Roseivivax lentus sp. nov., isolated from a tidal flat sediment, and emended description of the genus *Roseivivax* Suzuki *et al.* 1999

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A Gram-negative-staining, aerobic, non-motile and rod-shaped bacterial strain, S5-5^T, was isolated from a tidal flat sediment at Saemankum on the west coast of Korea and subjected to a polyphasic taxonomic investigation. Strain S5-5^T grew optimally at pH 7.5–8.0, at 30 °C and in the presence of 2% (w/v) NaCl. It did not produce bacteriochlorophyll *a*. Phylogenetic analyses based on 16S rRNA gene sequences showed that strain S5-5^T is phylogenetically closely related to the genus *Roseivivax*, joining the cluster comprising the two recognized *Roseivivax* species. The 16S rRNA gene sequence similarity between strain S5-5^T and members of the genus *Roseivivax* was in the range 95.0–96.7%. Strain S5-5^T contained Q-10 as the predominant ubiquinone and C_{18:1}ω7c and 11-methyl C_{18:1}ω7c as the major fatty acids. The DNA G+C content was 68.2 mol%. Differential phenotypic properties, together with the phylogenetic distinctiveness, demonstrated that strain S5-5^T could be differentiated from *Roseivivax* species. On the basis of the data presented, strain S5-5^T is considered to represent a novel species of the genus *Roseivivax*, for which the name *Roseivivax lentus* sp. nov. is proposed. The type strain is S5-5^T (=KCTC 22708^T =CCUG 57755^T).

The genus *Roseivivax* was proposed by Suzuki *et al.* (1999) with the descriptions of two bacteriochlorophyll (BChl) *a*-containing species, *Roseivivax halodurans* and *Roseivivax halotolerans*. No further *Roseivivax* species with validly published names have been described to date. Phylogenetic analyses based on 16S rRNA gene sequences show that the genus *Roseivivax* belongs to the family *Rhodobacteraceae* (Suzuki *et al.*, 1999; Lee *et al.*, 2005). The two *Roseivivax* species were isolated from a salt lake (Suzuki *et al.*, 1999). In this study, we describe a bacterial strain, designated S5-5^T, which was isolated from a tidal flat sediment on the west coast of Korea. Comparative 16S rRNA gene sequence analysis indicated that strain S5-5^T is phylogenetically affiliated to the genus *Roseivivax*. The aim of the present work was to determine the exact taxonomic position of strain S5-5^T by using a polyphasic characterization that included the determination of chemotaxonomic and phenotypic properties and a detailed phylogenetic investigation based on 16S rRNA gene sequences.

Strain S5-5^T was isolated by means of the dilution plating technique on marine agar 2216 (MA; Difco) at 25 °C. The type strains of the two recognized *Roseivivax* species were used as reference strains for phenotypic characterization and the analyses of fatty acids and polar lipids. *R. halodurans* KCTC 22255^T was obtained from the Korean Collection for Type Cultures, Taejeon, Korea, and *R. halotolerans* JCM 10271^T was obtained from the Japan Collection of Microorganisms, Saitama, Japan. The morphological, physiological and biochemical characteristics of strain S5-5^T were investigated using routine cultivation on MA at 30 °C. Cell morphology was examined by using light microscopy (E600; Nikon) and transmission electron microscopy (CM-20; Philips). Flagellation was determined by using transmission electron microscopy with cells from exponentially growing cultures. Gliding motility was investigated as described by Bowman (2000). The Gram reaction was determined by using the bioMérieux Gram-stain kit according to the manufacturer's instructions. Growth under anaerobic conditions was determined after incubation in a Forma anaerobic chamber on MA and on MA supplemented with 0.1% (w/v) potassium nitrate, both of which had been prepared anaerobically under a nitrogen atmosphere. Growth at 4, 15, 20, 25, 30, 37, 40 and 45 °C was measured on MA. Growth in the absence of NaCl and in the presence of 0.5, 1.0, 2.0 and 3.0% (w/v) NaCl was investigated by using trypticase soy broth prepared

Abbreviation: BChl, bacteriochlorophyll.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain S5-5^T is FJ875966.

