Genus

Pseudomonadota/Alphaproteobacteria/Rhodobacterales/Roseobacteraceae/

Mangrovicoccus

Yu et al. 2018^{VP}

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Man.gro.vi.coc'cus. N.L. neut. n. *mangrovum*, mangrove; N.L. masc. n. *coccus*, a grain or berry; N.L. masc. n. *Mangrovicoccus*, a coccus bacterium from mangrove.

The genus *Mangrovicoccus* classified within the family *Roseobacteraceae*, order *Rhodobacterales*, class *Alphaproteobacteria*, and in the phylum *Pseudomonadota*, currently includes two species with validly published names. Gram-stain-negative, oxidase- and catalase-positive bacteria. Cells are coccoid or ellipsoid-shaped and divide through binary fission. Aerobic or facultatively aerobic, chemoorganotrophs. Slightly halophilic or haloduric, mostly grow well in the salinity range of 0.5–13.0% (w/v) NaCl, with the optimum of 2.0–4.0%. Grow at pH range from 6.0 to 10.0, with an optimum at approx. pH 7.0–8.0. Mesophilic, optimal growth at 35–40°C, growth range 10–50°C. The colony color is beige. The major respiratory quinone is Q-10. The predominant (>25% of the total) fatty acid is $C_{18:1}$ ω7*c*. The major polar lipids are phosphatidylethanolamine (PE), phosphatidylglycerol (PG), diphosphatidylglycerol (DPG), and phosphatidylmonomethylethanolamine (PME). Known habitats are marine environment, such as sediment from a mangrove forest and brown algae.

DNA G + C content (mol%): 67.9–68.8.

Type species: **Mangrovicoccus ximenensis** Yu et al. 2018^{VP}.

Description

Gram-stain-negative, oxidase- and catalase-positive bacteria. Cells are coccoid or ellipsoid-shaped and divide through binary fission. Colonies are beige, circular, and convex with regular edges. All species are **aerobes**; one species are strict aerobes, but **facultative anaerobes exist**. Chemoorganotrophs. Slightly halophilic or haloduric, grow well in the salinity range of 0.5–13.0% (w/v) NaCl, with the optimum of 2.0–4.0%. Grow at pH range from 6.0 to 10.0, with an optimum at approx. pH 7.0–8.0. **Mesophilic**, optimal growth at 35–40°C, growth range 10–50°C. **One species produces alginate lyase**. The major respiratory quinone is Q-10. The predominant (>25% of the total) fatty acid is $C_{18:1}$ ω7*c*. The major polar lipids are phosphatidylethanolamine (PE), phosphatidylglycerol (PG), diphosphatidylglycerol (DPG), and phosphatidylmonomethylethanolamine (PME). **Known habitats are marine environment**, such as sediment from a mangrove forest and brown algae.

DNA G + C content (mol%): 67.9–68.8.

Size of sequenced genomes (Mb): 4.4–5.97.

Type species: **Mangrovicoccus ximenensis** Yu et al. 2018^{VP}.

Number of species with validly published names: 2.

Family classification: The genus *Mangrovicoccus* is classified within the family *Roseobacteraceae*.

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DOI: 10.1002/9781118960608.gbm01935. Published by John Wiley & Sons, Inc., in association with Bergey's Manual Trust.

Further descriptive information

Cell morphology and ultrastructure

Totally, two species with validly published names in the genus *Mangrovicoccus* are proposed. Two currently described species, that is *M. ximenensis* and *M. algicola*, were isolated from sediment from a mangrove forest and brown alga, respectively. Cells of all species divide through binary fission (Yu et al., 2018; Shi et al., 2021). Cells of *M. ximenensis* are motile, coccoid, approximately 0.7–1.1 μm in diameter (Yu et al., 2018). Cells of *M. algicola* are nonmotile, ellipsoid, 1.3–2.0 μm in length and 1.2–1.5 μm in width (Shi et al., 2021).

Colonial and cultural characteristics

The type strain of *M. ximenensis* T1lg56^T was isolated firstly by marine agar 2216 (MA; Difco), while the type strain of *M. algicola* HB182678^T was isolated by MA supplemented with 0.5% sodium alginate. After picking and purification, visible colonies of genus *Mangrovicoccus* species appear after 2 days of incubation at 30°C. Colonies are beige, circular, and convex with regular edges (Yu et al., 2018; Shi et al., 2021) (Table 1). No pigment and bacteriochlorophyll were detected in *M. ximenensis* (Yu et al., 2018).

