The genus *Delftia*, belonging to the family *Comamonadaceae* within the order *Burkholderiales* of the class Betaproteobacteria, was created by the relocation of *[Comamonas] acidovorans* on the basis of phylogenetic and phenotypic analyses (Wen et al., 1999). At the time of writing, this genus comprised three recognized species: *Delftia acidovorans*, isolated from soil (Wen et al., 1999); *Delftia tsuruhatensis*, isolated from activated sludge (Shigematsu et al., 2003); and *Delftia lacustris*, isolated from freshwater (Jørgensen et al., 2009). Members of the genus *Delftia* are characterized as Gram-negative, aerobic, rod-shaped, motile by means of polar or bipolar tufts of one to five flagella, poly-β-hydroxybutyrate-accumulating, oxidase-positive and catalase-positive; chemotaxonomically, they have a high metabolic versatility, having hexadecanoic acid (C16:0), hexadecenoic acid (C16:1) and octadecenoic acid (C18:1) as predominant fatty acids, possessing Q-8 as the main isoprenoid quinone and a DNA G+C content of 67–69 mol% (Wen et al., 1999). *D. acidovorans* is the most well-known wild-type bacterium that can efficiently accumulate poly-β-hydroxybutyrate (Loo & Sudesh, 2007; Siew et al., 2009).

During the characterization of micro-organisms from a freshwater shrimp culture pond (GPS location: 22°34′41″ N 120°36′15″ E; pH 8.5, 25 °C) in Pingtung countryside, southern Taiwan, strain wsw-7T was isolated and selected for detailed analysis. In this study, we describe the morphological, biochemical and phylogenetic characteristics of the isolate and propose that it represents a novel species in the genus *Delftia*.  

# Delftia litopenaei sp. nov., a poly-β-hydroxybutyrate-accumulating bacterium isolated from a freshwater shrimp culture pond

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A Gram-negative, short-rod-shaped, motile, non-sporing and poly-β-hydroxybutyrate-accumulating bacterial strain, designated wsw-7T, was isolated from a freshwater shrimp culture pond in Taiwan and was characterized using a polyphasic taxonomic approach. Phylogenetic analyses based on 16S rRNA gene sequences showed that the closest relatives of strain wsw-7T were *Delftia lacustris* 332T, *Delftia tsuruhatensis* T7T and *Delftia acidovorans* ATCC 15668T, with sequence similarities of 98.5, 98.4 and 97.9%, respectively. Phylogenetic trees obtained with 16S rRNA gene sequences or the polyhydroxyalkanoate synthase (phaC) gene sequences revealed that strain wsw-7T and these three closest relatives formed an independent phylogenetic clade within the order *Burkholderiales*. Strain wsw-7T contained summed feature 3 (comprising C16:1ω7c and/or C18:1ω6c), C16:0 and C18:1ω7c as predominant fatty acids. The major isoprenoid quinone was Q-8 and the DNA G+C content was 67.6 mol%. The polar lipid profile consisted of a mixture of phosphatidylethanolamine, phosphatidylglycerol, diphosphatidylglycerol, an uncharacterized aminolipid and several uncharacterized phospholipids. On the basis of the genotypic, chemotaxonomic and phenotypic data, strain wsw-7T represents a novel species in the genus *Delftia*, for which the name *Delftia litopenaei* sp. nov. is proposed; the type strain is wsw-7T (=BCRC 80212T=LMG 25724T).

## Abbreviations

AL, aminolipid; CM-cellulose, carboxymethylcellulose; DPG, diphosphatidylglycerol; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PL, phospholipid.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA and phaC gene sequences of *Delftia litopenaei* strain wsw-7T are GU721027 and JF894309, respectively; those for the phaC gene sequences of *Delftia tsuruhatensis* T7T and *Delftia lacustris* 332T are JN165747 and JN165748, respectively.

Two supplementary figures are available with the online version of this paper.

