Micrococcus endophyticus sp. nov., isolated from surface-sterilized *Aquilaria sinensis* roots

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A Gram-positive bacterial strain, designated YIM 56238^T, was isolated from plant roots (*Aquilaria sinensis*), and characterized by using a polyphasic approach. Strain YIM 56238^T grew optimally at pH 7.0–8.0 and at 28 °C. Analysis of the 16S rRNA gene sequence of strain YIM 56238^T indicated that it belongs to the genus *Micrococcus*. Chemotaxonomic data strongly supported the classification of this strain within the genus *Micrococcus*: the cell-wall peptidoglycan contained lysine, glutamic acid, alanine and glycine; the predominant menaquinones were MK-8(H₂) (63.6 %) and MK-7(H₂) (21.1 %); the phospholipids were diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol and an unknown ninhydrin-negative phospholipid; and the major cellular fatty acids were iso-C_{15:0} (30.95 %) and anteiso-C_{15:0} (53.75 %). The G+C content of the genomic DNA was 72.9 mol%. A number of physiological features were found that clearly distinguished strain YIM 56238^T from recognized species of the genus *Micrococcus*. DNA–DNA hybridization studies suggested that the novel strain represents a separate genomic species. On the basis of the data, therefore, strain YIM 56238^T represents a novel species of the genus *Micrococcus*, for which the name *Micrococcus endophyticus* sp. nov. is proposed. The type strain is YIM 56238^T (=DSM 17945^T=KCTC 19156^T).

Recent studies have indicated that endophytic bacteria are common among the resident microflora of the healthy inner tissues of various species of plants (Coombs *et al.*, 2004; Gu *et al.*, 2006; Trujillo *et al.*, 2006; Tian *et al.*, 2007), in which these micro-organisms play an important role in plant growth. The genus *Micrococcus* was first described by Cohn (1872) and since then the description of the genus has been revised repeatedly (Stackebrandt *et al.*, 1995; Wieser *et al.*, 2002). Members of the genus *Micrococcus* are aerobic, Gram-positive and catalase-positive. Cells are spherical, non-motile and do not produce endospores.

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The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain YIM 56238^T is EU005372.

A scanning electron micrograph of cells of strain YIM 56238^T grown on TSA medium is available as a supplementary figure with the online version of this paper.

The G+C contents of the DNA range from 66.3 to 73.3 mol%. At the time of writing, the genus *Micrococcus* encompasses four species: *Micrococcus luteus*, *Micrococcus lylae*, *Micrococcus antarcticus* and *Micrococcus flavus* (Stackebrandt *et al.*, 1995; Kloos *et al.*, 1974; Liu *et al.*, 2000; Liu *et al.*, 2007). These species are phylogenetically closely related to each other. The aim of this study was to determine the exact taxonomic position of a novel *Micrococcus* strain by means of a polyphasic characterization including phenotypic and chemotaxonomic determinations and a detailed phylogenetic analysis based on 16S rRNA gene sequences.

Strain YIM 56238^T was isolated from the roots of a plant, *Aquilaria sinensis* (traditionally used in Chinese medicine), collected in the tropical rainforest of Yunnan Province in south-west China. Samples were washed in running water to remove soil particles and were sterilized using an

established procedure (Coombs & Franco, 2003). After being surface-sterilized, the root samples were sliced into pieces for plating on tap water-yeast extract agar (TWYE) plates, which were incubated at 28 °C for 3–7 weeks. The micro-organisms were observed around the root samples under a light microscope. Pure cultures were obtained by means of repeated streaking on plates containing TWYE agar. The purified strain (YIM 56238^T) was picked and then maintained on trypticase soy agar (TSA; BD) slants at 4 °C and as 20% (w/v) glycerol suspensions at –20 °C. Biomass for chemical and molecular studies was obtained by means of cultivation according to Stackebrandt *et al.* (1995).

Gram staining was carried out using the standard Gram reaction and was confirmed with the KOH test (Moaledj, 1986). Morphology and motility were examined by using light microscopy (BH-2; Olympus) and scanning electron microscopy (LEO 1455VP; Zeiss) with cells from exponentially growing cultures. Colony morphology was observed on TSA after incubation at 28 °C for 3 days. Physiological characteristics of strain YIM 56238^T and its closest neighbours were tested in parallel by using the following procedures. Growth was tested on TSA at 4, 15, 20, 28, 37, 45, 50 and 55 °C. Growth at various NaCl concentrations (0, 1, 3, 5, 7, 10, 15 and 20%, w/v) was tested. The pH range and optimum for growth were investigated at pH 4.0–10.0 using the buffer system described by Xu *et al.* (2005) and trypticase soy broth as the basal medium. Metabolic properties were determined using API 50 CH test kits according to the manufacturer's instructions (bioMérieux). Other physiological and biochemical tests were performed as described previously (Barrow & Feltham, 1993; Wieser *et al.*, 2002).

