Reclassification of *Leuconostoc gasicomitatum* as *Leuconostoc gelidum* subsp. *gasicomitatum* comb. nov., description of *Leuconostoc gelidum* subsp. *aenigmaticum* subsp. nov., designation of *Leuconostoc gelidum* subsp. *gelidum* subsp. nov. and emended description of *Leuconostoc gelidum*

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In the present study we investigated the taxonomic status of 20 lactic acid bacteria (LAB) originating from packaged meat. On the basis of 16S rRNA gene sequence similarity, these strains were shown to belong to the genus *Leuconostoc* with *Leuconostoc gelidum*, *Leuconostoc inhae* and *Leuconostoc gasicomitatum* as the closest phylogenetic relatives. The novel strains shared more than 70% DNA–DNA relatedness with type and reference strains of both *L. gelidum* and *L. gasicomitatum*. The DNA–DNA relatedness values between *L. gelidum* type and reference strains and *L. gasicomitatum* type and reference strains were also above 70%, showing that all these strains belonged to the same species. Sequence analyses of concatenated *atpA*, *pheS*, and *rpoA* genes demonstrated that the novel strains as well as type and reference strains of *L. gelidum* and *L. gasicomitatum* are phylogenetically closely related, but form three clearly separated subgroups. Numerical analysis of *Hind*III ribopatterns and phenotypic tests supported this subdivision. Based on the data presented in this study, we propose to reclassify *Leuconostoc gasicomitatum* as *Leuconostoc gelidum* subsp. *gasicomitatum* comb. nov. (type strain, LMG 18811ᵀ = DSM 15947ᵀ). The novel strains isolated in the present study represent a novel subspecies, for which the name *Leuconostoc gelidum* subsp. *aenigmaticum* subsp. nov. is proposed, with POUF4dᵀ (=LMG 27840ᵀ = DSM 19375ᵀ) as the type strain. The proposal of these two novel subspecies automatically creates the subspecies *Leuconostoc gelidum* subsp. *gelidum* subsp. nov. (type strain, NCFB 2775ᵀ = DSM 5578ᵀ). An emended description of *Leuconostoc gelidum* is also provided.

**During characterization of spoilage microbiota of packaged meat, we isolated 20 lactic acid bacteria (LAB) strains from vacuum-packaged pork, vacuum-packaged turkey and modified atmosphere-packaged (MAP) broiler that remained unidentifed in the numerical analysis of *Hind*III ribopatterns (Fig. S1, available in the online Supplementary Material). The 20 LAB strains formed a tight cluster that was close to but clearly separated from *Leuconostoc gelidum* and *Leuconostoc gasicomitatum*. *L. gasicomitatum* and *L. gelidum* are closely related and form a phylogenetic branch within the genus *Leuconostoc* together with *Leuconostoc inhae*, *Leuconostoc kimchii*, *Leuconostoc carnosum*, and the recently described species *Leuconostoc miyukkimchii* (Björkroth & Holzapfel, 2006; Lee et al., 2012). Characteristic for these species of the genus *Leuconostoc*, with the**
exception of *L. kimchii*, is the ability to grow at low temperatures, which enables them to grow in chill-stored food (Björkroth & Holzapfel, 2006). *L. gelidum* and *L. gasicomitatum* often form part of the dominant microbiota in late shelf-life, packaged meat, and have been associated with spoilage of a variety of meat and meat products (Björkroth & Holzapfel, 2006).

The purpose of the present study was to resolve the taxonomic status of the novel strains by a polyphasic approach including phenotypic tests, sequence analysis of 16S rRNA, *atpA*, *pheS* and *rpoA* genes, and DNA–DNA hybridization. In this study we show that the strains represent a novel subspecies of the species *L. gelidum*. We also propose to reclassify the species *L. gasicomitatum* as a subspecies of *L. gelidum*.

The 20 strains were isolated from MAP meat by growth on Man-Rogosa-Sharpe agar (MRS; Oxoid) at 25 °C for 5 days under anaerobic conditions [Anaerogen (Oxoid); 9–13 % CO₂ according to the manufacturer]. All isolates were maintained in MRS broth at 2°C and grown in MRS broth and agar at 25 °C in anaerobic jars. The sources of the isolates of the genus *Leuconostoc* are presented in Fig. S1.

