First published in: Int J Syst Evol Microbiol, 2009. 60(3) 537-541. doi:10.1099/ijs.0.014142-0

Promicromonospora umidemergens sp. nov., isolated from moisture from indoor wall material

K. Martin,[1] J. Schäfer[2] and P. Kämpfer[2]

Correspondence
P. Kämpfer
peter.kaempfer@umwelt.uni-giessen.de

[1]Institut Leibniz-Institut für Naturstoff-Forschung und Infektionsbiologie eV, Hans-Knöll-Institut, D-07745 Jena, Germany

[2]Institut für Angewandte Mikrobiologie, Justus-Liebig-Universität Giessen, D-35392 Giessen, Germany

A Gram-positive, yellow-pigmented, branched-hyphae-forming micro-organism, strain 09-Be-007^T, was isolated from the wall of an indoor environment. Based on 16S rRNA gene sequence similarity studies, strain 09-Be-007^T belonged to the genus *Promicromonospora*. The novel isolate showed sequence similarities of 98.8 % to *Promicromonospora aerolata* V54A^T, 98.9 % to *Promicromonospora vindobonensis* V45^T, 98.1 % to *Promicromonospora sukumoe* DSM 44121^T, 98.2 % to *Promicromonospora kroppenstedtii* RS16^T, 96.7 % to *Promicromonospora flava* CC 0387^T and 97.8 % to *Promicromonospora citrea* DSM 43110^T, the type strain of the type species of this genus. Cell wall sugars of strain 09-Be-007^T were galactose, rhamnose and glucose. The diagnostic diamino acid of the cell-wall peptidoglycan was lysine. The major menaquinones detected were MK-9(H_4) and MK-9(H_6). Major polar lipids were diphosphatidylglycerol, phosphatidylglycerol and phosphatidylinositol. Major fatty acids were iso-$C_{15:0}$ and anteiso-$C_{15:0}$; moderate amounts of anteiso-$C_{17:0}$, iso-$C_{16:0}$ and iso-$C_{15:1}$ were also found. All these data supported the affiliation of strain 09-Be-007^T to the genus *Promicromonospora*. DNA–DNA hybridization values and physiological and biochemical data enabled strain 09-Be-007^T to be differentiated genotypically and phenotypically from the six recognized species of the genus *Promicromonospora*. For these reasons, strain 09-Be-007^T represents a novel species, for which the name *Promicromonospora umidemergens* sp. nov. is proposed, with 09-Be-007^T (=DSM 22081^T=CCM 7634^T) as the type strain.

The genus *Promicromonospora* currently harbours six species: *Promicromonospora citrea* (Krasil'nikov *et al.*, 1961), *Promicromonospora sukumoe* (Takahashi *et al.*, 1987), *Promicromonospora aerolata* and *Promicromonospora vindobonensis* (Busse *et al.*, 2003), *Promicromonospora kroppenstedtii* (Alonso-Vega *et al.*, 2008), and *Promicromonospora flava* (Jiang *et al.*, 2009). Two species originally described as members of the genus *Promicromonospora* have been transferred to other genera: *Promicromonospora enterophila* (Jäger *et al.*, 1983) was transferred to the genus *Oerskovia* as *Oerskovia enterophila* (Stackebrandt *et al.*, 2002), and *Promicromonospora pachnodae* (Cazemier *et al.*, 2003) was reclassified as *Xylanimicrobium pachnodae* (Stackebrandt & Schumann, 2004). *P. citrea, P. sukumoe* and *P. kroppenstedtii* were isolated from soil samples, whereas *P. aerolata* and *P. vindobonensis* were isolated from the air of the medieval Virgilkapelle in Vienna. *P. flava* was isolated from sediment from the Baltic Sea in Germany.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain 09-Be-007^T is FN293378.

