Agrococcus terreus sp. nov. and *Micrococcus terreus* sp. nov., isolated from forest soil

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Two bacterial strains, DNG5^T and V3M1^T, isolated from forest soil of the Changbai mountains in China, were characterized using a polyphasic approach. Analysis of their 16S rRNA gene sequences indicated that strains DNG5^T and V3M1^T were phylogenetically related to members of the genus *Agrococcus* (96.0–98.4 % similarity) and *Micrococcus* (96.7–98.0 % similarity), respectively, within the order *Actinomycetales*. Strains DNG5^T and V3M1^T were Gram-stain-positive and strictly aerobic and formed yellow colonies on LB agar. Cells of strain DNG5^T were short, non-motile rods, 0.4–0.5×0.8–1.0 µm. Strain DNG5^T contained MK-10 and MK-11 as the major respiratory quinones and anteiso-C_{15:0} (49.2 %) and iso-C_{16:0} (22.4 %) as the major fatty acids. The diamino acid in the peptidoglycan of strain DNG5^T was 2,4-diaminobutyric acid and the murein was of the acetyl type. Cells of strain V3M1^T were cocci, 0.6–0.7 µm in diameter. The cell-wall peptidoglycan of strain V3M1^T contained the amino acids lysine, glutamic acid, alanine and glycine. Strain V3M1^T contained MK-7, MK-7(H₂), MK-8 and MK-8(H₂) as respiratory quinones and anteiso-C_{15:0} (78.2 %) and iso-C_{15:0} (13.1 %) as the major cellular fatty acids. The DNA G + C contents of strains DNG5^T and V3M1^T were 75.9 and 67.2 mol%, respectively. The DNA–DNA relatedness of strain DNG5^T to *Agrococcus jejuensis* DSM 22002^T, *A. jenensis* JCM 9950^T, *A. baldri* JCM 12132^T and *A. citreus* JCM 12398^T was 58.3, 43.9, 36.1 and 54.1 %, respectively. The DNA–DNA relatedness of strain V3M1^T to *Micrococcus luteus* CGMCC 1.2299^T, *M. antarcticus* CGMCC 1.2373^T and *M. lylae* CGMCC 1.2300^T was 57.5, 45.4 and 39.0 %, respectively. Combining phenotypic and genotypic traits, strain DNG5^T represents a novel species of the genus *Agrococcus*, for which the name *Agrococcus terreus* sp. nov. is proposed, with DNG5^T (=CGMCC 1.6960^T =NBRC 104260^T) as the type strain. Strain V3M1^T represents a novel species of the genus *Micrococcus*, for which the name *Micrococcus terreus* sp. nov. is proposed, with V3M1^T (=CGMCC 1.7054^T =NBRC 104258^T) as the type strain.

Within the order *Actinomycetales*, the genus *Agrococcus* is a member of the family *Microbacteriaceae* and the genus *Micrococcus* is assigned to the family *Micrococcaceae*. The genus *Agrococcus* was created by Groth *et al.* (1996) and, at the time of writing, includes seven species with validly published names (<http://www.bacterio.cict.fr/a/agrococcus>).

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains DNG5^T and V3M1^T are respectively FJ423764 and FJ423763.

Maximum-parsimony 16S rRNA gene sequence-based trees and an extended neighbour-joining tree, results of 2D TLC of polar lipids of the novel strains and detailed fatty acid profiles are available as supplementary material with the online version of this paper.

Members of the genus *Agrococcus* have been isolated from various environments including soil samples (Groth *et al.*, 1996; Wieser *et al.*, 1999; Mayilraj *et al.*, 2006), cheese surfaces (Bora *et al.*, 2007), potato plants (Behrendt *et al.*, 2008) and dried seaweed (Lee, 2008), as well as from the air (Zlamala *et al.*, 2002). Chemotaxonomically, species of *Agrococcus* contain 2,4-diaminobutyric acid as the characteristic cell-wall diamino acid, phosphatidylglycerol and diphosphatidylglycerol as the major lipids (polar lipids have not been determined for *Agrococcus versicolor*), anteiso-C_{15:0} as the major fatty acid and acetyl-type murein.

