Aeribacillus composti sp. nov., a thermophilic bacillus isolated from olive mill pomace compost

Ilaria Finore,1 Alessia Gioiello,1 Luigi Leone,1 Pierangelo Orlando,2 Ida Romano,1 Barbara Nicolaus1 and Annarita Poli1,*

Abstract
A Gram-stain-positive, aerobic, endospore-forming, thermophilic bacterium, strain N.8T, was isolated from the curing step of an olive mill pomace compost sample, collected at the Composting Experimental Centre (CESCO, Salerno, Italy). Strain N.8T, based on 16S rRNA gene sequence similarities, was most closely related to Aeribacillus pallidus strain H12T (=DSM 3670T) (99.8% similarity value) with a 25% DNA–DNA relatedness value. Cells were rod-shaped, non-motile and grew optimally at 60°C and pH 9.0, forming cream colonies. Strain N.8 was able to grow on medium containing up to 9.0% (w/v) NaCl with an optimum at 6.0% (w/v) NaCl. The cellular membrane contained MK-7, and C16:0 (48.4%), iso-C17:0 (19.4%) and anteiso-C17:0 (14.6%) were the major cellular fatty acids. The DNA G+C content was 40.5 mol%. Based on phenotypic characteristics, 16S rRNA gene sequences, DNA–DNA hybridization values and chemotaxonomic characteristics, strain N.8T represents a novel species of the genus Aeribacillus, for which the name Aeribacillus composti sp. nov. is proposed. The type strain is N.8T (=KCTC 33824T =JCM 31580T).

The genus Aeribacillus was first proposed by Miñana-Galbis et al. [1] when Geobacillus pallidus [2, 3] was reclassified in a novel genus, as Aeribacillus pallidus. This genus belongs to the phylum Firmicutes, order Bacillales and family Bacillaceae, and is most closely related to the genera Geobacillus and Arxoxybacillus [4, 5]. At the time of writing, Aeribacillus pallidus strain H12T (=DSM 3670T) was the sole species of the genus Aeribacillus. Cells are Gram-positive, spore-forming rods, that occur singly, in pairs or in chains; it is catalase and oxidase-positive, aerobic, thermophilic and alkalitolerant, possessing menaquinone MK-7 as the predominant quinone and anteiso-C16:0 as a major cellular fatty acid. Aeribacillus pallidus strain DSM 3670T possessed diphosphatidylglycerol, phosphatidylglycerol, two unidentified glycolipids and an unidentified glycopolypholpid. The DNA G+C content of Aeribacillus pallidus strain DSM 3670T ranged from 39 to 41 mol% [2]. The aim of the present work was to determine the exact taxonomic position of strain N.8T, which was isolated from a composting site in the Cilento National Park, (Italy).

Samples of compost were collected from the Composting Experimental Centre (CESCO) in Cilento National Park, Salerno, Italy (Latitude N 40°18’17” E 15°21’39.057’’).

The composted waste biomass came from an olive oil mill and contained both wastewater and pomace. The waste material was firstly collected in a biocanister for the bio-oxidation phase (2 days, 55–65°C), and was then accumulated in semi-aerated conditions, underwent ‘curing’ (30 days) and was completely composted after 60–90 days. Strain N.8T was isolated from a compost sample of curing step (T sampling=51°C). The compost sample (1 g) was dissolved in 200 ml sterilised 50 mM phosphate buffer (pH 7.0) with agitation (120 r.p.m.) for 24 h at 60°C. The suspension obtained was used to inoculate 10 ml growth medium A containing (l−1): peptone, 8 g; yeast extract 4 g and NaCl, 2 g. After 48 h at 60°C, the growth that had occurred was used as an inoculum for the same solid medium obtained by adding agar [1.8% (w/v)]. After 48 h incubation at 60°C growth had occurred and colonies were purified by using the serial dilution-plating method at 60°C followed by restreaking on the same solid medium. Strain N.8T represented the fastest growing microorganism in medium A and it was the only colony-forming strain at the highest dilutions. Sub-culturing was conducted in Trypton Soy Broth–TSB (Oxoid) for 24 h at 60°C, and maintained as glycerol stocks at −20°C for further study.

