Chryseobacterium aahli sp. nov., isolated from lake trout (Salvelinus namaycush) and brown trout (Salmo trutta), and emended descriptions of Chryseobacterium ginsenosidimutans and Chryseobacterium gregarium

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Two strains (T68ᵀ and T62) of a Gram-reaction-negative, yellow-pigmented bacterium containing flexirubin-type pigments were recovered from the kidney of a cultured lake trout (Salvelinus namaycush) and necrotic fins of a brown trout (Salmo trutta) during disease surveillance in 2009. Both isolates possessed catalase and cytochrome oxidase activities and degraded multiple substrates (e.g. gelatin, casein, elastin and Tweens 20 and 80). The mean DNA G+C content of strain T68ᵀ was 34.1 mol%. 16S rRNA gene sequencing demonstrated that strains T68ᵀ and T62 had nearly identical sequences (>99% similarity) and placed the bacterium within the genus Chryseobacterium, where Chryseobacterium ginsenosidimutans THG 15ᵀ (97.8%), C. gregarium DSM 19109ᵀ (97.7%) and C. soldanellicola PSD1-4ᵀ (97.6%) were its closest relatives. Subsequent phylogenetic analyses using neighbour-joining, maximum-parsimony and Bayesian methodologies demonstrated that strains T68ᵀ and T62 formed a well-supported clade (bootstrap values of 100 and 97%; posterior probability 0.99) that was distinct from other species of the genus Chryseobacterium. The major fatty acids of strains T68ᵀ and T62 were characteristic of the genus Chryseobacterium and included iso-C₁₅ : 0, summed feature 3 (C₁₆ : 1ω6c and/or C₁₆ : 1ω7c), iso-C₁₇ : 0 3-oh, C₁₆ : 0 and C₁₆ : 0 3-oh. The mean DNA–DNA relatedness of strain T68ᵀ to C. ginsenosidimutans JCM 16719ᵀ and C. gregarium LMG 24952ᵀ was 24 and 21%, respectively. Based on the results from our polyphasic characterization, strains T68ᵀ and T62 represent a novel species of the genus Chryseobacterium, for which the name Chryseobacterium aahli sp. nov. is proposed. The type strain is T68ᵀ (≡LMG 27338ᵀ ≡ATCC BAA-2540ᵀ). Emended descriptions of Chryseobacterium ginsenosidimutans and Chryseobacterium gregarium are also proposed.

Members of the family Flavobacteriaceae (Reichenbach, 1992; Bernardet et al., 1996) occupy an extremely wide range of ecological niches (reviewed by Bernardet & Nakagawa, 2006) and can be associated with disease in invertebrates (Li et al., 2010), amphibians (Xie et al., 2009), reptiles (Hernandez-Divers et al., 2009), birds (Segers et al., 1993) and mammals (Haburjak & Schubert, 1997), including humans (Benedetti et al., 2011). In fish, serious diseases are caused by many species within the family Flavobacteriaceae, such as species of the genera Flavobacterium (Shotts & Starliper, 1999; Starliper, 2011), Tenacibaculum (Suzuki et al., 2001) and Chryseobacterium (Mudarris & Austin, 1989); the latter are an emerging problem across several continents (Bernardet et al., 2005). Since its original description by Vandamme et al. (1994), the genus Chryseobacterium has expanded rapidly to encompass more than 65 species (Bernardet et al., 2011), and emended descriptions have been proposed (Kämpfer et al., 2009; Wu et al., 2013). Concurrent with this rapid expansion are descriptions of numerous fish-associated species of the genus Chryseobacterium, such as Chryseobacterium piscium (de Beer et al., 2006), C. piscicola (Iardi et al., 2009), C. chaponense (Kämpfer et al., 2011), C. viscerum (Zamora et al., 2012a), C. oncorhynchi (Zamora et al., 2012b) and C.

Abbreviations: MP, maximum-parsimony; NJ, neighbour-joining.
The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain T68ᵀ is JX287893.