The genus *Micrococcus* was first described by Cohn (1872). The description of this genus has been emended several

times with reference to glucose utilization and fermentation, G+C content of the genomic DNA and phylogenetic analysis of the 16S rRNA gene (detailed by Wieser *et al.*, 2002). At the time of writing, the genus includes four species with validly published names, *Micrococcus luteus*, *M. lylae* (Stackebrandt *et al.*, 1995; Kloos *et al.*, 1974), *M. antarcticus* (Liu *et al.*, 2000) and *M. flavus* (Liu *et al.*, 2007). Members of this genus are yellow- or white-pigmented, non-fermentative, Gram-positive and non-motile and are characterized by the presence of anteiso-C_{15:0} and iso-C_{15:0} as major fatty acids and MK-8 and MK-8(H₂) as respiratory quinones.

In this note, we report the isolation and identification of two novel isolates, strains DNG5^T and V3M1^T, from a forest soil sample. In an attempt to study the microbial diversity and cultivability of forest soil of the Changbai mountains, Heilongjiang Province, China, bacterial strains were isolated by using the serial dilution method (Janssen *et al.*, 2002). DNG medium used in this study contained 0.15 g Bacto tryptic soy broth and 1.5 g gellan in 100 ml water. V3M medium was modified from VL55 medium (Sait *et al.*, 2002) by addition of 5 ml amino acid mixture (Davis *et al.*, 2005), 1 ml vitamin solution 1 and 3 ml vitamin solution 2 (Janssen *et al.*, 1997), 100 µl solution 1, 3 ml solution 2 and 3 ml solution 3 per litre of medium, and using 1.5 % gellan as solidifying agent (Davis *et al.*, 2005). Solution 1 contained the following ingredients (l⁻¹): 4 mg SrCl₂, 3 mg NaSiO₃·9H₂O, 3 mg TiO₂, 2 mg Cd(NO₃)₂·4H₂O and 2 mg SnCl₂·H₂O. Solution 2 contained (l⁻¹) 30 mg DL-glyceraldehyde, 20 mg chromotropic acid, 70 mg gallic acid, 30 mg ascorbic acid, 10 mg sodium thioglycolate, 50 mg sodium succinate, 50 mg DL-malic acid, 50 mg saligenin, 50 mg sorbitol, 40 mg salicin, 20 mg barbital, 20 mg aconitic acid, 30 mg creatine and 30 mg sodium deoxycholate. Solution 3 contained (l⁻¹) 26 mg L-rhamnose, 58 mg melezitose, 38 mg raffinose, 24 mg galactose, 37 mg melibiose, 64 mg inulin, 24 mg arabinose, 43 mg xylose and 54 mg cellobiose. Plates were inoculated with 10⁻⁵ to 10⁻⁹ dilutions and were sealed with Parafilm. Strains DNG5^T and V3M1^T were obtained from DNG agar and V3M agar plates, respectively, inoculated with the 10⁻⁷ dilution after 1 week of incubation at 25 °C and were obtained by repeated streaking.

Nearly complete 16S rRNA genes of strains DNG5^T (1516 bp) and V3M1^T (1514 bp) were amplified and sequenced as described by Zhang *et al.* (2003). DNA BLAST searches on NCBI (Altschul *et al.*, 1990) showed that strains DNG5^T and V3M1^T were phylogenetically related to members of the genera *Agrococcus* and *Micrococcus*, respectively. Alignments of 16S rRNA gene sequences were performed with the CLUSTAL_X program (version 1.64b; Thompson *et al.*, 1997) and alignment positions with insertions or deletions were excluded from our calculations. Phylogenetic trees based on 16S rRNA gene sequence analysis were constructed by the neighbour-joining and maximum-parsimony methods with Kimura's two-parameter calculation model in MEGA version 3.1 (Kumar *et al.*, 2004).

Analysis of 16S rRNA gene sequences indicated that strain DNG5^T was phylogenetically related to members of the genus *Agrococcus*, with similarities ranging from 96.0 to 98.4 %. In particular, strain DNG5^T was closely related to *Agrococcus jejuensis* SSW1-48^T (98.4 %), *A. jenensis* DSM 9580^T (98.1 %), *A. baldri* V-108^T (98.1 %) and *A. citreus* IAM 15145^T (97.9 %). The phylogenetic tree (Fig. 1a) also indicated that strain DNG5^T clustered with *Agrococcus* species; the topology of the maximum-parsimony tree was essentially the same (Supplementary Fig. S1, available in IJSEM Online).

