Yimella lutea gen. nov., sp. nov., a novel actinobacterium of the family Dermacoccaceae

Shu-Kun Tang,1† Jin-Yuan Wu,1† Yun Wang,2 Peter Schumann3 and Wen-Jun Li1,4

1The Key Laboratory for Microbial Resources of the Ministry of Education, and Laboratory for Conservation and Utilization of Bio-Resources, Yunnan Institute of Microbiology, Yunnan University, Kunming 650091, PR China
2Xinjiang Institute of Microbiology, Xinjiang Academy of Agricultural Science, Urumqi, Xinjiang 830091, PR China
3DSMZ – Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, Inhoffenstrasse 7B, D-38124 Braunschweig, Germany
4Guangdong Key Laboratory of Marine Materia Medica, South China Sea Institute of Oceanology, Chinese Academy of Sciences, Guangzhou 510301, PR China

A Gram-stain-positive, coccoid, non-motile, halotolerant actinobacterium, designated YIM 45900T, was found as a contaminant on an agar plate in the laboratory of Yunnan Institute of Microbiology, China. The peptidoglycan type was A4α with an L-Lys–L-Ser–D-Asp interpeptide bridge. The cell-wall sugars contained galactose and fucose. The predominant menaquinone was MK-8(H4). The major fatty acids were iso-C15:0, anteiso-C15:0 and anteiso-C17:0. The polar lipids contained diphosphatidylglycerol, phosphatidylinositol, a glucosamine-containing phospholipid and an unknown phospholipid. The DNA G+C content was 65.8 mol%.

Phylogenetic analysis based on 16S rRNA gene sequences revealed that the organism falls within the radius of the suborder Micrococcineae and its closest phylogenetic neighbours are the genera of the family Dermacoccaceae. Strain YIM 45900T showed 16S rRNA gene sequences similarity values of 93.1–95.9% with members of the genera Dermacoccus, Demetria and Kytococcus. On the basis of the phylogenetic and phenotypic characteristics of the actinobacterium, a novel genus and species, Yimella lutea gen. nov., sp. nov., are proposed. The type strain of Yimella lutea is YIM 45900T (=DSM 19828T =KCTC 19231T =CCTCC AB 207007T).

The family Dermacoccaceae was first proposed by Stackebrandt & Schumann (2000) and its pattern of 16S rRNA signature nucleotides was emended by Zhi et al. (2009). At the time of writing, the family Dermacoccaceae comprises the genera Dermacoccus (Stackebrandt et al., 1995), Demetria (Groth et al., 1997) and Kytococcus (Stackebrandt et al., 1995). Most strains have been isolated from human skin. They are Gram-positive, aerobic, non-encapsulated, non-endospore-forming, catalase-positive, non-halophilic, coccoid actinobacteria and the peptidoglycan type is variation A4x.

Strain YIM 45900T, a Gram-stain-positive, coccoid, non-motile, halotolerant actinobacterium, was found in the laboratory of Yunnan Institute of Microbiology, China, as a contaminant on a modified ISP medium 5 (Shirling & Gottlieb, 1966) agar plate (containing 1l−1 distilled water: 1 g L-asparagine, 10 g glycerol, 5 g yeast extract, 1 g K2HPO4, 5 g KNO3, 50 g NaCl, 15 g agar; final pH 7.5). NaCl was sterilized separately before being added to the medium. Strain YIM 45900T was maintained on ISP 2 (Shirling & Gottlieb, 1966) agar slants at 4°C and in 20% (w/v) glycerol suspensions at −20°C. Biomass for chemical and molecular studies was obtained by cultivation in shaken flasks (about 150 r.p.m.) using ISP 2 broth (pH 7.5) at 28°C for about 1 week.

