Labrys wisconsinensis sp. nov., a budding bacterium isolated from Lake Michigan water, and emended description of the genus Labrys

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Two facultatively anaerobic, budding bacterial strains, designated W1215-PCA4T and SRNK-1, were isolated from water from Lake Michigan, USA. The two strains showed identical ERIC-PCR-generated genomic fingerprints and shared 99.9 % 16S rRNA gene sequence similarity. Strain W1215-PCA4T showed highest 16S rRNA gene sequence similarities to Labrys monachus VKM B-1479T (95.8 %), Labrys methylaminophilus DSM 16812T (95.1 %), Labrys okinawensis MAFF 210191T (96.0 %), Labrys miyagienis G24103T (95.4 %), Labrys neptuniae BCRC 17578T (95.7 %) and Labrys portucalensis DSM 17916T (95.8 %). Data suggested that the two strains were members of a single novel species of the genus Labrys. The major cellular fatty acids of the two isolates were C18 : 1v7c, C19 : 0cyclov8c and C16 : 0. Their polar lipid profiles were highly similar to that of Labrys monachus DSM 5896T. The primary quinone was ubiquinone Q-10, with minor amounts of Q-9 and Q-11. sym-Homospermidine was the predominant polyamine, with putrescine present in moderate amounts. The two strains were identical in terms of their biochemical and physiological traits, but were distinguishable from other species of the genus Labrys. Hence, the description of a novel species in this genus appears to be justified. The name Labrys wisconsinensis sp. nov. is proposed; the type strain is W1215-PCA4T (=DSM 19619T =NRRL B-51088T).

The microbial diversity of freshwater environments is distinct and, based upon culture-independent techniques, the members of the communities are primarily affiliated with the Alphaproteobacteria, Betaproteobacteria, Actinobacteria, Bacteroidetes, Cyanobacteria, Verrucomicrobia, OP-10 and Planctomycetes (Zwart et al., 2002). Typically, Betaproteobacteria are the most common, but Actinobacteria and Bacteroidetes can be almost as common (Cottrell et al., 2005; Van der Gucht et al., 2005; Allgaier & Grossart, 2006 Newton et al., 2006; Schauer et al., 2005; Eiler & Bertilsson, 2004).

The five lakes, collectively known as the Great Lakes, found in the upper midwest of the USA, comprise the largest amount of surface freshwater in the world. One of those lakes, Lake Michigan, which is the second largest Great Lake, contains nearly 4900 km³ of freshwater. Lake Michigan serves as a source of potable water for over 7 million people.

Very little is known about the Lake Michigan microbial community; to our knowledge, there is only one published study characterizing this community. This study reported that members of the Betaproteobacteria were predominant, followed by Bacteroidetes and Alphaproteobacteria (Mueller-Spitz et al., 2009). Characterization of the members of the microbial community found in Lake Michigan potable water has, to our knowledge, not been reported. Other sources of potable water have been found to be composed of a bacterial community dominated by members of the Alphaproteobacteria and Betaproteobacteria (Santo Domingo et al., 2003; Williams et al., 2004).

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequences of strains W1215-PCA4T and SRNK-1 are EF382666 and FJ707292, respectively.

Micrographs of cells of strain W1215-PCA4T are available as supplementary figures with the online version of this paper.
During a taxonomic investigation of the bacterial population in samples of Lake Michigan water that were collected on August 14, 2006, and June 25, 2007, from the Port Washington community water system, Wisconsin, USA, two strains, designated W1215-PCA4T and SRNK-1, were isolated. Based upon 16S rRNA gene sequencing, both strains appeared to be novel species of the genus Labrys. The genus Labrys currently contains six recognized species of budding bacteria, including Labrys monachus (Vasil’eva & Semenov, 1984), Labrys methylaminophilus (Miller et al., 2005), Labrys okinawensis (Islam et al., 2007), Labrys miyagienesis (Islam et al., 2007), Labrys neptuniae (Chou et al., 2007) and Labrys portucalensis (Carvalho et al., 2008), all of which were isolated from a variety of soil and sediment samples.

In this paper, the isolation and characterization of strains W1215-PCA4T and SRNK-1 are reported. Samples were plated onto plate count agar (PCA; Difco) and incubated at 32 °C for 5 days. Cultures were purified by subculturting and stored at ~80 °C in growth medium supplemented with 20% glycerol. L. monachus DSM 5896T, obtained from the DSMZ, was used as a reference strain.