Nutrition and growth conditions

Strains of *Mangrovicoccus* species usually grow well in or on marine broth 2216 (MB, Difco; BD) and marine agar 2216 (MA, Difco;BD).

Optimal growth temperatures, pH, and concentration of NaCl vary between species (Table 1). The optimum temperature for growth varies among species, ranging from 35 to 40°C. The maximal and minimum growth temperatures are 40–50°C and 10°C, respectively (Table 1). The species of the *Mangrovicoccus* strains are slightly halophilic or haloduric, growing at a wide range (0.5–13.0%, w/v) of NaCl, with optimum of 2.0–4.0%. The pH range for growth is 6.0–10.0, with optimum at approx. pH 6.5–8.0.

Two species are aerobes. *M. ximenensis* T1lg56^T was described as strictly aerobic, but *M. algicola* HB182678^T shows properties of facultatively anaerobic with anaerobic growth on MA.

Chemoheterotrophic. The *Mangrovicoccus* strains can grow on MB or MA media, which contain peptone and yeast extract as organic nutrients (Yu et al., 2018; Shi et al., 2021). The *Mangrovicoccus* strains use organic acids and carbohydrates as sole sources of carbon for energy and growth. Although there is a limited amount of data for some species, two species can utilize gluconate and citrate as sole carbon and energy sources in API 20NE (Table 1). They also produce enzymes, and show some other characteristics typical of organotrophic bacteria, as shown in Table 1.

Chemotaxonomic characteristics

Mangrovicoccus species have Q-10 as the predominant isoprenoid quinone. In addition, ubiquinone-9 (Q-9) was also found as minor amount of respiratory quinone. The fatty acid profiles of *Mangrovicoccus* species vary depending on the growth conditions. However, the main component is stable (Table 2). The predominant fatty acid is $C_{18:1}$ ω7*c*, comprising 72–82.6% of the total fatty acids, and $C_{16:0}$ also occurs as major fatty acid (7.8–11.6%).

Two species of the genus *Mangrovicoccus* contain phosphatidylethanolamine (PE), phosphatidylglycerol (PG), diphosphatidylglycerol (DPG), and phosphatidylmethylethanolamine (PME) as major polar lipids. Some minor components distinguished the two species. *M. algicola* HB182678^T had unidentified phospholipids (PL), two unidentified glycolipids (GL1–GL2), and three unidentified aminolipids (AL1–AL3) as minor components, but *M. ximenensis* T1lg56^T had two unidentified phospholipids (PL1 and PL2) and five unidentified lipids (L1–5).

Genome features

The information on genomes is summarized in Table 3, including accession numbers and features. The genome sizes are 4.4 Mb and 5.97 Mb for *M. algicola* HB182678^T and *M. ximenensis* T1lg56^T, respectively. The G + C content are 67.9 mol% for *M. ximenensis* T1lg56^T and 68.8 mol% for *M. algicola* HB182678^T. The assembled genome of *M. ximenensis* T1lg56^T was 5,971,869 bp in size and comprised 34 contigs. A total of 6,350 genes and 44 tRNAs were detected. No rRNA genes were detected. The assembled genome of *M. algicola* HB182678^T was 4,397,334 bp in size and comprised 146 contigs. A total of 4,239 genes, three rRNAs (one each for 5S, 16S, and 23S rRNA) and 50 tRNAs were detected. For *M. algicola* HB182678^T, a total of 146 proteins were matched with the CAZy database, including 49 glycoside hydrolases, 40 glycosyl transferases, 26 carbohydrate esterases, 11 carbohydrate-binding modules, 12 auxiliary activities, and eight polysaccharide lyases (including three alginate lyases).