Cell morphology was determined on cultures grown for 6, 12, 24, 48 and 72 h on ISP 2 agar medium at 28°C. Gram staining was carried out by the standard Gram reaction and was confirmed by using KOH lysis (Cerny, 1978). Spore formation was determined by staining with malachite green. Cell motility was confirmed by the development of turbidity throughout a tube containing semisolid medium (Leifson, 1960). Morphological characteristics of the strain were observed by light microscopy (model BH 2; Olympus).
and by transmission electron microscopy (model H-800; Hitachi). The growth temperature was tested at 4–55 °C at intervals of 2 °C on ISP medium 2. For NaCl tolerance experiments, ISP medium 2 was used as the basal medium and salt concentrations ranging from 0 to 20% (w/v) at intervals of 1% were tested. The pH growth range was investigated between pH 4.0 and 10.0 at intervals of 1 pH unit, using the following buffer systems: pH 4–5 0.1 M citric acid/0.1 M sodium citrate; pH 6–8 0.1 M KH2PO4/0.1 M NaH2PO4; pH 9–10 0.1 M NaHCO3/0.1 M Na2CO3. Catalase activity was determined by production of bubbles after the addition of a drop of 3% H2O2. Oxidase activity was observed by oxidation of tetramethyl-p-phenylenediamine. Methyl red and Voges–Proskauer tests and tests for melanin production and milk peptoneization and hydrolysis of ascesulin, casein, cellulose, chitin, dextrin, DNA, gelatin, starch, urea and Tweens 20, 40, 60 and 80 were performed as described by Cowan & Steel (1965). Oxidation of different substrates was tested using GP2 MicroPlates (Biolog). Enzyme activities and acid production from carbohydrates were determined by using the API 20E, API ZYM and API 50CH systems (bioMérieux) according to the manufacturer’s instructions. Anaerobic growth was determined using the GasPak Anaerobic System (BBL) according to the manufacturer’s instructions. The morphological, cultural and physiological properties of strain YIM 45900T are given in the genus and species descriptions. The organism can be distinguished from members of the family Dermacoccaceae using a range of phenotypic properties (Table 1).

The peptidoglycan structure of the cell wall of strain YIM 45900T was determined by using established procedures (Schleifer & Kandler, 1972; Schleifer, 1985; MacKenzie, 1987). Sugar analysis of the purified cell wall followed procedures described by Staneck & Roberts (1974). Polar lipids were extracted, examined by two-dimensional TLC and identified using described procedures (Minnikin et al., 1984). Menaquinones were isolated according to Minnikin et al. (1984) and separated by HPLC (Kroppenstedt, 1982). For fatty acid analyses, cells of strain YIM 45900T were cultured on tryptic soy agar (Difco) at 28°C for 4 days. Cellular fatty acids analysis was performed as described by Sasser (1990) using the Microbial Identification System (MIDI).

The peptidoglycan of strain YIM 45900T contained Ala, Gly, Ser, Asp, Ghu and Lys in a molar ratio of 1.6:1.0:0.7:0.8:1.0:1.2. The peptide Lys–Ser, which is stable under hydrolytic conditions in 4 M HCl at 100 °C for 16 h, was detected. Aspartic acid was revealed by dinitrophenylation to represent the N terminus of the interpeptide bridge. From these data, it was concluded that strain YIM 45900T contained the peptidoglycan type A4\(\alpha\) with a L-Lys–L-Ser–D-Asp interpeptide bridge and a glycline residue bound to the α-carboxyl group of D-glutamic acid at position 2 of the peptide subunit. The cell-wall sugars were galactose and fucose (with a minor amount of mannose and traces of glucose). The polar lipids consisted of diposphatidylglycerol, phosphatidylinositol, glucosamine-containing phospholipid and one unknown phospholipid. The predominant menaquinone was MK-8(H4) (97.2%); a minor amount of MK-8(H6) (2.8%) was detected. Strain YIM 45900T had a cellular fatty acid profile that contained major amounts (>10%) of branched fatty acids, iso-C15:0 (35.2%), anteiso-C15:0 (12.1%) and anteiso-C17:0 (11.1%), and minor amounts of branched, straight-chain, unsaturated and methyl fatty acids, iso-C13:0 (4.2%), anteiso-C13:0 (2.4%), iso-C14:0 (0.5%), C14:0 (3.0%), C15:0 (1.0%), iso-C16:0 (0.5%), iso-C16:0 (4.8%), C16:0 cis-9 (3.3%), C16:0 (5.7%), C16:0 9-methyl (2.0%), anteiso-C17:0 (0.8%), iso-C17:0 (5.5%), C17:1 cis-9 (1.0%), C17:0 (0.5%), C18:1 cis-9 (2.0%) and C18:1 2-OH (1.6%).

