Runella limosa sp. nov., isolated from activated sludge

Seung Hyun Ryu,1 Thi Thu Hien Nguyen,1 Woojun Park,2 Chang-Jin Kim3 and Che Ok Jeon1

Correspondence Che Ok Jeon cojeon@gnu.ac.kr

1Division of Applied Life Science, EB-NCRC, PMBBRC, Gyeongsang National University, Jinju 660-701, Republic of Korea
2Division of Environmental Science and Ecological Engineering, Korea University, Seoul 136-701, Republic of Korea
3Korea Research Institute of Bioscience and Biotechnology, 52 Oeundong, Yusong, Daejeon 305-333, Republic of Korea

A Gram-negative bacterium, designated strain EMB111T, was isolated from activated sludge performing enhanced biological phosphorus removal in a sequencing batch reactor. Cells were long and rod-shaped. The isolate was strictly aerobic and non-motile. The strain grew optimally at 25–30°C and pH 7–8. The predominant fatty acids of strain EMB111T were iso-C15:0, C16:1ω5c, iso-C17:0 3-OH, iso-C16:0 3-OH, C16:0 3-OH, C16:0 and summed feature 3 (C16:1ω7c and/or iso-C15:0 2-OH). The strain contained a large amount of phosphatidylglycerol and small amounts of two unknown phospholipids (PL1, PL2) as the polar lipids. The major isoprenoid quinone was menaquinone-7. The G+C content of the genomic DNA was 42.7 mol%. Phylogenetic analysis showed that strain EMB111T formed a phyletic cluster with members of the genus Runella within the family Flexibacteraceae and was most closely related to Runella slithyformis ATCC 29530T with a 16S rRNA gene sequence similarity of 94.8%. On the basis of chemotaxonomic data and molecular properties, strain EMB111T represents a novel species within the genus Runella, for which the name Runella limosa sp. nov. is proposed. The type strain is EMB111T (=KCTC 12615T = DSM 17973T).

The genus Runella, a member of the family Flexibacteraceae, phylum Bacteroidetes (formerly Flexibacter–Bacteroides–Flavobacterium), was first erected by Larkin & Williams (1978). At the time of writing, the genus comprised two recognized species, Runella slithyformis and Runella zeae (Larkin & Williams, 1978; Chelius et al., 2002). R. slithyformis has an aquatic lifestyle; by contrast, R. zeae was isolated from the stems of surface-sterilized maize (Zea mays). This suggests that members of the genus Runella can be isolated from diverse environmental habitats. In this study, we describe a novel species of the genus Runella isolated from an activated sludge process performing enhanced biological phosphorus removal.

Strain EMB111T was isolated from activated sludge performing enhanced biological phosphorus removal in a laboratory-scale sequencing batch reactor. Sodium acetate was supplied as the sole carbon source, and the operation of the reactor was as described by Jeon et al. (2003). A sludge sample was serially diluted in 1% (w/v) saline solution, spread on R2A agar (Difco) and incubated at 20°C for 5 days. Subcultivation was on R2A agar at 25°C for 3 days. Gram staining was performed using the bioMérieux Gram stain kit according to the manufacturer’s instructions. Cell morphology and motility were studied by using phase-contrast microscopy and transmission electron microscopy (JEM-1010; JEOL) as described by Jeon et al. (2005). Physiological characteristics of strain EMB111T were examined by growing the isolate on R2A medium at different temperatures and pH values. R2A media with different pH values were prepared as described by Gomori (1955). Oxidase activity was tested by oxidation of 1% (w/v) tetramethyl-p-phenylenediamine (Merck) and catalase activity was evaluated by production of oxygen bubbles in 3% (v/v) aqueous hydrogen peroxide solution. Hydrolysis of tyrosine, Tween 20 and 80, aesculin, casein, starch, gelatin and urea was assessed on R2A agar after 5 days incubation according to the methods described by Lanyi (1987) and Gerhardt et al. (1994). Nitrate reduction was performed according to the method of Lanyi (1987) and

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain EMB111T is DQ372985. A transmission electron micrograph showing the general morphology of negatively stained cells of strain EMB111T is available as a supplementary figure in IJSEM Online.
acid production from carbohydrates was tested as described by Leifson (1963). Additional enzyme activities and biochemical characteristics were determined by using the API ZYM and API 20E kits as recommended by the manufacturer (bioMérieux). Strain EMB111T on R2A agar formed slightly raised, circular, salmon-pink colonies when grown at 25 °C for 3 days. Growth was observed at temperatures between 15 and 40 °C, with an optimum growth temperature range of 25–30 °C. The strain grew at pH 6.0–9.0, with an optimum pH range of 7.5–8.0. Cells of the isolate were non-motile, long rods (0.7–0.9 μm wide and 4.0–10.0 μm long) that lacked flagella (see Supplementary Fig. S1 in IJSEM Online). Cells of strain EMB111T were Gram-negative, oxidase-negative and catalase-positive and did not reduce nitrate to nitrite. The isolate was negative for production of indole, H₂S and acetoin and for utilization of citrate (API 20E). Growth was not observed under anaerobic conditions over a 7-day incubation period at 30 °C on R2A agar.