Photos of TLC plates showing polar lipids of strain S5-5^T and *Roseivivax* type strains are available as supplementary material with the online version of this paper.

according to the formula of the Difco medium except for supplementation with 0.45 % (w/v) $\text{MgCl}_2 \cdot 6\text{H}_2\text{O}$ or 0.06 % (w/v) KCl and exclusion or addition of NaCl as necessary. Growth at various NaCl concentrations (2.0–15.0 %, w/v, in increments of 1.0 %) was investigated in marine broth 2216 (MB; Difco). The pH range for growth was determined in MB adjusted to pH 4.5–9.5 (in increments of 0.5 pH units) by the addition of HCl or Na_2CO_3 . Catalase and oxidase activities were investigated as described by Cowan & Steel (1965). Hydrolysis of casein, starch, hypoxanthine, xanthine and tyrosine was tested on MA using substrate concentrations described by Cowan & Steel (1965). Hydrolysis of aesculin, gelatin, Tweens 20, 40, 60 and 80 and urea and reduction of nitrate were investigated as described by Lányi (1987) with the modification that artificial seawater (l^{-1} distilled water: 23.6 g NaCl, 0.64 g KCl, 4.53 g $\text{MgCl}_2 \cdot 6\text{H}_2\text{O}$, 5.94 g $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ and 1.3 g $\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$; Bruns *et al.*, 2001) was used for medium preparation. Cellulase and xylanase activities were investigated on MA containing 0.5 % (w/v) CM-cellulose (Sigma) or xylan (Sigma), respectively, and detected according to the method of Teather & Wood (1982). DNase activity was examined by using DNase test agar with methyl green (Difco) with the modification that artificial seawater was used for medium preparation. Acid production from carbohydrates was determined as described by Leifson (1963). Utilization of substrates as sole carbon and energy sources was tested as described by Baumann & Baumann (1981), using supplementation with 2 % (v/v) Hutner's mineral base (Cohen-Bazire *et al.*, 1957) and 1 % (v/v) vitamin solution (Staley, 1968). H_2S production was tested as described by Bruns *et al.* (2001). Susceptibility to antibiotics was investigated on MA plates using antibiotic discs containing the following (μg per disc unless otherwise stated): polymyxin B (100 U), streptomycin (50), penicillin G (20 U), chloramphenicol (100), ampicillin (10), cephalothin (30), gentamicin (30), novobiocin (5), tetracycline (30), kanamycin (30), lincomycin (15), oleandomycin (15), neomycin (30) and carbenicillin (100). Enzyme activities were determined after incubation for 4 h at 30 °C by using the API ZYM system (bioMérieux). Additional biochemical tests were performed using the API 20E system (bioMérieux); strips were inoculated with cells suspended in artificial seawater. For pigment absorption-spectrum analysis, strain S5-5^T was cultivated aerobically in the dark at 30 °C in MB. *R. halodurans* KCTC 22255^T and *R. halotolerans* JCM 10271^T were used as positive controls for the pigment absorption-spectrum analysis. The culture was centrifuged, washed twice using a MOPS buffer (0.01 M MOPS/NaOH, 0.1 M KCl, 0.001 M MgCl_2 ; pH 7.5) and disrupted by sonication with a Branson 450 sonifier. After removal of cell debris by centrifugation, the absorption spectrum of the supernatant was determined with a Beckman Coulter DU800 spectrophotometer. An aliquot of the culture was also centrifuged, the pigments from the cells were extracted using acetone/methanol (7:2, v/v) and the absorption spectrum of the pigments was determined with a Beckman Coulter DU800 spectrophotometer.