Strain 09-Be-007^T was enriched and recovered from a wall that was colonized with moulds. After extraction of 1 g sample material by shaking for 15 min in 10 ml 0.9 % NaCl solution containing 0.01 % (v/v) Tween 80, aliquots of this suspension were spread on agar plates containing organic medium M79 agar (Prauser & Falta, 1968) and incubated for 2 weeks at 28 °C. The new strain was maintained on M79 agar and preserved at −80 °C by mixing well-grown M79 broth cultures in a 1 : 1 ratio with glycerol preservation medium (Salser, 1978) containing K_2HPO_4 (1.26 %), KH_2PO_4 (0.36 %), $MgSO_4.7H_2O$ (0.01 %), sodium citrate (0.09 %), $(NH_4)_2SO_4$ (0.18 %) and glycerol (8.80 %). Stock cultures of the isolate in liquid M79 supplemented with 5 % DMSO were also maintained in the vapour phase of liquid nitrogen.

Morphological properties, Gram-staining and cell morphology were observed microscopically as described by Kämpfer & Kroppenstedt (2004). Strain 09-Be-007^T formed yellow-pigmented colonies with characteristic wrinkly and shining surfaces. Branching septate hyphae, which grew on the agar surface and penetrated into the

agar, were observed microscopically. Aerial mycelium was not observed. In older cultures, hyphae broke up into non-motile fragments of various sizes. One-day-old cultures stained Gram-positive.

DNA isolation was performed with a commercial DNA extraction kit (GenElute Plant Genomic DNA kit; Sigma) after disruption of cells by a 1 min bead-beating step with 1 g Zirconia beads (0.1 mm diameter) at maximum speed.

Multiple sequence alignment and analysis of the data were performed using the software package MEGA version 4 (Tamura *et al.*, 2007), the ARB software package (version December 2007; Ludwig *et al.*, 2004) and the corresponding SILVA SSURef 95 database (version July 2008; Pruesse *et al.*, 2007). Genetic distance calculations (distance options according to the Kimura-2 model) and clustering were determined with the neighbour-joining method (Fig. 1) and the maximum-likelihood method with FASTDNAML (Olsen *et al.*, 1994; results not shown). Bootstrap values were based on 1000 replications. The 16S rRNA gene sequence of strain 09-Be-007^T was a continuous stretch of 1327 bp.

Sequence similarity calculations after pairwise local alignment indicated that the closest relatives of strain 09-Be-007^T were *P. aerolata* V54A^T (98.8 % 16S rRNA gene sequence similarity) and *P. vindobonensis* V45^T (98.9 % similarity).

Bacterial biomass for chemotaxonomic investigations was prepared by cultivating strain 09-Be-007^T for 24–48 h in shake flasks in liquid organic medium M79 at 180 r.p.m. and 28 °C. For fatty acid analysis, cells were grown on tryptic soy agar (TSA) at 28 °C for 48 h.

Cell-wall amino acids were determined by TLC according to Schleifer & Kandler (1972). The peptidoglycan hydrolysates contained the diagnostic diamino acid lysine together with glutamic acid and alanine. Whole-cell sugars, determined by TLC (Becker *et al.*, 1965), were galactose, rhamnose and glucose. The same composition was reported for *P. vindobonensis* and *P. aerolata*. *P. flava* contained ribose in addition to these sugars, whereas *P. citrea* contained only galactose and *P. kroppenstedtii* contained galactose plus rhamnose (Table 1).

Menaquinones were extracted as described by Collins *et al.* (1977) and analysed by HPLC (Groth *et al.*, 1996). In contrast to previously described species of the genus *Promicromonospora*, which contain MK-9(H_4) as the predominant menaquinone, strain 09-Be-007^T exhibited a quinone system with a high amount of MK-9(H_6) (48 %), followed by MK-9(H_4) (36 %). Minor amounts of MK-8(H_4) (6 %) and MK-9(H_2) (2 %) were also detected. Menaquinone MK-8(H_4) has also been found in *P. kroppenstedtii* and *P. flava*, but not in the other four species of the genus *Promicromonospora*. *P. citrea* contained only one nonhydrated menaquinone with nine isoprenoid units (MK-9).

Polar lipids were extracted according to Minnikin *et al.* (1979). Major lipids were diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol, three unknown glycolipids and one unknown phospholipid. The same complex pattern of phospholipids with the major components and some unknown glyco- and phospholipids was also described for *P. kroppenstedtii*. Diphosphatidylglycerol is found in all species of the genus *Promicromonospora*, except *P. citrea*, and phosphatidylglycerol has not been reported for *P. sukumoe* (Table 1).