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tructae (Zamora et al., 2012c). In fish, species of the genus Chryseobacterium are associated with skin and muscle ulcerations (Bernardet et al., 2005; Iardi et al., 2010; Kämpfer et al., 2011), gill haemorrhage and hyperplasia (Mudarris & Austin, 1989; Mudarris et al., 1994) and general signs of septicaemia (Mudarris & Austin, 1989; Mudarris et al., 1994; Bernardet et al., 2005). Herein, we describe a novel fish-associated member of the genus Chryseobacterium recovered from diseased salmonids in Michigan that is genotypically and phenotypically distinct from all other described species of the genus.

Strain T62 was recovered from necrotic fins of a hatchery-reared yearling brown trout (Salmo trutta; Harrietta State Fish Hatchery, Wexford County, MI, USA) and strain T68T was isolated from the kidney of a systemically infected yearling lake trout (Salvelinus namaycush; Marquette State Fish Hatchery, Marquette County, MI, USA). Tissues from affected organs were collected using sterile 1 µl disposable loops (Sigma), inoculated directly onto Hsu–Shotts medium (HSM; Bullock et al., 1986) and incubated at 22 °C for 72 h, after which <60 c.f.u. from the fin culture and 2 c.f.u. from the kidney culture were observed. The semi-translucent colonies were golden yellow, 1.0–1.5 mm in diameter and low-convex with entire margins. Both isolates were then subcultured onto HSM for purity and incubated for 24–48 h at 22 °C for initial morphological and phenotypic characterization. All reagents were purchased from Remel unless noted otherwise. Cells of both isolates were Gram-reaction-negative rods (1.5–2.0 µm long) that had cytochrome oxidase (Pathotec test strips) and catalase (using 3 % H2O2) activities, contained flexirubin-type pigments (using 3 % KOH) and did not have cell-wall-associated galactosamine glycans (0.01 % Congo red solution; Bernardet et al., 2002). Both isolates were non-motile in sulfur-indole-motility (SIM) deeps and did not glide under a light microscope according to the hanging-drop technique as described by Bernardet et al. (2002). Isolates were cryopreserved at −80 °C in Hsu–Shotts broth supplemented with 20 % glycerol.

In order to determine the taxonomic position of the two bacterial strains, a polyphasic characterization was performed. Bacterial colonies from pure 48 h cultures on HSM were harvested and genomic DNA was extracted using a Qiangen DNeasy tissue kit according to the manufacturer’s protocol for Gram-negative bacteria. Quantification of extracted DNA was performed using the Quant-iT DS DNA assay kit in conjunction with a Qubit fluorometer (Invitrogen). Amplification of the nearly complete 16S rRNA gene was conducted by PCR using the universal primers 8F and 1492R (Sacchi et al., 2002) as described previously (Loch & Faisal, 2014). Amplicon purification was conducted as described by Loch et al. (2011) and gene sequencing was carried out at the Genomics Technology Support Facility of Michigan State University using the following primers: 8F, 1492R (Sacchi et al., 2002), 518F (5′-TACCAGGTTATCTATCC-3′), 800R (5′-CAAGCAGGCGCGGTATATTG-3′) and 1205F (5′-AATCATCAGGGCTTACGC-3′). Contigs were assembled in the BioEdit sequence alignment editor (Hall, 1999) using the contig assembly program (CAP). Generated sequences (1380–1417 bp) were initially analysed using the BLASTN software from the NCBI to assess similarity with other bacterial sequences contained within the NCBI nucleotide database. Sequences for members of all formally described species of the genus Chryseobacterium, as well as for Elizabethkingia miricola ATCC 862T, Elizabethkingia meningoseptica ATCC 13253T and Empedobacter brevis LMG 4011T (used as an outgroup), were downloaded from NCBI and the EzTaxon-e database (Kim et al., 2012) and subsequently aligned with the sequences of strains T68T and T62. Neighbour-joining (NJ) analysis was then performed (Saitou & Nei, 1987) using the MEGA software (version 5.0), with evolutionary distances being calculated using the maximum composite likelihood method (Tamura et al., 2004). The robustness of the topology was evaluated by bootstrap analysis based upon 1000 resamplings of the sequences. In order to confirm the phylogenetic validity of the initial NJ analysis, sequences of strains T68T and T62 and the 13 most closely related members of the genus Chryseobacterium, along with members of the genus Chryseobacterium recovered from fish/fish products, the type species (Chryseobacterium gleum) and members of the genera Elizabethkingia and Empedobacter (used as an outgroup), were aligned as described previously and further analysed using Bayesian and maximum-parsimony (MP) analyses. Bayesian analysis was conducted in MrBayes 3.1.2 (Ronquist & Huelsenbeck, 2003) and MP analysis in PAUP 4.0 (Swofford, 2001) as described by Loch & Faisal (2014). Results from Bayesian and MP analyses were visualized in FigTree version 1.3.1 (Rambaut, 2009).