Cell biomass of strain S5-5^T for DNA extraction and for the analyses of isoprenoid quinones and polar lipids was obtained from cultures grown in MB at 30 °C. Chromosomal DNA was extracted and purified by the procedure described by Yoon *et al.* (1996), with the modification that RNase T1 was used in combination with RNase A to minimize contamination with RNA. Amplification of the 16S rRNA gene sequence was performed using two universal primers as described previously (Yoon *et al.*, 1998) and the PCR products were purified by using a QIAquick PCR purification kit (Qiagen). Sequencing of the amplified 16S rRNA gene and phylogenetic analysis were performed as described by Yoon *et al.* (2003). Isoprenoid quinones were analysed as described by Komagata & Suzuki (1987), using reversed-phase HPLC and a YMC ODS-A (250 × 4.6 mm) column. Polar lipids were extracted according to the procedures described by Minnikin *et al.* (1984) and identified by two-dimensional TLC followed by spraying with appropriate detection reagents (Minnikin *et al.*, 1984; Komagata & Suzuki, 1987). For cellular fatty acid analysis, cell mass of strain S5-5^T, *R. halodurans* KCTC 22255^T and *R. halotolerans* JCM 10271^T was harvested from MA plates after cultivation for 3 days at 30 °C. The fatty acids were extracted and fatty acid methyl esters were prepared according to the standard protocol of the Microbial Identification System (Sasser, 1990). The DNA G+C content was determined using the method of Tamaoka & Komagata (1984) with the modification that DNA was hydrolysed using nuclease P1 (Sigma) and the resultant nucleotides were analysed by reversed-phase HPLC.

The morphological, cultural, physiological and biochemical characteristics of strain S5-5^T are given in the species description and in Table 1. Strain S5-5^T did not produce BChl *a* during aerobic growth in the dark. The 16S rRNA gene sequence of strain S5-5^T determined in this study comprised 1385 nucleotides, representing approximately 96 % of the *Escherichia coli* 16S rRNA gene sequence. In the neighbour-joining phylogenetic tree based on 16S rRNA gene sequences, strain S5-5^T joined the cluster comprising the type strains of the two *Roseivivax* species with a bootstrap confidence level of 69.4 %, and this relationship was also maintained in the tree constructed using the maximum-likelihood algorithm (Fig. 1). Strain S5-5^T exhibited 16S rRNA gene sequence similarity of 96.7 and 95.0 % to *R. halotolerans* OCh 210^T and *R. halodurans* OCh 239^T, respectively. The DNA G+C content of strain S5-5^T was 68.2 mol%.

The predominant ubiquinone detected in strain S5-5^T was ubiquinone-10 (Q-10), with a peak area ratio of approximately 93 %, which is the same as that of *Roseivivax* species (Suzuki *et al.*, 1999). The cellular fatty acid profile of strain S5-5^T is shown in Table 2, in which the cellular fatty acid profiles of the two *Roseivivax* type strains analysed in this study are also given. The fatty acid profile of strain S5-5^T was similar with those of the *Roseivivax* type strains in that $\text{C}_{18:1}\omega 7c$ is the predominant fatty acid, but there were also

Table 1. Differential phenotypic characteristics of strain S5-5^T and the type strains of *Roseivivax* species

Strains: 1, *Roseivivax lentus* sp. nov. S5-5^T; 2, *R. halodurans* KCTC 22255^T; 3, *R. halotolerans* JCM 10271^T. Data were taken from this study unless indicated. All three strains are Gram-negative-staining and positive for oxidase*, catalase*, hydrolysis of Tweens 20, 40 and 60 (weakly positive for *R. halodurans* JCM 10271^T), activity of alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase and naphthol-AS-BI-phosphohydrolase and susceptibility to ampicillin, streptomycin, novobiocin, cephalothin, neomycin, carbenicillin, penicillin G and chloramphenicol. All three strains are negative for production of H₂S*, hydrolysis of CM-cellulose, casein, DNA, starch*, xanthine and xylan, acid production from D-sorbitol, myo-inositol, melezitose, trehalose, D-fructose, sucrose and raffinose, activity of lipase (C14), 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 and susceptibility to polymyxin B and lincomycin. +, Positive; w, weakly positive; –, negative.