TABLE 1. Characteristics of the species in the genus *Mangrovicoccus*

Characteristics	*M. ximenensis* T1lg56^T (Yu et al., 2018; Shi et al., 2021)	*M. algicola* HB182678^T (Shi et al., 2021)
Colony morphology	Beige, circular, and convex with regular edges	Beige, circular, and convex with regular edges
Cell morphology	Coccoid	Ellipsoid-shaped
Cell size (μm)	0.7–1.1 μm in diameter	1.3–2.0 × 1.2–1.5 μm
Motile	+	–
Cell division	Binary fission	Binary fission
Type of metabolism	Aerobic	Facultative anaerobic
Growth range of pH (optimum)	6.0–9.5 (6.5)	6–10 (8)
Growth range of NaCl (optimum, %)	0.5–12.0 (2–4)[a]	0.5–13.0 (2.0–4.0)
Growth range of temperature (optimum, °C)	20–40 (35)	10–50 (37–40)
Oxidase	+	+
Catalase	+	+
Nitrate reduction	v	w
Urease	+	+
Alginate lyase	–	+
Arginine dihydrolase	v	w
Gelatinase activities	–	–
Indole production	–	–
Fermentation/oxidation of D-glucose	–	–
API ZYM results		
Alkaline phosphatase	+	+
Esterase (C4)	+	+
Esterase lipase (C8)	+	+
Lipase (C14)	w	–
Leucine arylamidase	+	+
Valine arylamidase	+	w
Cystine arylamidase	w	–
Trypsin	–	–
α-Chymotrypsin	–	–
Acid phosphatase	+	+
Naphthol-AS-Bl-phosphohydrolase	v	w(+)[b]
α-Galactosidase	–	–
β-Galactosidase	–	–
β-Glucuronidase	–	w(+)[b]
α-Glucosidase	–	w(+)[b]
N-Acetyl-β-glucosaminidase	–	–
α-Mannosidase	–	–
α-Fucosidase	–	–
Assimilation of (API 20NE)		
D-glucose	v	+
L-Aarabinose	+	–
D-Mannitol	+	–
N-Acetylglucosamine	+	–
Potassium gluconate	v	+

TABLE 1. *(continued)*

Characteristics	*M. ximenensis* T1lg56^T (Yu et al., 2018; Shi et al., 2021)	*M. algicola* HB182678^T (Shi et al., 2021)
Malic acid	v	+
Trisodium citrate	v	+
D-Mannose	v	−
Maltose	−	−
Capric acid	−	−
Phenylacetic acid	−	−
Adipic acid	w	−
Isoprenoid quinones	Q-10, Q-9	Q-10, Q-9
Major fatty acid (>5.0%)	$C_{18:1}$ $\omega 7c$, $C_{16:0}$	$C_{18:1}$ $\omega 7c$, $C_{16:0}$, $C_{18:0}$ and $C_{19:0}$ cyclo $\omega 8c$
Major polar lipids[c]	DPG, PG, PE, PME, PL, GL, L1–L3	DPG, PG, PE, PME, PL, GL1–GL2, AL1–AL3
DNA G + C content (mol%, by genome)	67.9	68.8

+, Positive; −, negative; w, weakly positive; w(+), weakly positive or positive; v, variable results from different literatures.

[a] Data obtained from Shi et al. (2021).

[b] Variable results from Shi et al. (2021), "weak" in description of the *Mangrovicoccus algicola* and "+" in Table 1.

[c] DPG, diphosphatidylglycerol; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PME, phosphatidylmonomethylethanolamine; AL, unidentified aminolipid; PL, unidentified phospholipid; GL, unidentified glycolipid; AL, unidentified aminolipid; L, unidentified lipid.

Ecology

Mangrovicoccus species are found in marine environments (Yu et al., 2018; Shi et al., 2021). The type strains of *M. ximenensis* were isolated from a sediment sample collected from Ximen Island mangrove forest (Yu et al., 2018). The type strain of *M. algicola* was isolated from brown alga (Shi et al., 2021). Three cultivation-dependent strains closely related to the genus *Mangrovicoccus* (with >97% 16S rRNA gene similarity) were found and were all from marine environments, such as mangrove sediment (*Poseidonocella* sp. strain 161398, MH001979 and *Ruegeria* sp. strain 161399, MH001980) and marine sediment (*Alphaproteobacteria* sp. ML20, JN791347).

Further use of cultivation-independent 16S rRNA gene-based methods from IMNGS (https://www.imngs.org/) demonstrated that *Mangrovicoccus* species are widely distributed in various environments and *Mangrovicoccus*-like 16S rRNA gene sequences also could be retrieved from human gut, soil, food, freshwater, fish, and terrestrial metagenomes.