The isolation of DNA and generation of PCR products for 16S rRNA gene sequence analysis were performed using the MicroSeq full gene protocol. DNA sequence data were analysed and assembled with Auto Assembler software (Applied Biosystems) (Albert et al., 2005). Strains W1215-PCA4T and SRNK-1 shared 99.9% 16S rRNA gene sequence similarity. The suggested relationship between the two strains at the species level was confirmed by ERIC-PCR analysis of strains. Lanes: 1, negative control; M, 100 bp ladder; 2, SRNK-1; 3, W1215-PCA4T; 4, Labrys monachus DSM 5896T.

Fig. 1. ERIC-PCR analysis of strains. Lanes: 1, negative control; M, 100 bp ladder; 2, SRNK-1; 3, W1215-PCA4T; 4, Labrys monachus DSM 5896T.

The phylogenetic relationships between strain W1215-PCA4T and related strains, including members of the genus Labrys, are shown in Fig. 2. The tree was reconstructed by using the maximum-likelihood algorithm (calculation parameters are reported in the legend to Fig. 2). Examination of the phylogenetic tree indicated that W1215-PCA4T comprised the deepest branch in the Labrys clade (Fig. 2), which was initially revealed by sequence similarities.

Phenotypic characterization of the two strains was accomplished by examination of physiological, biochemical and chemotaxonomic traits. The physiological and biochemical characteristics reported in Table 1 were carried out as follows. All tests were performed at 25 °C, except growth temperature range, using 24- to 48 h-old cultures grown on PCA (Difco). Inoculum for tests utilizing cell suspensions was prepared in phosphate-buffered water (Maturin & Peeler, 2001). Motility testing, catalase activity, oxidase testing and Gram staining were performed using standard procedures (Smibert & Krieg, 1994). Capsule staining was performed by using the method of Murray et al. (1994). Temperature growth range was determined by visual examination for growth on PCA plates. Prior to inoculation, plates were incubated at the test temperature for 24 h. After inoculation, plates were incubated for up to 7 days. The ability to utilize various carbohydrates as growth substrates and various nitrogen sources was evaluated according to Islam et al. (2007) with some modifications. Tubes containing 5 ml growth medium were incubated with shaking aeration for 7 days. Growth was compared visually with controls, which did not contain either a carbohydrate source or a nitrogen source. Anaerobic growth was determined by visually monitoring growth in tubes containing plate count broth (PCB; Difco) supplemented with 0.075% agar (Difco). Prior to inoculation, tubes containing 25 ml PCB were incubated under anaerobic conditions for 48 h. Anaerobic conditions were generated by using H2 and CO2 GasPaks (BBL) in anaerobe jars. Cell suspensions were used to inoculate tubes containing the test medium. After inoculation, the tubes were placed in the anaerobe jars and anaerobic conditions were regenerated using H2 and CO2 GasPaks. After 10 days, tubes were removed from the anaerobic condi-
tions and examined visually for growth. Turbidity was used to indicate growth. Samples from all tubes were streaked onto PCA to determine the identity of the bacterium present. Growth in various NaCl concentrations (w/w) was determined by inoculating tubes containing 5 ml PCB with NaCl concentrations of 0.0–1.5 %, in 0.1 % increments. After inoculation, the tubes were incubated with shaking aeration for up to 7 days. Appearance of turbidity was used to indicate growth. Samples from all tubes were streaked onto PCA to determine the identity of the bacterium present.

Results for the physiological and biochemical characterization performed as part of this study (reported in Table 1) showed that strains W1215-PCA4 T and SRNK-1 had both similarities and differences to other members of the genus Labrys. A significant difference was that both strains W1215-PCA4 T and SRNK-1 were able to grow anaerobically, whereas all recognized species of the genus Labrys have been reported to be obligate aerobes. Members of the genus Labrys reported to reduce nitrate are L. monachus, L. methylaminophilus and L. neptuniae (Miller et al., 2005; Chou et al., 2007). Strains W1215-PCA4 T and SRNK-1 were able to grow in a wider range of NaCl concentrations (0.0–1.2 %), whereas the NaCl range for growth of L. okinawensis MAFF 210191 T and L. miyagiensis G24103 T was 0.0–0.3 % NaCl.

The cellular fatty acid profile was determined by growing the strains on R2A (Difco) for 48 h at 25 °C. After growth, bacteria were saponified and the liberated fatty acids were methylated and analysed by capillary GLC (Hewlett Packard 6890) by the Sherlock system (MIDI 4.5), according to the manufacturer’s instructions. The cellular fatty acid profile of the two strains is reported in Table 2. Examination of the results indicated that three cellular fatty acids, C18 : 1 ω7 c, C 19 : 0 cyclo ω8 c and C16 : 0 comprised over found to be negative in this test. Even though this is the first report of members of the genus Labrys able to grow anaerobically, the ability to grow anaerobically is implied by the ability to reduce nitrate. Members of the genus Labrys reported to reduce nitrate are L. monachus, L. methylaminophilus and L. neptuniae (Miller et al., 2005; Chou et al., 2007). Strains W1215-PCA4 T and SRNK-1 were able to grow in a wider range of NaCl concentrations (0.0–1.2 %), whereas the NaCl range for growth of L. okinawensis MAFF 210191 T and L. miyagiensis G24103 T was 0.0–0.3 % NaCl.

