Micrococcus lactis sp. nov., isolated from dairy industry waste

Chittipurna, Pradip K. Singh, Dipti Verma, Anil Kumar Pinnaka, Shanmugam Mayilraj and Suresh Korpole

Correspondence

Suresh Korpole
suresh@imtech.res.in

Microbial Type Culture Collection and Gene bank, Institute of Microbial Technology, Sector 39A, Chandigarh – 160 036, India

A Gram-positive, yellow-pigmented, actinobacterial strain, DW152^T, was isolated from a dairy industry effluent treatment plant. 16S rRNA gene sequence analysis indicated that strain DW152^T exhibited low similarity with many species with validly published names belonging to the genera *Micrococcus* and *Arthrobacter*. However, phenotypic properties including chemotaxonomic markers affiliated strain DW152^T to the genus *Micrococcus*. Strain DW152^T had ai-C_{15:0} and i-C_{15:0} as major cellular fatty acids, and MK-8(H₂) as the major menaquinone. The cell-wall peptidoglycan of strain DW152^T had L-lysine as the diagnostic amino acid and the type was A4 α . The DNA G+C content of strain DW152^T was 68.0 mol%. In 16S rRNA gene sequence analysis, strain DW152^T exhibited significant similarity with *Micrococcus terreus* NBRC 104258^T, but the mean value of DNA–DNA relatedness between these strains was only 42.3%. Moreover, strain DW152^T differed in biochemical and chemotaxonomic characteristics from *M. terreus* and other species of the genus *Micrococcus*. Based on the above differences, we conclude that strain DW152^T should be treated as a novel species of the genus *Micrococcus*, for which the name *Micrococcus lactis* sp. nov. is proposed. The type strain of *Micrococcus lactis* sp. nov. is DW152^T (=MTCC10523^T =DSM 23694^T).

The genus *Micrococcus* was first described by Cohn (1872) and was subsequently emended repeatedly (Stackebrandt *et al.*, 1995; Wieser *et al.*, 2002). It comprises Gram-positive, non-spore-forming, aerobic, non-motile cocci. All species of the genus with validly published names were isolated from different environments, such as a wall painting, air, activated sludge (Wieser *et al.*, 2002; Liu *et al.*, 2007), roots of plants (Chen *et al.*, 2009; Zhao *et al.*, 2009) and soil (Liu *et al.*, 2000; Zhang *et al.*, 2010). The genus *Micrococcus* is phylogenetically closely related to other genera of the family *Micrococcaceae* and exhibits similarity in many properties, including chemotaxonomic markers (Stackebrandt *et al.*, 1995). In the present study we isolated a strain designated DW152^T from an industrial effluent plant of the dairy industry located at Hyderabad, India. The polyphasic characterization of this strain indicated that it represents a novel species of the genus *Micrococcus*.

Strain DW152^T was isolated from liquid samples obtained from a dairy waste treatment plant. Upon transfer of the

samples to the laboratory, they were serially diluted and plated onto nutrient agar (Hi-Media). After incubation at 30 °C, a yellow-pigmented colony was isolated, subcultured and preserved at –70 °C for further studies. Morphological characteristics like cell shape and size were observed under a phase-contrast microscope (Axiophot; Zeiss). An active culture was assigned for Gram staining using the Hi-Media kit according to the instructions of the manufacturer. Physiological tests such as growth at different temperatures and pH were determined using nutrient broth (Hi-Media), measuring the growth as OD at 660 nm by using a spectrophotometer (Lambda 25, Perkin Elmer). To determine salt tolerance, nutrient agar without NaCl was supplemented with different concentrations of NaCl. Assimilation of different substrates by strain DW152^T was determined using the Biolog Microlog system (release 4.2) according to the manufacturer's instructions except that the strain was grown on tryptone soya agar (TSA; Hi-Media) medium instead of Biolog universal agar. Biochemical tests for catalase and oxidase were determined as described by Cowan & Steel (1965). Hydrolysis of aesculin, indole, Voges–Proskauer and methyl red tests, H₂S production and nitrate reduction were performed as described by Lanyi (1987). Utilization of various carbon compounds and casein, gelatin, starch and Tween hydrolysis were determined as described by Smibert & Krieg (1994). Further ability to produce acid from different sugars was checked on medium containing (g per

Abbreviations: DPG, diphosphatidylglycerol; PG, phosphatidylglycerol; PI, phosphatidylinositol; PC, phosphatidylcholine.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain DW152^T is FN673681.