The fatty acid profile (Table 2) of strain 09-Be-007^T was very similar to those of the other species with predominant

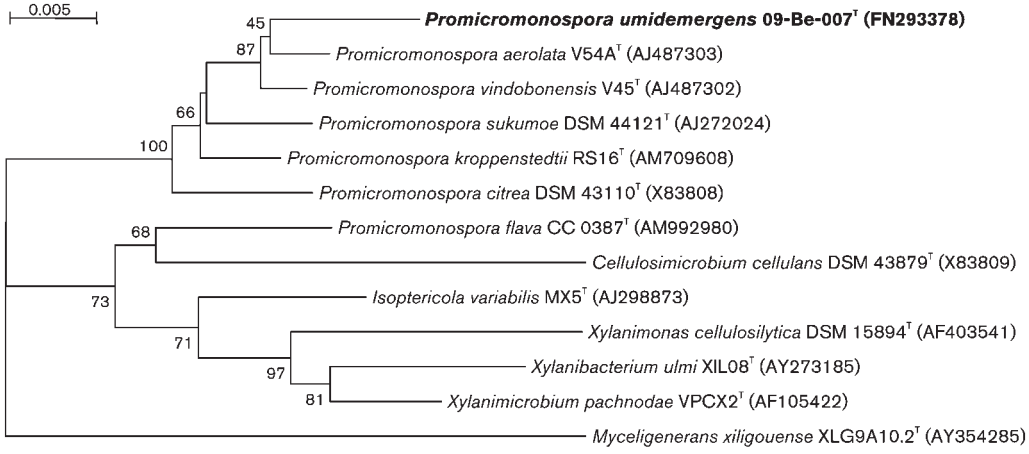

Fig. 1. Neighbour-joining tree based on 16S rRNA gene sequences showing the phylogenetic relationships between strain 09-Be-007^T, other members of the genus *Promicromonospora* and closely related taxa of the family *Promicromonosporaceae*. Numbers at the nodes are bootstrap percentages (1000 replications). All nodes of the *Promicromonospora* branch were also seen in the maximum-likelihood tree. Bar, 0.005 changes per nucleotide position.

Table 1. Chemotaxonomic characteristics that differentiate the type strains of members of the genus *Promicromonospora*

Strains: 1, 09-Be-007^T; 2, *P. vindobonensis* V45^T; 3, *P. aerolata* V54A^T; 4, *P. kroppenstedtii* RS16^T; 5, *P. citrea* DSM 43110^T; 6, *P. sukumoe* DSM 44121^T; 7, *P. flava* CC 0387^T. Data are from this study, Takahashi *et al.* (1987), Kalakoutskii *et al.* (1989), Busse *et al.* (2003) and Jiang *et al.* (2009).

Characteristic	1	2	3	4	5	6	7
Menaquinone composition (%)	MK-9(H_6), 48; MK-9(H_4), 36; MK-8(H_4), 6; MK-9(H_2), 2	MK-9(H_4), 92; MK-9(H_2), 4; MK-9(H_6), 4	MK-9(H_4), 93; MK-9(H_2), 7	MK-9(H_4), 64; MK-9(H_6), 15; MK-8(H_4), 10; MK-9(H_2), 2	MK-9	MK-9(H_4), MK-9, MK-9(H_2), MK-9(H_6)	MK-9(H_4), 86; MK-8(H_4), 7; MK-9(H_2), 5; MK-9, 3
Polar lipids*	PG, DPG, PI, unknown PL, 3 unknown GL	DPG, PG, unknown GL, PGL	DPG, PG, 2 unknown GL, 2 unknown PGL, unknown PL	PG, DPG, PI, GL and PGL	PG, PI, unidentified glucosamine-phospholipid	PI, DPG	DPG, PG, unknown GL, unknown PL
Cell-wall composition†	Lys (Glu, Ala)	Glu : Gly : Ala : Lys (0.98 : 0.69 : 2.88 : 1.0) (A3α)	Glu : Gly : Ala : Lys (1.05 : 0.43 : 3.4 : 1.0) (A3α)	Ala : Glu : Lys (2.3 : 2.0 : 1.0) (A4α)	Lys-Ala (A3α)	Lys (A3α)	Lys (Ala)
Cell-wall sugars‡	rha, gal, glu§	rha, gal, glu	rha, gal, glu	gal, rha	gal	rha, glu, rib§	rha, gal, glu, rib§