The nearly complete 16S rRNA gene sequence of three representative unknown strains was determined to confirm the genus level identification of the isolates as described by Vihavainen & Björkroth (2007). DNA for all analyses was extracted as described by Pitcher *et al.* (1989) with modifications as described by Björkroth & Korkeala (1996). Sequences of the isolates were subjected to the BLAST search program (Altschul *et al.*, 1997), the 16S rRNA sequences of the type strains of species within the genus *Leuconostoc* were retrieved from the GenBank database (http://www.ncbi.nlm.nih.gov), and all the sequences were aligned with CLUSTAL_X (Thompson *et al.*, 1994). A phylogenetic tree was reconstructed by PALM (Chen *et al.*, 2009) by using the maximum-likelihood method with bootstrap values based on 1000 replications.

Sequence analysis of the 16S rRNA gene clearly showed that the isolates belonged to the genus *Leuconostoc* (Fig. 1). The 16S rRNA gene sequences of the unknown strains POUF4dT, AMKR32 and POKY4-4 were identical, and most similar to *L. gelidum* DSM 5578T, *L. gasicomitatum* LMG 18811T, and *L. inhae* KCTC 3774T (99.8, 99.7 and 99.2 % sequence similarity, respectively). The similarity between *L. gelidum* DSM 5578T and *L. gasicomitatum* LMG 18811T was 99.4 %. The high 16S rRNA gene sequence similarity within the *L. gelidum* lineage has been reported before (Björkroth *et al.*, 2000).

Multilocus sequence analysis (MLSA) of housekeeping genes *atpA*, *pheS* and *rpoA* has been successfully applied for

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**Fig. 1.** Maximum-likelihood tree based on 16S rRNA gene sequences of three representative novel strains and 13 type and reference strains of species of the genus *Leuconostoc*, with *Leuconostoc fallax* LMG 13177T as an outgroup. GenBank accession numbers are given in parentheses. Bootstrap values >50 % after 1000 resamplings are shown at branching points. Bar, 0.1 substitutions per nucleotide position.
differentiation of species of the genus Leuconostoc, and the discriminatory resolution of these genes was shown to be substantially higher compared to the sequence of the 16S rRNA gene (De Bruyne et al., 2007). Sequences of the atpA, pheS and rpoA genes of the unknown strains were determined to investigate the taxonomic position of the isolates. Amplification and sequencing was performed as described by Naser et al. (2005a, b). The sequences were assembled using the BioNumerics software package (Applied Maths), subjected to the BLAST search program (Altschul et al., 1997), and aligned with sequences of type strains of species of the genus Leuconostoc retrieved from the GenBank database using CLUSTAL_X software (Thompson et al., 1994). GenBank/EMBL accession numbers for the atpA, pheS and rpoA genes used in this study are given in Table S1. Phylogenetic trees were reconstructed using the maximum-likelihood method (Fig. 2) as described above for 16S rRNA gene sequence analysis and by CLUSTAL_X using the neighbour-joining method (Fig. S2).

In the maximum-likelihood tree based on concatenated sequences of atpA, pheS and rpoA genes, the six representative unknown strains formed a distinct branch close to two clusters formed by the four strains of L. gasicomitatum and the three strains of L. gelidum (Fig. 2). The topology of the trees reconstructed using maximum-likelihood and neighbour-joining methods are mostly congruent except for the position of L. citreum (with low bootstrap values in both trees) and the relative positions of the novel strains, L. gasicomitatum and L. gelidum in spite of their clustering in the same clade (Fig. S2). In the analysis of the partial pheS sequences (Fig. S3), which is the most discriminatory locus, the similarity between strains POUF4dT and AMKR32 was 98.7 %, and the similarity between strains POUF4dT and both L. gasicomitatum LMG 18811T and L. gelidum LMG 18297T was 96.1 %. Between L. gasicomitatum LMG 18811T and L. gelidum LMG 18297T, the pheS sequence similarity was 93.2 %, and for L. inhae LMG 22919T, the similarity with strain POUF4dT, L. gasicomitatum LMG 18811T and L. gelidum LMG 18297T, was 89.6, 89.9 and 90.6 %, respectively. This correlates with the study by De Bruyne et al. (2007), who reported that species of the genus Leuconostoc were delineated above 93 % pheS sequence similarity.