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

100 ml): KCl, 0.01; yeast extract, 0.01; KH_2PO_4 , 0.025; $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 0.025; $(\text{NH}_4)_2\text{SO}_4$, 0.2; Bromocresol Purple (BCP, pH indicator), 0.02; and supplemented with 1.0 % of each filter-sterilized carbon compound.

Microscopic studies revealed that cells of strain DW152^T were Gram-positive and non-spore-forming cocci, present in pairs, and their appearance as diplococci indicated that cell division was by binary fission (Supplementary Fig. S1 available in IJSEM Online). They could grow at 10 °C but not at 42 °C and growth was observed between pH 4.5 and 9.0. Strain DW152^T could not grow at high salinity in comparison to other strains that grew with 10 % NaCl. The casein hydrolysis activity of strain DW152^T may allow it to utilize casein present in dairy waste. Other properties of strain DW152^T along with those of closely related species are given in Table 1.

Total cellular fatty acid methyl esters were extracted from culture grown on nutrient agar at 30 °C for 48 h (Sato & Murata, 1988) and analysed by using the Microbial Identification System (MIDI). The analysis was performed according to the instructions of MIDI (Sasser, 1990). Menaquinones and polar lipids were extracted from freeze-dried cells and analysed as described by Minnikin *et al.* (1984). Peptidoglycan was extracted according to Komagata & Suzuki (1987) and amino acids were identified by comparison with standards. The type of peptidoglycan was identified according to the classification system described by Schleifer & Kandler (1972). The G + C content of genomic DNA was estimated spectrophotometrically (Lambda 25; Perkin Elmer) as described by Mandel & Marmur (1968).

The total cellular fatty acid profile was obtained for strain DW152^T along with other closely related strains after growth under identical conditions and the compositions are compared in Table 2. The FAME analysis indicated that fatty acid ai-C_{15:0} was the common major fatty acid amongst all species of the genus *Micrococcus*. Other fatty acids observed in significant quantities for strain DW152^T were i-C_{16:1} H and ai-C_{17:1} ω9c, representing 8.73 and 6.92 % of the total, respectively. Interestingly, these were found to be absent in other close relatives like *M. terreus* NBRC 104258^T and *M. lylae* DSM 20315^T. However, saturated fatty acids were predominant in all strains. Respiratory isoprenoid quinone analysis indicated the presence of MK-8(H₂) as major quinone and MK-7(H₂), MK-9(H₂) and MK-7 as minor menaquinones. Cell-wall peptidoglycan analysis revealed that strain DW152^T contained the amino acids lysine, aspartic acid, alanine and glycine. The presence of L-lysine as the diagnostic amino acid classified the peptidoglycan as type A4α, which is characteristic of the genus *Micrococcus*. Total polar lipid analysis of strain DW152^T indicated that it had diphosphatidylglycerol (DPG), phosphatidylglycerol (PG), phosphatidylinositol (PI), phosphatidylcholine (PC), one unknown phospholipid and two unknown glycolipids (Supplementary Fig. S2). Strain DW152^T differed in biochemical and chemotaxonomic properties from closely related species of the genus

Micrococcus (Table 1). The total genomic DNA G + C content of strain DW152^T was 68.0 mol%, as estimated by the *T_m* method, which is within the limits of the DNA G + C content reported for other species of the genus.

PCR amplification of the 16S rRNA gene was done using primers 8-27f (5'-AGAGTTTGATCCTGGCTCAG-3') and 1492r (5'-TACGGYTACCTTGTACGACTT-3') as described by Pandey *et al.* (2002). The amplified PCR product was purified and sequenced as described by Suresh *et al.* (2006). The almost complete sequence of the 16S rRNA gene (1429 bp continuous stretch) was obtained and used for the initial BLAST search. Closely related sequences were retrieved from the EMBL database. Sequence alignment was done using CLUSTAL X (Thompson *et al.*, 1997) and results obtained were edited manually. Phylogenetic trees were reconstructed using the maximum-likelihood algorithm using the PhyML program (Guindon & Gascuel, 2003). The stability among the groupings of the phylogenetic tree was assessed by taking 100 replicates. *Actinomyces bovis* CCUG 31996^T was used as an outgroup.