*DPG, Diphosphatidylglycerol; GL, glycolipid; PG, Phosphatidylglycerol; PGL, phosphoglycolipid; PI, phosphatidylinositol; PL, phospholipid.
†Ala, Alanine; Glu, glutamic acid; Gly, glycine; Lys, lysine. Amino acids given in parentheses are minor components.
‡gal, Galactose; glu, glucose; rha, rhamnose; rib, ribose.
§Whole-cell sugars.

amounts of iso-$C_{15:0}$ (between 30 and 41 %) and anteiso-$C_{15:0}$ (between 34 and 52 %). The newly described species *P. flava* is an exception, showing a higher proportion of anteiso-$C_{15:0}$ (57.2 %) and less than 20 % iso-$C_{15:0}$ (16.3 %). It should be mentioned here that *P. flava* may not belong to the genus *Promicromonospora* and should be studied again for its taxonomic allocation (see Tables 1 to 3 and Fig. 1).

Table 2. Fatty acid contents of strain 09-Be-007^T and the type strains of all other species of the genus *Promicromonospora* grown under the same conditions

Strains: 1, 09-Be-007^T; 2, *P. vindobonensis* V45^T; 3, *P. aerolata* V54A^T; 4, *P. kroppenstedtii* RS16^T; 5, *P. sukumoe* DSM 44121^T; 6, *P. citrea* DSM 43110^T; 7, *P. flava* CC 0387^T. All strains were grown on TSA for 48 h at 28 °C and analysed using the MIDI system (Kämpfer & Kroppenstedt, 1996). −, Not detected. Data are from this study except where indicated.

Fatty acid	1	2	3	4	5	6	7*
$C_{13:0}$	−	−	−	0.2	−	−	−
$C_{14:0}$	−	1.5	0.8	1.8	1.3	0.6	−
iso-$C_{14:0}$	0.5	−	0.3	1.5	0.9	1.2	−
iso-$C_{15:1}$ G	7.0	−	0.4	0.5	3.4	−	−
anteiso-$C_{15:1}$ A	2.5	−	0.4	1.2	4.4	−	−
iso-$C_{15:0}$	38.6	36.7	30.8	39.7	36.6	40.6	16.3
anteiso-$C_{15:0}$	34.8	46.5	51.1	43.2	38.0	38.9	57.2
$C_{15:0}$	−	−	−	1.0	1.6	1.0	−
$C_{16:0}$ N alcohol	−	−	−	−	0.4	−	−
iso-$C_{16:0}$	4.8	2.2	2.2	4.4	3.9	4.0	−
$C_{16:0}$	1.0	6.0	3.8	1.9	2.4	0.8	−
Summed feature 5†	−	2.0	1.4	−	−	−	−
iso-$C_{17:0}$	3.5	1.3	1.5	1.2	2.0	3.1	−
anteiso-$C_{17:0}$	6.8	3.8	6.7	3.4	4.6	9.7	−
$C_{18:1}\omega 9c$	−	−	0.5	−	−	−	−
$C_{18:3}\omega 6,9,12c$	−	−	−	−	0.4	−	−

*Data from Jiang *et al.* (2009).
†Summed feature 5 contains $C_{18:2}\omega 6,9c$ and/or anteiso-$C_{18:0}$, which could not be separated by GLC with the MIDI system.

Table 3. Biochemical characteristics of type strains of members of the genus *Promicromonospora*

Strains: 1, 09-Be-007^T; 2, *P. kroppenstedtii* RS16^T; 3, *P. vindobonensis* V45^T; 4, *P. aerolata* V54A^T; 5, *P. sukumoe* IFO 14650^T; 6, *P. citrea* IFO 12397^T; 7, *P. flava* CC 0387^T. +, Positive; (+), weakly positive; −, negative; ND, not determined. Data are from this study except where indicated.