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Keywords: Aeribacillus; olive mill pomace; compost; Composting Experimental Center (CESCO).
Abbreviations: CMC, carboxymethyl-cellulose; DPG, Diphosphatidylglycerol; ESI/MS, electrospray ionization-mass spectrometry; FAME, fatty acid methylester; 1H-NMR, Proton nuclear magnetic resonance; LC/MS, liquid chromatography–mass spectrometry; TM, melting point temperature.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain N.8T is LT594972.

Two supplementary tables and three supplementary figures are available with the online Supplementary Material.

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The 16S rRNA gene sequence was determined at the BMR Genomics Service (Padova University, Italy) by using the following primers for amplification: 3′-CCA GCA GGC GCG GTA AT-5′ and 5′-ATT ACC GCG GCT GCT GG-3′. A phylogenetic tree was reconstructed by using the software package MEGA version 5 [6] after multiple alignments of the data by CLUSTAL X [7]. Distances (distance options according to Kimura’s two-parameter model) [8] and clustering were based on the neighbour-joining and maximum likelihood algorithms [6, 9]. Tree topologies were re-examined by the bootstrap method of resampling [10] using 1000 replications.

The isolate was identified using the EzTaxon-e server (https://www.ezbiocloud.net/taxonomy), based on 16S rRNA gene sequence data [11]. Data suggested that strain N.8T belongs to the genus Aeribacillus and, based on the gene sequence similarities, it was most closely related to Aeribacillus pallidus H12T (=DSM 3670T) (99.8 %), Anoxybacillus vitaminiplus 5nPT (=CMC 16594T) (96.7 %), Anoxybacillus calidus C161aT (=DSM 25220T) (95.7 %), Anoxybacillus rupiensis R270T (=DSM 17127T) (95.1 %) and Saccharococcus thermophilus 657T (=ATCC 43125T) (95.0 %). The phylogenetic tree reconstructed using the neighbour-joining method showed that strain N.8T is a member of the genus Aeribacillus (Fig. 1). Analogous phylogenetic information for strain N.8T was obtained by using the maximum-likelihood algorithms (Fig. S1, available in the online Supplementary Material).