BLAST analysis of the 16S rRNA gene sequence (1429 bp) using the EZ Taxon server indicated that strain DW152^T exhibited 97.03 % similarity with *M. terreus* V3M1^T. Further, pairwise comparative analysis of the sequence indicated that it had low similarity with the type strains of different species belonging to the genera *Micrococcus* and *Arthrobacter*. Both of these genera belong to the family *Micrococcaceae* of the class *Actinobacteria* (Stackebrandt *et al.*, 1997) and it was observed that different families belonging to this class have high similarity in the primary structure of their 16S rRNA genes. However, strain DW152^T was affiliated to the genus *Micrococcus* due to the absence of a rod-coccus cycle, presence of chemotaxonomic markers similar to those found in members of the genus *Micrococcus*, and high similarity of the 16S rRNA gene sequence with that of *M. terreus* NBRC 104258^T. In particular, MK-8(H₂) as major menaquinone, the polar lipids DPG, PG, PI and unknown glycolipids, ai-C_{15:0} and i-C_{15:0} as major fatty acids and L-lysine as diagnostic amino acid were observed for strain DW152^T, characteristic of the genus *Micrococcus*. DNA-DNA hybridization results for strain DW152^T with *M. terreus* NBRC 104258^T revealed a mean value of 42.3 % relatedness. According to accepted criteria, more than 3 % difference in 16S rRNA gene sequence represents similarity of less than 70 % at the whole-genome level (Stackebrandt & Goebel, 1994) and thus it is assumed that whole-genome DNA similarity amongst other species would be quite low. Further, phylogenetic analysis of the 16S rRNA gene sequence assigned strain DW152^T to the genus *Micrococcus* as it formed a distinct clade in the maximum-likelihood phylogenetic tree with a bootstrap value of 90 % (Fig. 1). An additional maximum-likelihood phylogenetic tree reconstructed for strain DW152^T along with species of closely related genera belonging to family *Micrococcaceae* also revealed that strain DW152^T formed a distinct clade (Supplementary Fig. S3). The differences in phenotypic properties, low DNA similarity and phylogenetic analysis readily differentiated strain DW152^T from the nearest

Table 1. Physiological and biochemical characteristics of strain DW152^T and related species of the genus *Micrococcus*

Strains: 1, DW152^T; 2, *M. terreus* NBRC 104258^T; 3, *Micrococcus lylae* DSM 20315^T; 4, *Micrococcus luteus* MTCC106^T; 5, *Micrococcus yunnanensis* YIM 65004^T; 6, *Micrococcus antarcticus* AS 1.2372^T; 7, *Micrococcus flavus* LW4^T. All strains are non-motile and catalase-positive. +, Positive; –, negative; NR, not reported; w, weakly positive; UL1, unknown phospholipid; GL1–3, unknown glycolipids.

Characteristic	1	2	3	4	5 ^{a*}	6 ^{b,c}	7 ^{c,d}
Growth at/with:							
10 °C	+	–	–	–	+	+	–
42 °C	–	–	+	+	+	NR	–
4 % NaCl	+	+	+	+	NR	NR	NR
6 % NaCl	–	–	+	+	+	+	–
pH 4.5	+	–	+	–	–	NR	NR
Simmons citrate agar	–	+	+	–	NR	+	–
Nitrate reduction	+	–	+	+	–	+	–
Voges-Proskauer reaction	–	–	–	–	–	+	–
Indole	–	–	–	–	–	+	–
Hydrolysis of:							
Tween 20	–	+	–†	–†	NR	+	–
Tween 80	–	+	–†	–	+	+	–
Casein	+	+§	–	+	NR	NR	NR
Starch	–	–	–	–	–	+	+
Urea	+	+§	+†	–†	–	–	–
Acid production from:							
Glucose	–	–	–	+	NR	–	–
Sucrose	–	+	–	+	NR	–	–
Assimilation of:							
N-Acetyl-D-glucosamine	–	–	–	+†	NR	NR	NR
L-Arabinose	–	+	–	–	NR	NR	NR
D-Glucose	–	+	+	+	NR	–	–
Glycerol	+	–	+	+	NR	NR	NR
Trehalose	–	–	+‡	+	+	–	+
β-Hydroxybutyric acid	+	+	+	–	NR	NR	NR
α-Ketoglutaric acid	–	–	+	w	NR	–	–
L-Lactic acid	–	–	+	+	NR	NR	–
L-Malic acid	+	–§	+‡	–	NR	+	–
Maltose	+	+	+	+	NR	+	–
N-Acetyl-L-glutamic acid	–	–	+	–	NR	NR	NR
L-Glutamic acid	+	+	–	–	NR	NR	–
2'-Deoxyadenosine	–	+	+	–	NR	NR	NR
Thymidine	–	–	+	–	NR	NR	NR
Menaquinones	MK-8(H2), MK-7(H2), MK-9(H2), MK-7	MK-7, MK-7(H2), MK-8, MK-8(H2)	MK-8(H2)	MK-8, MK-8(H2)	MK-8(H2), MK-7(H2)	MK-8, MK-8(H2)	MK-8(H2), MK-7(H2)
Polar lipids	DPG, PG, PC, PI, UPL1, GL1, GL2	DPG, PG, PC, PI, UPL1§, GL1, GL2, GL3	DPG, PG, PI, UPL1, UPL2	DPG, PG, PI, UPL1, UPL2, GL1, GL2	DPG, PG, PI, UPL1	NR	NR
DNA G + C content (mol%)	68.0	69.0	70.0	67.2	71.7	66.4	71.4