The sequences of strains T68T and T62 were nearly identical (≥99 %) across 1380 bp of the sequenced portion of the 16S rRNA gene. Initial searches using BLASTN demonstrated that strains T68T and T62 were members of the genus Chryseobacterium and that strain T68T was most closely related to C. ginsenosidimutans THG 15T (97.8 % 16S rRNA gene sequence similarity), C. gregarium DSM 19109T (97.7 %), C. soldanellicola PSD1-4T (97.6 %), C. gambrini 5-1St1aT (97.5 %), C. delfluvii B2T (97.4 %), C. piperi CTM1 (97.3 %), C. indolthenticum LMG 4025T (97.2 %), C. wyanjuense R2A10-2T (97.1 %) and C. soli JS6-6T (97.1 %), and its sequence was 94.0 % similar to that of the type strain of the type species of the genus Chryseobacterium, C. gleum ATCC 35910T. Similarities were <97 % for sequences of all other recognized species of the genus Chryseobacterium within the NCBI database. Interestingly, the most similar sequences of strains of the genus Chryseobacterium recovered from diseased fish by Bernardet et al. (2005) were those of Chryseobacterium sp. JIP 13/00 (2) (97.4 %) and Chryseobacterium sp. FRGDSA 4580/97 (96.8 %) (data not shown), which were recovered from muscle lesions of neon tetras (Paracheirodon innesi) and Siberian sturgeon (Acipenser baeri) fry, respectively. NJ, MP and Bayesian phylogenetic analyses yielded similar topologies (as indicated by filled circles when a node was present in all three trees Fig. 1) and demonstrated that
strains T68<sup>T</sup> and T62 formed a robustly supported clade (bootstrap values of 100 and 97%; posterior probability 0.89) that was distinct from all other members of the genus *Chryseobacterium*.

Further morphological, physiological and biochemical characterization was performed as recommended by Bernardet *et al.* (2002) for strains T68<sup>T</sup> and T62, *C. ginsenosidimutans* JCM 16719<sup>T</sup> and *C. gregarium* LMG 24952<sup>T</sup> and included the following: colony morphology on cytophaga agar (CA; Anacker & Ordal, 1955), growth on cetrimide and nutrient agars (Sigma), marine agar (Becton Dickinson Microbiology Systems), trypticase soy agar (TSA), TSA supplemented with 5% sheep erythrocytes (sheep-blood agar; SBA) and MacConkey agar; growth on HSM at pH 6.0–8.0 (in increments of 0.5 pH units, adjusted using 1 M HCl and 1 M NaOH); growth at 4, 15, 22, 37 and 42 °C; growth on HSM supplemented with 0–5.0% (w/v) NaCl (in 1% increments); production of acid/gas from glucose (1% final concentration, phenol red broth base); hydrolysis of aesculin (bile aesculin agar); production of indole and/or hydrogen sulfide on SIM medium; degradation of haemoglobin (0.1%, w/v), casein (5%, w/v) and elastin (0.5%, w/v) as modified from Shotts *et al.* (1985) using HSM as the basal medium; activities of gelatinase (Whitman, 2004) and amylase [modified from Lin *et al.* (1988), using HSM as basal medium]; degradation of L-tyrosine and brown pigment production from L-tyrosine (0.5%, w/v) [modified from Pacha & Porter (1968), using HSM as basal medium];
and degradation of agar on TSA. When HSM was used as the basal medium in morphological, physiological and biochemical assays, no gelatin or neomycin was added. Commercially available identification galleries (API 20E, API 20NE, API ZYM and API 50CH; bioMérieux) were inoculated according to the manufacturer’s protocol with the following modification: tests were incubated at 22 °C and were read from 24 h after inoculation up until 7 days with the exception of the API ZYM gallery, which was read at 72 h. The morphological, physiological and biochemical characteristics of strains T68T and T62 are presented in the species description, while those characters that distinguish them from Chryseobacterium JCM 16719T and C. gregarium LMG 24952T are listed in Table 1.

