Mameliella alba gen. nov., sp. nov., a marine bacterium of the *Roseobacter* clade in the order *Rhodobacterales*

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A Gram-negative, non-motile, rod-shaped bacterial strain, JLT354-W^T, that accumulates poly- β -hydroxybutyrate granules was isolated from the South China Sea. Phylogenetic analysis based on 16S rRNA gene sequences showed that the strain was related to members of the genera *Antarctobacter*, *Sagittula*, *Oceanicola* and *Loktanella*; levels of similarity between strain JLT354-W^T and members of the above genera were less than 92.0 %. The predominant fatty acid of strain JLT354-W^T was C_{18:1 ω 7c} (83.1 %); significant amounts of C_{18:0} (7.9 %) and C_{12:1} 3-OH (3.7 %) were also present. The predominant respiratory ubiquinone was Q-10. The DNA G + C content of strain JLT354-W^T was 63.7 mol%. The isolate was distinguishable from members of the order *Rhodobacterales* based on phenotypic and biochemical characteristics. On the basis of the taxonomic data presented, strain JLT354-W^T is considered to represent a novel species of a new genus, for which the name *Mameliella alba* gen. nov., sp. nov. is proposed. The type strain of *Mameliella alba* is JLT354-W^T (=LMG 24665^T=CGMCC 1.7290^T).

Members of the *Roseobacter* clade (Wagner-Döbler *et al.*, 2003) in the order *Rhodobacterales* of the class *Alphaproteobacteria* are abundant in marine environments. Many novel genera and species of this clade have been described recently, for example *Oceanicola* (Cho & Giovannoni, 2004), *Thalassobacter* (Macián *et al.*, 2005a), *Dinoroseobacter* (Biebl *et al.*, 2005), *Yangia* (Dai *et al.*, 2006), *Wenxinia* (Ying *et al.*, 2007), *Ponticoccus* (Hwang & Cho, 2008), *Tropicibacter* (Harwati *et al.*, 2009) and *Nautella* (Vandecastelaere *et al.*, 2009). The abundance and diverse physiological characteristics within this group suggest that they play important roles in marine ecosystems, such as the degradation of aromatic compounds (Buchan *et al.*, 2001, 2005) and the biogeochemical cycles of carbon and sulfur (Buchan *et al.*, 2005; Wagner-Döbler & Biebl, 2006).

During surveys of the biodiversity of bacteria in the South China Sea, strain JLT354-W^T was obtained during cruise 908 in July 2006 after direct plating of seawater dilutions. It was incubated in a rich organic (RO) medium (Yurkov *et al.*, 1999) at room temperature (25 °C) for 10 days.

Cell morphology was examined by using transmission electron microscopy (JEM 2100; JEOL). The Gram reaction was determined on cells grown on RO medium at 25 °C for 24 h according to the method described by Gerhardt *et al.* (1994). Colonies were white, 0.5–1.5 mm in diameter, uniformly circular, convex and opaque after growth on RO medium at 25 °C for 3 days. Cells were Gram-negative, non-motile rods, 2.0–3.2 μ m long and 0.7–0.9 μ m wide, which divided by binary fission (Fig. 1).

Salt requirement for growth was tested in RO medium with final NaCl concentrations of 0, 2, 5, 10, 15, 20, 25 and 30 % (w/v) (at pH 7.8 and 25 °C). pH and temperature conditions for growth were determined by adjusting the final pH of the RO medium to 0, 2, 4, 6, 7, 8, 10, 12 and 14 with HCl or NaOH (2 % NaCl, 25 °C), and by incubation at 4, 10, 15, 25, 28, 37 and 45 °C (2 % NaCl, pH 7.8). The temperature range for growth was 10–30 °C (optimum, 25 °C), the pH range for growth was 6.0–9.0 (optimum, pH 8.0) and the NaCl concentration range for growth was 1–10 % (w/v) (optimum 1.0–2.0 %).

Oxidase activity of strain JLT354-W^T was tested according to Smibert & Krieg (1994) and catalase activity was determined by using 3 % (v/v) hydrogen peroxide solution

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain JLT354-W^T is EU734592.

Fig. 1. Micrographs of negatively stained cells of strain JLT354- W^T observed by using transmission electron microscopy. Bars, 0.5 μ m.

(Dong & Cai, 2001). Nitrite and nitrate reduction were tested in RO medium by growing the strain in the presence of NO_2^- and NO_3^- , respectively (Dong & Cai, 2001). Hydrolysis of starch, gelatin and Tween 80, and urease activity were determined as described by Dong & Cai (2001). H_2S production was tested in RO medium supplemented with 0.01% L-cysteine, the indicator being a strip of paper impregnated with lead acetate placed in the neck of the tube (Clarke, 1953; Mata *et al.*, 2002). Methyl red and Voges–Proskauer reaction tests were performed by using methyl red and Barritt's reagent (Barritt, 1936; Mata *et al.*, 2002). Accumulation of poly- β -hydroxybutyrate granules was determined by using the Sudan Black staining method (Smibert & Krieg, 1994). Growth on sole carbon and nitrogen sources was examined according to the procedures of Williams *et al.* (1983) on RO medium without organic compounds at 25 °C for 7–14 days.