*Data from: a, Zhao *et al.* (2009); b, Liu *et al.* (2000); c, Zhang *et al.* (2010); d, Liu *et al.* (2007).

†Different results obtained by Wieser *et al.* (2002) using similar methods.

‡Different results obtained by Wieser *et al.* (2002) who used different methods.

§Different results obtained by Zhang *et al.* (2010) who used different methods.

Table 2. Cellular fatty acid compositions of strain DW152^T and the type strains of species of the genus *Micrococcus*

Strains: 1, DW152^T; 2, *M. terreus* NBRC 104258^T; 3, *M. lylae* DSM 20315^T; 4, *M. luteus* MTCC106^T; 5, *M. yunnanensis* YIM 65004^T; 6, *M. antarcticus* AS 1.2372^T; 7, *M. flavus* LW4^T. Values were obtained in this study unless indicated and are expressed as percentages of total fatty acids; all strains were grown on nutrient agar at 30 °C for 48 h. –, Absent.

Fatty acid	1	2	3	4	5*	6*	7*
i-C _{13:0}	–	–	1.33	–	–	0.06	3.98
ai-C _{13:0}	–	–	–	0.86	–	0.09	2.78
C _{14:0}	1.00	–	0.72	–	–	0.63	0.78
i-C _{14:0}	2.45	3.14	1.51	1.30	7.41	6.19	3.98
i-C _{15:0}	7.25	11.05	40.11	9.95	13.04	12.34	23.35
ai-C _{15:0}	68.06	72.23	48.04	78.38	61.98	63.66	41.92
i-C _{16:1} H	8.73	–	–	2.61	–	–	1.13
i-C _{16:0}	2.86	3.55	5.26	0.82	14.25	8.29	0.34
C _{16:0}	–	2.20	0.86	–	–	1.00	–
ai-C _{17:1} ω9c	6.92	–	–	2.61	–	–	1.27
ai-C _{17:0}	0.86	1.42	2.16	1.03	3.32	4.17	–
Summed feature 1†	1.77	–	–	2.97	–	–	17.56

*Data from Zhao *et al.* (2009).

†Summed feature 1 comprises i-C_{15:1} H and/or C_{13:0} 3OH.

species. Therefore, based on these differences, it is proposed that strain DW152^T should be recognized as a novel species of the genus *Micrococcus*, for which the name *Micrococcus lactis* sp. nov. is proposed.

Description of *Micrococcus lactis* sp. nov.

Micrococcus lactis (lac'tis. L. gen. n. *lactis* from milk, pertaining to the isolation source 'dairy waste').