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Table 1. Morphological and physiological characteristics that differentiate strains W1215-PCA4<sup>T</sup> and SRNK-1 from strains of related species

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
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<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
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<tbody>
<tr>
<td>Motility</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Temperature growth range (°C)</td>
<td>10-40</td>
<td>5-40</td>
<td>10-35</td>
<td>16-37</td>
<td>15-35</td>
<td>15-32</td>
<td>15-32</td>
</tr>
<tr>
<td>NaCl growth range (% w/w)</td>
<td>0.0-1.2</td>
<td>0.0-0.7</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>0.0-0.3</td>
<td>0.0-0.3</td>
</tr>
<tr>
<td>Capsule formation</td>
<td>+</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>ND</td>
</tr>
<tr>
<td>Anaerobic growth</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Oxidase</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
<td>ND</td>
</tr>
<tr>
<td>Catalase</td>
<td>(+)</td>
<td>(+)</td>
<td>+</td>
<td>+</td>
<td>(+)</td>
<td>(+)</td>
<td>(+)</td>
</tr>
</tbody>
</table>

Assimilation of carbon sources:
- D-Ribose: (+) + ND ND ND ND ND ND
- D-Xylose: (+) + ND ND ND + +
- Sucrose: (+) + + + ND + + +
- L-Arabinose: (+) + ND ND + + +
- Cellobiose: (+) + + ND ND ND + +
- Fructose: + + + ND + + +
- Lactose: - - - + ND ND ND

Nitrogen sources:
- L-Histidine: + + ND ND ND + +
- L-Leucine: (+) - ND ND ND - +
- L-Lysine: (+) + ND ND ND + +
- L-Valine: (+) (+) ND ND ND ND + +
- L-Isoleucine: (+) - ND ND ND - -
- L-Methionine: (+) - + ND ND + +
- L-Phenylalanine: (+) (+) + ND ND + +
- L-Threonine: - - + ND ND + +
- L-Aspartic acid: + - + ND ND + -

All taxa are positive for assimilation of D-glucose and D-mannitol and have short-rod-shaped cells.

85% total fatty acids, with C<sub>18:1</sub>ω7c comprising approximately 75% and the other two accounting for ~5% and ~10%, respectively. The same three cellular fatty acids accounted for approximately 80% of the cellular fatty acids in L. monachus DSM 5896<sup>T</sup>, although the relative amounts were different, with C<sub>18:1</sub>ω7c, C<sub>19:0</sub> cyclo ω8c and C<sub>16:0</sub> accounting for ~48%, ~30% and ~10%, respectively. Other studies have also reported that these fatty acids are the primary fatty acids for members of the genus Labrys. Differences in relative amounts of C<sub>18:1</sub>ω7c and C<sub>19:0</sub> cyclo ω8c cannot be considered to be of relevance for discrimination between species. It has been shown for several taxa that C<sub>19:0</sub> cyclo ω8c is synthesized from C<sub>18:1</sub>ω7c when cells are approaching the stationary growth phase (Auran & Schmidt, 1972; Martinez-Rodriguez & Mackey, 2005). There can be significant differences in the fatty acid profiles of members of the genus Labrys. For example, Miller et al. (2005) reported that L. monachus DSM 5896<sup>T</sup> contained 11.9% C<sub>20:1</sub>ω9, whereas this study and Islam et al. (2007) did not find this fatty acid. This study reported the presence of very low levels (~1%) of C<sub>16:0</sub> 2-OH and C<sub>18:1</sub> 2-<OH in L. monachus DSM 5896<sup>T</sup>, which have not been reported previously. This is probably because other authors did not report fatty acids at <1% of the total. In addition, differences in fatty acid profiles can be due to differences in growth conditions, including

Table 2. Cellular fatty acid profiles of strains W1215-PCA4<sup>T</sup>, SRNK-1 and Labrys monachus DSM 5896<sup>T</sup>