Enrichments and isolation procedures

After the collection of the samples, a standard dilution plating technique is used to isolate strains. For *M. ximenensis* T1lg56^T, the marine sediment sample was serially diluted with artificial seawater (ASW; 3% sea salts), spread on marine agar 2216 (MA; Difco), and incubated at 30°C for 2–4 days. For *M. algicola* HB182678^T, 10 g mashed sample was diluted with 90 ml sterile aged seawater and kept shaking at 200 r.p.m for 30 min. Then, suspension liquid was serially diluted with sterile aged seawater and spread on modified 2216E agar (MA; Difco BD) supplemented with 0.5% sodium alginate. Plates were incubated at 30°C for 7 days and monitored at 24 h intervals.

Colonies appearing on the plates are selected and repeatedly streaked onto the same medium to obtain pure cultures. Since there are no other *Mangrovicoccus* strains reported, the procedure mentioned above can be applied for the genus *Mangrovicoccus*. Two members of genus *Mangrovicoccus* can grow on marine agar 2216 (MA; Difco; BD) or in marine broth 2216 (MB; Difco; BD).

Maintenance procedures

In order to store the *Mangrovicoccus* species, marine agar 2216 (MA; Difco; BD) or marine broth 2216 (MB; Difco; BD) and mid-exponential phase cultures are routinely used. For long-term preservation, the strains can be stored at −80°C in broth medium supplemented with 15–25% (v/v) glycerol suspension or by freeze-drying storage method.

TABLE 2. Fatty acid compositions (%) of type strains of *Mangrovicoccus* species

Fatty acid (%)	*M. ximenensis* T1lg56^T (incubated on Mb at 30°C for 2 days)	*M. ximenensis* T1lg56^T (grown on TSA plates (containing 2% NaCl) at 30°C for 2 days)	*M. algicola* HB182678^T (grown on TSA plates (containing 2% NaCl) at 30°C for 2 days)
$C_{12:0}$	TR	0.2	0.2
$C_{14:0}$	–	0.2	–
$C_{16:0}$	**11.6**	**7.8**	**8.2**
$C_{17:0}$	–	–	0.4
$C_{18:0}$	1.1	1.4	**5.6**
iso-$C_{16:0}$	–	0.3	–
$C_{10:0}$ 3OH	2.4	2.3	2.5
$C_{18:1}$ ω7*c*	**72.0**	**82.6**	**74.6**
$C_{18:1}$ ω7*c* 11-methyl	TR	0.4	–
$C_{19:0}$ cyclo ω8*c*	–	–	**5.5**
$C_{20:1}$ ω7*c*	–	–	0.2
ECL 11.799[a]	4.2	–	–
Summed feature 2[b]	2.4	1.5	1.8
Summed feature 3[c]	3.8	2.6	1.0

TR, Trace amount (<1%); –, not detected. Major components (>5.0%) are highlighted in bold.

[a] Unknown fatty acids are designated by their equivalent chain length.

[b] Summed features represent two or three fatty acids that cannot be separated by the MIDI.

[c] Summed feature 2 consisted of 12:0 aldehyde and/or unknown 10.9525. Summed feature 3 consisted of $C_{16:1}$ ω7*c* and/or $C_{16:1}$ ω6*c*.

TABLE 3. Genomic information for the type strains of *Mangrovicoccus* species

Species	*M. ximenensis* T1lg56^T (QBKZ00000000)	*M. algicola* HB182678^T (JACVXA000000000)
Genome size (Mb)	5.97	4.4
DNA G + C content (mol%)	67.9[a]	68.8
Protein count	5,049	4,047
rRNA	0	3
tRNA	44	50
Other RNA	3	3
Genes	6,350	4,239
Pseudogenes	1,254	136
GenBank assembly accession	GCA_003056725.1 (QBKZ00000000)	GCA_014903745.1 (JACVXA000000000)
Scaffolds/Contigs	34/34	146/146
References	Yu et al. (2018)	Shi et al. (2021)