Cells are cocci with diameter of about 1.0 µm, stain Gram-positive, are non-motile and strictly aerobic. Growth is observed between temperatures of 10 and 40 °C but not at 42 °C and between pH 4.5 and 9.5, the optimum being 7.5. Growth occurs with between 0 and 4 % NaCl. No growth is observed on MacConkey agar. Catalase-positive but

oxidase-negative. Exhibits urease activity. Cannot hydrolyse starch, aesculin or Tweens 20, 40, 60 or 80. Positive in the Vitek2 system (bioMérieux) for leucine, alanine, L-proline, tyrosine and L-aspartate arylamidases but negative for ala-phe-pro arylamidase. Positive for α-glucosidase but negative for arginine dihydrolase, β-glucuronidase, β-galactopyranosidase, α-galactosidase, β-galactosidase-mannosidase, phosphatase, and arginine dihydrolase. Exhibits L-lactate alkalization. Cannot utilize D-ribose, raffinose, cyclodextrin, D-sorbitol, lactose, D-mannitol, salicin, D-mannose, sucrose, trehalose, N-acetyl-D-glucosamine, methyl β-D-glucopyranoside, D-galactose or pullulan. Sensitive to novobiocin, optochin, polymyxin and bacitracin. Positive for oxidation of the following substrates in Biolog plates: acetate, dextrin, α-hydroxybutyric acid, glycerol, inosine, lactate, pyruvic acid, pyruvic acid methyl ester, L-pyrogutamic acid, adenosine, maltose, maltotriose, α-ketovaleric acid, D-ribose, sucrose, succinamic acid, succinic acid, succinic acid monomethyl ester, turanose, Tween 40, Tween 80 and glycerol. Cannot oxidize α-cyclodextrin, β-cyclodextrin, inulin, mannan, N-acetyl-β-D-mannosamine, L-arabinose, D-arabitol, arbutin, amygdalin, cellobiose, D-fructose, L-fucose, glycogen, D-galactose, D-galacturonic acid, gentiobiose, D-glucose 6-phosphate, D-gluconic acid, myo-inositol, α-lactose, lactulose, D-mannitol, D-mannose, melezitose, melibiose, methyl α-D-galactoside, methyl β-D-galactoside, 3-methyl-D-glucose, methyl α-D-glucoside, methyl β-D-glucoside, methyl α-D-mannoside, palatinose, D-psicose, salicin, sedoheptulosan, D-sorbitol, stachyose, D-tagatose, xylitol, γ-hydroxybutyric acid, D-lactic acid methyl ester, thymidine 5'-monophosphate, lactamide, D-malic acid, L-alaninamide, D-alanine, L-alanine, glycyl L-glutamic acid, putrescine, adenosine 5'-monophosphate, D-glucose 6-phosphate, uridine 5'-monophosphate, D-fructose 6-phosphate or α-D-glucose 1-phosphate. The cell wall peptidoglycan of the type strain is type A4α with L-Lys-Asp. The polar lipid pattern includes DPG, PG, PI, PC, an unknown phospholipid and two unknown glycolipids. The predominant menaquinone is MK-8(H₂). The major cellular fatty acids are ai-C_{15:0}, i-C_{16:1} H, i-C_{15:0} and ai-C_{17:1}ω9c. The G + C content of the genomic DNA of the type strain is 68.0 mol%.

The type strain, DW152^T (=MTCC10523^T =DSM 23694^T), was isolated from dairy industry waste.

Fig. 1. Maximum-likelihood phylogenetic tree based on 16S rRNA gene sequences showing the relationship of strain DW152^T with members of the genus *Micrococcus*. Numbers at nodes are bootstrap values >50 %. *Actinomyces bovis* CCUG 31996^T was used as an outgroup. Bar, 0.01 substitutions per nucleotide position.

Acknowledgements

We thank the Council of Scientific and Industrial Research (CSIR) and Department of Biotechnology, Government of India for financial assistance. Financial help from CSIR network project (NWP006) is also duly acknowledged. We would like to thank Mr Deepak for his excellent help in sequencing DNA. This is communication number 058/2010 of the Institute of Microbial Technology.

