Zoogloea caeni sp. nov., a floc-forming bacterium isolated from activated sludge

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Two floc-forming, nitrogen-fixing bacteria, strains EMB43T and EMB61, obtained from activated sludge of a domestic wastewater treatment plant in Korea, were characterized. The two strains were very closely related, sharing 99.7 % 16S rRNA gene sequence similarity and showing a level of DNA–DNA relatedness of 93 %, which suggests that they represent members of a single species. Phylogenetic analysis based on 16S rRNA gene sequences showed that the two novel isolates formed a distinct phyletic lineage within the genus Zoogloea and were related most closely to Zoogloea resiniphila DhA-35T and Zoogloea oryzae A-7T, with sequence similarities of 97.2 %. Levels of DNA–DNA relatedness between strain EMB43T and Zoogloea resiniphila DhA-35T and Zoogloea oryzae A-7T were 12.8 and 7.4 %, respectively. Cells of strains EMB43T and EMB61 were facultatively aerobic, rod-shaped, Gram-negative and motile by means of a polar flagellum. The strains grew at temperatures of 15–40 °C (optimum: 25–30 °C) and at pH 6.0–9.0 (optimum: pH 6.5–7.5). The predominant fatty acids were C₁₆ : 0, C₁₀ : 03-OH and summed feature 3 (C₁₆ : 1ω7c and/or iso-C₁₅ : 0 2-OH), and the predominant polar lipid was phosphatidylethanolamine. The genomic DNA G+C content was 64.9–65.0 mol% and the major isoprenoid quinone was ubiquinone-8 (Q-8). On the basis of phenotypic, chemotaxonomic and molecular data, the isolates are considered to represent a novel species of the genus Zoogloea, for which the name Zoogloea caeni sp. nov. is proposed. The type strain is EMB43T (=KCTC 22084T=DSM 19389T).

Bacteria of the genus Zoogloea, a member of the family Rhodocyclaceae, are known to form characteristic cell aggregates embedded in gelatinous matrices, often called zoogloeal matrices (Dugan et al., 1992). Historically, the criteria used for taxonomic classification in this genus were based on phenotypic characteristics, which has resulted in confusion in identifying members of the genus and led to Zoogloea ramigera ATCC 25935 (=IAM 12670) being transferred to Duganella zoogloeoides based on molecular approaches (Hiraishi et al., 1997). At the time of writing, the genus Zoogloea comprises three recognized species, namely Z. ramigera (Crabtree & McCoy, 1967), Zoogloea resiniphila (Mohn et al., 1999) and Zoogloea oryzae (Xie & Yokota, 2006).

Activated-sludge processes have been used to remove organic compounds as well as nutrients from wastewater, and insight into the bacterial communities is a prerequisite for understanding activated-sludge processes. Therefore, efforts have been made in our laboratory to isolate and characterize members of the bacterial community in activated sludge (Jeon et al., 2003; Lu et al., 2006; Park et al., 2007; Ryu et al., 2007). In the present study, we describe a novel species of the genus Zoogloea isolated from an activated-sludge process treating domestic sewage.

Strains EMB43T and EMB61 were isolated from floc sludge of a domestic wastewater treatment plant in Pohang, South Korea.
Korea. The sludge sample was diluted serially with 1 % (w/v) saline solution, spread on R2A agar (Difco) and incubated at 20 °C for 7 days for isolation of bacteria. Subcultivation was performed on R2A agar at 30 °C for 5 days.

Gram staining was performed by using a 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 previously (Jeon et al., 2005). Physiological characteristics of strains EMB43T and EMB61 were examined by growing the isolates on R2A agar at different temperatures (5–50 °C at 5 °C intervals) and in R2A broth adjusted to different pH values (5.0–10.0 at 0.5 pH unit intervals). R2A media with different pH values were prepared as described by Gomori (1955). The formation of flocs was determined by test-tube growth in R2A broth after 3 days incubation and was confirmed by examination with a phase-contrast microscope. Oxidase activity was tested based on oxidation of 1 % (w/v) tetramethyl-p-phenylenediamine (Merck) and catalase activity was evaluated based on production of oxygen bubbles in 3 % (v/v) aqueous hydrogen peroxide solution. Hydrolysis of casein, gelatin, Tweens 80 and 20, aesculin, urea, tyrosine, and starch was investigated on R2A agar broth medium (Stanier et al., 1966) containing 0.2 % (w/v) sodium acetate, and on R2A agar or R2A agar minimal medium agar (Stanier et al., 1966) containing 0.1 % (w/v, 11.7 mM) NaNO3, when strains EMB43T and EMB61 were incubated in R2A broth medium (Stanier et al., 1966) containing 0.1 % (w/v) nitrate, small colonies were obtained after 7 days incubation both on R2A agar and on minimal medium agar containing 0.2 % (w/v) sodium acetate, indicating that denitrification contributed more to growth than to fermentation. Several phenotypic features of strains EMB43T and EMB61 were presented and compared with those of related Zoogloea species in Table 1. Some phenotypic features of strains EMB43T and EMB61, such as urease activity and utilization of glucose and mannitol, were different, which shows that the species represented by these two strains (see below) is metabolically diverse.