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sys816@mail.nkmu.edu.tw
at 25 °C for 48–72 h. On this medium, strain wsw-7\(^T\) was able to grow at 4–40 °C. It was preserved at −80 °C in R2A broth with 20% (v/v) glycerol or by lyophilization. *D. acidovorans* ATCC 15668\(^T\) and *D. tsuruhatensis* T7\(^T\) were obtained from the Bioresource Collection and Research Center (BCRC) and *D. lacustris* 332\(^T\) was obtained from the Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ). These three type strains were selected as reference strains for phenotypic and genotypic tests.

Genomic DNA was isolated using a bacterial genomic kit and the 16S rRNA gene sequence was analysed as described previously by Chen et al. (2001). Primers FD1 (5'-AGAGTTTGATCCTGGCTCAG-3') and RD1 (5'-AAGGAGGGT-GATCCAGGC-3') were used for amplification of bacterial 16S rRNA genes by PCR. These primers correspond to nucleotide positions 8–27 and 1525–1541 of the 16S rRNA genes by PCR. These primers can be used for amplifying the nearly full-length 16S rRNA gene, respectively, and can be used for the EzTaxon server (Chun et al., 2007), the Ribosomal Database Project (Maidak et al., 2001) and GenBank (http://blast.ncbi.nlm.nih.gov/Blast.cgi). Analysis of the sequence data was performed by using the software package BioEdit (Hall, 1999) and MEGA version 5 (Tamura et al., 2011), after multiple alignments of the data by CLUSTAL_X (Thompson et al., 1997). Distances (corrected according to Kimura’s two-parameter model; Kimura, 1983) were calculated and clustering was performed with the neighbour-joining method (Saitou & Nei, 1987). The maximum-likelihood (Felsenstein, 1981) and maximum-parsimony (Cluge & Farris, 1969) trees were generated by using the treeing algorithms contained in the PHYLIP software package (Felsenstein, 1993). In each case, bootstrap values were calculated based on 1000 replications.

Phylogenetic analyses based on 16S rRNA gene sequences revealed that strain wsw-7\(^T\) was closely related to members of the genera *Delftia* (97.9–98.5% sequence similarity), *Comamonas* (96.8–95.8%) and *Diaphorobacter* (96.5–96.4%). Strain wsw-7\(^T\) formed a deep phyletic cluster with *D. acidovorans* ATCC 15668\(^T\), *D. tsuruhatensis* T7\(^T\) and *D. lacustris* 332\(^T\) within the order *Burkholderiales* in the neighbour-joining tree (Fig. 1). The overall topologies of the phylogenetic trees obtained with the maximum-likelihood and maximum-parsimony methods were similar. Sequence similarity calculations (over 1400 bp) indicated that strain wsw-7\(^T\) was closely related to *D. lacustris* 332\(^T\) (98.5% sequence similarity), *D. tsuruhatensis* T7\(^T\) (97.9%) and *D. acidovorans* ATCC 15668\(^T\) (97.9%). In addition, sequence similarity calculations also showed that strain wsw-7\(^T\) was very closely related to an arsenite-resistant bacterial strain, *Delftia* sp. TS40 (99.8% sequence similarity; Cai et al., 2009), and strain wsw-7\(^T\) formed a deep monophyletic clade with this strain in the phylogenetic tree (shown in Fig. 1).

A PCR technique to detect the polyhydroxyalkanoate synthase gene (*phaC*) has been employed for rapid identification of *Delftia* species in the laboratory and in the field. The PCR approach allows for rapid identification of the target bacteria using the primers *phaC*-F (5'-CAAGAGAAGGATTTGGTTGACGATG-3') and *phaC*-R (5'-CGTTGCCTTCTCCAACGATACGTA-3'). The amplicon is 627 bp long and is specific to *Delftia* species. The amplification protocol consists of an initial denaturation step at 94°C for 2 min, followed by 30 cycles of 94°C for 1 min, 60°C for 1 min, and 72°C for 1 min, with a final extension step at 72°C for 10 min.