Analysis of 16S rRNA gene sequences indicated that strain V3M1^T was phylogenetically related to members of the genus *Micrococcus*. In particular, strain V3M1^T was closely related to *M. luteus* DSM 20030^T (98.0 %), *M. antarcticus* T2^T (97.6 %), *M. lylae* DSM 20315^T (97.5 %) and *M. flavus* LW4^T (96.7 %). Phylogenetic trees (Fig. 1b and Supplementary Fig. S2) also indicated that strain V3M1^T clustered with *Micrococcus* species, and the topology of the maximum-parsimony tree was essentially the same (Supplementary Fig. S3).

The morphological, physiological and biochemical characteristics of strains DNG5^T and V3M1^T were investigated using routine cultivation on LB agar at 30 °C. Gram staining was performed according to Gerhardt *et al.* (1994) with cells grown on LB agar at 30 °C for 2 days. Morphological observation was performed by scanning electron microscopy (FEI Quanta 200). The presence of flagella, gliding motility and growth under anaerobic conditions were examined according to Dong & Cai (2001). The growth temperature range was determined with a TN3F temperature-gradient incubator (Advantec) at 9, 10, 11, 12, 13, 14, 15.5, 16, 17.5, 19, 20, 22, 24, 27, 28, 29, 31, 34, 35, 38, 40, 45, 49, 51, 56 and 61 °C. The pH range for growth was tested at pH 4.0, 4.8, 5.5, 6.0, 6.5, 7.0, 7.5, 8.0, 8.5, 9.0 and 9.8 in LB broth. The pH was adjusted by addition of 5 M NaOH or HCl and verified after autoclaving. Tolerance of NaCl was examined in LB broth supplemented with 0, 0.25, 0.5, 1, 2, 4 and 5 % (w/v) NaCl. Tests for catalase and oxidase activities, the Voges-Proskauer reaction, the methyl red test and hydrolysis of casein, starch, tyrosine and Tweens 20 and 80 were carried out according to Dong & Cai (2001). In addition, strains DNG5^T and V3M1^T were characterized by using API 20NE, API 50CH and API ZYM identification systems (bioMérieux) at 30 °C.

Strain DNG5^T was strictly aerobic. Cells of strain DNG5^T were Gram-stain-positive, non-motile, short rods, 0.4–0.5 µm in diameter and 0.8–1.0 µm long. Strain V3M1^T was also strictly aerobic. Cells of strain V3M1^T were non-motile, Gram-stain-positive cocci, 0.6–0.7 µm in diameter. Detailed physiological and biochemical characteristics of strains DNG5^T and V3M1^T are provided in the species descriptions; differential properties from other *Agrococcus* and *Micrococcus* species, respectively, are listed in Tables 1 and 2.

Fig. 1. Phylogenetic trees constructed with the neighbour-joining method showing (a) that strain DNG5^T and other members of the genus *Agrococcus* are clustered together and (b) that strain V3M1^T and other members of the genus *Micrococcus* are clustered together. GenBank accession numbers are given in parentheses. Numbers represent percentage confidence levels (values >50 % are shown) from bootstrap resampling with 1000 replicates. Outgroups were the sequences of *Arthrobacter globiformis* JCM 1332^T (a) and *Kytococcus sedentarius* DSM 20547^T (b). Bars, evolutionary distances (K_{nuc}) of 0.005.