Characteristic	1	2	3	4	5	6	7*
Assimilation of:							
N-Acetyl-D-glucosamine	+	+†	+	(+)	+	+	ND
Trehalose	+	+†	+	(+)	+	+	+
Cellobiose	+	+†	(+)	+	+	+	ND
D-Fructose	+	+‡	(+)	+	+	+	−
D-Glucose, D-xylose	+	+†	+	−	+	+	+
Maltose	+	+‡	+	−	+	+	−
D-Mannose, salicin	+	+‡	(+)	−	+	−	ND
D-Ribose, sucrose	+	+†	(+)	−	+	−	+
D-Sorbitol	+	+†	(+)	−	+	−	−
L-Arabinose	+	+†	−	−	+	+	ND
L-Aspartate, L-histidine	+	−	−	−	+	+	ND
Pyruvate	+	+	(+)	(+)	+	(+)	ND
L-Proline	+	(+)	+	(+)	+	(+)	ND
DL-3-Hydroxybutyrate, DL-lactate, L-malate	+	+	(+)	(+)	+	+	ND
Fumarate	+	+	(+)	−	+	+	ND
L-Alanine	−	−	−	−	+	(+)	ND
L-Rhamnose	+	−	(+)	(+)	−	+	−
Glutarate	(+)	−	(+)	(+)	−	−	ND
Propionate	(+)	−	+	−	−	−	ND
Hydrolysis of:†§							ND
pNP-phenylphosphonate, L-proline-pNA, L-alanine-pNA, pNP-β-D-xylopyranoside, pNP-β-D-glucopyranoside	+	+	+	−	+	+	ND
Aesculin	+	+†	(+)	−	+	+	ND
bis-pNP phosphate	+	+	−	−	+	+	ND
pNP-β-D-galactopyranoside	+	+†	−	−	(+)	(+)	ND

*Data from Jiang *et al.* (2009).
†Data for *P. kroppenstedtii* are congruent with those from Alonso-Vega *et al.* (2008).
‡Data for *P. kroppenstedtii* are not congruent with those from Alonso-Vega *et al.* (2008).
§pNA, *p*-Nitroanilide; pNP, *p*-nitrophenyl.

Although the 16S rRNA gene sequence similarity studies clearly supported the affiliation of strain 09-Be-007^T to the genus *Promicromonospora*, some chemotaxonomic markers differed from those of previously described species of this genus. The results of the comparative physiological characterization carried out using identical test conditions are given in Table 3 and in the species description, with methods as described previously (Kämpfer *et al.*, 1991). The observed chemotaxonomic (Table 1) and physiological (Table 3) differences between the type strains of the recognized members of the genus *Promicromonospora* and strain 09-Be-007^T clearly warrant the creation of a separate species.

DNA–DNA hybridization experiments were performed with strain 09-Be-007^T and *P. aerolata* V54A^T, *P. vindobonensis* V45^T and *P. kroppenstedtii* RS16^T using the method described by Ziemke *et al.* (1998) with a minor variation in the nick translation step (2 μg DNA was labelled during a 3 h incubation at 15 °C). Strain 09-Be-007^T showed low DNA–DNA hybridization with *P. aerolata* V54A^T (42.4 %, reciprocal 56 %), *P. vindobonensis* V45^T (42.2 %, reciprocal 46 %) and *P. kroppenstedtii* RS16^T (36 %, reciprocal 23.2 %).

Description of *Promicromonospora umidemergens* sp. nov.

Promicromonospora umidemergens (u.mi.de.mer′gens. L. adj. *umidus* moist; L. part. adj. *emergens* emerging, rising; N.L. part. adj. *umidemergens* rising moisture).