<table>
<thead>
<tr>
<th>Fatty acid</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>C&lt;sub&gt;14:0&lt;/sub&gt; 3-OH/16:1 iso 1</td>
<td>4.6</td>
<td>5.0</td>
<td>3.3</td>
</tr>
<tr>
<td>C&lt;sub&gt;16:1&lt;/sub&gt;ω7c/15 iso 2-OH</td>
<td>1.1</td>
<td>1.2</td>
<td>1.0</td>
</tr>
<tr>
<td>C&lt;sub&gt;16:0&lt;/sub&gt;</td>
<td>10.1</td>
<td>9.7</td>
<td>10.4</td>
</tr>
<tr>
<td>C&lt;sub&gt;16:0&lt;/sub&gt; 2-&lt;OH</td>
<td>ND</td>
<td>ND</td>
<td>0.3</td>
</tr>
<tr>
<td>C&lt;sub&gt;16:0&lt;/sub&gt; 3-OH</td>
<td>2.5</td>
<td>2.6</td>
<td>3.4</td>
</tr>
<tr>
<td>C&lt;sub&gt;18:1&lt;/sub&gt;ω7c</td>
<td>76.8</td>
<td>74.0</td>
<td>48.5</td>
</tr>
<tr>
<td>C&lt;sub&gt;18:0&lt;/sub&gt;</td>
<td>0.9</td>
<td>1.1</td>
<td>0.5</td>
</tr>
<tr>
<td>C&lt;sub&gt;19:0&lt;/sub&gt; cyclo ω8c</td>
<td>4.1</td>
<td>5.5</td>
<td>30.6</td>
</tr>
<tr>
<td>C&lt;sub&gt;18:1&lt;/sub&gt; 2-&lt;OH</td>
<td>0.2</td>
<td>0.3</td>
<td>0.9</td>
</tr>
</tbody>
</table>

Strains: 1, W1215-PCA4<sup>T</sup>; 2, SRNK-1; 3, L. monachus DSM 5896<sup>T</sup>. All data are from this study and results are the means of two runs. Strains were grown on R2A (Difco) at 25 °C for 48 h. ND, Not detected.
medium used, incubation time and temperature (Albert et al., 2007).

Polar lipids, quinones and polyamines were extracted from cells grown on PYE medium (0.3 % peptone from casein, 0.3 % yeast extract, pH 7.2) at 28 °C. Polar lipids and quinones were extracted and analysed as described previously (Tindall, 1990a, b; Altenburger et al., 1996). Polyamines were extracted and analysed as described by Busse & Auling (1988). HPLC analyses were carried out using the equipment described by Stolz et al. (2007). The polar lipid profiles of strains W1215-PCA4T and SRNK-1 were almost indistinguishable from each other and with one exception exhibited only quantitative differences (results not shown) from the profile of L. monachus DSM 5896T. The profile of L. monachus DSM 5896T (Fig. 3) consisted of the major compounds phosphatidylmonomethylethanolamine, phosphatidylmethylmethylethanolamine, diphasphatidylglycerol, phosphatidylglycerol, phosphatidylcholine and an unknown phospholipid (PL1, also staining positively with Dragendorff reagent, indicating the presence of a quaternary nitrogen in this lipid), moderate amounts of an unknown aminophospholipid (APL1), an unknown aminolipid (AL1), polar lipid (L2) and an unknown phosphoglycolipid (PGL1), and minor to trace amounts of two unknown aminolipids (AL2 and 3), an unknown phosphoglycolipid (PGL2) and an unknown polar lipid (L1). AL1 exhibited chromatographic behaviour that was similar to that of phosphatidylethanolamine, but it did not stain positively with molybdenum blue, which is characteristic of phosphatidylethanolamine.