**Fig. 1.** Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showing the position of *D. litopenaei* wsw-7\(^T\) and related taxa in the order *Burkholderiales* of the class *Betaproteobacteria*. Numbers at nodes are bootstrap percentages ≥ 70% based on the neighbour-joining (above nodes) and maximum-parsimony (below nodes) tree-making algorithms. Filled circles indicate branches of the tree that were also recovered using the maximum-likelihood and maximum-parsimony tree-making algorithms. Open circles indicate that the corresponding nodes were also recovered in the tree generated with the maximum-parsimony algorithm. *Neisseria gonorrhoeae* NCTC 8375\(^T\) was used as an outgroup. Bar, 0.01 substitutions per nucleotide position.
D. lacustris strain was closely related to sequence similarity calculations indicated that the novel formed a distinct phylogenetic cluster (Fig. 2). Partial phaC gene sequence similarities (<73.0%) were found with representative members of all other genera shown in Fig. 2. The phylogenetic tree obtained based on phaC sequences reflected the major branches of the tree obtained with the 16S rRNA gene. These results suggested a strong phylogenetic relationship among these taxa. Based on phylogenetic data obtained using these two sequences, the three closest relatives, D. acidovorans DS-17 (86.7%), D. acidovorans SPH-1 (85.6%). Lower sequence similarities (<73.0%) were found with representative members of all other genera shown in Fig. 2.

The phylogenetic tree obtained based on phaC sequences was constructed as described above except that it was based on partial phaC gene sequences; the tree revealed that strain wsw-7T and the closely related members of the genus Delftia formed a distinct phylogenetic cluster (Fig. 2). Partial phaC sequence similarity calculations indicated that the novel strain was closely related to D. lacustris 332T (87.0% similarity), D. tsuruhatensis T7T (86.9%), D. acidovorans DS-17 (86.7%) and D. acidovorans SPH-1 (85.6%). Lower sequence similarities (<73.0%) were found with representative members of all other genera shown in Fig. 2.

Cell morphology was observed by phase-contrast microscopy (DM 2000; Leica) at lag, exponential and stationary phases of growth. The Gram Stain Set S kit (BD Difco) and the Ryu non-staining KOH method (Powers, 1995) were used for testing the Gram reaction. Motility was tested by the hanging drop method (Murray et al., 1994). The Spot Test Flagega Stain (BD Difco) was used for flagellum staining. Poly-β-hydroxybutyrate granule accumulation was observed under light microscopy after staining of the cells with Sudan black (Schlegel et al., 1970) and visualized by UV illumination after directly staining growing bacteria on plates containing Nile red (Spiekermann et al., 1999).

Colonies morphology was observed on marine agar using a stereoscopic microscope (SMZ 800; Nikon).

The pH range for growth was determined by measuring the optical densities (wavelength 600 nm) of R2A broth cultures. The pH was adjusted prior to sterilization to pH 4–10 (at intervals of 1.0 pH unit) using appropriate biological buffers (Breznak & Costilow, 1994): citrate/Na2HPO4 buffer, pH 4.0–5.0; phosphate buffer, pH 6.0–7.0; Tris buffer, pH 8.0–9.0; no buffer, pH 10.0. Verification of pH values after autoclaving revealed only minor changes. The temperature range for growth was determined on R2A broth at 4–50 °C. To investigate tolerance to NaCl, R2A broth was prepared according to the formula of the BD Difco medium with NaCl concentration adjusted to 0%, 0.5% and 1.0–8.0%, w/v (at intervals of 1.0%). Growth under anaerobic conditions was determined after incubating strain wsw-7T on R2A agar in the OXoid AnaeroGen system.