The morphological characteristics of strain N.8T were investigated using cultures grown on TSB with Aeribacillus pallidus strain DSM 3670T as a reference strain. The phenotypic characteristics were analysed following the criteria proposed by Logan et al. [12]. Cells of strain N.8T were grown at 60 °C for 24 h and their morphology was observed using phase-contrast microscopy (Nikon Eclipse E400) and by Scanning Electron Microscopy (SEM) (Philips: XL 30 ESEM). For SEM analysis samples were fixed for 24 h in 2.5 % (w/v) glutaraldehyde and subsequently dehydrated in a graded series of ethyl alcohol they were critical-point dried and gold coated by sputtering. Colony morphology was analysed on a solid medium by stereomicroscopy (M8, Leica). Gram-staining was performed according to Dussault [13]. Growth was tested at different temperatures (37, 45, 50, 55, 60, 65, 70, 80 °C). An anaerobic growth test was carried out in TSB medium in an anaerobic chamber for 5 days at 60 °C, as described by Poli et al. [14]. All biochemical tests were performed at the optimal growth temperature, pH and NaCl concentration: 60 °C, pH 9.0 and 6 % (w/v) NaCl, respectively. Carbon and nitrogen source usage of strain N.8T was evaluated using BIOLOG Phenotype MicroArray plates PM1, PM2A and PM3B (Biolog). Ionic and osmotic sensitivities and the optimum pH for growth were studied using BIOLOG Phenotype MicroArray plates PM9 and PM10, respectively, prepared as recommended by the manufacturers. Unless stated otherwise, the pH of the optimal growth medium was 9.0. Oxidase activity was determined by assessing the oxidation of tetramethyl-p-phenylenediamine, and catalase activity was determined by assessing bubble production in a 3 % (v/v) hydrogen peroxide solution. For nitrate and nitrite reduction, optimal medium (TSB containing 0.1 % (w/v) KNO3 or 0.001 % (w/v) NaN3O2), was used, respectively. Acid and gas production from D-glucose were tested as reported in Poli et al. [14]. Hydrolysis of hippurate was tested by using 1.0 % (w/v) sodium hippurate. Tyrosine degradation was tested on solidified growth medium containing 0.45 % (w/v) l-tyrosine. Indole formation was tested using Kovac’s reagent. Maltose, mannose and sucrose were tested as a sole carbon source for the exopolysaccharide production; 1 % (w/v) of each substrate was added in a medium, according to Radchenkova et al. [15]. Starch hydrolysis was tested by flooding cultures with Lugol’s iodine solution on solid TSB medium containing 0.2 % (w/v) starch. Xylan and cellulose hydrolysis were tested by flooding cultures with 0.1 % Congo red followed by 1 M NaCl on solid TSB medium containing 0.2 % (w/v) xylan and carboxymethyl-cellulose (CMC), respectively. For casein hydrolysis, solid TSB medium plus 5.0 % (w/v) skimmed milk was used. For gelatin hydrolysis and sensitivity to lysozyme, 10 % (w/v) gelatine and 0.001 % (w/v) lysozyme were used, respectively. Phenylalanine degradation was tested by flooding cultures with 10 % (w/v) FeCl3 solution on solid TSB medium containing 0.2 % (w/v) phenylalanine. The urease activity test was performed according to Rustigian and Stuart [16]. For the endospore formation test, 0.001 % (w/v) MnCl2·4H2O was added in liquid medium as the stimulating agent and checked by optical microscopy after 24 and 48 h of incubation. The Voges-Proskauer test was performed according to the Clark and Lubs method [17]. The motility test was assessed by using test-tubes containing semi-solid TSB medium with agar (0.5 %, w/v) [18]. The sensitivity of the strain to antibiotics was tested by using solid TSB medium and Sensi-discs (6 mm; Oxoid) containing streptomycin (25 µg), gentamicin (30 µg), bacitracin (10 U), novobiocin (30 µg), penicillin (10 U), ampicillin (25 µg), erythromycin (30 µg), tetracycline (30 µg), neomycin (30 µg), fusidic acid (10 µg), lincomycin (15 µg), vancomycin (30 µg), chloramphenicol (10 µg), kanamycin (30 µg) and nistatin (100 µg) [19].

Cells of strain N.8T were aerobic, Gram-stain-positive, straight rods (0.5–0.6×1.5–5 µm) with a tendency to chain. Spherical endospores located terminally and of diameter of approximately 0.3–0.4 µm were present (Fig. S2). Strain N.8T was susceptible to all the antibiotics tested except for nistatin. Colonies on solid TSB medium were cream, smooth, circular and shiny and of approximately 1 mm in diameter at 60 °C after 24 h, while colonies of Aeribacillus pallidus DSM 3670T were pale and circular at 50 °C in the same growth media. The optimal growth temperature for strain N.8T was 60 °C (optimal temperature range for growth 50–65 °C), while for Aeribacillus pallidus DSM 3670T it was 50 °C (optimal temperature range for growth 30–70 °C). Strain N.8T was a non-motile rod, while Aeribacillus pallidus DSM 3670T was a motile rod. Strain N.8T and...
**Aeribacillus pallidus** DSM 3670T were both positive for hippurate hydrolysis, oxidase and catalase activities, and spor formation, but negative for xylanase, cellulase, urease, protease, gelatin and phenylalanine hydrolysis, indole formation, nitrate and nitrite reduction, and the Voges-Proskauer reaction. For both strains, the pH range for growth was 5.5–10.0 with an optimum pH for growth of 9.0. Strain N.8T was not able to produce exopolysaccharides using maltose, mannose and sucrose as the sole carbon source. The differential physiological, biochemical and molecular properties of strain N.8T and its nearest phylogenetic neighbour *Aeribacillus pallidus* DSM 3670T are presented in Table 1. Other information regarding carbon and nitrogen sources utilization, ionic and osmotic sensitivity and the optimum pH values for growth are given in Table S1.