For fatty acid profiling, strain T68T, C. ginsenosidimutans JCM 16719T and C. gregarium LMG 24952T were cultured on a medium containing 30 g tryptcase soy broth and 15 g Bacto agar (Difco) per litre distilled water for 24 h at 28 °C. Bacterial cells were then harvested according to Sassser (1990) to ensure that age standardization was accounted for and then saponified, methylated to fatty acid methyl esters and extracted according to the standard procedure of the Sherlock Microbial Identification System (MIDI, version 4.0). Separation of fatty acid methyl esters was conducted by GC on an Agilent 6890A series instrument (Agilent Technologies). The carrier gas was H2 and peak identification/integration was performed using the Agilent Chemstation and MIDI software (Agilent Technologies) and the Microbial Identification System database (Sasser, 1990). The major fatty acid constituents of strain T68T were iso-C15:0 (30.5%), summed feature 3 (C16:1ω6c and/or C16:1ω7c; 27.0%), iso-C17:0 3-OH (15.8%), C16:0 (7.0%) and C16:0 3-OH (5.2%); smaller amounts of other fatty acids were also present (Table 2). The predominant fatty acids typical of the genus Chryseobacterium are iso-C15:0, iso-C17:1ω9c, iso-C17:0 3-OH and summed feature 4 (iso-C15:0 2-OH and/or C16:1ω7c) (Bernardet et al., 2011). Strain T68T was quite distinct from C. ginsenosidimutans JCM 16719T and C. gregarium LMG 24952T in that it had much higher percentages of summed feature 3 (C16:1ω6c and/or C16:1ω7c), C16:0 and C16:0 3-OH and also had a lower percentage of iso-C17:1ω9c (Table 2). Interestingly, strain T68T even contained a higher percentage of summed feature 3 than is typical of members of the genus Elizabethkingia (17.0–19.6%; Kim et al., 2005).

For DNA–DNA hybridization experiments and DNA G+C content determination, total DNA from strain T68T, C. ginsenosidimutans JCM 16719T and C. gregarium LMG 24952T was isolated according to Wilson (1987) as modified by Cleenwerck et al. (2002). The mean DNA G+C content of strain T68T, as determined by three independent analyses using the methods of Mesbah et al. (1989), was 34.1 mol%, and in accordance with those of members of the genus Chryseobacterium (Bernardet et al., 2011). Hybridizations were carried out in 50% formamide at 35 °C (Goris et al., 1998; Cleenwerck et al., 2002) as modified from Ezaki et al. (1989). Reciprocal reactions

Table 1. Biochemical and physiological characteristics of strains T68T and T62 that were distinct from their two closest relatives in the genus Chryseobacterium

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
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<tbody>
<tr>
<td>Growth on HSM suplemented</td>
<td>w</td>
<td>w</td>
<td>w</td>
<td>[−]</td>
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<tr>
<td>with 2% NaCl</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Starch hydrolysis</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Enzyme activity (API strips)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Arginine dihydrolase</td>
<td>−</td>
<td>−</td>
<td>w</td>
<td>−</td>
</tr>
<tr>
<td>Esterase</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Cystine arylamidase</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>α-Chymotrypsin</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Acid production from (API 50CH):</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Arbutin</td>
<td>−</td>
<td>−</td>
<td>w</td>
<td>w</td>
</tr>
<tr>
<td>Maltose</td>
<td>−</td>
<td>−</td>
<td>w</td>
<td>w</td>
</tr>
</tbody>
</table>

Table 2. Cellular fatty acid profiles of strain T68T and the two most closely related members of the genus Chryseobacterium