A Gram-stain-positive, aerobic, chemo-organotrophic bacterium. Forms yellow-pigmented colonies with characteristic wrinkly and shining surfaces. Possesses branched septate hyphae that grow on the agar surface and penetrate into the agar. Aerial mycelium is not observed. Hyphae break up into non-motile fragments of various sizes. The major components of the quinone system are MK-9(H_6) and MK-9(H_4). The diagnostic diamino acid of the cell-wall peptidoglycan is lysine; glutamic acid and alanine are

also found. The polar lipid profile consists of diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol, three unknown glycolipids and one unknown phospholipid as major lipids. Fatty acid composition is dominated by iso- and anteiso-branched fatty acids. Major fatty acids are iso-$C_{15:0}$ and anteiso-$C_{15:0}$; moderate amounts of iso-$C_{15:1}$, anteiso-$C_{15:1}$, iso-$C_{17:0}$ and anteiso-$C_{17:0}$ are also found. Carbon source utilization patterns and differential characteristics of *P. umidemergens* and related *Promicromonospora* species (determined under identical conditions) are indicated in Table 3.

The type strain is 09-Be-007^T (=DSM 22081^T=CCM 7634^T), isolated by C. Trautmann, Berlin, Germany, from the wall of a house with rising damp and colonized with moulds.

Acknowledgements

We are grateful to Carmen Schult and Gundula Will for excellent technical assistance. We are grateful to Jean Euzéby for support with the nomenclature and to Dr Martha Trujillo for supplying the type strain of *P. kroppenstedtii*. The study was supported in part by the Federal Environment Agency (Umweltbundesamt) grant number FKZ 20562236.

References

Alonso-Vega, P., Santamaría, R., Martínez-Molina, E. & Trujillo, M. E. (2008). *Promicromonospora kroppenstedtii* sp. nov., isolated from a sandy soil. *Int J Syst Evol Microbiol* **58**, 1476–1481.

Becker, B., Lechevalier, M. P. & Lechevalier, H. A. (1965). Chemical composition of cell-wall preparations from strains of various form-genera of aerobic actinomycetes. *Appl Microbiol* **13**, 236–243.

Busse, H.-J., Zlamala, C., Buczolits, S., Lubitz, W., Kämpfer, P. & Takeuchi, M. (2003). *Promicromonospora vindobonensis* sp. nov. and *Promicromonospora aerolata* sp. nov., isolated from the air of the medieval 'Virgilkapelle' in Vienna. *Int J Syst Evol Microbiol* **53**, 1503–1507.

Cazemier, A. E., Verdoes, J. C., Reubsaet, F. A. G., Hackstein, J. H. P., van der Drift, C. & Op den Camp, H. J. M. (2003). *Promicromonospora pachnodae* sp. nov., a member of the (hemi) cellulolytic hindgut flora of larvae of the scarab beetle *Pachnoda marginata*. *Antonie van Leeuwenhoek* **83**, 135–148.

Collins, M. D., Pirouz, T., Goodfellow, M. & Minnikin, D. E. (1977). Distribution of menaquinones in actinomycetes and corynebacteria. *J Gen Microbiol* **100**, 221–230.

Groth, I., Schumann, P., Weiss, N., Martin, K. & Rainey, F. A. (1996). *Agrococcus jenensis* gen. nov., sp. nov., a new genus of actinomycetes with diaminobutyric acid in the cell wall. *Int J Syst Bacteriol* **46**, 234–239.

Jäger, K., Márialigeti, K., Hauck, M. & Barabás, G. (1983). *Promicromonospora enterophila* sp. nov., a new species of monospore actinomycetes. *Int J Syst Bacteriol* **33**, 525–531.

Jiang, Y., Wiese, J., Cao, Y.-R., Xu, L.-H., Imhoff, J. F. & Jiang, C.-L. (2009). *Promicromonospora flava* sp. nov., isolated from sediment of the Baltic Sea. *Int J Syst Evol Microbiol* **59**, 1599–1602.

Kalakoutskii, L. V., Agre, N. S., Prauser, H. & Evtushenko, L. I. (1989). Genus *Promicromonospora* Krasil'nikov, Kalakoutskii and Kirillova 1961a, 107^{AL}. In *Bergey's Manual of Systematic Bacteriology*, vol. 4, pp. 2392–2395. Edited by S. T. Williams, M. E. Sharpe & J. G. Holt. Baltimore: Williams & Wilkins.