Genomic DNA was extracted and purified from bacterial cell cultures (approximately 200 mg of dry pellet) using the Genomic- DNA-Buffer Set and Genomic-tip-100/G columns (QIAGEN), according to the manufacturer’s instructions, as reported by Poli et al. [20]. The DNA G+C content was evaluated as previously described [20] on the basis of the DNA thermodenaturatation profile and melting point temperature (TM) evaluation (mol%). Bacterial DNA samples of known G+C % content, ranging from 30 to 60 %, were used for the construction of a standard G+C % versus TM curve (linear correlation coefficient greater than 0.99 %) and the G+C % content of the unidentified value was extrapolated from the curve [21]. DNA–DNA filter hybridization and per cent sequence homology evaluations were performed as previously described [22]. The type strain of *Aeribacillus pallidus* H12T (DSM 3670T) was obtained from the Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ), Braunschweig, Germany. The strain was grown in medium recommended by the culture collection and it was used for comparative purposes.

DNA–DNA hybridization, evaluated by filter hybridization was carried out between strain N.8T and a strain of the closely related species, *Aeribacillus pallidus* DSM 3670T. Strain N.8T demonstrated a 25 % DNA–DNA relatedness value with respect to *Aeribacillus pallidus* DSM 3670T. This

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**Fig. 1.** Neighbour-joining phylogenetic tree, based on 16S rRNA gene sequences, showing the relationship between strain N.8T and related taxa. *Aneuribacillus thermoaeophilus* DSM 3670T (X94196) was used as an outgroup.

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*Aeribacillus pallidus* DSM 3670T were both positive for hippurate hydrolysis, oxidase and catalase activities, and spor formation, but negative for xylanase, cellulase, urease, protease, gelatin and phenylalanine hydrolysis, indole formation, nitrate and nitrite reduction, and the Voges-Proskauer reaction. For both strains, the pH range for growth was 5.5–10.0 with an optimum pH for growth of 9.0. Strain N.8T was not able to produce exopolysaccharides using maltose, mannose and sucrose as the sole carbon source. The differential physiological, biochemical and molecular properties of strain N.8T and its nearest phylogenetic neighbour *Aeribacillus pallidus* DSM 3670T are presented in Table 1. Other information regarding carbon and nitrogen sources utilization, ionic and osmotic sensitivity and the optimum pH values for growth are given in Table S1.
Table 1. Differential characteristics of strain N.8\textsuperscript{T} and a strain of the most closely related species, Aeribacillus pallidus

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Strain N.8\textsuperscript{T}</th>
<th>Aeribacillus pallidus DSM 3670\textsuperscript{T}</th>
</tr>
</thead>
<tbody>
<tr>
<td>NaCl range (%)</td>
<td>2.0–9.0</td>
<td>1.0–9.0</td>
</tr>
<tr>
<td>Colony colour</td>
<td>Cream</td>
<td>Pale</td>
</tr>
<tr>
<td>Motility</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Optimal temperature for growth (°C)</td>
<td>60</td>
<td>50</td>
</tr>
<tr>
<td>Temperature range for growth (°C)</td>
<td>50–65</td>
<td>30–70</td>
</tr>
<tr>
<td>Assimilation substrates\textsuperscript{†}</td>
<td></td>
<td></td>
</tr>
<tr>
<td>L-Asparagine</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>L-Valine</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>L-Aspartate</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>L-Isoleucine</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>L-Leucine</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>L-Tryptophan</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>L-Lysine</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>L-Arginine</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>L-Threonine</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>L-Isoleucine</td>
<td>+</td>
<td>–</td>
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<tr>
<td>L-Serinine</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>L-Proline</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>D-Aspartate</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>L-Valine</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>L-Isoleucine</td>
<td>+</td>
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<td>L-Threonine</td>
<td>–</td>
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<tr>
<td>L-Serinine</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>L-Proline</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>DNA G+C content (mol%)</td>
<td>40.5</td>
<td>39–41</td>
</tr>
</tbody>
</table>

\textsuperscript{a}Data from present study.

\textsuperscript{†}Data from Scholz et al [2].