Major differences in the polar lipid profiles of strains W1215-PCA4T and SRNK-1 compared to that of L. monachus DSM 5896T were the relative lower amounts of phosphatidylglycerol, phosphatidylmethylmethylethanolamine and PL1 and absence of unknown lipid L2. A polar lipid profile lacking phosphatidylethanolamine, but containing phosphatidylmethylmethylethanolamine as a major compound is rather rare among alphaproteobacteria and, to the best of our knowledge, a phospholipid exhibiting the chromatographic behaviour of PL1 is also rare among alphaproteobacteria that have been studied to date. Fritz et al. (2004) reported the presence of phosphatidyl acid, phosphatidylglycerol, phosphatidylmethylmethylethanolamine, phosphatidylcholine and an unknown type of phospholipid in L. monachus VKM B-1479T. Results from this study confirm the presence of phosphatidylglycerol, phosphatidylmethylmethylethanolamine and phosphatidylcholine in L. monachus DSM 5896T. However, this study did not detect a lipid that stained positive only for phosphate, which would be expected for phosphatidyl acid. The unknown phospholipid reported by Fritz et al. (2004) may correspond to any of the phosphate group-containing lipids shown in Fig. 3. However, based upon the results of this study, the polar lipid profile of species of the genus Labrys appears to be much more complex than that suggested by Fritz et al. (2004). The polar lipid profiles of the Labrys strains studied here appeared to be characteristic for the genus and supported the affiliation of strains W1215-PCA4T and SRNK-1 to the genus Labrys, although deeply branching on this lineage (Fig. 2). Strains W1215-PCA4T and SRNK-1 exhibited similar quinone systems consisting of ubiquinone Q-10 (96 and 95 %, respectively), Q-9 (3 and 4 %, respectively) and Q-11 (1 % each). The polyamine profiles of L. monachus DSM 5896T and strains W1215-PCA4T and SRNK-1 contained sym-homospermidine [86.7, 41.8 and 80.4 μmol (g dry weight)\(^{-1}\), respectively] as the major compound, moderate amounts of putrescine [5.5, 17.6 and 5.9 μmol (g dry weight)\(^{-1}\), respectively], and low amounts of spermidine [1.9, 3.5 and 2.7 μmol (g dry weight)\(^{-1}\), respectively] and spermine [0.1, 0.7 and 1.0 μmol (g dry weight)\(^{-1}\), respectively]. Similar polyamine profiles have been reported for numerous members of the class Alphaproteobacteria (Busse & Auling, 1988; Hamana & Takeuchi, 1998; Hamana et al., 2003, 2006).

On the basis of almost identical 16S rRNA gene sequences, identical physiological and biochemical traits and identical genomic fingerprints, the two new strains can be considered to be representatives of a single species. The phylogenetic position and distinctive polar lipid profile, which was qualitatively identical to that of L. monachus DSM 5896T, suggested the assignment of the novel species to the genus Labrys. In contrast, the ability to grow anaerobically is unique among species of the genus Labrys and could be considered as a key characteristic of a novel separate genus. However, since additional strains and species more related to strains W1215-PCA4T and SRNK-1
and that share the ability to grow anaerobically are not available, the proposal of a novel genus at this time is premature. Hence, a novel species of the genus *Labrys* is described to accommodate strains W1215-PCA4T and SRNK-1, which can be distinguished from other species of the genus by low 16S rRNA gene sequence similarities and distinct physiological traits. The name *Labrys wisconsinensis* sp. nov. is proposed for the novel species.

**Emended description of the genus *Labrys***

The characteristics of the genus are those described by Vasil’eva & Semenov (1984) and Islam et al. (2007). However, members are aerobes or facultative anaerobes. The primary polar lipids are diphosphatidylglycerol, phosphatidylmonomethylethanolamine and phosphatidylcholine. The major polyamine is sym-homospermidine.

**Description of *Labrys wisconsinensis* sp. nov.**

*Labrys wisconsinensis* (wis.con.si.nen’sis. N.L. masc. adj. *wisconsinensis* referring to Wisconsin, the state in the USA where the bacterium was isolated).

Cells are rod-shaped, 2.0–3.0 μm in length and 1.0–1.5 μm wide, and occur singly or in pairs and produce capsules (see Supplementary Fig. S1 in IJSEM Online). Cells stain Gram-negative. Isolated colonies on PCA after 48 h incubation are 1–2 mm in diameter. Colonies are circular, semi-translucent and entire with a viscous consistency. Cells produce large amounts of extracellular slime. Growth is observed at 10–40 °C and in 0.0–1.2 % (w/w) NaCl. Facultatively anaerobic and positive for catalase (weakly) and oxidase. Other physiological and biochemical characteristics are listed in Table 1. The primary cellular fatty acids are C18:1iso7c, C16:0 and C19:0 cyclo ω8c. The polar lipid profile consists of the major compounds phosphatidylmonomethylethanolamine, phosphatidylglycerol, diphosphatidylglycerol and phosphatidylcholine, and moderate amounts of phosphatidylglycerol, an unidentified phosphoglycolipid, an unidentified polar lipid, an unidentified phospholipid and three unknown aminophospholipids. Other lipids are present in trace amounts. The major quinone is ubiquinone Q-10, with minor amounts of Q-9 and Q-11. The major polyamine is sym-homospermidine, with moderate amounts of putrescine.

The type strain, W1215-PCA4T (=DSM 19619T=NRRL B-51088T), was isolated from a Lake Michigan water sample in south-eastern Wisconsin, USA. The reference strain, SRNK-1 (=NRRL B-59233), was isolated from the same source.

**Acknowledgements**

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spermidine within the classes Deltaproteobacteria and Epsilonproteobacteria. *Ann Ganna Health Sci* 27, 1–16.