<table>
<thead>
<tr>
<th>Fatty acid</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>iso-C13:0</td>
<td>TR</td>
<td>1.9</td>
<td>1.1</td>
</tr>
<tr>
<td>iso-C15:0</td>
<td>30.5</td>
<td>45.1</td>
<td>32.2</td>
</tr>
<tr>
<td>anteiso-C15:0</td>
<td>2.7</td>
<td>2.5</td>
<td>9.2</td>
</tr>
<tr>
<td>Summed feature 3</td>
<td>27.0</td>
<td>8.5</td>
<td>10.5</td>
</tr>
<tr>
<td>C16:1ω5c</td>
<td>1.6</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>C16:0</td>
<td>7.0</td>
<td>2.0</td>
<td>1.6</td>
</tr>
<tr>
<td>iso-C15:0 3-OH</td>
<td>2.4</td>
<td>3.2</td>
<td>2.5</td>
</tr>
<tr>
<td>iso-C17:1ω9c</td>
<td>1.5</td>
<td>5.8</td>
<td>18.5</td>
</tr>
<tr>
<td>iso-C17:0</td>
<td>TR</td>
<td>3.8</td>
<td>TR</td>
</tr>
<tr>
<td>C16:0 3-OH</td>
<td>5.2</td>
<td>1.0</td>
<td>1.5</td>
</tr>
<tr>
<td>iso-C17:0 3-OH</td>
<td>15.8</td>
<td>23.5</td>
<td>15.7</td>
</tr>
<tr>
<td>C17:0 2-OH</td>
<td>1.8</td>
<td>TR</td>
<td>4.0</td>
</tr>
</tbody>
</table>

*As indicated by Montero-Calasanz et al. (2013), summed features are groups of two or three fatty acids that are treated together for the purpose of evaluation in the MIDI System and include both peaks with discrete equivalent chain-lengths (ECLs) as well as those where the ECLs are not reported separately. Summed feature 3 was listed as C16:1ω6c and/or C16:1ω7c.
were performed and the percentage of DNA–DNA relatedness is reported as the mean of a minimum of six hybridizations. The mean DNA–DNA relatedness of strain T68T to C. ginsenosidimutans JCM 16719T and C. gregarium LMG 24952T was 24.0 and 21 %, respectively; these values are far below the threshold of 70 % that is generally used to delineate genomic species (Wayne et al., 1987).

The results of the polyphasic characterization conducted in this study demonstrate that the two new isolates recovered from salmonids in Michigan indeed represent a novel species of the genus Chryseobacterium, for which the name Chryseobacterium aahli sp. nov. is proposed. Pathogenicity studies with strain T68T have demonstrated previously that it is facultatively pathogenic to multiple Great Lakes salmonid species (Loch, 2012). Emended descriptions of Chryseobacterium ginsenosidimutans and Chryseobacterium gregarium are also proposed on the basis of new data obtained in this study.

**Emended description of Chryseobacterium ginsenosidimutans Im et al. 2011**

The description is as given by Im et al. (2011) with the following additions. Does not grow on marine agar, but does grow on HSM, CA and SBA. Does not produce gas from glucose. Degrades haemoglobin and elastin, produces a brown pigment in the presence of tyrosine (in the absence of tyrosine degradation) and degrades Tweens 20 and 80 and does not produce H2S or acetoin or produce acid from glucose, mannitol, inositol, sorbitol, rhamnose, melibiose or arabinose. Produces acid weakly from amygdalin. In contrast to the original description of Im et al. (2011), grows weakly at 4°C but not at 37°C on HSM and grows weakly on HSM supplemented with 2 % NaCl.

**Emended description of Chryseobacterium gregarium Behrendt et al. 2008**

The description is as given by Behrendt et al. (2008) with the following additions. Does not absorb Congo red or grow on marine agar, but does grow on HSM, CA and SBA. Can grow on HSM supplemented with up to 1 % NaCl, but not higher concentrations, and is able to degrade haemoglobin, elastin and Tween 20.

**Description of Chryseobacterium aahli sp. nov.**

Chryseobacterium aahli (aah’li. N.L. arbitrary gen. n. aahli of Aahl1, in honour of the Aquatic Animal Health Laboratory of Michigan State University, where the first strains were characterized).