Cells of strain YIM 56238^T were Gram-positive, aerobic, non-motile, non-endospore-forming and coccoid (0.5–0.7 µm in diameter) (see Supplementary Fig. S1, available in IJSEM Online). The colonies were yellow, circular, slightly convex, opaque and had a maximum diameter of about 2 mm after incubation at 28 °C for 48 h on TSA. No diffusible pigments were produced on any of the media tested. The novel isolate could grow at temperatures in the range 15–37 °C and at pH 6–9. Optimal growth was observed at 28 °C and at around pH 7.0–8.0. The isolate was catalase-positive and gave a positive oxidase reaction. Detailed physiological and biochemical properties are given in Table 1 and in the species description. It is evident from Table 1 that there were some phenotypic differences between YIM 56238^T and recognized species of the genus *Micrococcus*.

Peptidoglycan was purified and the cell-wall amino acids and peptides in cell-wall hydrolysates were analysed by two-dimensional ascending TLC on cellulose plates using the solvent system of Schleifer & Kandler (1972). The cell-wall sugars were analysed according to the procedures developed by Hasegawa *et al.* (1983). Phospholipids were extracted, examined by two-dimensional TLC and iden-

tified using previously described procedures (Minnikin *et al.*, 1984). Menaquinones were isolated as described by Minnikin *et al.* (1984) and separated by HPLC (Kroppenstedt, 1982). Cellular fatty acid analysis was performed using the Sherlock Microbial Identification System (MIDI) according to the manufacturer's instructions. The results indicated that the cell-wall peptidoglycan of strain YIM 56238^T contained lysine, glutamic acid, alanine and glycine. The phospholipids consisted of diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol and an unknown ninhydrin-negative phospholipid. The menaquinones were MK-8(H₂) (63.6%) and MK-7(H₂) (21.1%). The major fatty acids were iso-C_{15:0} and anteiso-C_{15:0}, the profile being very similar to those described for recognized species of the genus *Micrococcus* (Table 2).

Extraction of genomic DNA, PCR amplification and sequencing of the 16S rRNA gene were performed as described by Li *et al.* (2007). Multiple alignments with sequences from the most closely related actinobacteria and calculations of sequence similarity were carried out using CLUSTAL_X (Thompson *et al.*, 1997). A phylogenetic tree (Fig. 1) was constructed by means of the neighbour-joining method of Saitou & Nei (1987), from *K*_{nuc} values (Kimura, 1980), using MEGA, version 3.1 (Kumar *et al.*, 2004). Alignment positions with insertions or deletions were excluded from the calculations. The topology of the phylogenetic tree was evaluated by using the bootstrap resampling method of Felsenstein (1985) with 1000 replicates.

The almost-complete 16S rRNA gene sequence (1438 bp) of strain YIM 56238^T was determined. Phylogenetic analysis revealed that the closest relatives of strain YIM 56238^T were *M. luteus* DSM 20030^T, *M. antarcticus* T2^T, *M. lylae* DSM 20315^T and *M. flavus* LW4^T, which showed 16S rRNA gene sequence similarities of 99.06, 98.05, 97.56 and 97.79%, respectively. The results of the comparative 16S rRNA gene sequence analysis clearly demonstrated that strain YIM 56238^T is a member of the genus *Micrococcus*. The chemotaxonomic characteristics of strain YIM 56238^T, such as peptidoglycan type, menaquinones, major fatty acids, phospholipids and DNA G+C content, were consistent with its assignment to the genus *Micrococcus*.

DNA–DNA relatedness was studied using the fluorometric micro-well method (Ezaki *et al.*, 1989; Christensen *et al.*, 2000; He *et al.*, 2005). Fluorescence intensities were measured using a fluorescence microplate reader (SpectraMax Gemini XPS; Molecular Devices). Hybridizations were performed using six replications for each sample. The DNA hybridization rate was calculated according to the method of He *et al.* (2005). The DNA–DNA hybridization values for strain YIM 56238^T with respect to *M. luteus* DSM 20030^T, *M. antarcticus* CGMCC 1.2372^T, *M. lylae* DSM 20315^T and *M. flavus* CGMCC 1.5361^T were 27.3, 50.3, 30.1 and 54.2%, respectively. The G+C content of genomic DNA was determined by using