Characteristic	1	2	3
Colony colour on MA	Greyish yellow	Greyish yellow	Reddish orange
Production of BChl <i>a</i>	–	+	+
Presence of flagella	–	+	+
NaCl range for growth (%)	2–13	0–20*	0.5–20*
Anaerobic growth	–	+	+
Nitrate reduction	+	+	–
Indole production	–	+	+
Hydrolysis of:			
Aesculin	–	+	+
Gelatin	–	–	+
Hypoxanthine	–	+	+
Tween 80	+	–	–
Tyrosine	–	+	+
Urea	–	–	+
Acid production from:			
L-Arabinose	–	+	+
Cellobiose	–	+	–
D-Galactose	–	+	w
D-Glucose	–	+	–
Lactose	–	+	–
Maltose	–	+	–
D-Mannitol	–	w	–
D-Mannose	–	+	–
Melibiose	–	+	–
L-Rhamnose	–	w	–
D-Ribose	–	+	–
D-Xylose	–	+	–
Acid phosphatase activity	–	–	+
Antibiotic susceptibility			
Oleandomycin	–	–	+
Kanamycin	+	+	–
Tetracycline	–	+	–
Gentamicin	+	+	–
Major polar lipids†	PG, PE, AL, PL, L	PG, PE, PL, L	PG, PE, AL, PL, L
Presence of DPG†	+	+	–
DNA G + C content (mol%)	68.2	64.4*	59.7*

*Data for *R. halodurans* OCh 239^T and *R. halotolerans* OCh 210^T from Suzuki *et al.* (1999).

†AL, Unknown aminolipid; DPG, diphosphatidylglycerol; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PL, unidentified phospholipid; L, unidentified lipids.

differences in the proportions of some fatty acids, particularly 11-methyl C_{18:1}ω7c and C_{19:0} cyclo ω8c. The major polar lipids found in strain S5-5^T were phosphatidylglycerol, phosphatidylethanolamine, an unidentified aminolipid, an unidentified phospholipid and two unidentified lipids (Table 1 and Supplementary Fig. S1, available

in IJSEM Online). The polar lipid profiles of *R. halodurans* KCTC 22255^T and *R. halotolerans* JCM 10271^T were similar to that of strain S5-5^T in that phosphatidylglycerol, phosphatidylethanolamine, an unidentified phospholipid and two unidentified lipids are the major polar lipids (Table 1 and Supplementary Fig. S1). An unidentified

Fig. 1. Neighbour-joining tree based on 16S rRNA gene sequences showing the positions of strain S5-5^T, the type strains of the two *Roseivivax* species and some other related taxa. Bootstrap values (>50%) based on 1000 replications are shown at branch nodes. Filled circles indicate that the corresponding nodes were also recovered in trees generated with the maximum-likelihood and maximum-parsimony algorithms. Open circles indicate that the corresponding node was also recovered in the tree generated with the maximum-likelihood algorithm. *Stappia stellulata* IAM 12621^T was used as an outgroup. Bar, 0.01 substitutions per nucleotide position.

aminolipid was present as a major polar lipid in strain S5-5^T and *R. halotolerans* JCM 10271^T but absent in *R. halodurans* KCTC 22255^T. A minor amount of diphosphatidylglycerol was detected in strain S5-5^T and *R. halodurans* KCTC 22255^T but not detected in *R. halotolerans* JCM 10271^T. Differences in polar lipid profiles among members of the same genus have been reported many times. There were no distinct chemotaxonomic properties that served to differentiate strain S5-5^T from the two recognized *Roseivivax* species. Accordingly, in view of the combined phylogenetic and chemotaxonomic data, it appears to be reasonable to classify strain S5-5^T within the genus *Roseivivax*.

The phylogenetic distinctiveness is sufficient to categorize strain S5-5^T as a member of a species that is distinct from the recognized *Roseivivax* species (Stackebrandt & Goebel, 1994). Strain S5-5^T is also distinguishable from *Roseivivax* species by differences in phenotypic characteristics, including colony colour, presence of flagella, production of Bchl *a*, susceptibility to antibiotics and hydrolysis of, utilization

Table 2. Cellular fatty acid compositions of strain S5-5^T and the type strains of *Roseivivax* species

Strains: 1, *Roseivivax lentus* sp. nov. S5-5^T; 2, *R. halodurans* KCTC 22255^T; 3, *R. halotolerans* JCM 10271^T. Values are percentages of total fatty acids, obtained in this study. Fatty acids that represented <0.5% in all strains were omitted. —, Not detected.