\textsuperscript{‡}by BIOLOG Phenotype Microarray plate PM1, PM2A, PM3B.

value was below the 70 % threshold value generally accepted for species delineation [23], hence supporting the distinct position of strain N.8\textsuperscript{T} within the genus Aeribacillus. The DNA G+C content of strain was 40.5 mol%, which is close to that reported for Aeribacillus pallidus DSM 3670\textsuperscript{T} [3].

The lipid extract of N.8\textsuperscript{T} was obtained using 1.26 g of freeze-dried cells harvested at the stationary growth phase after growth at 60 °C in TSB medium. Aeribacillus pallidus DSM 3670\textsuperscript{T} [1] was used for chemo-taxonomic comparison and was grown in TSB medium at 50 °C and collected at the stationary growth phase. Quinones were extracted from freeze-dried cells with n-hexane and were purified by TLC on silica gel (0.25 mm, F254, Merck) eluted with n-hexane/ethylacetate (96 : 4, v/v). The purified UV-band from TLC was then analysed by Liquid Chromatography/Mass Spectrometry (LC/MS) on a reversed-phase RP-18 Lichrospher column eluted with n-hexane/ethylacetate (99 : 1, v/v) with a flow rate of 1.0 ml min\textsuperscript{−1} and identified by Electrospray Ionization-Mass Spectrometry (ESI/MS) and \textsuperscript{1}H-NMR spectra [24, 25]. NMR spectra, recorded at the NMR Service of the Institute of Biomolecular Chemistry of CNR (Pozzuoli, Italy), were acquired on a Bruker DPX-300 operating at 300 MHz, using a dual probe. The residual cellular pellet, after n-hexane extraction of freeze-dried cells, was subjected to a further extraction with CHCl\textsubscript{3}/MeOH/H\textsubscript{2}O (65 : 25 : 4, by vol.) for polar lipid recovery. The polar lipid extract was analysed by TLC on silica gel (0.25 mm, F254, Merck) eluted in the first dimension with CHCl\textsubscript{3}/MeOH/H\textsubscript{2}O (65 : 25 : 4, by vol.) and in the second dimension with CHCl\textsubscript{3}/MeOH/acetic acid/H\textsubscript{2}O (80 : 12 : 15 : 4, by vol.). All polar lipids were detected by spraying the plates with 0.1 % (w/v) Ce(SO\textsubscript{4})\textsubscript{2}, in 1 M H\textsubscript{2}SO\textsubscript{4}, or with 3 % (w/v) methanolic solution of molybdophosphoric acid followed by heating at 100 °C for 5 min. Phospholipids and aminolipids were detected by spraying thin layer chromatographs with Dittmer-Lester and ninhydrin reagents, respectively, and glycolipids were visualized with α-naphthol [24, 25].

The total lipid contents of strain N.8\textsuperscript{T} and Aeribacillus pallidus DSM 3670\textsuperscript{T} were 19 and 17 % of the total dry weight of cells grown at 60 and 50 °C in TSB medium, respectively (when harvested at the stationary phase of growth). Chromatographic analysis of quinone revealed the presence of a UV-absorbing band. The \textsuperscript{1}H-NMR spectrum of strain N.8\textsuperscript{T} showed the presence of menaquinone (MK) signals that were similarly reported for Aeribacillus pallidus DSM 3670\textsuperscript{T}. The LC/MS analysis gave one molecular peak for respiratory quinones, which was identified as MK-7, as reported for Aeribacillus pallidus DSM 3670\textsuperscript{T}. Three major phospholipids were found in strain N.8\textsuperscript{T}: 1,2-DPPA, 1,2-Dipalmitoyl-sn-glycero-3-phosphate; PC(1,2,3)-dipalmitoyl-sn-glycerol-1-phosphocholine and DPG(1,3-sn-phosphatidyl)rac-glycerol. A similar phospholipid pattern was found for Aeribacillus pallidus DSM 3670\textsuperscript{T}. The bidimensional TLC analysis of strain N.8\textsuperscript{T} showed the presence of two unidentified glycolipids, an unidentified glycosphospholipid and an unidentified phospholipid (Fig. S3a–f).
Fatty acid methyl esters (FAMEs) of strain N.8\(^T\) and *Aeribacillus pallidus* DSM 3670\(^T\) were obtained from total lipids by acid methanolysis and analysed using a Hewlett Packard 5890A gas chromatograph fitted with a FID detector, as previously reported [24]. The FAME profile of N.8\(^T\) showed C\(_{16:0}\) (48.4 %), iso-C\(_{17:0}\) (19.4 %) and anteiso-C\(_{17:0}\) (14.6 %) to be major cellular fatty acids. The cellular fatty acids of strain N.8\(^T\) and *Aeribacillus pallidus* DSM 3670\(^T\) [1] are compared in Table S2. C\(_{16:0}\) was the common and the most abundant fatty acid in both strain N.8\(^T\) and in *Aeribacillus pallidus* DSM 3670\(^T\). Iso-C\(_{17:0}\) was found in both species, even though with a higher abundance in strain N.8\(^T\). Strain N.8\(^T\) did not demonstrate the presence of anteiso-C\(_{14:0}\), iso-C\(_{14:0}\), C\(_{14:0}\) and C\(_{15:0}\), all of which were found in *Aeribacillus pallidus* DSM 3670\(^T\).