For DNA–DNA hybridization (DDH), DNA was isolated using a French pressure cell (Thermo Spectronic) and was purified by chromatography on hydroxyapatite as described by Cashion et al. (1977). DDH was carried out as described by De Ley et al. (1970) under consideration of

**Fig. 2.** Maximum-likelihood tree based on concatenated atpA, pheS and rpoA sequences of Leuconostoc gelidum subsp. aenigmaticum subsp. nov. and 16 type and reference strains of species of the genus Leuconostoc with Leuconostoc fallax LMG 13177T as an outgroup. Bootstrap values >50 % after 1000 resamplings are shown at branching points. Bar, 0.07 substitutions per site.
the modifications described by Huss et al. (1983) using a model Cary 100 Bio UV/VIS-spectrophotometer equipped with a Peltier-thermostatted 6 × 6 multicell changer and a temperature controller with in situ temperature probe (Varian). The DDH experiment was repeated in another laboratory with the same spectrophotometric method of De Ley et al. (1970) as described by De Bruyne et al. (2007). The DNA base composition analysis of strain POUF4dT was performed as described by De Bruyne et al. (2007).

The DDH values between strain POUF4dT and L. gasicomitatum LMG 18811T, L. gelidum DSM 5578T, and L. inhae LMG 22919T were 75 ± 2, 76 ± 3 and 45 ± 4 %, respectively. This shows that strain POUF4dT belongs to the same species as L. gasicomitatum LMG 18811T and L. gelidum DSM 5578T, and does not belong to the same species as L. inhae LMG 22919T when the cut-off point of 70 % DNA–DNA relatedness for species delineation is considered (Wayne et al., 1987). Strains POUF4dT and AMKR32 showed a DDH value of 87 ± 4 %. The DDH values for L. gasicomitatum LMG 18811T with L. gasicomitatum LMG 19597T, L. gelidum DSM 5578T and L. gelidum AMKR21 were 82 ± 7, 80 ± 4, and 80 ± 1 %, respectively, indicating that these strains belong to the same species. The DDH values for L. gasicomitatum LMG 18811T with L. inhae LMG 22919T and L. mesenteroides DSM 20343T were 51 ± 3 and 35 ± 2 %, respectively. Thus, these strains do not represent the same species. The DNA–DNA relatedness values obtained for L. gasicomitatum LMG 18811T and L. gelidum DSM 5578T were clearly higher than those reported by Björkroth et al. (2000) and Kim et al. (2000), who assigned these strains to different species. We thus repeated the DDH experiment in another laboratory, which confirmed our results (Table S2). The DNA G + C content of strain POUF4dT was 37 mol%, which is within the expected range of the genus Leuconostoc.

Phenotypic characteristics were tested for six representative strains (AMKR32, APM2b4, POKY4-4, POKY4-10, POUF4dT and POUF4h). Growth at 0, 5, 10, 15, 25, 30 and 37 °C, pH 2–10 and with 2, 4, 6.5, and 8 % NaCl was tested in MRS broth (Oxoid) until growth was observed or for at least 21 days. The carbohydrate fermentation profiles of the strains were studied using API 50 CHL and API Strept (bioMérieux) according to the manufacturer’s instructions. Tests for production of ammonia from arginine, gas from glucose and slime from sucrose were performed as described by Koort et al. (2004). Like other Leuconostocs, cells were Gram-positive, catalase-negative, facultatively anaerobic, oval cocci. The API 50CH profiles of the novel strains were similar to the profile of the type strain of L. gasicomitatum (Table 1). Like L. gasicomitatum, and unlike L. gelidum, the novel strains did not ferment amygdalin, arbutin or salicin. All strains produced gas from glucose, and none of the strains produced ammonium from arginine. The strains grew at 5 °C and at 25 °C, but not at 37 °C; two out of six strains grew at 30 °C. The strains grew in 4 % NaCl, and at pH 5–8. Unlike L. gasicomitatum, five

### Table 1. Phenotypic characteristics of *Leuconostoc gelidum* subsp. *aenigmaticum* subsp. nov. and its closest phylogenetic relatives