Fatty acid	1	2	3
Straight-chain			
C _{16:0}	6.5	6.4	2.9
C _{17:0}	3.2	0.8	0.2
C _{18:0}	4.8	7.8	4.2
Branched			
iso-C _{15:0}	—	0.9	—
Unsaturated			
C _{18:1} ω7c	68.2	59.1	69.7
C _{20:1} ω7c	0.3	0.3	1.1
C _{20:2} ω6,9c	—	1.3	—
Hydroxy			
C _{10:0} 3-OH	1.2	—	0.2
C _{12:0} 3-OH	0.5	3.3	2.1
C _{12:1} 3-OH	1.0	—	1.5
C _{19:0} cyclo ω8c	2.4	15.7	12.8
11-Methyl C _{18:1} ω7c	10.7	3.8	3.9
Summed feature 7*	0.2	—	1.0

*Summed features represent groups of two or three fatty acids that cannot be separated by the Microbial Identification System. Summed feature 7 consisted of one or more of C_{19:1}ω6c, C_{19:0} cyclo ω10c and an unknown fatty acid (equivalent chain-length 18.846).

of and acid production from various substrates (Table 1). Therefore, on the basis of the phenotypic, chemotaxonomic and phylogenetic data, strain S5-5^T is considered to represent a novel species of the genus *Roseivivax*, for which the name *Roseivivax lentus* sp. nov. is proposed.

Emended description of the genus *Roseivivax* Suzuki *et al.* 1999

The description of the genus *Roseivivax* is as given by Suzuki *et al.* (1999) with the following amendments. Motile or non-motile. Bchl *a* may or may not be produced. Anaerobic growth may or may not occur. Common major polar lipids are phosphatidylglycerol, phosphatidylethanolamine, an unidentified phospholipid and unidentified lipids. The DNA G + C content is 59.7–68.2 mol%.

Description of *Roseivivax lentus* sp. nov.

Roseivivax lentus (len' tus. L. masc. adj. *lentus* slow, delayed, referring to the slow growth of the micro-organism).

Cells are Gram-negative-staining, aerobic, non-flagellated, non-gliding and rod-shaped, 0.5–1.0 μm in diameter and 1.0–3.0 μm long. Colonies on MA are circular, slightly convex, glistening, smooth and greyish yellow. Optimal growth temperature is 30 °C; growth occurs at 10 and

40 °C, but not at 4 or 45 °C. Optimal pH for growth is between pH 7.5 and 8.0; growth occurs at pH 5.5, but not at pH 5.0. Growth occurs in the presence of 2.0–13.0 % (w/v) NaCl with an optimum of approximately 2.0 % (w/v) NaCl. BChl *a* is not produced. D-Fructose, D-galactose, D-glucose, acetate, succinate, L-malate and L-glutamate are utilized as sole carbon and energy sources, but L-arabinose, cellobiose, maltose, D-mannose, sucrose, trehalose, D-xylose, citrate, benzoate, pyruvate, salicin and formate are not. The predominant ubiquinone is Q-10. The major polar lipids are phosphatidylglycerol, phosphatidylethanolamine, an unidentified aminolipid, an unidentified phospholipid and two unidentified lipids. The major cellular fatty acids (>10 % of total fatty acids) are C_{18:1}ω7c and 11-methyl C_{18:1}ω7c. Other phenotypic characteristics are given in Table 1. The DNA G+C content of the type strain is 68.2 mol% (determined by HPLC).

The type strain, S5-5^T (=KCTC 22708^T =CCUG 57755^T), was isolated from a tidal flat sediment at Saemankum on the west coast of Korea.