On the basis of the physiological, biochemical and phylogenetic properties presented here, and considering that the DNA–DNA % relatedness values were below the 70 % threshold generally accepted for species delineation, strain N.8\(^T\) represents a novel species within the genus *Aeribacillus*, for which the name *Aeribacillus composti* sp. nov. is proposed.

**DESCRIPTION OF AERIBACILLUS COMPOSTI SP. NOV.**

*Aeribacillus composti*, (com.posti. N.L. gen. n. composti of compost).

Gram-stain-positive rods of size 0.5–0.6×1.5–5µm, obligately aerobic, chemoorganotroph, hetero-fermentative using sugars and amino acids for growth. Halo-alkaliphilic and moderately thermophilic, non-motile and endospore-forming. Colonies on solid medium are cream, smooth, circular and shiny and approximately 1 mm in diameter at 60°C after 24 h. Growth occurs at 50–65°C, pH 5.5–10.0 and with 2–9 % (w/v) NaCl present. Optimum conditions for growth are 60°C, pH 9.0, with 6 % NaCl (w/w; on TSB medium). Catalase- and oxidase-positive, but negative for urease and indole formation. Does not reduce nitrate and nitrite. Hydrolyses L-tyrosine and hippurate, but not xylan, CMG, starch, casein, gelatine, phenylalanine and urea. Positive for aminopeptidase tests. Negative result in the Voges–Proskauer reaction. It was able to utilise D-L-arabinose, D-sorbitol, trehalose, glycerol, L-fucose, D-ribose, suc- cinic acid, fumaric acid, L-rihamnose, D-xylene, pyruvic acid, L-lactic acid, D-mannose, maltose, D-mannitol, maltotriose, sucrose, xylitol, D-glucose, 2-deoxy-D-ribose as sole carbon sources. It was able to utilise L-alanine, L-arginine, L-asparagine, L-aspartic acid, L-glutamic acid, L-glutamine, glycine, L-histidine, L-isoleucine, L-leucine, L-lysine, L-methionine, L-phenylalanine, L-threonine, L-tryptophan, L-serine, L-tyrosine, L-valine, hydroxyl-L-proline, L-ornithine, L-arginine and L-serine as the sole nitrogen source. It produces acid from D-glucose, but no gas. Major fatty acids are C\(_{16:0}\), iso-C\(_{17:0}\) and anteiso-C\(_{17:0}\). The menaquinone is MK-7; polar lipids are 1,2-DPPA 1,2-dipalmitoyl-sn-glycero-3-phosphatidylrac-glycerol, two unidentified glycolipids, an unidentified glycosphospholipid and an unidentified phospholipid.

The type strain, N.8\(^T\) (=KCTC 33824\(^T\)=JCM 31580\(^T\)), was isolated from a pomace compost sample from an olive mill. The DNA C+G content of the type strain is 40.5 mol%.

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**Conflicts of interest**

The authors declare that there are no conflicts of interest.

**References**


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