References

- Chen, H.-H., Zhao, G.-Z., Park, D.-J., Zhang, Y.-Q., Xu, L.-H., Lee, J.-C., Kim, C.-J. & Li, W.-J. (2009). *Micrococcus endophyticus* sp. nov., isolated from surface-sterilized *Aquilaria sinensis* roots. *Int J Syst Evol Microbiol* **59**, 1070–1075.
- Cohn, F. (1872). Untersuchungen über Bakterien. *Beitr Biol Pflanz* **1**, 127–224 (in German).
- Cowan, S. T. & Steel, K. J. (1965). *Manual for the Identification of Medical Bacteria*. London: Cambridge University Press.
- Guindon, S. & Gascuel, O. (2003). A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood. *Syst Biol* **52**, 696–704.
- Komagata, K. & Suzuki, K. (1987). Lipid and cell wall analysis in bacterial systematics. *Methods Microbiol* **19**, 161–207.
- Lanyi, B. (1987). Classical and rapid identification methods for medically important bacteria. *Methods Microbiol* **19**, 1–67.
- Liu, H., Xu, Y., Ma, Y. & Zhou, P. (2000). Characterization of *Micrococcus antarcticus* sp. nov., a psychrophilic bacterium from Antarctica. *Int J Syst Evol Microbiol* **50**, 715–719.
- Liu, X.-Y., Wang, B.-J., Jiang, C.-Y. & Liu, S.-J. (2007). *Micrococcus flavus* sp. nov., isolated from activated sludge in a bioreactor. *Int J Syst Evol Microbiol* **57**, 66–69.
- Mandel, M. & Marmur, J. (1968). Use of ultraviolet absorbance-temperature profile for determining the guanine plus cytosine content of DNA. *Methods Enzymol* **12B**, 195–206.
- Minnikin, D. E., O'Donnell, A. G., Goodfellow, M., Alderson, G., Athalye, M., Schaal, K. & Parlett, J. H. (1984). An integrated procedure for the extraction of bacterial isoprenoid quinones and polar lipids. *J Microbiol Methods* **2**, 233–241.
- Pandey, K. K., Mayilraj, S. & Chakrabarti, T. (2002). *Pseudomonas indica* sp. nov., a novel butane-utilizing species. *Int J Syst Evol Microbiol* **52**, 1559–1567.
- Sasser, M. (1990). *Identification of bacteria by gas chromatography of cellular fatty acids*. MIDI Technical note 101. Newark, DE: MIDI Inc.
- Sato, N. S. & Murata, N. (1988). Membrane lipids. *Methods Enzymol* **167**, 251–259.
- Schleifer, K. H. & Kandler, O. (1972). Peptidoglycan types of bacterial cell walls and their taxonomic implications. *Bacteriol Rev* **36**, 407–477.
- Smibert, R. M. & Krieg, N. R. (1994). Phenotypic characterization. In *Methods for General and Molecular Bacteriology*, pp. 607–654. Edited by P. Gerhardt. Washington, DC: American Society for Microbiology.
- 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.
- Stackebrandt, E., Koch, C., Gvozdiak, O. & Schumann, P. (1995). Taxonomic dissection of the genus *Micrococcus*: *Kocuria* gen. nov., *Nesterenkonia* gen. nov., *Kytococcus* gen. nov., *Dermacoccus* gen. nov., and *Micrococcus* Cohn 1872 gen. emend. *Int J Syst Bacteriol* **45**, 682–692.
- Stackebrandt, E., Rainey, F. A. & Ward-Rainey, N. L. (1997). Proposal for a new hierarchic classification system, *Actinobacteria* classis nov. *Int J Syst Bacteriol* **47**, 479–491.
- Suresh, K., Mayilraj, S. & Chakrabarti, T. (2006). *Effluviibacter roseus* gen. nov., sp. nov., isolated from muddy water, belonging to the family 'Flexibacteraceae'. *Int J Syst Evol Microbiol* **56**, 1703–1707.
- Thompson, J. D., Gibson, T. J., Plewniak, F., Jeanmougin, F. & Higgins, D. G. (1997). The CLUSTAL_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Res* **25**, 4876–4882.
- Wieser, M., Denner, E. B. M., Kämpfer, P., Schumann, P., Tindall, B., Steiner, U., Vybiral, D., Lubitz, W., Maszenan, A. M. & other authors (2002). Emended descriptions of the genus *Micrococcus*, *Micrococcus luteus* (Cohn 1872) and *Micrococcus lylae* (Kloos et al. 1974). *Int J Syst Evol Microbiol* **52**, 629–637.
- Zhang, J.-Y., Liu, X.-Y. & Liu, S.-J. (2010). *Agrococcus terreus* sp. nov. and *Micrococcus terreus* sp. nov., isolated from forest soil. *Int J Syst Evol Microbiol* **60**, 1897–1903.
- Zhao, G.-Z., Li, J., Qin, S., Zhang, Y.-Q., Zhu, W.-Y., Jiang, C.-L., Xu, L.-H. & Li, W.-J. (2009). *Micrococcus yunnanensis* sp. nov., a novel actinobacterium isolated from surface-sterilized *Polyspora axillaris* roots. *Int J Syst Evol Microbiol* **59**, 2383–2387.