Cell mass of strains DNG5^T and V3M1^T used for chemotaxonomic analyses was produced on TSB agar and LB agar, respectively, at 30 °C for 2 days. Cellular fatty acids were extracted, methylated and analysed by using the Sherlock Microbial Identification System following the manufacturer's instructions. Polar lipids were extracted by the modified method of Kamekura (1993) and separated by TLC on Merck Kieselgel 60-HPTLC by two-dimensional development as described by Ross *et al.* (1985). Phospholipids were detected with the Zinzadze reagent of Dittmer & Lester (1964). Glycolipids were detected by spraying the plate with 0.5 % 1-naphthol in methanol/water (1:1, v/v) and then with sulfuric acid/ethanol (1:1, v/v), followed by heating at 120 °C for 5–10 min (Xin *et al.*, 2001). The acyl type of cellular murein of DNG5^T was determined as described by Uchida & Aida (1984), with *Nocardioideus albus* CGMCC 4.1230^T as a reference strain in a parallel experiment. Isoprenoid quinones of strains DNG5^T and V3M1^T, *A. jenensis* JCM 9950^T, *A. baldri* JCM 12132^T

were extracted and purified in parallel according to the method of Collins (1985) and were analysed with HPLC (Wu *et al.*, 1989; Hu *et al.*, 2004), with a previously characterized mixture of various menaquinones and ubiquinones. Cell-wall analysis of DNG5^T and V3M1^T was carried out as described by Stanek & Roberts (1974) and Dong & Cai (2001), with lysine, glutamic acid, alanine, glycine and aspartic acid as reference substances and *A. baldri* JCM 12132^T as a reference strain in a parallel experiment.

The most abundant cellular fatty acids of strain DNG5^T were anteiso- $C_{15:0}$ (49.2 %) and iso- $C_{16:0}$ (22.4 %). The complete fatty acid profiles of strain DNG5^T and other *Agrococcus* species are summarized in Supplementary Table S1. The major fatty acids of strain DNG5^T was similar to those of *Agrococcus* species, although strain DNG5^T contained a significant amount (1.8 %) of anteiso- $C_{15:1}$, in contrast to other *Agrococcus* species. The major respiratory quinones of strain DNG5^T were MK-10 (39 %) and MK-11

Table 1. Phenotypic characteristics that differentiate strain DNG5^T from the type strains of other *Agrococcus* species

Strains: 1. *A. terreus* sp. nov. DNG5^T; 2. *A. jejuensis* SSW1-48^T; 3. *A. baldri* V-108^T; 4. *A. jenensis* 2002-39/1^T; 5. *A. citreus* D-1/1a^T; 6. *A. versicolor* K114/01^T; 7. *A. lahaulensis* K22-21^T; 8. *A. casei* R-17892t2^T. Data were taken from Groth *et al.* (1996), Wieser *et al.* (1999), Zlamala *et al.* (2002), Mayilraj *et al.* (2006), Bora *et al.* (2007), Behrendt *et al.* (2008), Lee (2008) and this study. *A. terreus* DNG5^T, *A. jejuensis* DSM 22002^T, *A. baldri* JCM 12132^T, *A. jenensis* JCM 9950^T and *A. citreus* JCM 12398^T were tested in parallel with the API 20NE system in this study. All strains are positive for catalase activity and negative for oxidase activity, the Voges–Proskauer reaction and assimilation of citrate. +, Positive; –, negative; (+), weakly positive; ND, no data available.

Characteristic	1	2	3	4	5	6	7	8
Cell morphology	Short rods	Short rods	Irregular coccoids to rods	Irregular spherical or ovoid to short rods	Irregular spherical, ovoid or rods	Short to ovoid rods	Irregular spherical rods	Irregular ovoid to short rods
Cell size (µm)								
Length	0.8–1.0	1.3–1.5	1.1–1.7	0.7–1.7	1.1–1.7	0.5–0.6	1.0–1.5	0.8–1.0
Width	0.4–0.5	0.3–0.4	0.7–1.0	0.7–1.0	0.7–1.0	0.8–1.2	0.6–1.0	0.3–0.4
Colony colour	Yellow	Yellow	Light yellow	White or orange	Yellow	Yellow to dark pink	Lemon	Cream
Optimum growth temperature (°C)	30	30	28	28	28	21	30	30
Hydrolysis of:								
Starch	–	–	+	+	+	–	+	+
Casein	–	+	–	–	–	+	+	–
Tween 80	–	–	+	–	+	–	–	+
Tyrosine	–	–	–	+	+	–	–	–
Gelatin	+	+	–	–	–	+	+	ND
Aesculin	+	+	+	+	+	+	–	–
Nitrate reduction	–	–	–	–	–	ND	–	ND
Assimilation of:								
D-Glucose	–	+	+	+	–	+	–	ND
L-Arabinose	+	–	+	+	+	+	+	–
D-Mannose	–	+	+	+	+	+	–	ND
N-Acetyl-D-glucosamine	–	+	+	–	–	+	–	–
Gluconate	+	–	+	+	+	+	–	–
Acid produced from:								
D-Glucose	+	+	+	–	+	(+)	ND	+
D-Fructose	+	+	–	+	+	(+)	+	–
D-Mannose	+	+	–	–	–	(+)	ND	+
Mannitol	+	–	+	+	+	–	–	–
Cellobiose	+	+	+	+	+	–	–	–
Maltose	(+)	+	+	–	+	–	–	–
Sucrose	+	+	+	–	–	(+)	–	–
Trehalose	+	+	+	–	+	–	+	–
Major menaquinones	10, 11, 9	10, 9	12, 11	12, 11	12, 11	10, 11	10, 11, 12	11, 12
DNA G + C content (mol%)	75.9	73	73.8–74.9	74	74	ND	74.1	65