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
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<tbody>
<tr>
<td>Growth in 6.5 % NaCl</td>
<td>(83)</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>+</td>
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<td>Haem-stimulated aerobic growth</td>
<td>–</td>
<td>+*</td>
<td>–</td>
<td>ND</td>
<td>ND</td>
<td>+</td>
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<tr>
<td>Acid production from:</td>
<td></td>
<td></td>
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<tr>
<td>Amygdalin</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>–</td>
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<tr>
<td>l-Arabinose</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
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<td>+</td>
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<tr>
<td>Arbutin</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>+</td>
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<tr>
<td>Raffinose</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
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<tr>
<td>D-Xylose</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
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<tr>
<td>Salicin</td>
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<td>–</td>
<td>+</td>
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</tbody>
</table>

*Data from this study.*
all be differentiated in both genotypic and phenotypic analyses. On the basis of data presented in this study, the novel strains represent a novel subspecies of the species *L. gelidum* for which the name *Leuconostoc gelidum* subsp. *aeinigmaticum* subsp. nov. is proposed. In addition, we propose to reclassify *L. gasicomitatum* as *Leuconostoc gelidum* subsp. *gasicomitatum* comb. nov. The proposal of these two novel subspecies automatically creates the subspecies *Leuconostoc gelidum* subsp. *gelidum* subsp. nov. An emended description of *L. gelidum* is also provided.

**Emended description of *Leuconostoc gelidum* Shaw & Harding 1989**

The emendation of the species description is based on the present study and the publication by Björkroth et al. (2000). Cells are Gram-stain-positive, catalase-negative, non-spore-forming, non-motile, oval cocci. Colonies are small and greyish-white. Growth occurs at 5°C, but not at 37°C. Gas is produced from glucose. Arginine is not hydrolysed. Most strains produce slime from sucrose. All strains hydrolyse aesculin. Acid is produced from L-arabinose, cellobiose, D-fructose, D-mannose, melibiose, methyl D-glucoside, raffinose, sucrose, trehalose and D-xylose, but not from D-arabinose, dulcitol, erythritol, glycerol, inositol, lactose, mannitol, melezitose, rhamnose, sorbitol or D-sorbitol. Fermentation of amygdalin, arbutin, gluconate, galactose, maltose, ribose and salicin is strain-dependent.

The type strain is NCFB 2775T (=DSM 5578T), isolated from vacuum-packaged meat.

**Description of *Leuconostoc gelidum* subsp. *aeinigmaticum* subsp. nov.**

*Leuconostoc gelidum* subsp. *aeinigmaticum* (ae.nig.ma’ti.-cum. Gr. n. aenigma riddle; N.L. neut. adj. aenigmaticum enigmatic, as its role in spoilage of packaged meat is unclear).

The following characteristics allow differentiation from *L. gelidum* subsp. *gelidum* and *L. gelidum* subsp. *gasicomitatum*: amygdalin, arbutin and salicin are not fermented; ribose is fermented; majority of the strains grow in 6.5% NaCl; aerobic growth is not stimulated by haem (Table 1).

The type strain is POUF4dT (=LMG 27840T =DSM 19375T) isolated from MAP pork in Helsinki, Finland. The G+C content of the DNA of the type strain is 37 mol%.

**Description of *Leuconostoc gelidum* subsp. *gasicomitatum* (Björkroth et al. 2001) comb. nov.**

*Leuconostoc gelidum* subsp. *gasicomitatum* (ga.si.co.mi.ta’tum. N.L. neut. n. gasum gas; L. part. adj. comitatum accompanied; N.L. neut. part. adj. gasicomitatum accompanied by gas).

Basonym: *Leuconostoc gasicomitatum* Björkroth et al. 2001

The description is as given for *Leuconostoc gasicomitatum* by Björkroth et al. (2000). The following characteristics allow differentiation from *L. gelidum* subsp. *gelidum* and *L. gelidum* subsp. *aeinigmaticum*: amygdalin, arbutin and salicin are not fermented; ribose is fermented; does not grow in 6.5% NaCl; haem stimulates aerobic growth.

The type strain is LMG 18811T (=DSM 15947T), isolated from MAP marinated broiler. The G+C content of the DNA of the type strain is 37 mol%.

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**REFERENCES**