Table 1. Differential phenotypic characteristics of strain YIM 56238^T and related species of the genus *Micrococcus*

Strains: 1, YIM 56238^T; 2, *M. luteus* DSM 20030^T; 3, *M. antarcticus* CGMCC 1.2372^T; 4, *M. flavus* CGMCC 1.5361^T; 5, *M. lylae* DSM 20315^T. Data were obtained during this study under identical growth conditions, except where indicated otherwise. All strains are positive for acid production from mannose, maltose, sucrose, D-glucose and 5-ketogluconate, but negative for acid production from L-xylose, methyl β -D-xyloside, amygdalin, D-arabitol, L-arabitol, L-fucose, 2-ketogluconate and xylitol.

Characteristic	1	2	3	4	5
Growth at/with:					
4 °C	—	—	+	—	—
45 °C	—	—	—	—	+
7 % NaCl	+	+	+	—	—
Nitrate reduction	+	—	+	—	—
Voges–Proskauer reaction	—	—	+	—	—
Hydrolysis of:					
Tween 80	—	—	+	—	—
Starch	—	—	+	+	—
Assimilation of:					
D-Mannose	—	+	—	—	—
Trehalose	+	—	—	+	+
Acid production from:					
N-Acetylglucosamine	+	—	+	—	—
Adonitol	—	—	—	—	+
Aesculin	+	—	+	+	—
D-Arabinose	+	+	—	—	—
L-Arabinose	+	—	+	—	—
Arbutin	+	+	+	—	—
Cellobiose	+	—	+	+	—
Dulcitol	—	—	—	+	+
Erythritol	—	—	—	+	—
Fructose	+	+	+	—	+
D-Fucose	—	—	—	—	+
Galactose	+	—	+	—	—
β -Gentiobiose	—	—	+	—	+
Gluconate	—	—	—	+	—
Glycerol	—	+	+	—	+
Glycogen	—	—	+	—	+
Inositol	—	—	+	—	—
Inulin	—	—	—	—	+
Lactose	—	—	+	+	+
D-Lyxose	+	—	+	—	+
Mannitol	—	—	—	—	+
Melezitose	—	—	—	—	+
Melibiose	—	—	+	—	—
Methyl α -D-glucoside	+	+	—	—	—
Methyl α -D-mannoside	—	—	—	+	—
Raffinose	+	—	—	—	—
Rhamnose	—	—	+	—	+
Ribose	+	—	+	+	—
Salicin	—	+	+	+	+
Sorbitol	+	—	—	—	+
Sorbose	—	—	—	—	+
Starch	—	—	+	+	+
D-Tagatose	—	—	+	—	—
Trehalose	+	+	—	+	+
D-Xylose	—	—	+	—	—
Predominant menaquinone(s)	MK-8(H ₂), MK-7(H ₂)	MK-8, MK-8(H ₂)*	MK-8, MK-8(H ₂)*	MK-8(H ₂), MK-7(H ₂)*	MK-8(H ₂)*
DNA G + C content (mol%)	72.9	70.0*	66.4*	71.4*	69*

*Data for the type strains were taken from Liu *et al.* (2007).

Table 2. Comparative fatty acid compositions of strain YIM 56238^T and related species in the genus *Micrococcus*

Strains: 1, YIM 56238^T; 2, *M. luteus* DSM 20030^T; 3, *M. antarcticus* CGMCC 1.2372^T; 4, *M. flavus* CGMCC 1.5361^T; 5, *M. lylae* DSM 20315^T. Data were obtained during this study; growth conditions were identical for all strains. –, Not detected.

Fatty acid	1	2	3	4	5
iso-C _{13:0}	0.91	0.32	0.06	3.98	0.76
anteiso-C _{13:0}	0.89	0.50	0.09	2.78	0.24
Summed feature 1*	4.19	0.39	–	17.56	–
iso-C _{14:0}	2.59	1.88	6.19	3.98	2.46
C _{14:1} ω5c	–	0.27	–	0.66	–
C _{14:0}	0.35	1.05	0.63	0.78	0.57
iso-C _{15:1} G	–	–	0.46	–	–
anteiso-C _{15:1} A	–	–	2.52	–	–
iso-C _{15:0}	30.95	14.67	12.34	23.35	36.34
anteiso-C _{15:0}	53.75	63.16	63.66	41.92	50.03
C _{15:1} ω6c	0.18	–	–	0.95	–
iso-C _{16:1} H	0.77	1.03	–	1.13	–
iso-C _{16:0}	1.42	5.22	8.29	0.34	5.33
C _{16:0}	0.30	0.90	1.00	–	0.57
Summed feature 3*	0.45	2.53	–	1.31	–
anteiso-C _{17:1} ω9c	0.81	1.46	–	1.27	–
iso-C _{17:0}	0.58	0.40	0.40	–	0.59
anteiso-C _{17:0}	1.36	6.03	4.17	–	2.81