Extraction of genomic DNA and PCR amplification of the 16S rRNA gene sequence were performed as described by Li et al. (2007). Multiple alignments with sequences from the most closely related members of the suborder Micrococcineae and calculations of levels of sequence similarity were carried out using the EzTaxon server 2.0 (Chun et al., 2007). Phylogenetic analyses were performed using three tree-making algorithms, the neighbour-joining (Saitou & Nei, 1987), maximum-likelihood (Felsenstein, 1981) and maximum-parsimony (Fitch, 1971) methods. A phylogenetic tree was constructed using the neighbour-joining method from K_{nuc} values (Kimura, 1980) using MEGA version 4.0 (Tamura et al., 2007). The topology of the phylogenetic tree was evaluated by the bootstrap resampling method of Felsenstein (1985) with 1000 resamplings. The genomic DNA of strain YIM 45900T for the determination of G+C content was prepared according to the method of Marmur (1961). The G+C content of the DNA was determined by reversed-phase HPLC of nucleosides according to Mesbah et al. (1989).

An almost-complete 16S rRNA gene sequence (1446 bp) was determined for strain YIM 45900T. Comparative 16S rRNA gene sequence analysis showed that strain YIM 45900T fell within the radius of the suborder Micrococcineae (Fig. 1). Its closest phylogenetic neighbours were members of the genera of the family Dermacoccaceae. Strain YIM 45900T showed 16S rRNA gene sequence similarities of 95.9, 95.9, 95.7, 95.6, 94.0, 93.5 and 93.1% to the type strains of Dermacoccus profundus, Dermacoccus barathri, Dermacoccus abyssi, Dermacoccus nishinomiya-ensis, Demetria terragena, Kytococcus selenitarius and Kytococcus schroeteri, respectively. This relationship was supported by all three tree-making methods (data not shown). The G+C content of the DNA was 65.8 mol%.

Strain YIM 45900T was similar to members of the genera of the family Dermacoccaceae (Dermacoccus, Kytococcus and Demetria), which have lysine as the diagnostic diamino acid, and different from members of the genera of the family Dermabacteraceae (Dermabacter and Brachybacterium) and Dermatophilaceae (Dermatophilus and Kineosphaera), which have meso-A2pm as the diagnostic
diamino acid. In the phylogenetic tree based on the neighbour-joining algorithm, all of the type strains of the family Dermacoccaceae together with strain YIM 45900T clustered in a distinct clade that was strongly supported by a bootstrap value of 60%. All of the above data confirmed that the isolate should be assigned to the family Dermacoccaceae. However, strain YIM 45900T formed a monophyletic branch within the radiation occupied by the three genera of the family Dermacoccaceae. Moreover, strain YIM 45900T could be differentiated from the genera Dermacoccus and Kytococcus in some chemotaxonomic properties (Table 1), i.e. strain YIM 45900T had L-Lys–L-Ser–D-Asp as the interpeptide bridge of the peptidoglycan and MK-8(H₄) as the predominant menaquinone, whereas the members of genus Dermacoccus show L-Lys–L-Ser₁–₂–D-Glu or L-Lys–L-Ser₁–₂–L-Ala–D-Glu as the interpeptide bridge and MK-8(H₂) as the predominant menaquinone and the genus Kytococcus contains L-Lys–Glu₂ as the interpeptide bridge and MK-8, MK-9 and MK-10 as the predominant menaquinones. Although strain YIM 45900T was similar to the genus Demetria in containing L-Lys–L-Ser–D-Asp as the interpeptide bridge and MK-8(H₄) as the