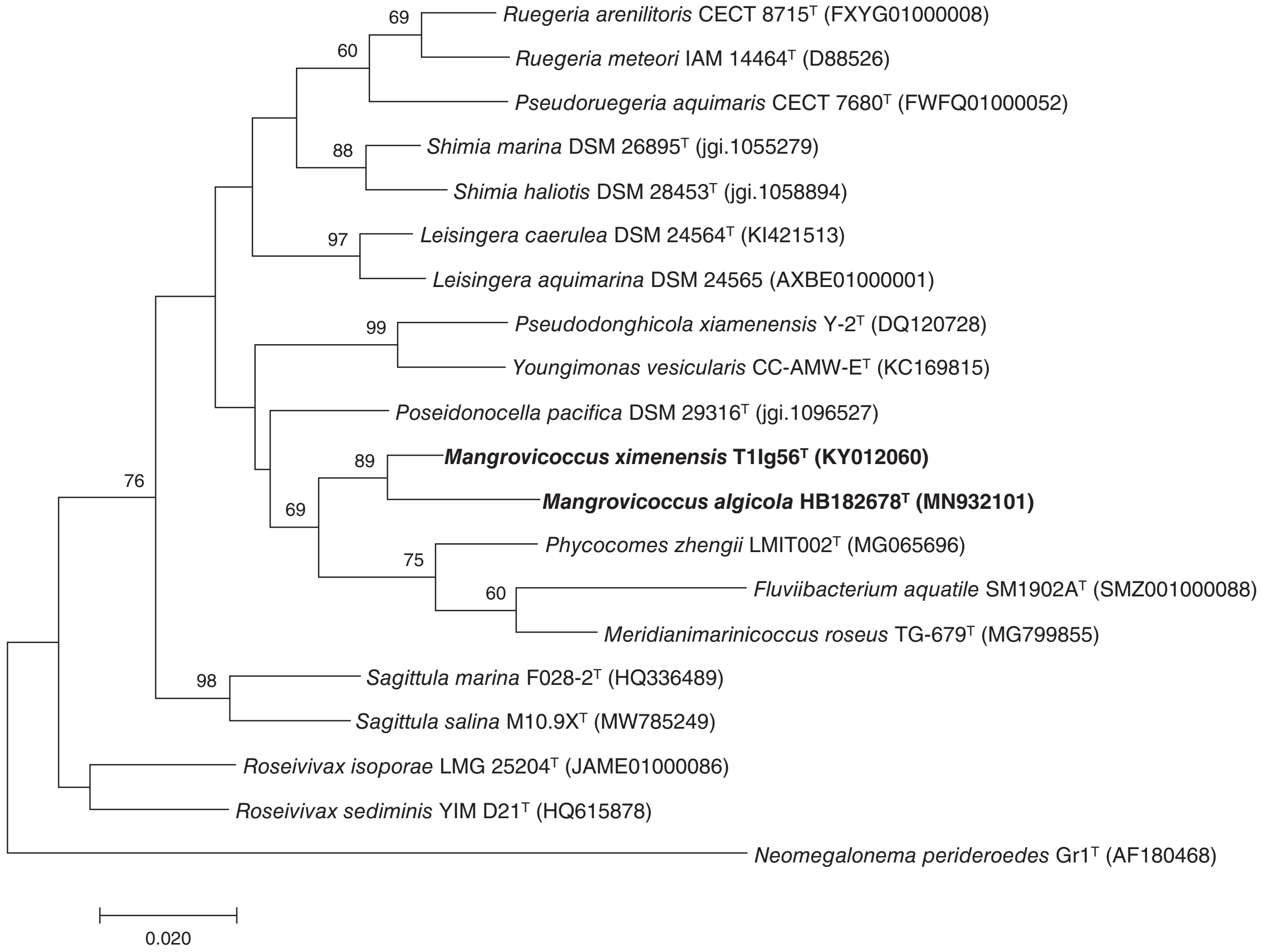
[a] Data obtained from NCBI GenBank Database accession number of QBKZ00000000.

Differentiation of the genus *Mangrovicoccus* from other genera

The 16S rRNA gene sequence similarity analysis revealed that the closest genera were genus *Poseidonocella* with *M. ximenensis* T1lg56^T and *Ruegeria* with *M. algicola* HB182678^T. The *Mangrovicoccus* species form an independent group that is well separated from the members of other genera based on 16S rRNA genes and whole-genome sequences. The maximum-likelihood phylogenetic trees based on 16S rRNA genes and whole-genome sequences are given (Figures 1 and 2).