Kämpfer, P. & Kroppenstedt, R. M. (1996). Numerical analysis of fatty acid patterns of coryneform bacteria and related taxa. *Can J Microbiol* **42**, 989–1005.

Kämpfer, P. & Kroppenstedt, R. M. (2004). *Pseudonocardia benzenivorans* sp. nov. *Int J Syst Evol Microbiol* **54**, 749–751.

Kämpfer, P., Steiof, M. & Dott, W. (1991). Microbiological characterization of a fuel-oil contaminated site including numerical identification of heterotrophic water and soil bacteria. *Microb Ecol* **21**, 227–251.

Krasil'nikov, N. A., Kalakoutskii, L. V. & Kirillova, N. F. (1961). A new genus of *Actinomycetales*, *Promicromonospora* gen. nov. *Bull Acad Sci USSR Ser Biol* **1**, 107–112.

Ludwig, W., Strunk, O., Westram, R., Richter, L., Meier, H., Yadhukumar, Buchner, A., Lai, T., Steppi, S. & other authors (2004). ARB: a software environment for sequence data. *Nucleic Acids Res* **32**, 1363–1371.

Minnikin, D. E., Collins, M. D. & Goodfellow, M. (1979). Fatty acid and polar lipid composition in the classification of *Cellulomonas*, *Oerskovia* and related taxa. *J Appl Bacteriol* **47**, 87–95.

Olsen, G. J., Matsuda, H., Hagstrom, R. & Overbeek, R. (1994). fastDNAml: a tool for construction of phylogenetic trees of DNA sequences using maximum likelihood. *Comput Appl Biosci* **10**, 41–48.

Prauser, H. & Falta, R. (1968). Phagensensibilität, Zellwand-Zusammensetzung und Taxonomie von Actinomyceten. *Z Allg Mikrobiol* **8**, 39–46.

Pruesse, E., Quast, C., Knittel, K., Fuchs, B. M., Ludwig, W., Peplies, J. & Glöckner, F. O. (2007). SILVA: a comprehensive online resource for quality checked and aligned ribosomal RNA sequence data compatible with ARB. *Nucleic Acids Res* **35**, 7188–7196.

Salser, W. (1978). Cloning DNA sequences: a general technique for propagating eukaryotic gene sequences in bacterial cells. In *Genetic Engineering*, Chapter 3, pp. 53–81. Edited by A. M. Chakrabarty. West Palm Beach, FL: CRC Press.

Schleifer, K. H. & Kandler, O. (1972). Peptidoglycan types of bacterial cell walls and their taxonomic implications. *Bacteriol Rev* **36**, 407–477.

Stackebrandt, E. & Schumann, P. (2004). Reclassification of *Promicromonospora pachnodae* Cazemier *et al.* 2004 as *Xylanimicrobium pachnodae* gen. nov., comb. nov. *Int J Syst Evol Microbiol* **54**, 1383–1386.

Stackebrandt, E., Breymann, S., Steiner, U., Prauser, H., Weiss, N. & Schumann, P. (2002). Re-evaluation of the status of the genus *Oerskovia*, reclassification of *Promicromonospora enterophila* (Jäger *et al.* 1983) as *Oerskovia enterophila* comb. nov. and description of *Oerskovia jenensis* sp. nov. and *Oerskovia paurometabola* sp. nov. *Int J Syst Evol Microbiol* **52**, 1105–1111.

Takahashi, Y., Tanaka, Y., Iwai, Y. & Ōmura, S. (1987). *Promicromonospora sukumoe* sp. nov., a new species of the *Actinomycetales*. *J Gen Appl Microbiol* **33**, 507–519.

Tamura, K., Dudley, J., Nei, M. & Kumar, S. (2007). MEGA4: Molecular evolutionary genetics analysis (MEGA) software version 4.0. *Mol Biol Evol* **24**, 1596–1599.

Ziemke, F., Höfle, M. G., Lalucat, J. & Rosselló-Mora, R. (1998). Reclassification of *Shewanella putrefaciens* Owen's genomic group II as *Shewanella baltica* sp. nov. *Int J Syst Bacteriol* **48**, 179–186.