Table 1. Differential phenotypic and chemotaxonomic characteristics of the genus Yimella gen. nov. and related genera of the family Dermacoccaceae

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cell/colony characteristics</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cell size (µm)</td>
<td>0.7–0.9 x 1.3–1.8</td>
<td>0.8 x 1.2 or 0.8 x 3.0</td>
<td>0.9 x 1.6</td>
<td>0.8 x 1.1</td>
</tr>
<tr>
<td>Cell morphology</td>
<td>Coccoid</td>
<td>Coccoid or rods</td>
<td>Coccoid</td>
<td>Coccoid</td>
</tr>
<tr>
<td>Colony pigmentation</td>
<td>Orange</td>
<td>White to pale yellow</td>
<td>Bright orange</td>
<td>Orange</td>
</tr>
<tr>
<td>Water-soluble pigment</td>
<td>–</td>
<td>ND</td>
<td>Orange</td>
<td>Brownish</td>
</tr>
<tr>
<td>Conditions for growth</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NaCl range (% w/v)</td>
<td>0–8</td>
<td>0–12</td>
<td>0–7</td>
<td>0–10</td>
</tr>
<tr>
<td>pH range</td>
<td>5.0–9.0</td>
<td>ND</td>
<td>5.4–6.9</td>
<td>ND</td>
</tr>
<tr>
<td>Facultatively anaerobic</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Methyl red test</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Oxidase test</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>Nitrate reduction</td>
<td>+</td>
<td>–</td>
<td>V</td>
<td>V</td>
</tr>
<tr>
<td>Hydrolysis of:</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Aesculin</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Gelatin</td>
<td>+</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Starch</td>
<td>–</td>
<td>+</td>
<td>V</td>
<td>–</td>
</tr>
<tr>
<td>Tween 80</td>
<td>+</td>
<td>+</td>
<td>V</td>
<td>–</td>
</tr>
<tr>
<td>Urea</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Acid production from</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>D-Fructose</td>
<td>+</td>
<td>+</td>
<td>ND</td>
<td>–</td>
</tr>
<tr>
<td>D-Galactose</td>
<td>–</td>
<td>+</td>
<td>ND</td>
<td>–</td>
</tr>
<tr>
<td>D-Glucose</td>
<td>+</td>
<td>+</td>
<td>ND</td>
<td>–</td>
</tr>
<tr>
<td>Maltose</td>
<td>+</td>
<td>–</td>
<td>ND</td>
<td>–</td>
</tr>
<tr>
<td>Trehalose</td>
<td>+</td>
<td>–</td>
<td>ND</td>
<td>–</td>
</tr>
<tr>
<td>Sucrose</td>
<td>+</td>
<td>–</td>
<td>ND</td>
<td>–</td>
</tr>
<tr>
<td>D-Xylose</td>
<td>–</td>
<td>–</td>
<td>ND</td>
<td>–</td>
</tr>
<tr>
<td>Cell-wall sugar(s)</td>
<td>Galactose, fucose</td>
<td>Galactose</td>
<td>Galactose</td>
<td>ND</td>
</tr>
<tr>
<td>Predominant menaquinone(s)</td>
<td>MK-8(H₄)</td>
<td>MK-8(H₄)</td>
<td>MK-8(H₂)</td>
<td>MK-8, MK-9, MK-10</td>
</tr>
<tr>
<td>Polar lipids*</td>
<td>DPG, PI, GlcN-PL, PL</td>
<td>DPG, PG, PE, PI, PL</td>
<td>DPG, PG, PI</td>
<td>DPG, PG, PI</td>
</tr>
<tr>
<td>Major fatty acids (≥10%)</td>
<td>i-C₁₅:₀, ai-C₁₅:₀, C₁₈:₁, C₁₇:₀, C₁₈:₀</td>
<td>i-C₁₇:₀, ai-C₁₇:₀, i-C₁₇:₁, i-C₁₅:₀</td>
<td>i-C₁₇:₀, ai-C₁₇:₀, C₁₅:₀, i-C₁₇:₁</td>
<td>i-C₁₇:₀, ai-C₁₇:₀, C₁₅:₀, i-C₁₇:₁</td>
</tr>
<tr>
<td>DNA G+C content (mol%)</td>
<td>65.8</td>
<td>66</td>
<td>66–71†</td>
<td>68–69†</td>
</tr>
</tbody>
</table>

