). The nearly complete (at least 1,400 bases sequenced) 16S rRNA gene was amplified by PCR with a universal primer pair, F3-27 (5′-AGAGTTTGTATCTGCGCGT-AG-3′) and R1541-1522 (5′-AAGAGGTTGATCCTGGCAGCGA-3′). Sequencing of the purified (QIAquick PCR purification kit; QIAGEN, Venlo, The Netherlands) PCR product from both directions was performed by Sanger’s dideoxynucleotide chain termination method using primers F19-35 (5′-CTGGCG TACGAGYAGAACGGTCTG-3′), F926 (5′-AATCTCAAGAAATGTACGGG-3′), R519 (5′-GTAATACGACTCACTATAGG-3′), and R1541-1522. Samples were run in a 1% agarose gel (2.4% sequencing device with c-Seq 2.0 software (LiCor, Lincoln, NE)) according to the manufacturer’s instructions. The consensus sequences of these strains (created with AlignIR software; LiCor) and representative strains belonging to the same phylogenetic group (retrieved from GenBank [http://www.ncbi.nlm.nih.gov/]) using BLASTN 2.2.6 [1]) were aligned, and a phylogenetic tree was constructed based on the neighbor-joining method using the BioNumerics 3.5 software package (Applied Maths, Sint-Martens-Latem, Belgium). Figure 2 shows the accession numbers of the 16S rRNA gene sequences used and deposited during the study.

DNA base composition and DNA-DNA hybridization. For the determination of the G+C content, DNA was enzymatically degraded into nucleosides as described by Mesbah et al. (16). The obtained nucleoside mixture was then separated by HPLC using a Waters SymmetryShield C8 column thermostated at 37°C. The solvent was 0.02 M NH4H2PO4 with 1.5% acetonitrile. Nonmethylated λ phage DNA (Sigma) was used as the calibration reference. DNA-DNA hybridizations were performed with photothiobiotin-labeled probes in microplate wells as described by Ezaki et al. (10) using an HST7000 bioassay reader (Perkin-Elmer) for the fluorescence measurements. The hybridization temperature was 35°C in 50% formamide.

Ribotyping and numerical analyses of ribopatterns. HindIII and EcoRI enzymes were used for the digestion of DNA as specified by the manufacturer (New England Biolabs, Beverly, MA). Restriction enzyme analysis, Southern blotting, hybridization, and detection of the digoxigenin label were performed as described previously (2). Labeling of the cDNA probe used was done by avidin biotinylated Cy5 dye (Promega and Dig labeling kit; Roche Molecular Biochemicals, Mannheim, Germany) (7). Scanned (Hewlett Packard Scan Jet 4c/T, Palo Alto, CA) ribopatterns were analyzed using the BioNumerics 3.5 software package. The similarity between all pairs was expressed by the Dice coefficient correlation, and unweighted-pair group method using average linkages clustering was used for construction of the dendrograms. Based on the use of internal controls, a position tolerance of 1.5% was allowed for the bands.

Morphology and phenotypical tests. All strains were Gram stained. For the size and precise morphology determination by transmission electron microscopy, cells of strains AMKR26, AMKR32, and 557 were suspended in physiological NaCl, negatively stained with 1% of phosphotungstic acid, and examined using the JEM 100 electron microscope (JEOL, Toyo, Japan). All the phenotypical tests were done at 25°C, unless otherwise stated, and each test was carried out at least twice. Growth at different temperatures (4, 15, and 37°C) or in the presence of NaCl (2%, 4%, and 6.5%, wt/vol) was tested in MRS broth (Difco) incubated until growth was observed or otherwise at least for 21 days. Configuration of lactic acid was determined enzymatically by using the UV method according to Hohorst (12) and Stetter (20). Carbohydrate fermentation profiles were tested using API 50 CHL (bioMérieux, Marcy l’Etoile, France) according to the manufacturer’s instructions. Gas formation from glucose was tested according to the manufacturer’s instructions. Gas formation from glucose was tested according to the method of Gibson and Abdel-Malek (11).
Confirmation of biogenic amine formation. The amine-forming capacity was studied by a liquid chromatographic method described by Maijala and Eerola (15) and Eerola et al. (9). The potential formation of histamine, tyramine, tryptamine, phenylethylamine, putrescine, and cadaverine was tested. Strains were adapted for 24 h at 25°C in MRS broth (pH 6.3) containing 2.0 g/liter of each precursor amino acid (separately). The precursor amino acids were L-histidine, L-tyrosine, L-tryptophane, L-phenylalanine, L-lysine (monohydrchloride), and L-ornithine (monohydrochloride). Next, 100 µl of broth was further transferred to another tube of the same medium and incubated at 25°C for 48 h. One ml of each fermented broth was extracted with (0.4%) perchloric acid and analyzed by accredited the high-performance liquid chromatography method (SFS-EN ISO/IEC 17025) by their dansyl derivatives using a Hewlett Packard (Waldbronn, Germany) HPLC system 1090 M. The results were confirmed by positive controls.