*Summed features represent groups of two or three fatty acids that could not be separated by GLC with the MIDI system. Summed feature 1 contained iso-C_{15:1} H and/or C_{13:0} 3-OH; summed feature 3 contained C_{16:1}ω7c and/or C_{16:1}ω6c.

the HPLC method (Mesbah *et al.*, 1989) with *Escherichia coli* JM-109 as the reference strain, and a value of 72.9 mol% was derived.

The values for DNA–DNA relatedness among strains YIM 56238^T, *M. luteus* DSM 20030^T, *M. antarcticus* CGMCC 1.2372^T, *M. lylae* DSM 20315^T and *M. flavus* CGMCC 1.5361^T were all below 70 %, which indicates that the novel isolate represents a distinct genospecies (Wayne *et al.*, 1987) of the genus *Micrococcus*. Thus, on the basis of the differential phenotypic properties mentioned above and the character-

istics shown in Tables 1 and 2, strain YIM 56238^T represents a novel species of the genus *Micrococcus*, for which the name *Micrococcus endophyticus* sp. nov. is proposed.

Description of *Micrococcus endophyticus* sp. nov.

Micrococcus endophyticus (en.do.phy'ti.cus. Gr. pref. *endo*- within; Gr. neutr. n. *phyton* plant; N.L. adj. *endophyticus* within plant, pertaining to the original isolation from plant tissues).

Fig. 1. Neighbour-joining phylogenetic dendrogram, based on 16S rRNA gene sequences, showing the relationships between strain YIM 56238^T and related taxa. Numbers at branch points are bootstrap percentages (based on 1000 resamplings). *Kytococcus sedentarius* DSM 20547^T was used as an outgroup. Bar, 0.005 substitutions per nucleotide position.

Cells are spherical, Gram-positive, aerobic, non-endospore-forming, coccoid and 0.5–0.7 µm in diameter. Motility is not observed. Colonies on TSA are yellow, slimy, smooth and circular with entire margins. No pigment is produced. The temperature, pH and NaCl ranges for growth are 15–37 °C, pH 6–9 and 0–10 % (w/v). Optimal growth occurs at 28 °C and at around pH 7.0–8.0. Catalase-positive and oxidase-positive. Gelatin is hydrolysed, but starch is not hydrolysed. The Voges–Proskauer reaction is negative and the reduction of nitrate is positive. The cell-wall peptidoglycan of the type strain contains lysine, glutamic acid, alanine and glycine. The phospholipids consist of diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol and an unknown ninhydrin-negative phospholipid. The predominant menaquinones are MK-8(H₂) (63.6 %) and MK-7(H₂) (21.1 %). The major cellular fatty acids are iso-C_{15:0} and anteiso-C_{15:0}. Other characteristics of the species are indicated in Tables 1 and 2.

The type strain, YIM 56238^T (=DSM 17945^T=KCTC 19156^T), was isolated from surface-sterilized roots of the plant *Aquilaria sinensis*, collected in the tropical rainforest of Yunnan Province in south-west China. The G+C content of the genomic DNA of the type strain is 72.9 mol%.