(53 %), with MK-9 (8 %) as a minor component. The diamino acid in the peptidoglycan was 2,4-diaminobutyric acid; alanine, glycine, glutamic acid and aspartic acid were also detected. The murein was of the acetyl type, and the major lipids were phosphatidylglycerol, diphosphatidylglycerol and two unknown glycolipids (Supplementary Fig. S4), which are typical characteristics of the genus *Agrococcus*.

The most abundant cellular fatty acids of strain V3M1^T were anteiso-C_{15:0} (78.2 %) and iso-C_{15:0} (13.1 %). This

fatty acid profile was similar to those of *Micrococcus* species, and the detailed fatty acid compositions of strain V3M1^T and the other *Micrococcus* species are given in Supplementary Table S2. The major polar lipids were diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol and an unidentified phospholipid that showed similar migration behaviour to phosphatidylcholine during TLC. Three unknown glycolipids were also detected (Supplementary Fig. S5). This polar lipid pattern was similar to those of *M. lylae* DSM 20315^T and *M. luteus*

Table 2. Phenotypic characteristics that differentiate strain V3M1^T from the type strains of other *Micrococcus* species

Strains: 1, *M. terreus* sp. nov. V3M1^T; 2, *M. luteus* CGMCC 1.2299^T; 3, *M. antarcticus* CGMCC 1.2373^T; 4, *M. lylae* CGMCC 1.2300^T; 5, *M. flavus* CGMCC 1.5361^T. All five strains were tested in parallel in this study for oxidase and catalase activities, casein hydrolysis and reactions in API 20NE and API ZYM tests. Other data were taken from Liu *et al.* (2000, 2007) and Wieser *et al.* (2002). +, Positive; –, negative; (+), weakly positive. All strains are positive for assimilation of maltose and malate and activities of catalase, leucine arylamidase, trypsin, α -glucosidase and valine arylamidase. All strains are negative for motility, nitrate reduction, indole production, hydrolysis of casein and aesculin, glucose fermentation, assimilation of D-mannitol, N-acetyl-D-glucosamine and caprate and activities of arginine dihydrolase, esterase (C₄), esterase lipase (C₈), lipase (C₁₄), α -galactosidase, N-acetyl- β -glucosaminidase, β -galactosidase, β -glucuronidase, β -glucosidase and α -fucosidase.