For analysis of fatty acid methyl esters, cells of strains EMB43T and EMB61 were harvested from R2A agar plates after incubation for 3 days. 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 by using the methods described by Komagata & Suzuki (1987). The DNA G+C content of strains EMB43T and EMB61 was determined by using a high-performance liquid chromatograph fitted with a reversed-phase column (GROM-SIL 100 ODS-2FE; GROM) according to the method of Tamaoka & Komaga (1984). The major respiratory lipoquinone of strains EMB43T and EMB61 was ubiquinone-8 (Q-8). The cellular membrane of strains EMB43T and EMB61 contained C16:0, C10:0 3-OH and summed feature 3 (C16:1ω7c and/or iso-C15:0 2-OH) as major fatty acids (see Supplementary Table S1, available in IJSEM Online). Polar lipids were dominated by a large amount of phosphatidylethanolamine, but a small amount of an amino group-containing lipid was also present. The DNA G+C contents of strains EMB43T and EMB61 were 64.9 and 65.0 mol%, respectively. Strains EMB43T and EMB61 were able to grow in nitrogen-free minimal broth medium (Stanier et al., 1966) containing 0.2 % (w/v) sodium acetate. PCR amplifications of the nifH gene by using the forward primer PolF, 5'-TGGCAYCCSAARGCBGACTC-3' and the reverse primer PolR, 5'-ATSGCCATCATYTCRCCGGA-3' (Poly et al., 2001), on DNA extracted from strains EMB43T and EMB61, Z. oryzae A-7T, Z. resinihiphila Dha-35T and Z. ramigera ATCC 19544T were carried out to confirm their
Table 1. Characteristics of strains EMB43T and EMB61 and related Zoogloea species

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1*</th>
<th>2*</th>
<th>3</th>
<th>4</th>
<th>5</th>
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<tbody>
<tr>
<td>Cell diameter (μm)</td>
<td>0.6–0.9</td>
<td>0.6–0.9</td>
<td>0.5–0.7</td>
<td>1.0</td>
<td>1.0–1.2</td>
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<td>Growth at 45 °C</td>
<td>–</td>
<td>–</td>
<td>+*</td>
<td>–</td>
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<tr>
<td>Catalase</td>
<td>+</td>
<td>+</td>
<td>–*</td>
<td>+</td>
<td>+</td>
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<tr>
<td>Urease</td>
<td>–</td>
<td>+</td>
<td>–*</td>
<td>+</td>
<td>+</td>
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<tr>
<td>Denitrification</td>
<td>+ (slow)</td>
<td>+ (fast)</td>
<td>–*</td>
<td>+</td>
<td>+</td>
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<td>Hydrolysis of:</td>
<td></td>
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<tr>
<td>Gelatin</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>+</td>
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<tr>
<td>Casein</td>
<td>–</td>
<td>–</td>
<td>+*</td>
<td>+</td>
<td>+</td>
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<td>Utilizes as sole carbon source:</td>
<td></td>
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<tr>
<td>Acetate</td>
<td>+</td>
<td>+</td>
<td>+*</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Citrate</td>
<td>–</td>
<td>–</td>
<td>–*</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Glucose</td>
<td>+</td>
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<td>+*</td>
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<td>–</td>
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<tr>
<td>Mannitol</td>
<td>–</td>
<td>+</td>
<td>+*</td>
<td>–</td>
<td>+</td>
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<tr>
<td>DNA G+C content (mol%)</td>
<td>64.9</td>
<td>65.0</td>
<td>NA</td>
<td>65.1</td>
<td>65.3</td>
</tr>
</tbody>
</table>

*Data from the present study.