Cellular fatty acid analysis was carried out as described by Komagata & Suzuki (1987). Isoprenoid quinones were analysed as described by Hiraiishi *et al.* (1998) by using a UPLC-Q-TOF-MS spectrometer and electrospraying ionization (Romano *et al.*, 2006). Tests of antimicrobial susceptibility were performed by using the disc-diffusion plate (Kirby–Bauer) method according to Fraser & Jorgensen (1997) and Andrews (2008), and with the antimicrobial compounds suggested by Mata *et al.* (2002). Strain JLT354- W^T was sensitive to gentamicin, ciprofloxacin, clindamycin, chloramphenicol, streptomycin, cefoperazone and ampicillin, but was resistant to cephalothin. The predominant fatty acid was $\text{C}_{18:1}\omega 7\text{c}$ (83.1% of the total); $\text{C}_{18:0}$ (7.9%), $\text{C}_{12:1}$ 3-OH (3.7%), $\text{C}_{16:0}$ (2.0%), 11-methyl $\text{C}_{18:1}\omega 7\text{c}$ (1.4%), $\text{C}_{17:1}\omega 8\text{c}$ (0.9%), $\text{C}_{20:1}\omega 7\text{c}$ (0.7%) and $\text{C}_{15:0}$ (0.5%) were also present. The predominant respiratory ubiquinone was Q-10.

Additional phenotypic properties are given in Table 1 and in the genus and species descriptions below.

Genomic DNA was extracted in accordance with the method of Marmur (1961) from cells grown in RO medium for 2 days at 28 °C and subsequently washed and resuspended in TE buffer. Purity was assessed by A_{280}/A_{260} and A_{230}/A_{260} ratios (Johnson, 1994). Phylogenetic analyses based on 16S rRNA gene sequences were performed as described by Ying

et al. (2007). The 16S rRNA gene was amplified with universal bacterial primers 27F (5'-AGAGTTTGATCC-TGGCTCAG) and 1492R (5'-GGTTACCTTGTTACGAC-TT) (Embley, 1991). The 16S rRNA gene sequence of strain JLT354- W^T was compared with those available from the GenBank database by using the BLAST program (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>; NCBI) to determine its approximate phylogenetic affiliation. The 16S rRNA gene sequence of strain JLT354- W^T was aligned with those of related species and phylogenetic trees were constructed by using the neighbour-joining and maximum-parsimony methods within the MEGA software package (Kumar *et al.*, 2004). The nearly complete 16S rRNA gene sequence of strain JLT354- W^T (1394 bp) was determined and used for phylogenetic analyses. The strain formed a monophyletic branch at the periphery of the evolutionary radiation occupied by the genus *Antarctobacter* (Fig. 2). Phylogenetic analysis based on 16S rRNA gene sequences showed that strain JLT354- W^T was related most closely to species of various genera: *Antarctobacter heliothermus* EL-219 T (91.7% similarity) (Labrenz *et al.*, 1998), *Sagittula stellata* E-37 T (91.3%) (Gonzalez *et al.*, 1997), *Pelagibaca bermudensis* HTCC2601 T (91.1%) (Cho & Stephen, 2006), *Tateyamaria omphalii* MKT107 T (90.7%) (Kurahashi & Yokota, 2007), *Oceanicola batsensis* HTCC2597 T (89.7%) (Cho & Giovannoni, 2004), *Leisingera methylohalidivorans* MB2 T (89.4%) (Schaefer *et al.*, 2002) and *Jannaschia rubra* 4SM3 T (89.3%) (Macián *et al.*, 2005b).

The genomic DNA G + C content of strain JLT354- W^T was estimated from the midpoint value (T_m) of the thermal denaturation profile, as described by Mandel *et al.* (1970). The DNA G + C content of strain JLT354- W^T was 63.7 mol%.

On the basis of the data presented, strain JLT354- W^T is considered to represent a novel species of a new genus within the *Roseobacter* clade of the order *Rhodobacterales*, for which the name *Mameliella alba* gen. nov., sp. nov. is proposed.

Description of *Mameliella* gen. nov.

Mameliella (Ma.me.li.el'la. N.L. fem. dim. n. *Mameliella* arbitrary name derived from the acronym MMEL, marine microbial ecology laboratory).

Table 1. Characteristics that differentiate strain JLT354-W^T from related members of the *Roseobacter* clade

Taxa: 1, strain JLT354-W^T; 2, *Antarctobacter heliothermus* (data from Labrenz *et al.*, 1998); 3, *Sagittula stellata* (Gonzalez *et al.*, 1997); 4, *Oceanicola batsensis* (Cho & Giovannoni, 2004); 5, *Leisingera methylohalidivorans* (Schaefer *et al.*, 2002); 6, *Wenxinia marina* (Ying *et al.*, 2007); 7, *Ponticoccus litoralis* (Hwang & Cho, 2008); 8, *Tropicibacter naphthalenivorans* (Harwati *et al.*, 2009). +, Positive; –, negative; w, weakly positive; v, variable; ND, not determined.