Strain wsw-7T was examined for a broad range of phenotypic properties. Activities of catalase, oxidase, DNase, urease and

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**Fig. 2.** Neighbour-joining tree based on partial phaC gene sequences of D. litopenaei wsw-7T and related taxa in the order *Burkholderiales* of the class *Betaproteobacteria*. Numbers at nodes are bootstrap percentages (>70%) based on the neighbour-joining tree-making algorithm. Bar, 0.01 substitutions per nucleotide position.
lipase (corn oil), and hydrolysis of starch, casein, gelatin and Twents 20, 40, 60 and 80 were determined using standard methods (Smibert & Krieg, 1994). Chitin hydrolysis activity was determined by chitinase-detection agar plate (CDA plate). Chitin hydrolysis was visualized by the formation of clear zone around the colonies in CDA plates; CDA plates were prepared as described earlier by Wen et al. (2002). Hydrolysis of carboxymethylcellulose (CM-cellulose) was tested as the method described by Bowman (2000) using R2A agar as the basal medium. Peptidoglycan from Bacillus subtilis BCRC 10255T was purified according to the method of Pelz et al. (1998) and degradation of extracellular peptidoglycan was examined as described by Jørgensen et al. (2009) using solid medium. Additional biochemical tests were performed using API ZYM and API 20NE kits (bioMérieux) and carbon source utilization was evaluated using the GN2 microplate (Biolog). All commercial phenotypic tests were performed according to the manufacturers’ recommendations.

Sensitivity of strain wsw-7T, D. acidovorans ATCC 15668T, D. tsuruhatensis T7T and D. lacustris 332T to antibiotics was tested by the disc diffusion method after spreading cell suspensions (0.5 McFarland) on R2A agar (BD Difco) plates. The discs (Oxoid) contained the following antibiotics: ampicillin (10 μg), chloramphenicol (30 μg), gentamicin (10 μg), kanamycin (30 μg), nalidixic acid (30 μg), novobiocin (30 μg), rifampicin (5 μg), penicillin G (10 μg), streptomycin (10 μg), sulfamethoxazole (23.75 μg) plus trimethoprim (1.25 μg) and tetracycline (30 μg). The effect of antibiotics on cell growth was assessed after 2 days at 30 °C. The diameter of the antibiotic discs was 8 mm and strains were considered susceptible when the diameter of the inhibition zone was >13 mm, intermediate at 10–12 mm and resistant at <10 mm, as described by Nokhal & Schlegel (1983).

The fatty acid profiles of strain wsw-7T, D. acidovorans ATCC 15668T, D. tsuruhatensis T7T and D. lacustris 332T were determined using cells grown on R2A agar at 30 °C for 2 days. Fatty acid methyl esters were prepared and separated according to the instructions of the Microbial Identification System (MIDI; Sasser, 1990), and identified by MIDI version 6.0 and the RTSBA6.00 database. The fatty acid profile of strain wsw-7T was similar to those of the other three Delftia species, although there were differences in the proportions of some components (Table 1). The major fatty acids of strain wsw-7T were summed feature 3 (comprising C16:1ω7c and/or C16:1ω6c 38.6 %), C16:0 (25.5 %) and C18:1ω9c (18.0 %). In addition, significant amounts of C10:0 3-OH (3.8 %), C12:0 (3.2 %), cyclopropanoic acid (C17:0 cyclo; 2.2 %), C14:0 (1.2 %) and C18:0 (1.0 %) were detected. However, in contrast to its closest relatives, D. acidovorans ATCC 15668T, D. tsuruhatensis T7T and D. lacustris 332T, strain wsw-7T had a much higher proportion of fatty acid summed feature 3. Furthermore, the quantities of fatty acids C16:0 and C17:0 cyclo in strain wsw-7T were much lower than those found in its closest relatives.

<table>
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<th>Fatty acid</th>
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<th>3</th>
<th>4</th>
</tr>
</thead>
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<tr>
<td>C10:0 3-OH</td>
<td>3.8</td>
<td>3.0</td>
<td>3.0</td>
<td>2.8</td>
</tr>
<tr>
<td>C12:0</td>
<td>3.2</td>
<td>2.9</td>
<td>2.9</td>
<td>2.8</td>
</tr>
<tr>
<td>C14:0</td>
<td>1.2</td>
<td>1.5</td>
<td>1.6</td>
<td>1.5</td>
</tr>
<tr>
<td>C16:0</td>
<td>25.5</td>
<td>32.5</td>
<td>36.4</td>
<td>34.3</td>
</tr>
<tr>
<td>C17:0 cyclo</td>
<td>2.2</td>
<td>11.7</td>
<td>15.0</td>
<td>12.4</td>
</tr>
<tr>
<td>C18:0</td>
<td>1.0</td>
<td>1.1</td>
<td>1.1</td>
<td>2.6</td>
</tr>
<tr>
<td>C18:1ω7c</td>
<td>18.0</td>
<td>15.3</td>
<td>14.5</td>
<td>15.3</td>
</tr>
<tr>
<td>Summed feature 3*</td>
<td>38.6</td>
<td>27.4</td>
<td>22.5</td>
<td>23.5</td>
</tr>
</tbody>
</table>