RESULTS

16S rRNA gene sequence comparison, mean base composition of DNA, and DNA-DNA reassociation studies. In the BLAST analysis, the 16S rRNA gene sequences of the isolates 423, 553, 557, MARL13, AMKR26, and AMKR18T possessed the highest similarities with L. durianis type strain LMG 19193T (similarity between 95.0 and 96.3%), Lactobacillus vaccinostercus (92.7%), and Lactobacillus suebicus (from 95.8 to 96.0%). These species belongs to the L. reuteri phylogenetic group of the genus Lactobacillus. Figure 2 shows the distance matrix tree based on the 16S rRNA gene similarities, and the accession numbers of the 16S rRNA gene sequences used and deposited are also shown in the figure. However, it should be noted that the sequence (AJ417735) of L. vaccinostercus deposited into GenBank is relatively short (508 bp) compared to the other sequences (about 1,500 bp) used in the study. The C+G content of the strains studied was 35.3 to 39.9%. Table 2 presents the DNA-DNA hybridization results. Reassociation values between Lactobacillus oligofermentans isolates and L. durianis LMG 19193T varied from 3 to 15%, whereas values among the eight L. oligofermentans isolates varied from 67 to 96%.

Numerical analyses of ribopatterns. Figure 1a to c shows the dendograms and banding patterns based on the HindIII (Fig. 1a) and EcoRI (Fig. 1b) ribotypes together with the dendrogram obtained by combining the unweighted pattern information of both EcoRI and HindIII ribotypes into one numerical analysis (Fig. 1c). In all numerical analyses, L. oligofermentans strains clustered together but clearly apart from the other
species. The strain division between the different \textit{L. oligofermentans} EcoRI clusters resembled the division between the six HindIII clusters detected earlier, with the exception that HindIII-deficient cluster IV was further divided into two subclusters, IVa and IVb. The pattern similarity levels among the \textit{L. oligofermentans} clusters varied from 70.1 to 75.8\%, depending on the analysis. The highest similarity between the \textit{L. oligofermentans} clusters and the other species was with the patterns of \textit{L. reuteri} (56.4\% in HindIII and 42.5\% in combined HindIII-EcoRI) or the \textit{L. durianis} and \textit{Lactobacillus vaccinostercus} (59.0\% in EcoRI) type strains.

**Phenotypic properties.** All isolates studied were gram-positive rods. Figure 3 shows the transmission electron microscopy picture of cells of isolates AMKR26, AMKR18T, and 557. All isolates grew at 4 and 15°C; none grew at 37°C, indicating the psychrotrophic nature of these strains. All isolates grew in the presence of 2\% NaCl but none in the presence of 6.5\% NaCl. According to the Gibson and Abdel-Malek (11) test, all isolates produced gas from glucose. However, in the API 50 CHL test, the utilization of D-glucose, gluconate, and N-acetylglucosamine was very weak or delayed. Positive reactions were obtained after a 5-day incubation period, and even then, some of the strains produced weak reactions. Detailed results of the utilization of carbohydrates are given in the species description below. The ratio of L- and D-lactic acids produced was approximately 70/30. None of the isolates produced ammonia from arginine.

**DISCUSSION**

The results of the present study indicate that the LAB strains detected in various MAP broiler meat products belong to a novel species to which we propose the name \textit{Lactobacillus oligofermentans} sp. nov. (see the species description below). Phylogenetic analysis (Fig. 2) clearly assigned this novel species to the genus \textit{Lactobacillus} and, specifically, to the \textit{L. reuteri} phylogenetic group, with \textit{L. durianis}, \textit{L. vaccinostercus}, and \textit{L. suebicus} as its closest neighbors. The DNA-DNA reassociation experiments, however, clearly distinguished \textit{L. oligofermentans} strains and \textit{L. durianis} type strain LMG 19193\textsuperscript{T} as two different species. This finding was expected because of the relatively low (identities, 96.3 to 96.2\%) 16S rRNA gene sequence similarities between the 6 \textit{L. oligofermentans} strains and the \textit{L. durianis} type strain.