The selected phenotypic properties useful for distinguishing the genus *Mangrovicoccus* and the closely related genera *Ruegeria* and *Poseidonocella* are compared in Table 4. None definitively distinguished *Mangrovicoccus* from the closely related genera *Ruegeria* and *Poseidonocella* (Table 4). Currently, the best approach to distinguish *Mangrovicoccus* species from other genera is based on the 16S rRNA gene and whole-genome sequences.

FIGURE 1. 16S rRNA gene-based maximum-likelihood tree showing the phylogenetic position of *Mangrovicoccus* species in relation to other representatives of the *Roseobacteraceae*. Bootstrap values were expressed as a percentage of 1,000 replicates, and only those higher than 60% were given at the branch points. Bar, 0.02 substitutions per nucleotide position.



Taxonomic comments

The genus *Mangrovicoccus* was proposed by Yu et al. (2018). The type strain *M. ximenensis* T1lg56^{T} shares the highest 16S rRNA sequence similarity (95.7%) with *Poseidonocella pacifica* KMM 9010^{T}. Initially, the genus *Mangrovicoccus* was reported belonging to the family *Rhodobacteraceae*. In 2021, whole-genome phylogenetic and genotypic analyses combined with a meta-analysis of phenotypic data to review taxonomic classifications of 331 type strains (under 119 genera) within the *Rhodobacteraceae* family was performed, and a new family, *Roseobacteraceae* fam. nov. was proposed (Liang et al., 2021). Unfortunately, the genus *Mangrovicoccus* was not included in this analysis and not reclassified into the *Roseobacteraceae* family at this time.

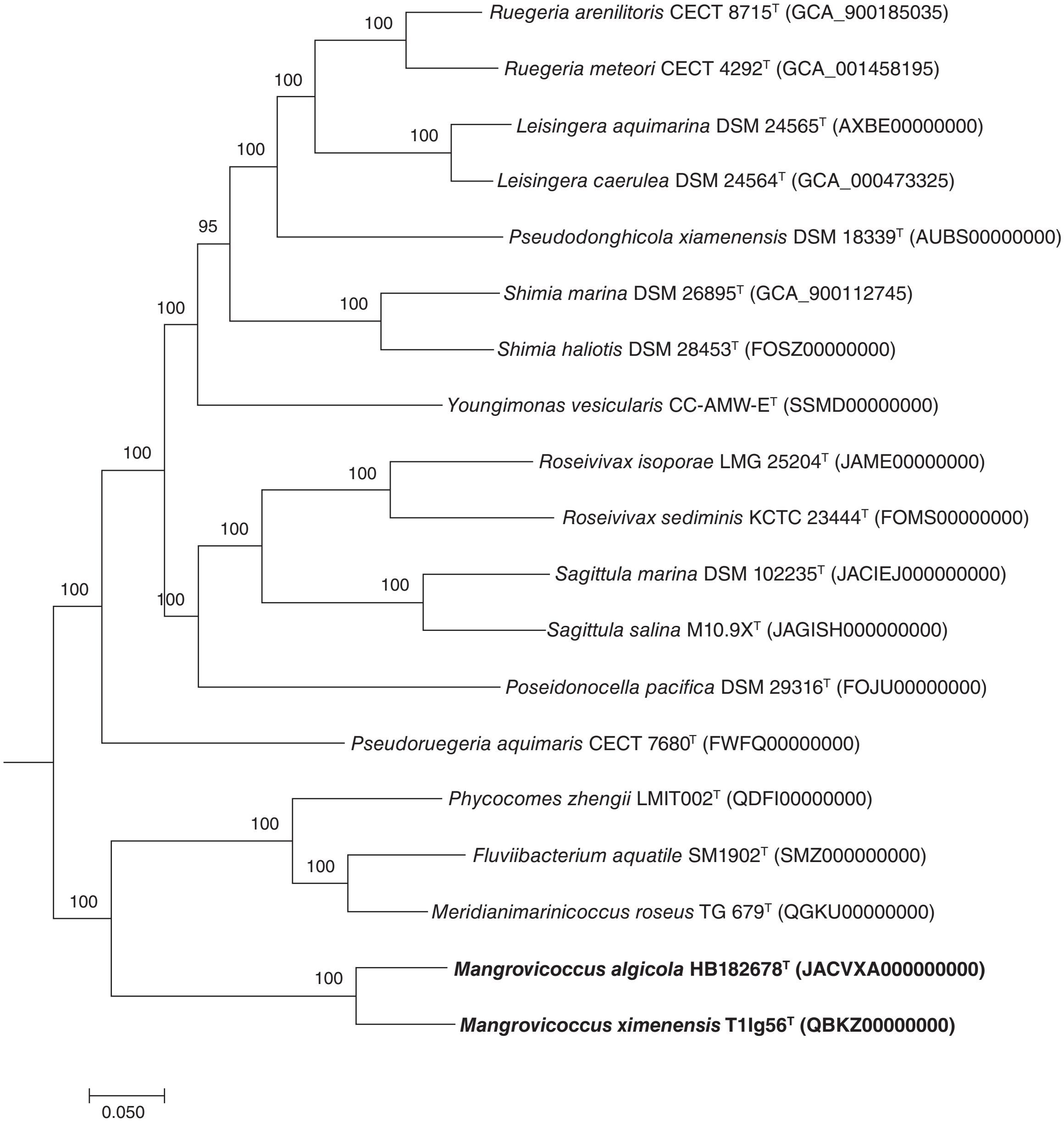
The phylogenetic trees of the 16S rRNA genes and genomes indicated that the genus *Mangrovicoccus* should belong to *Roseobacteraceae* family. Two species, *M. ximenensis and M. algicola,* are included in the genus *Mangrovicoccus.* Average nucleotide identity (ANI) among the two type strains is 84.3%, and *in silico* DNA–DNA hybridization is 27.2% (Shi et al., 2021).