*Summed features are groups of two or three fatty acids that cannot be separated by GLC using the MIDI system. Summed feature 3 comprises C16:1ω7c and/or C16:1ω6c.

Isoprenoid quinones were extracted and purified according to the method of Collins (1985) and analysed by HPLC. Strain wsw-7T, D. tsuruhatensis T7T and D. lacustris 332T had Q-8 as their major respiratory quinone, which is the same as that of the type species of the genus Delftia (Wen et al., 1999). The DNA G+C content of strain wsw-7T, determined by HPLC according to Mesbah et al. (1989), was 67.6 ± 1.0 mol%.

Polar lipids were extracted and analysed by two-dimensional TLC according to Embley & Wait (1994). Molybdophosphoric acid was used for detection of all lipids, ninhydrin reagent was used for lipids containing free amino groups, Zinzadze reagent was used for phosphorus-containing lipids and α-naphthol reagent was used for glycolipids. Strain wsw-7T exhibited a complex polar lipid profile consisting of phosphatidylethanolamine (PE), phosphatidyglycerol (PG), diphosphatidylglycerol (DPG), an uncharacterized aminolipid (AL) and several uncharacterized phospholipids (PL1–PL4) (see Supplementary Fig. S1 available in IJSEM Online). Compared with its closest relatives, D. acidovorans ATCC 15668T, D. tsuruhatensis T7T and D. lacustris 332T, strain wsw-7T exhibited a very similar polar lipid profile, and they all had PE, PG, DPG, AL, PL1 and PL2. However, PL3 was absent in D. tsuruhatensis T7T and D. lacustris 332T, but present in strain wsw-7T and D. acidovorans ATCC 15668T. An uncharacterized phospholipid, PL4, was detected in strain wsw-7T but was not detected in the three reference strains. The results suggested that there are some differences in the polar lipid profiles among them, although they belong to the same genus and have very similar profiles.

DNA–DNA hybridization experiments of strain wsw-7T with D. acidovorans ATCC 15668T, D. tsuruhatensis T7T and
D. lacustris 332\textsuperscript{T} were carried out by the method of Ezaki et al. (1989). The signal produced by self-hybridization was taken as 100\%, and relatedness values (\%) were calculated from duplicate samples. The levels of DNA–DNA relatedness of strain wsw-7\textsuperscript{T} with D. acidovorans ATCC 15668\textsuperscript{T}, D. tsuruhatensis T7\textsuperscript{T} and D. lacustris 332\textsuperscript{T} were 47.2 \pm 3.1\% (41.9 \pm 4.5\% in a reciprocal experiment), 41.3 \pm 3.8\% (44.7 \pm 3.5\%) and 54.4 \pm 3.5\% (49.8 \pm 6.2\%), respectively. Since the recomended DNA–DNA relatedness threshold for the definition of a species is 70\% (Wayne et al., 1987), these results indicate that strain wsw-7\textsuperscript{T} does not belong to any known species of the genus Delftia.