Cells are non-motile, non-gliding, Gram-reaction-negative rods (1.5–2.0 μm long) that do not contain cell-wall-associated galactosamine glycans (i.e. do not absorb Congo red). On CA, colonies are semi-translucent, golden yellow due to the presence of flexirubin-type pigments, circular (1.0–1.5 mm in diameter) and low-convex with entire margins. Growth occurs on nutrient agar, TSA, HSM, CA and SBA, but not on marine agar, MacConkey agar or cetrimide agar at 22°C. Grows well at pH 6.0–8.0 and at 4, 15 and 22°C, but not at 37 or 42°C. Growth occurs on HSM supplemented with 0–2 % (w/v) NaCl (weakly with 2 % NaCl), but not on HSM supplemented with 3–5 % NaCl. Does not produce indole or acid from glucose in phenol red broth (1 % final carbohydrate solution). Produces catalase, cytochrome oxidase, gelatinase, caseinase and elastase, but not amylase. Able to lyse haemoglobin and hydrolyse aesculin and Tweens 20 and 80, but unable to degrade agar and L-tyrosine. Yields a brown pigment from tyrosine. On the API 20E gallery, negative for activities of β-galactosidase, arginine dihydrolase, lysine and ornithine decarboxylases, tryptophan deaminase and does not produce H2S, indole or acetoin or produce acid from glucose, mannitol, inositol, sorbitol, rhamnose, melibiose, amygdalin or arabinose. Able to utilize citrate and degrade gelatin but does not reduce nitrate to nitrite or nitrogen gas. On the API 20NE gallery, does not reduce nitrate, produce indole, urease or arginine dihydrolase, ferment glucose or utilize p-nitrophenyl β-D-galactopyranoside, but does hydrolyse gelatin and aesculin. Unable to assimilate D-mannitol, N-acetylglucosamine, maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate or phenylacetic acid. Very weak assimilation of D-glucose, L-arabinose and D-mannose. On the API ZYM gallery, positive for activities of alkaline phosphatase, esterase, esterase lipase, leucine arylamidase, valine arylamidase, cystine arylamidase, ε-chymotrypsin, acid phosphatase, naphthol-AS-BI-phosphohydrolase, β-glucosidase and N-acetyl-β-glucosaminidase, but negative for lipase, β-galactosidase, β-glucuronidase, α-mannosidase and α-fucosidase. Variable for activities of trypsin and α-glucosidase (strain T68T positive, strain T62 very weakly positive for both). On the API 50CH gallery (using CHB/E medium), does not produce acid from glycerol, erythritol, 1, 3- or L-arabinose, D- or L-ribose, D- or L-xylene, D-adonitol, methyl β-D-xylopyranoside, D-galactose, L-sorbose, dulcitol, inositol, D-mannitol, D-sorbitol, methyl α-D-mannopyranoside, methyl α-D-glucopyranoside, N-acetylglucosamine, arbutin, cellobiose, maltose, lactose, melibiose, inulin, melezitose, raffinose, starch, glycerogen, xylitol, turanose, D-lyxose, D-tagatose, D- or L-fucose, D- or L-arabitol, potassium gluconate, potassium 2-ketogluconate or potassium 5-ketogluconate. Acid is produced from ascorbin. Very weak acid production from D-glucose, trehalose and gentiobiose; acid production from sucrose is variable (strain T68T weakly positive, strain T62 negative). One of the known two strains gives a very weakly positive result for acid production from D-fructose (T68T), D-mannose (T62), L-rhamnose (T68T), amygdalin (T62) and salicin (T62). The fatty acid profile is comprised primarily of iso-C15:0 summed feature 3 (C16:1ω6c and/or C16:1ω7c), iso-C17:0 3-OH, C16:0 and C16:1ω9c.
The type strain is T68\(^T\) (=LMG 27338\(^T\)=ATCC BAA-2540\(^T\)), isolated from the kidney of a yearling lake trout (Salvelinus namaycush). An additional strain is T62, isolated from the fins of a hatchery-reared brown trout (Salmo trutta). The mean DNA G+C content of the type strain is 34.1 mol%.

Acknowledgements

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