Characteristic	1	2	3	4	5
Colony colour	Yellow	Yellow	Yellow	White	Yellow
Optimum growth temperature (°C)	33	37	16.8	37	31
Oxidase	–	+	(+)	+	+
Voges–Proskauer reaction	–	–	+	–	–
Methyl red test	–	+	+	–	–
Hydrolysis of:					
Starch	–	–	+	–	+
Tween 20	+	–	+	–	–
Tween 80	+	+	+	–	–
Biochemical characteristics (API 20 NE)					
Urease activity	–	+	–	+	–
Gelatin hydrolysis	+	–	–	–	–
Assimilation of (API 20NE):					
D-Glucose	+	+	–	+	+
L-Arabinose	–	–	+	–	–
D-Mannose	–	+	–	–	–
Gluconate	(+)	–	+	–	+
Adipate	+	–	–	–	–
Citrate	+	–	+	+	–
Phenylacetate	+	+	+	+	–
Enzyme activities (API ZYM)					
Alkaline phosphatase	–	–	–	+	–
Valine arylamidase	(+)	(+)	+	(+)	(+)
Cystine arylamidase	–	–	+	(+)	–
α -Chymotrypsin	(+)	–	–	–	–
Acid phosphatase	–	–	(+)	–	–
Naphthol-AS-BI-phosphohydrolase	(+)	(+)	(+)	–	+
α -Mannosidase	–	–	+	–	–
Major menaquinone(s)	7, 7(H ₂), 8, 8(H ₂)	8, 8(H ₂)	8, 8(H ₂)	8(H ₂)	7(H ₂), 8(H ₂)
DNA G + C content (mol%)	67.2	70.0	66.4	69.0	71.5

DSM 20030^T (Stackebrandt *et al.*, 1995; Wieser *et al.*, 2002). The predominant isoprenoid quinones were MK-7 (57.8 %), MK-7(H₂) (21.8 %), MK-8 (15.0 %) and MK-8(H₂) (5.4 %). The cell-wall peptidoglycan of strain V3M1^T contained the amino acids lysine, glutamic acid, alanine and glycine. These data were compatible with the typical characteristics of the genus *Micrococcus*.

The DNA base composition was determined by thermal denaturation (Marmur & Doty, 1962) and *Escherichia coli* K-12 was used as a reference. The DNA G + C content of strain DNG5^T was 75.9 mol%, which is close to but slightly higher than the range of values (65–74.9 mol%) reported for *Agrococcus* species. The DNA G + C content of strain V3M1^T was 67.2 mol%, which is within the range of values (66.4–71.5 mol%) reported for *Micrococcus* species.

Based on the above phenotypic and phylogenetic studies, it is clear that strains DNG5^T and V3M1^T are respectively members of the genera *Micrococcus* and *Agrococcus*. Strain DNG5^T showed a range of phenotypic characteristics that differentiated it from currently described *Agrococcus* species (Table 1), such as assimilation of various carbon sources, cellular fatty acids and respiratory quinones. To distinguish strain DNG5^T further from the phylogenetically highly related *Agrococcus* species, DNA–DNA hybridization was performed by the thermal denaturation and renaturation method of De Ley *et al.* (1970) as modified by Huß *et al.* (1983). Results showed that the DNA–DNA relatedness of strain DNG5^T to *A. jejuensis* DSM 22002^T, *A. jenensis* JCM 9950^T, *A. baldri* JCM 12132^T and *A. citreus* JCM 12398^T was 58.3, 43.9, 36.1 and 54.1 %, respectively. Therefore, it is concluded that bacterial strain DNG5^T

represents a novel species of the genus *Agrococcus*, for which the name *Agrococcus terreus* sp. nov. is proposed.

Strain V3M1^T showed a range of phenotypic characteristics that differentiated it from *Micrococcus* species with validly published names (Table 2), such as oxidase activity, major respiratory quinones, assimilation of various carbon sources and production of different enzymes. To distinguish strain V3M1^T further from other *Micrococcus* species, the DNA–DNA relatedness of strain V3M1^T to *M. luteus* CGMCC 1.2299^T, *M. antarcticus* CGMCC 1.2373^T and *M. lylae* CGMCC 1.2300^T was 57.5, 45.4 and 39.0 %, respectively. Therefore, it is concluded that bacterial strain V3M1^T represents a novel species of the genus *Micrococcus*, for which the name *Micrococcus terreus* sp. nov. is proposed.

Description of *Agrococcus terreus* sp. nov.

Agrococcus terreus (ter're.us. L. masc. adj. *terreus* of the earth).