*DPG, Diphosphatidylglycerol; GlcN-PL, glucosamine-containing phospholipid; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PI, phosphatidylinositol; PL, unknown phospholipid.
†Range of values for several strains, including the type strain.
predominant menaquinone, it could be differentiated from the genus *Demetria* by the occurrence of a glycine residue bound to the α-carboxyl group of D-glutamic acid of the peptide subunit and by the polar lipid pattern, as strain YIM 45900ᵀ contained a glucosamine-containing phospholipid but no phosphatidylethanolamine. In particular, strain YIM 45900ᵀ was quite different from the genus *Demetria* in its fatty acid profile, i.e. strain YIM 45900ᵀ contained major amounts of branched fatty acids (iso-C₁₅:₀, anteiso-C₁₅:₀ and anteiso-C₁₇:₀) whereas the genus *Demetria* contained major amounts of straight and unsaturated fatty acids (C₁₇:₀, C₁₈:₀ and C₁₈:₁).

Therefore, on the basis of chemotaxonomic and phylogenetic differentiation of the isolate from its closest neighbours in the family *Dermacoccaceae*, we propose that strain YIM 45900ᵀ represents a novel species in a new genus, *Yimella lutea* gen. nov., sp. nov.

**Description of the genus *Yimella* gen. nov.**

*Yimella* (Yi.mel.9a. L. fem. dim. suff. -ella; N.L. fem. dim. n. *Yimella* arbitrary name formed from the acronym of Yunnan Institute of Microbiology, YIM, where the first taxonomic studies of this taxon were performed).

Cells are Gram-stain-positive, coccoid, non-encapsulated, halotolerant, aerobic and facultatively anaerobic in the presence of KNO₃. They do not form endospores. The peptidoglycan is of the type A₄α with a L-Lys–L-Ser–D-Asp interpeptide bridge and a glycine residue bound to the α-carboxyl group of D-glutamic acid at position 2 of the peptide subunit. The cell-wall sugars contain galactose and fucose. The predominant menaquinone is MK-8(H₄). The polar lipids are diphosphatidylglycerol, phosphatidylinositol, a glucosamine-containing phospholipid and an unknown phospholipid. The major fatty acids are iso-C₁₅:₀, anteiso-C₁₅:₀ and anteiso-C₁₇:₀. The G+C content of the DNA is about 65–66 mol%. The type species is *Yimella lutea*.

**Description of *Yimella lutea* sp. nov.**

*Yimella lutea* (lu.te.9a. L. fem. adj. lutea orange-coloured).

Cells are approximately spherical (0.7–0.9 × 1.3–1.8 µm) on ISP 2 medium, non-motile and arranged in irregular clusters. The orange colonies on ISP 2 agar are circular, smooth, opaque and non-pigmented. Temperature, pH and NaCl tolerance ranges for growth are 22–42 °C, pH 5.0–9.0 and 0–8 % and optimal growth occurs at 28 °C, pH 6.0–7.0 and 0–1 %. Catalase and methyl red tests are positive. Oxidase and Voges–Proskauer tests are negative. Gelatin, cellulose and Tweens 20, 40, 60 and 80 are hydrolysed, but casein, dextrin, starch, DNA, chitin and urea are not hydrolysed. Nitrate reduction and melanin production are positive. Milk peptonization and coagulation, H₂S and indole production, arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase and tryptophan deaminase are negative. With the API ZYM system, positive for alkaline phosphatase, esterase (C₄), esterase lipase (C₈), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, x-chymotrypsin, naphthol-AS-BI-phosphohydrolase, β-glucuronidase and α-glucosidase, but negative for lipase (C₁₄), x- and β-galactosidases, β-glucosidase, N-acetyl-β-glucosaminidase, β-mannosidase and x-fucosidase. With Biolog GP2 MicroPlates, oxidizes Tweens 40 and 80, D-fructose, trehalose, α-D-glucose, D-mannose, sucrose, maltose, D-xylene, acetic acid, D-ribose, propanionic acid, pyruvic acid, glyceral, uridine, D-tagatose, turanose, L-arginine, glycine, L-histidine and xanthine. Acid is pro-