Also in the numerical analysis based on ribotyping, \textit{L. oligofermentans} strains were distinguished from the \textit{L. reuteri} phylogenetic group reference strains (Fig. 1). However, depending on the analysis, \textit{L. oligofermentans} strains possessed pattern variability between 24.3 and 29.9\% (Fig. 1). In the DNA-DNA

### Table 2. Results of \textit{L. oligofermentans} sp. nov. DNA-DNA reassociation experiments

<table>
<thead>
<tr>
<th>HindIII cluster</th>
<th>Strain</th>
<th>% DNA-DNA reassociation with:</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>LMG 19193\textsuperscript{T}</td>
<td>423 5-14 557 MARL13 AMKR18</td>
</tr>
<tr>
<td>IIa</td>
<td>423</td>
<td>3 93 93 90 90</td>
</tr>
<tr>
<td>IIa</td>
<td>5-14</td>
<td>6 93</td>
</tr>
<tr>
<td>IIb</td>
<td>557</td>
<td>7 90 90</td>
</tr>
<tr>
<td>V</td>
<td>518</td>
<td>14 ND 90 90</td>
</tr>
<tr>
<td>V</td>
<td>533</td>
<td>15 ND 80 96</td>
</tr>
<tr>
<td>III</td>
<td>MARL13</td>
<td>8 ND 72 ND ND 67</td>
</tr>
<tr>
<td>IV</td>
<td>AMKR18</td>
<td>8 74 ND 72 ND 67</td>
</tr>
<tr>
<td>I</td>
<td>AMKR26</td>
<td>4 82 ND 79 ND 90 72</td>
</tr>
</tbody>
</table>

\textsuperscript{a} LMG 19193\textsuperscript{T}, \textit{Lactobacillus durianis} type strain.

\textsuperscript{b} ND, not determined.
reassociation experiments, reassociation levels varying from 67 to 96% were detected. Between the strains from same RFLP cluster or subclusters, DNA-DNA reassociation values from 93 to 96% were obtained (Table 2) whereas the lowest value, 67%, was obtained between strains representing clusters III and IV. The variation in the DNA-DNA reassociation results, in the G+C content (35.3 to 39.9%), and in ribopatterns may indicate that L. oligofermentans is a heterogeneous species.

All of our L. oligofermentans isolates originated from MAP broiler meat products. We have not detected this species from other meat sources. These MAP broiler meat products have included various kinds of nonmarinated and marinated products, such as legs, meat strips, breast files, and minced meat. Even though the products harboring L. oligofermentans have been variable, most (46 of the 67 total) isolates originate from marinated products. We have not yet, however, detected this or other spoilage LAB species in the marinades used for poultry products. It is currently not clear to us why marinating supports the growth of L. oligofermentans. The other species, L. duriansis, L. vaccinostercus, and Lactobacillus suebicus, located in the same phylogenetic branch with L. oligofermentans based on the 16S rRNA gene sequences (Fig. 2) have been detected in fermented durian fruits (tempoyak), apple and pear mashe, and dried cow dungs, respectively. A common feature of these species is that they prefer pentose carbohydrates to hexoses and they all ferment xylose well and glucose poorly.

L. oligofermentans has been detected both in the initial LAB population associated with marinated MAP broiler legs (5) and in late-shelf-life (21) or spoiled products (6). However, two-thirds of the strains have been isolated from spoiled products where the total LAB counts have varied from 10^6 to 10^10 CFU/g (6). Even though the levels of L. oligofermentans have been high in those products, this species has never dominated the spoilage LAB populations. In the studies of Björkroth et al. (5, 6), L. oligofermentans formed 10 (as unidentified) and 18% (as Unknown VII, VIIIa, and VIIIb) of the spoilage LAB while L. oligofermentans the spoilage LAB populations. In the studies of Bjo¨rkroth et al. have been variable, most (46 of the 67 total) isolates originate from marinated products. We have not yet, however, detected this or other spoilage LAB species in the marinades used for poultry products. It is currently not clear to us why marinating supports the growth of L. oligofermentans. The other species, L. duriansis, L. vaccinostercus, and Lactobacillus suebicus, located in the same phylogenetic branch with L. oligofermentans based on the 16S rRNA gene sequences (Fig. 2) have been detected in fermented durian fruits (tempoyak), apple and pear mashe, and dried cow dungs, respectively. A common feature of these species is that they prefer pentose carbohydrates to hexoses and they all ferment xylose well and glucose poorly.