Strictly aerobic, Gram-stain-positive, heterotrophic, oxidase-negative and catalase-positive. Colonies on LB agar are circular, entire and yellow. Growth occurs at 20–40 °C (optimum, 30 °C), at pH 5.5–9.0 (optimum, pH 7.0) and in the presence of 0–4 % NaCl (optimum, 1.0 %). Nitrate is not reduced. Gelatin and aesculin are hydrolysed, but tyrosine, casein, starch and Tweens 20 and 80 are not. Urease and arginine dihydrolase activities are absent. Indole is not produced. The Voges–Proskauer reaction and methyl red test are negative. Assimilates L-arabinose, D-mannose, D-mannitol, gluconate and malate, but not D-glucose, maltose, N-acetyl-D-glucosamine, caprate, adipate, citrate or phenylacetate. In API 50 CH tests, acids are produced from glycerol, ribose, D-glucose, D-fructose, D-mannose, rhamnose, mannitol, aesculin, cellobiose, sucrose, trehalose and turanose and are produced weakly from salicin and maltose; all other API 50 CH tests are negative. Esterase lipase (C₈), leucine arylamidase, valine arylamidase, acid phosphatase, naphthol-AS-BI-phosphohydrolase and α-glucosidase activities are present. Weak cystine arylamidase activity is present. Alkaline phosphatase, esterase (C₄), lipase (C₁₄), trypsin, α-chymotrypsin, α-galactosidase, β-galactosidase, β-glucuronidase, N-acetyl-β-glucosaminidase, β-glucosidase, α-mannosidase and α-fucosidase activities are absent. The most abundant cellular fatty acids are anteiso-C_{15:0} and iso-C_{16:0}. The diamino acid in the peptidoglycan is 2,4-diaminobutyric acid; alanine, glycine, glutamic acid and aspartic acid are also present. The major respiratory quinones are MK-10 and MK-11, with MK-9 as a minor component. The murein is of the acetyl type, and the major lipids are phosphatidylglycerol, diphosphatidylglycerol and two unknown glycolipids. The DNA G+C content of the type strain is 75.9 mol% (T_m).

The type strain is DNG5^T (=CGMCC 1.6960^T =NBRC 104260^T), isolated from forest soil.

Description of *Micrococcus terreus* sp. nov.

Micrococcus terreus (ter're.us. L. masc. adj. *terreus* of the earth).

Strictly aerobic, Gram-stain-positive, heterotrophic, oxidase-negative and catalase-positive. Colonies on LB agar are circular, entire, smooth, yellow and 0.5–10 mm in diameter. Growth occurs at 20–35 °C (optimum, 33 °C), at pH 5.0–9.0 (optimum, pH 7.0) and in the presence of 0–2 % NaCl (optimum, 1.0 %). Nitrate is not reduced. Gelatin and Tweens 20 and 80 are hydrolysed, but casein, starch and aesculin are not. Urease and arginine dihydrolase activities are absent. Indole is not produced. The Voges–Proskauer reaction and methyl red test are negative. D-Glucose, maltose, adipate, malate, citrate and phenylacetate are assimilated and gluconate is assimilated weakly. L-Arabinose, D-mannose, D-mannitol, N-acetyl-D-glucosamine and caprate are not assimilated. In API 50 CH tests, acids are produced from maltose, sucrose, trehalose and turanose; all other API 50 CH tests are negative. Leucine arylamidase, trypsin and α-glucosidase activities are present. Weak valine arylamidase, α-chymotrypsin and naphthol-AS-BI-phosphohydrolase activities are present. Alkaline phosphatase, esterase (C₄), esterase lipase (C₈), lipase (C₁₄), cystine arylamidase, acid phosphatase, α-galactosidase, β-galactosidase, β-glucuronidase, β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase activities are absent. Cell-wall peptidoglycan contains the amino acids lysine, glutamic acid, alanine and glycine. The most abundant cellular fatty acids are anteiso-C_{15:0} and iso-C_{15:0}. MK-7, MK-7(H₂), MK-8 and MK-8(H₂) are the major respiratory quinones. The DNA G+C content of the type strain is 67.2 mol% (T_m).

The type strain is V3M1^T (=CGMCC 1.7054^T =NBRC 104258^T), isolated from forest soil.

Acknowledgements

This work was supported by grants from the National Nature Science Foundation of China (30725001) and the Chinese Academy of Sciences (KSCX2-YW-G-052).

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