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Table 1. Characteristics of strains EMB43T and EMB61 and related Zoogloea species

Strains: 1, EMB43T (data from the present study); 2, EMB61 (present study); 3, Z. resiniHila DhA-35T (present study and Mohn et al., 1999); 4, Z. oryzae A-7T (Xie & Yokota, 2006); 5, Z. ramigera ATCC 19544T (Unz, 1984; Xie & Yokota, 2006).

Symbols: +, positive; –, negative; NA, data not available. All are positive for nitrate reduction.

**nitrogen-fixing capabilities. Expected PCR product sizes (about 340 bp) of the *nifH* gene were detected for strains EMB43T, EMB61 and *Z. oryzae* A-7T, but not for *Z. resiniHila* DhA-35T or *Z. ramigera* ATCC 19544T (data not shown). The predominant fatty acids, major lipoquinone and polar lipids, and DNA G+C contents of strains EMB43T and EMB61 were in accordance with those of members of the genus *Zoogloea* (Unz, 1984; Mohn et al., 1999; Xie & Yokota, 2006).

Sequencing of the 16S rRNA gene was carried out as described by Lane (1991). The resulting 16S rRNA gene sequences (1460 nt) of strains EMB43T and EMB61 were compared with available 16S rRNA gene sequences from GenBank by using the BLAST program (http://www.ncbi.nlm.nih.gov/BLAST/) to determine an approximate phylogenetic affiliation, and gene sequences were aligned with those of closely related species by using the CLUSTAL W program (Thompson et al., 1994). Phylogenetic trees were constructed by using the neighbour-joining, maximum-likelihood and maximum-parsimony algorithms available in PHYLIP version 3.6 (Felsenstein, 2002). Sequence similarity values between the novel isolates and related strains were computed by using the FASTA3 program at EBI (http://www.ebi.ac.uk/ fasta33/nucleotide.html). Bootstrap analysis was performed according to the algorithm of the Kimura two-parameter model (Kimura, 1980) of the neighbour-joining method in the PHYLIP package. DNA–DNA hybridization was carried out to evaluate the level of genomic DNA relatedness among the two novel isolates and closely related *Zoogloea* species by using the fluorometric microplate method (Ezaki et al., 1989). Fluorometric data recorded after 30 min reaction of the substrates were used for calculation of DNA–DNA hybridization values. The signals produced by self-hybridization were inferred as 100% and the levels of DNA–DNA relatedness were calculated from the mean values of five replications.

Phylogenetic analysis based on 16S rRNA gene sequences indicated that strains EMB43T and EMB61 formed a distinct phyletic lineage within the genus *Zoogloea* (Fig. 1). The overall topology of the neighbour-joining tree was similar to that of the maximum-likelihood and maximum-parsimony trees (data not shown). Comparative 16S rRNA gene sequence analysis revealed that strains EMB43T and EMB61 were very closely related (99.7%), and they showed a level of DNA–DNA relatedness of 93%, which suggests that they represent members of a single species. Strains EMB43T and EMB61 were related most closely to *Z. oryzae* A-7T, *Z. resiniHila* DhA-35T and *Z. ramigera* ATCC 19544T, with 16S rRNA gene sequence similarities of 97.2, 97.2 and 96.6%, respectively. However, levels of DNA–DNA relatedness between strain EMB43T and *Z. resiniHila* DhA-35T and *Z. oryzae* A-7T were 12.8 and 7.4%, respectively, which are clearly below the 70% threshold generally accepted for species delineation (Rosselló-Mora & Amann, 2001; Stackebrandt et al., 2002). The physiological, biochemical and phylogenetic data presented suggest that strains EMB43T and EMB61 represent a single novel species of the genus *Zoogloea*, for which the name *Zoogloea caeni* sp. nov. is proposed.

**Description of Zoogloea caeni** sp. nov.

*Zoogloea caeni* (cae’ni. L. gen. n. caeni of mud, referring to the isolation of the type strain from activated sludge).

Colonies on R2A agar are white, glistening, translucent, raised and circular with entire margins. Cells are facultatively...
The type strain, EMB43T (AF233877) are shown as percentages of 1000 replicates; only values ≥50% are shown. Comamonas denitrificans 123T was used as an outgroup. Bar, 0.01 changes per nucleotide position.

Fig. 1. Neighbour-joining tree based on 16S rRNA gene sequences showing the phylogenetic relationships between strains EMB43T and EMB61 and related taxa. Bootstrap values are shown. Bar, 0.01 changes per nucleotide position.

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References