L. oligofermentans has been detected both in the initial LAB population associated with marinated MAP broiler legs (5) and in late-shelf-life (21) or spoiled products (6). However, two-thirds of the strains have been isolated from spoiled products where the total LAB counts have varied from 10^6 to 10^10 CFU/g (6). Even though the levels of L. oligofermentans have been high in those products, this species has never dominated the spoilage LAB populations. In the studies of Björkroth et al. (5, 6), L. oligofermentans formed 10 (as unidentified) and 18% (as Unknown VII, VIIIa, and VIIIb) of the spoilage LAB while L. oligofermentans the spoilage LAB populations. In the studies of Bjo¨rkroth et al. have been variable, most (46 of the 67 total) isolates originate from marinated products. We have not yet, however, detected this or other spoilage LAB species in the marinades used for poultry products. It is currently not clear to us why marinating supports the growth of L. oligofermentans. The other species, L. duriansis, L. vaccinostercus, and Lactobacillus suebicus, located in the same phylogenetic branch with L. oligofermentans based on the 16S rRNA gene sequences (Fig. 2) have been detected in fermented durian fruits (tempoyak), apple and pear mashe, and dried cow dungs, respectively. A common feature of these species is that they prefer pentose carbohydrates to hexoses and they all ferment xylose well and glucose poorly.

Description of Lactobacillus oligofermentans sp. nov. Lacto-
bacillus oligofermentans (o.li.go.fer.men’ tans, Gr. adj. oligos few or little, L. part. adj. fermentans fermenting, N.L. part. adj. oligofermentans fermenting few [substrates]).

Strains are gram-positive, round-ended rods. Size varies extremely, between 0.8 to 3.1 \mu m in width and 5.0 to 27.0 \mu m in length, when grown in MRS broth (Fig. 3). Colonies on MRS agar are white, the size varying from 0.5 mm to 2.5 mm. Strains grow well at 15°C and more slowly at 4°C, but no growth is observed at 37°C. All strains grow well in the presence of 2% NaCl, and most (not strains 406 and 423) in the presence of 4% NaCl. None of the strains grows in the presence of 6.5% NaCl.

L- and D-lactic acids are produced at a ratio of 70/30. All strains produced acid from ribose, L-arabinose, and D-xylene, but not from D-arabinose or L-xylene. Utilization of maltose, gluconate, D-glucose, and D- and L-fucose, D- and L-arabitol, L-saccharose, sucrose, salicine, sorbitol, trehalose, xylitol, D-fructose, D-lyxose, D-mannose, D-ribofuranose, D-tagatose, L-turanose, L-sorbose, and D- and L-fucose, D- and L-arabitol, L-arabinose, D- and L-mannose, and L-M-glucono-\(\delta\)-lactone are weak or de-

The G+C content of DNA is from 35.3 to 39.9%. The type strain is LMG 22743^T (also known as DSM 15707^T or AMRK18^T) isolated from late-shelf-life, modified-atmosphere-packaged, marinated broiler legs. Its G+C content is from 35.9%. Strains 406, 518, and AMKR33 have been deposited in the Belgian Coordinated Collections of Microorganisms LMG Bacteria Collection (Laboratorium voor Microbiologie, Ghent, Belgium) as LMG 22744^T, LMG 22745, and LMG 22746, respectively. Strains 423, 557, AMKR26, 5-14, and MARL13 have been deposited to the German Collection of Microorganisms and Cell Cultures as DSM 15704, DSM 15705, DSM 15706, DSM 15708, and DSM 15709, respectively. The strains originate from MAP raw broiler chicken products.
ACKNOWLEDGMENTS

We thank H. Niinivirta for her excellent technical assistance. Financial support from the Academy of Finland (project 100479) is gratefully acknowledged.

REFERENCES