List of species of the genus *Mangrovicoccus*

Mangrovicoccus algicola
Shi et al. 2021^{VP}

al.gi'co.la. L. fem. n. *alga*, seaweed, alga; L. masc./fem. n. suff. *-cola*, inhabitant, dweller; N.L. masc./fem. n. *algicola*, alga-dweller).

FIGURE 2. Maximum-likelihood phylogenetic tree of *Mangrovicoccus* species and other representatives of the *Roseobacteraceae* genomes. *Neomegalonema perideroedes* DSM 15528^{T} (ARFG00000000) was used as outgroup (data not shown). Bar, 0.05 substitutions per nucleotide position. The phylogenetic tree was constructed using IQ-TREE2 with LG+F+R6 model (Adapted from Minh et al. (2020)).



Cells are Gram-stain-negative, nonmotile, ellipsoid-shaped (1.3–2.0 × 1.2–1.5 μm) and divide through binary fission. Colonies on MA are beige, circular, and convex with regular edges. Anaerobic growth occurs on MA. The temperature range for growth is 10–50°C (optimum 37–40°C). The pH range for growth is 6–10 (optimum pH 8). Growth occurs at 0.5–13.0% (w/v) NaCl (optimum 2–4%). Nitrate can be reduced to nitrite weakly. Indole is not produced, and glucose is not fermented. Positive for oxidase, catalase, urease, β-glucosidase, alginate lyase, and arginine dihydrolase (weak); but negative for gelatinase and β-galactosidase. The following substrates are utilized for growth: D-glucose, gluconate, and citric acid. The following compounds are not utilized as sole carbon sources:

TABLE 4. Differentiation between genus *Mangrovicoccus* and its related genera in the family *Roseobacteraceae*

Characteristics	*Mangrovicoccus*	*Poseidonocella* (Romanenko et al., 2012)	*Ruegeria* (Wirth and Whitman, 2019)
Cell morphology	Coccoid, ellipsoid-shaped	Ovoid, rod	Rod
Colony color	Beige	Yellowish-beige, beige	Cream, colorless, beige, yellow, tan, or brownish
Cell division	Binary fission	Budding	Normal cell division
Fatty acid	$C_{18:1}$ ω7*c*	$C_{18:1}$ ω7*c*, 11-methyl $C_{18:1}$ ω7*c*	$C_{18:1}$ ω7*c*, or summed feature 8
Polar lipids[a]	DPG, PG, PE, PME, PL, GLs, ALs, Ls	PC, PG, DPG, PL, AL, Ls	PC, PG, Ls, ALs, DPG, PLs, PE
DNA G + C content (mol%)	67.9–68.8	60.5–65.4	55–68

+, Positive; −, negative; w, weakly positive.