Analysis of fatty acid methyl esters was performed according to the instructions of the Microbial Identification System (MIDI; Microbial ID, Inc.). Analyses of polar lipids and isoprenoid quinones were carried out using the methods described by Komagata & Suzuki (1984). The major respiratory lipoquinone of the isolate included iso-C₁₅ : 0 (29.7%), summed feature 3 (C₁₆ : 1ω7c and/or iso-C₁₅ : 0 2-OH; 19.5%), C₁₆ : 1ω5c (12.9%), iso-C₁₇ : 0 3-OH (9.2%), iso-C₁₅ : 0 3-OH (6.7%), C₁₆ : 0 3-OH (5.7%), C₁₆ : 0 (5.5%), C₁₅ : 0 (2.5%), iso-C₁₅ : 1G (2.4%), iso-C₁₅ : 0 (1.8%), anteiso-C₁₅ : 0 (1.7%), iso-C₁₆ : 0 3-OH (0.8%), iso-C₁₆ : 0 (0.8%), C₁₄ : 0 (0.8%), iso-C₁₇ : 0 (0.3%) and iso-C₁₄ : 0 (0.2%). The strain contained a large amount of phosphatidylglycerol (PG) and small amounts of two unknown phospholipids (PL₁, PL₂). The G+C content of the genomic DNA of strain EMB111T was 42.7 mol%.

The phenotypic characteristics of strain EMB111T are summarized and compared with those of the type strains of closely related taxa in Table 1.

Sequencing and assembling of the 16S rRNA gene were carried out as described by DeLong (1992). The resultant 16S rRNA gene sequence of strain EMB111T was compared with available sequences from GenBank using the BLAST program (http://www.ncbi.nlm.nih.gov/BLAST/) to determine an approximate phylogenetic affiliation, and the gene sequence was aligned with those of closely related strains using CLUSTAL W software (Thompson et al., 1994). Phylogenetic trees were constructed using three different methods, the neighbour-joining, maximum-likelihood and maximum-parsimony algorithms, which are available in the PHYLIP software, version 3.6 (Felsenstein, 2002). Sequence similarity values were computed by using Similarity Matrix version 1.1 (Ribosomal Database Project II; http://35.8.164.52/html; Cole et al., 2003). A bootstrap analysis was performed according to the algorithm of the Kimura two-parameter model (Kimura, 1980) of the neighbour-joining method using the PHYLIP package. Phylogenetic analysis using a nearly complete 16S rRNA gene sequence (1428 nt) of strain EMB111T indicated that the isolate formed a phylectic cluster with members of the genus Runella with 100% bootstrap support (Fig. 1). The strain was most closely related to R. slithyformis ATCC 29530T with a 16S rRNA gene sequence similarity of 94.8%. The topologies of phylogenetic trees built using the maximum-likelihood and maximum-parsimony algorithms also supported the notion that the isolate belongs to the genus Runella (data not shown).

Table 1. Differential characteristics of strain EMB111T and type strains of selected related species

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
</tr>
</thead>
<tbody>
<tr>
<td>Morphology</td>
<td>Long rods</td>
<td>Curved rods</td>
<td>Bent rods</td>
<td>Rods</td>
<td>Curved rods</td>
</tr>
<tr>
<td>Colony colour</td>
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<td>Salmon pink</td>
<td>Salmon pink</td>
<td>Yellow</td>
<td>Pink</td>
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<tr>
<td>Optimum temperature (°C)</td>
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<td>20–30</td>
<td>28</td>
<td>28</td>
<td>20–30</td>
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<tr>
<td>Oxidase</td>
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<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Catalase</td>
<td>+</td>
<td>(+)</td>
<td>+</td>
<td>+</td>
<td>(+)</td>
</tr>
<tr>
<td>Gelatin hydrolysis</td>
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<td>–</td>
<td>–</td>
<td>–</td>
<td>(+)</td>
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<tr>
<td>Starch hydrolysis</td>
<td>–</td>
<td>(+)</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Major cellular fatty acids</td>
<td>iso-C₁₅ : 0, C₁₆ : 1ω5c, NA</td>
<td>C₁₆ : 1ω5c, iso-C₁₅ : 0, C₁₆ : 1ω7c</td>
<td>iso-C₁₅ : 0</td>
<td>C₁₆ : 1ω5c, C₁₆ : 1ω7c</td>
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<tr>
<td>Summed feature</td>
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<td>3*</td>
<td>3*</td>
<td>3*</td>
<td>3*</td>
</tr>
<tr>
<td>DNA G+C content (mol%)</td>
<td>42.7</td>
<td>49</td>
<td>49</td>
<td>48</td>
<td>40</td>
</tr>
</tbody>
</table>

*Summed feature 3 comprises C₁₆ : 1ω7c and/or iso-C₁₅ : 0 2-OH.
shown). Therefore, the physiological, biochemical and phylogenetic properties of strain EMB111T suggest that it represents a novel species of the genus Runella within the family Flexibacteraceae, for which the name Runella limosa sp. nov. is proposed.

**Description of Runella limosa sp. nov.**

Runella limosa (l.im.o’sa. L. fem. adj. limosa muddy, pertaining to sludge, the natural habitat of the species).

Colonies are slightly raised, circular and salmon-pink in colour on R2A agar. Growth occurs optimally at 25–30 °C and pH 7.5–8.0. Cells are Gram-negative, non-motile, long rods, 0.7–0.9 μm wide and 4.0–10.0 μm long when grown at 25 °C on R2A agar. Nitrate is not reduced to nitrite. Catalase-positive and oxidase-negative. Tyrosine, Tween 80

**References**