The physiological, biochemical and morphological characteristics of strain wsw-7\textsuperscript{T} are given in the species description and Table 2. Phenotypic examination revealed many common traits between the novel strain and its closest relatives, D. acidovorans ATCC 15668\textsuperscript{T}, D. tsuruhatensis T7\textsuperscript{T} and D. lacustris 332\textsuperscript{T}. However, strain wsw-7\textsuperscript{T} could be clearly differentiated from these three species by the inability to degrade peptidoglycan (see Supplementary Fig. S2), by the absence of C4 esterase lipase activity, by the inability to assimilate arabinose, N-acetylglucosamine and citrate, and by susceptibility to ampicillin (Table 2). Strain wsw-7\textsuperscript{T} could also be differentiated from D. acidovorans ATCC 15668\textsuperscript{T} by the inability to assimilate mannose and by resistance to rifampicin. Phenotypic properties such as the inability to hydrolyse casein, the absence of valine arylamidase activity, the inability to assimilate maltose and caprate, and susceptibility to penicillin G, gentamicin and streptomycin distinguish strain wsw-7\textsuperscript{T} from D. tsuruhatensis T7\textsuperscript{T}. Some features of strain wsw-7\textsuperscript{T}, such as the absence of valine arylamidase, \(\alpha\)-glucosidase and \(\beta\)-glucosidase activities, the inability to assimilate mannose, and the susceptibility to kanamycin, penicillin G, gentamicin and streptomycin may be helpful for distinguishing the novel strain from D. lacustris 332\textsuperscript{T}.

Table 2. Differential characteristics of Delftia species

<table>
<thead>
<tr>
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</tr>
<tr>
<td>Range</td>
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<td>5.0–8.0</td>
<td>5.0–9.0</td>
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</tr>
<tr>
<td>Optimum</td>
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<td>6.0–7.0</td>
<td>7.0</td>
<td>6.0–7.0</td>
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<td></td>
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<tr>
<td>Range</td>
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<td>0–4.0</td>
<td>0–5.0</td>
</tr>
<tr>
<td>Optimum</td>
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<td>0–2.0</td>
<td>0–2.0</td>
<td>0–2.0</td>
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<tr>
<td>Optimal growth temperature ((\degree)C)</td>
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<td>Hydrolysis of:</td>
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<tr>
<td>Peptidoglycan</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Casein</td>
<td>–</td>
<td>–</td>
<td>+</td>
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<td>Enzymic activities:</td>
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<tr>
<td>C4 esterase</td>
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<td>–</td>
<td>+</td>
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<td>Valine arylamidase</td>
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<td>R</td>
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<td>R</td>
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<td>R</td>
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<td>R</td>
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<tr>
<td>Rifampicin</td>
<td>R</td>
<td>S</td>
<td>R</td>
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<tr>
<td>DNA G+C content (mol%)</td>
<td>67.6</td>
<td>63.4</td>
<td>66</td>
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</tr>
</tbody>
</table>

* S, Sensitive; R, Resistant.
wsw-7T constitutes the novel member of the genus *Delftia*. The name *Delftia litopenaei* sp. nov. is proposed for this taxon.

**Description of *Delftia litopenaei* sp. nov.**

*Delftia litopenaei* (li.to.pen ae’i. N.L. gen. n. Litopenaeus the scientific name of a genus of penaeid shrimp; N.L. gen. n. *litopenaei* of *Litopenaeus*, referring to the isolation of the type strain from a shrimp belonging to the genus *Litopenaeus*).