[a] DPG, diphosphatidylglycerol; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PME, phosphatidylmonomethylethanolamine; AL, unidentified aminolipid; PL, unidentified phospholipid; GL, unidentified glycolipid; AL, unidentified aminolipid; L, unidentified lipid.

L-arabinose, D-mannitol, mannose, *N*-acetyl-glucosamine, maltose, capric acid, adipic acid, and phenylacetic acid. In API ZYM strips, positive for alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, and acid phosphatase; weak reaction for valine arylamidase, naphthol-AS-BI-phosphohydrolase, β-glucuronidase, and α-glucosidase; negative for lipase (C14), cystine arylamidase, trypsin, α-chymotrypsin, α-galactosidase, β-galactosidase, β-glucosidase, *N*-acetyl-β-glucosaminidase, α-mannosidase, and α-fucosidase. The predominant respiratory quinone is Q-10. The major polar lipids are diphosphatidylglycerol, phosphatidylglycerol, phosphatidylethanolamine, phosphatidylmethylethanolamine, an unidentified phospholipid, two unidentified glycolipids, and three unidentified aminophospholipids. Major cellular fatty acids (>5%) are $C_{18:1}$ ω7*c*, $C_{16:0}$, $C_{18:0}$ and $C_{19:0}$ cyclo ω8*c*. The type strain was isolated from brown alga samples collected from Hainan.

DNA G + C content (mol%): 68.8 (genome analysis).

Type strain: HB182678, MCCC 1K04624, KCTC 82318.

EMBL/GenBank accession (16S rRNA gene): MN932101.

EMBL/GenBank accession (genome): JACVXA000000000.

Mangrovicoccus ximenensis Yu et al. 2018$^{\mathrm{VP}}$

xi.men.en'sis. N.L. masc./fem. adj. *ximenensis*, pertaining to Ximen.

In addition to the characteristics listed for the genus, the species is characterized by the following features. Cells are coccoid, approximately 0.7–1.1 μm in diameter. Colonies on MA are beige, circular, and convex with regular edges. Growth occurs at 18–42°C (optimum, 35°C), at pH 6.0–9.5 (optimum, pH 6.5), and in the presence of 0.5–12.0% (w/v) NaCl (optimum, 2.0–4.0%). Acid is produced from D-galactose, maltose, lactose, and sucrose but not from trehalose and starch. In API 20E strips, positive for citrate utilization, acetoin production, urease, and tryptophan deaminase activities; negative for ONPG, arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase and gelatinase activities, H_2S and indole production, and fermentation/oxidation of D-glucose, D-mannitol, inositol, D-sorbitol, L-rhamnose, sucrose, melibiose, amygdalin, and L-arabinose. In the API 20NE strips, positive for urease activity, hydrolysis of aesculin, assimilation of D-glucose, L-arabinose, D-mannitol, *N*-acetylglucosamine, potassium gluconate, malic acid, trisodium citrate, and D-mannose; negative for nitrate reduction, *p*-nitrophenyl-β-D-galactopyranosidase activity, assimilation of maltose, capric acid, and phenylacetic acid; weak reaction for assimilation of adipic acid. Results obtained with API 20NE for indole production, fermentation of glucose, activities of arginine dihydrolase, urease, and gelatinase are similar to those with API 20E. In API ZYM strips, positive for alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase, acid phosphatase, and naphthol-AS-BI-phosphohydrolase; weak reaction for lipase (C14) and cystine arylamidase; negative for trypsin, α-chymotrypsin, α-galactosidase, β-galactosidase, β-glucuronidase, α-glucosidase, β-glucosidase, *N*-acetyl-β-glucosaminidase, α-mannosidase, and α-fucosidase. In addition to the predominant fatty acid of $C_{18:1}$ ω7*c*, significant amounts of $C_{16:0}$ are also present. The major respiratory quinone is Q-10. The type strain was isolated from sediment of mangrove forest in the Ximen Island in China.

DNA G + C content (mol%): 67.9 (*genome analysis*).

Type strain: T1lg56, CCTCC AB 2016238, KCTC 52623.

EMBL/GenBank accession number (16S rRNA gene): KY012060.

EMBL/GenBank accession number (genome): QBKZ00000000.

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