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References

- Barrow, G. I. & Feltham, K. A. (1993). *Cowan and Steel's Manual for the Identification of Medical Bacteria*, 3rd edn. London: Cambridge University Press.
- Christensen, H., Angen, O., Mutters, R., Olsen, J. E. & Bisgaard, M. (2000). DNA–DNA hybridization determined in micro-wells using covalent attachment of DNA. *Int J Syst Evol Microbiol* **50**, 1095–1102.
- Cohn, F. (1872). Untersuchungen über Bakterien. *Beitr Biol Pflanz* **1**, 127–224 (in German).
- Coombs, J. T. & Franco, C. M. (2003). Isolation and identification of actinobacteria from surface-sterilized wheat roots. *Appl Environ Microbiol* **69**, 5603–5608.
- Coombs, J. T., Michelsen, P. P. & Franco, C. M. M. (2004). Evaluation of endophytic actinobacteria as antagonists of *Gaeumannomyces graminis* var. *tritici* in wheat. *Biol Control* **29**, 359–366.
- Ezaki, T., Hashimoto, Y. & Yabuuchi, E. (1989). Fluorometric deoxyribonucleic acid–deoxyribonucleic acid hybridization in micro-dilution wells as an alternative to membrane filter hybridization in which radioisotopes are used to determine genetic relatedness among bacterial strains. *Int J Syst Bacteriol* **39**, 224–229.
- Felsenstein, J. (1985). Confidence limits on phylogenies: an approach using the bootstrap. *Evolution* **39**, 783–789.
- Gu, Q., Luo, H., Zheng, W., Liu, Z. & Huang, Y. (2006). *Pseudonocardia oroxyli* sp. nov., a novel actinomycete isolated from surface-sterilized *Oroxylum indicum* root. *Int J Syst Evol Microbiol* **56**, 2193–2197.
- Hasegawa, T., Takizawa, M. & Tanida, S. (1983). A rapid analysis for chemical grouping of aerobic actinomycetes. *J Gen Appl Microbiol* **29**, 319–322.
- He, L., Li, W., Huang, Y., Wang, L. & Liu, Z. (2005). *Streptomyces jietaisiensis* sp. nov., isolated from soil in northern China. *Int J Syst Evol Microbiol* **55**, 1939–1944.
- Kimura, M. (1980). A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. *J Mol Evol* **16**, 111–120.
- Kloos, W. E., Tornabene, T. G. & Schleifer, K. H. (1974). Isolation and characterization of micrococci from human skin, including two new species: *Micrococcus lylae* and *Micrococcus kristinae*. *Int J Syst Bacteriol* **24**, 79–101.
- Kroppenstedt, R. M. (1982). Separation of bacterial menaquinones by HPLC using reverse phase (RP18) and a silver loaded ion exchanger as stationary phases. *J Liq Chromatogr* **5**, 2359–2367.
- Kumar, S., Tamura, K. & Nei, M. (2004). MEGA3: integrated software for molecular evolutionary genetics analysis and sequence alignment. *Brief Bioinform* **5**, 150–163.
- Li, W. J., Xu, P., Schumann, P., Zhang, Y. Q., Pukall, R., Xu, L. H., Stackebrandt, E. & Jiang, C. L. (2007). *Georgenia ruanii* sp. nov., a novel actinobacterium isolated from forest soil in Yunnan (China) and emended description of the genus *Georgenia*. *Int J Syst Evol Microbiol* **57**, 1424–1428.
- 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.
- Mesbah, M., Premachandran, U. & Whitman, W. B. (1989). Precise measurement of the G+C content of deoxyribonucleic acid by high-performance liquid chromatography. *Int J Syst Bacteriol* **39**, 159–167.
- 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.
- Moaledj, K. (1986). Comparison of Gram-staining and alternate methods, KOH test and aminopeptidase activity in aquatic bacteria: their application to numerical taxonomy. *J Microbiol Methods* **5**, 303–310.
- Saitou, N. & Nei, M. (1987). The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Mol Biol Evol* **4**, 406–425.
- Schleifer, K. H. & Kandler, O. (1972). Peptidoglycan types of bacterial cell walls and their taxonomic implications. *Bacteriol Rev* **36**, 407–477.
- 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 emend. *Int J Syst Bacteriol* **45**, 682–692.
- 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.

- Tian, X. L., Cao, L. X., Tan, H. M., Han, W. Q., Chen, M., Liu, Y. H. & Zhou, S. N. (2007). Diversity of cultivated and uncultivated actinobacterial endophytes in the stems and roots of rice. *Microb Ecol* 53, 700–707.
- Trujillo, M. E., Kroppenstedt, R. M., Schumann, P. & Martinez-Molina, E. (2006). *Kribbella lupini* sp. nov., isolated from the roots of *Lupinus angustifolius*. *Int J Syst Evol Microbiol* 56, 407–411.
- Xu, P., Li, W. J., Tang, S. K., Zhang, Y. Q., Chen, G. Z., Chen, H. H., Xu, L. H. & Jiang, C. L. (2005). *Naxibacter alkalitolerans* gen. nov., sp. nov., a novel member of the family 'Oxalobacteraceae' isolated from China. *Int J Syst Evol Microbiol* 55, 1149–1153.
- Wayne, L. G., Brenner, D. J., Colwell, R. R., Grimont, P. A. D., Kandler, O., Krichevsky, M. I., Moore, L. H., Moore, W. E. C., Murray, R. G. E. & other authors (1987). International Committee on Systematic Bacteriology. Report of the ad hoc committee on reconciliation of approaches to bacterial systematics. *Int J Syst Bacteriol* 37, 463–464.
- 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.