Cells are Gram-negative, aerobic, non-spore-forming, motile, short-rod-shaped and chemo-heterotrophic. Poly-β-hydroxybutyrate accumulation is observed. After 48 h of incubation on R2A agar at 30 °C, the mean cell size is approximately 0.5–0.8 μm in diameter and 1.5–2.0 μm in length. Colonies are semi-transparent, convex, round and smooth with entire edges. Colonies are approximately 1.0–1.7 mm in diameter on R2A agar after 72 h of incubation at 25 °C. Growth occurs at 4–40 °C (optimum, 25–35 °C), at pH 5.0–9.0 (optimum, pH 6.0–7.0) and with 0–3% NaCl (optimum, 0–1%). Positive for oxidase and catalase activities. Positive for hydrolysis of DNA, and Tween 20, 40 and 60. Negative for hydrolysis of urea, starch, gelatin, casein, chitin, CM-cellulose, peptidoglycan, corn oil and Tween 80. In API 20NE tests, positive for nitrate reduction, assimilation of glucose, mannitol, glucosone, adipate, malate and phenylacetate, and negative for indole production, glucose fermentation, asuscin and gelatin hydrolysis, arginine dihydrolase, urease and β-galactosidase activities and assimilation of arabinose, mannose, N-acetylglucosamine, maltose, caprate and citrate. In the API ZYM kit, alkaline phosphatase, C8 esterase lipase, leucine arylamidase, acid phosphatase and naphthol-AS-BI-phosphohydrolase activities are present and C4 esterase, C14 lipase, valine arylamidase, cystine arylamidase, trypsin, α-chymotrypsin, α-galactosidase, β-galactosidase, β-glucuronidase, α-glucosidase, β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase activities are absent. The following compounds are utilized as sole carbon sources in the GN2 microplate: dextrin, Tween 40 and 60. Negative for hydrolysis of urea, starch, gelatin, casein, chitin, CM-cellulose, peptidoglycan, corn oil and Tween 80. In API 20NE tests, positive for nitrate reduction, assimilation of glucose, mannitol, glucosone, adipate, malate and phenylacetate, and negative for indole production, glucose fermentation, asuscin and gelatin hydrolysis, arginine dihydrolase, urease and β-galactosidase activities and assimilation of arabinose, mannose, N-acetylglucosamine, maltose, caprate and citrate. In the API ZYM kit, alkaline phosphatase, C8 esterase lipase, leucine arylamidase, acid phosphatase and naphthol-AS-BI-phosphohydrolase activities are present and C4 esterase, C14 lipase, valine arylamidase, cystine arylamidase, trypsin, α-chymotrypsin, α-galactosidase, β-galactosidase, β-glucuronidase, α-glucosidase, β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase activities are absent. The following compounds are utilized as sole carbon sources in the GN2 microplate: dextrin, Tween 40, Tween 80, d-fructose, D-mannitol, D-psicose, pyruvic acid methyl ester, acetic acid, cis-aconitic acid, formic acid, D-gluconic acid, α-hydroxybutyric acid, β-hydroxybutyric acid, γ-hydroxybutyric acid, p-hydroxyphenylacetic acid, itaconic acid, z-ketobutyric acid, dl-lactic acid, propionic acid, quinic acid, sebacic acid, succinic acid, bromosuccinic acid, succinamic acid, L-alaninamide, D-alanine, L-alanine, L-asparagine, L-aspartic acid, L-glutamic acid, glycol-L-aspartic acid, glycol-L-glutamic acid, l-histidine, L-leucine, L-phenylalanine, L-proline, L-prolylglutamic acid, L-threonine, γ-aminobutyric acid, urocanic acid and DL-α-glycerol phosphate. All other substrates in the GN2 microplate are not utilized. Resistant to rifampicin and sensitive to penicillin G, ampicillin, chloramphenicol, gentamicin, kanamycin, tetracycline, novobiocin, streptomycin, sulfamethoxazole plus trimethoprim and nalidixic acid. The major fatty acids are summed feature 3 (comprising C16:1ω7c and/or C16:1ω6c), C16:0 and C18:1ω7c. The major cellular hydroxy fatty acid is C10:0 3-OH. Substantial amounts of C12:0, C14:0, C17:0 cyclo and C18:0 are also detected. The major respiratory quinone is Q-8. The polar lipid profile consists of a mixture of PE, PG, DPG, an uncharacterized AL and several uncharacterized PLs.

The type strain is wsw-7T (BCRC 80212T = LMG 25724T), isolated from a freshwater shrimp culture pond in Pingtung countryside, southern Taiwan. The DNA G+C content of the type strain is 67.6 mol%.

**References**


Jørgensen, N. O. G., Brandt, K. K., Nybroe, O. & Hansen, M. (2009). *Delftia lacustris* sp. nov., a peptidoglycan-degrading bacterium from fresh water, and emended description of *Delftia tsuruhatensis* as a