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References

- Baumann, P. & Baumann, L. (1981). The marine Gram-negative eubacteria: genera *Photobacterium*, *Beneckea*, *Alteromonas*, *Pseudomonas*, and *Alcaligenes*. In *The Prokaryotes*, pp. 1302–1331. Edited by M. P. Starr, H. Stolp, H. G. Trüper, A. Balows & H. G. Schlegel. Berlin: Springer.
- Bowman, J. P. (2000). Description of *Cellulophaga algicola* sp. nov., isolated from the surfaces of Antarctic algae, and reclassification of *Cytophaga uliginosa* (ZoBell and Upham 1944) Reichenbach 1989 as *Cellulophaga uliginosa* comb. nov. *Int J Syst Evol Microbiol* **50**, 1861–1868.
- Bruns, A., Rohde, M. & Berthe-Corti, L. (2001). *Muricauda ruestringensis* gen. nov., sp. nov., a facultatively anaerobic, appendaged bacterium from German North Sea intertidal sediment. *Int J Syst Evol Microbiol* **51**, 1997–2006.
- Cohen-Bazire, G., Sistrom, W. R. & Stanier, R. Y. (1957). Kinetic studies of pigment synthesis by nonsulfur purple bacteria. *J Cell Comp Physiol* **49**, 25–68.
- Cowan, S. T. & Steel, K. J. (1965). *Manual for the Identification of Medical Bacteria*. London: Cambridge University Press.
- Komagata, K. & Suzuki, K. (1987). Lipid and cell-wall analysis in bacterial systematics. *Methods Microbiol* **19**, 161–207.
- Lányi, B. (1987). Classical and rapid identification methods for medically important bacteria. *Methods Microbiol* **19**, 1–67.
- Lee, K.-B., Liu, C.-T., Anzai, Y., Kim, H., Aono, T. & Oyaizu, H. (2005). The hierarchical system of the 'Alphaproteobacteria': description of *Hyphomonadaceae* fam. nov., *Xanthobacteraceae* fam. nov. and *Erythrobacteraceae* fam. nov. *Int J Syst Evol Microbiol* **55**, 1907–1919.
- Leifson, E. (1963). Determination of carbohydrate metabolism of marine bacteria. *J Bacteriol* **85**, 1183–1184.
- Minnikin, D. E., O'Donnell, A. G., Goodfellow, M., Alderson, G., Athalye, M., Schaal, A. & Parlett, J. H. (1984). An integrated procedure for the extraction of bacterial isoprenoid quinones and polar lipids. *J Microbiol Methods* **2**, 233–241.
- Sasser, M. (1990). *Identification of bacteria by gas chromatography of cellular fatty acids*, MIDI Technical Note 101. Newark, DE: MIDI Inc.
- Stackebrandt, E. & Goebel, B. M. (1994). Taxonomic note: a place for DNA-DNA reassociation and 16S rRNA sequence analysis in the present species definition in bacteriology. *Int J Syst Bacteriol* **44**, 846–849.
- Staley, J. T. (1968). *Prosthecomicrobium* and *Ancalomicrobium*: new prosthecate freshwater bacteria. *J Bacteriol* **95**, 1921–1942.
- Suzuki, T., Muroga, Y., Takahama, M. & Nishimura, Y. (1999). *Roseivivax halodurans* gen. nov., sp. nov. and *Roseivivax halotolerans* sp. nov., aerobic bacteriochlorophyll-containing bacteria isolated from a saline lake. *Int J Syst Bacteriol* **49**, 629–634.
- Tamaoka, J. & Komagata, K. (1984). Determination of DNA base composition by reversed-phase high-performance liquid chromatography. *FEMS Microbiol Lett* **25**, 125–128.
- Teather, R. M. & Wood, P. J. (1982). Use of Congo red-polysaccharide interactions in enumeration and characterization of cellulolytic bacteria from the bovine rumen. *Appl Environ Microbiol* **43**, 777–780.
- Yoon, J.-H., Kim, H., Kim, S.-B., Kim, H.-J., Kim, W. Y., Lee, S. T., Goodfellow, M. & Park, Y.-H. (1996). Identification of *Saccharomonospora* strains by the use of genomic DNA fragments and rRNA gene probes. *Int J Syst Bacteriol* **46**, 502–505.
- Yoon, J.-H., Lee, S. T. & Park, Y.-H. (1998). Inter- and intraspecific phylogenetic analysis of the genus *Nocardioides* and related taxa based on 16S rDNA sequences. *Int J Syst Bacteriol* **48**, 187–194.
- Yoon, J.-H., Kim, I.-G., Shin, D.-Y., Kang, K. H. & Park, Y.-H. (2003). *Microbulbifer salipaludis* sp. nov., a moderate halophile isolated from a Korean salt marsh. *Int J Syst Evol Microbiol* **53**, 53–57.