Characteristic	1	2	3	4	5	6	7	8
Motility	–	+ / –	ND	–	+	–	–	+
Optimum temperature (°C)	25–28	16–26	30	30	27	34–38	30	37
Optimum NaCl (%)	1–2	2–6	ND	0.75–10	ND	1–4	3–5	5
Optimum pH	8.0	6.9–7.8	7.5	7.5–8.0	7.7	7.5–8.0	7	7.6
DNA G + C content (mol%)	63.7	62.3–62.8	65.0	67.3	60.5	69.4	67.9	64.6
Respiratory ubiquinone	Q-10	Q-10	ND	ND	ND	Q-10	Q-10	Q-10
Colony colour	White	Brownish yellow	Pale cream	Faint yellow	Non-pigmented	Faint pink	Creamy	Yellowish white
Nitrate reduction	+	v	–	ND	ND	+	+	+
Poly-β-hydroxybutyrate	+	+	+	ND	ND	ND	+	ND
Utilization of:								
D-Malonic acid	+	–	ND	+	–	–	ND	ND
myo-Inositol	+	–	ND	+	–	–	+	ND
Cellobiose	+	–	+	–	–	+	ND	+
L-Sorbose	–	ND	ND	+	–	–	ND	+
Sucrose	+	ND	–	–	–	+	+	+
L-Alanine	+	–	+	–	–	+	+	+
L-Threonine	w	ND	–	+	–	ND	ND	ND
Glycine	–	ND	ND	+	–	ND	ND	ND
Antibiotic susceptibility								
Gentamicin	–	ND	ND	+	ND	+	–	–
Streptomycin	–	–	–	+	ND	–	–	–
Major fatty acids (%)								
11-methyl C _{18:1} ω7c	1.36	–	–	–	ND	5.4	11.3	14.7
C _{12:1} 3-OH	3.65	3.1	3.6	–	ND	–	3.0	1.2
C _{16:0}	2.0	2.5	8.6	15.0	ND	16.5	6.4	17.9
C _{18:0}	7.9	1.0	6.8	2.4	ND	3.9	4.6	1.7
C _{18:1} ω7c	83.1	83.2	–	31.0	ND	57.1	71.4	50.9
cyclo C _{19:0}	–	2.4	–	40.4	ND	–	–	2.4

Fig. 2. Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationship between strain JLT354-W^T and representatives of the order *Rhodobacterales*. Bootstrap percentages from neighbour-joining (above nodes) and maximum-parsimony (below nodes) analyses based on 1000 replications are shown at nodes; only values >50 % are shown. Bar, 0.02 substitutions per nucleotide position.

Cells are Gram-negative, non-motile rods that multiply by binary fission. Accumulates poly- β -hydroxybutyrate granules. White colonies are formed on RO medium. Oxidase- and catalase-positive. Negative for urease activity, hydrolysis of starch and gelatin, and production of indole. The predominant respiratory ubiquinone is Q-10. The type species is *Mameliella alba*.

Description of *Mameliella alba* sp. nov.

Mameliella alba (al'ba. L. fem. adj. *alba* white).

Exhibits the following properties in addition to those given in the genus description. Cells are 2.0–3.2 μm long and 0.7–0.9 μm wide. Small (about 0.5–1.5 mm) colonies are produced on RO medium after incubation at 25 °C for 3–5 days. Colonies are smooth, convex and opaque. Growth occurs at 10–30 °C, at pH 6.0–9.0 and in the presence of 1.0–10 % NaCl; optimal growth occurs at 25 °C, at pH 8.0 and in the presence of 1.0–2.0 % NaCl. Positive for nitrate reduction. Negative for hydrolysis of Tween 80, casein, aerobic nitrite reduction, methyl red test and Voges–Proskauer reaction. Results for utilization of various substrates as sole carbon sources, and other differential characteristics, are listed in Table 1. Utilizes L-malic acid, D-malonic acid, sodium D-gluconate, acetic acid, citric acid, lactic acid, D-sorbitol, D-mannitol, glycerol, *myo*-inositol, cellobiose, trehalose dihydrate, maltose, D-glucose, sucrose, D-xylose, L-alanine and L-arginine, but not L-sorbose, lysine, glycine, α -D-lactose, D-fructose, D-xylose or L-threonine. Acid is produced from D-glucose, sucrose, D-sorbitol, trehalose and maltose. Sensitive to gentamicin, ciprofloxacin, clindamycin, chloramphenicol, streptomycin, cefoperazone and ampicillin. The predominant fatty acid is C_{18:1 ω 7c}; significant amounts of C_{18:0}, C_{12:1} 3-OH, C_{16:0} and 11-methyl C_{18:1 ω 7c} are also present. The DNA G+C content of the type strain is 63.7 mol% (T_m).

The type strain, JLT354-W^T (=LMG 24665^T=CGMCC 1.7290^T), was isolated from surface water of the South China Sea in China.

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