**Fig. 1.** Phylogenetic dendrogram obtained by distance-matrix analysis of 16S rRNA gene sequences, showing the position of strain YIM 45900ᵀ and its phylogenetic neighbours. Bootstrap values (≥50 %) based on 1000 resamplings are shown at branch nodes. The sequence of *Bifidobacterium gallicum* JCM 8224ᵀ was used as an outgroup. Bar, 1 % sequence divergence.
duced from aesculin, D-fructose, D-glucose, glycerol, D-
mannose, maltose, sucrose, D-tagatose, trehalose, turanose
and potassium 5-ketogluconate, but not from N-acetylgluco-
samine, D-adonitol, amygdalin, DL-arabitol, arbutin, DL-
arabinose, cellobiose, dulcitol, erythritol, DL-fucose, D-
galactose, gentiobiose, glycogen, inositol, inulin, lactose,
D-lyxose, D-mannitol, melezitose, melibiose, D-raffinose, L-
rhamnose, D-ribose, salicin, D-sorbitol, L-sorbose, starch,
DL-xylene, methyl β-D-xlyopyranoside, methyl α-D-manno-
pyranoside, methyl α-D-glucopyranoside, xylitol, potassium
gluconate or potassium 2-ketogluconate. The DNA G+C
content of the type strain is 65.8 mol%.

The type strain is YIM 45900T (=DSM 19828T =KCTC
19231T =CCTCC AB 207007T), isolated from a contami-
nated agar plate.

Acknowledgements

The authors are grateful to Dr Jean Euzéby for the Latin
construction of the generic name. This research was supported by the National
Basic Research Program of China (2010CB833800), the Key Project of
the National Natural Science Foundation of China (30860002, 30870005), the Key Project of
International Cooperation (2007DFB31620) and the National Natural
Science Foundation of China (30860002, 30870005).

References

Cerny, G. (1978). Studies on aminopeptidase for the distinction of
Gram-negative from Gram-positive bacteria. Eur J Appl Microbiol
Biotechnol 5, 113–122.

(2007). EzTaxon: a web-based tool for the identification of
prokaryotes based on 16S ribosomal RNA gene sequences. Int J Syst

Medical Bacteria. London: Cambridge University Press.


using the bootstrap. Evolution 39, 783–789.

Fitch, W. M. (1971). Toward defining the course of evolution:

Groth, I., Schumann, P., Rainey, F. A., Martin, K., Schuetze, B. &
genus of actinomycetes isolated from compost soil. Int J Syst Evol
Microbiol 47, 1129–1133.

of base substitutions through comparative studies of nucleotide

HPLC using reverse phase (RP18) and a silver loaded ion exchanger
as stationary phases. J Liq Chromatogr 5, 2359–2387.

Press.

Li, W. J., Xu, P., Schumann, P., Zhang, Y. Q., Pukall, R., Xu, L. H.,
Stackebrandt, E. & Jiang, C. L. (2007). Georgenia ruanti 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.

acids as the N-heptfluorobutyryl isobutyl esters. J Assoc Off Anal
Chem 70, 151–160.


measurement of the G+C content of deoxyribonucleic acid by high-
167.

Minnikin, D. E., O’Donnell, A. G., Goodfellow, M., Alderson, G.,
procedure for the extraction of isoprenoid quinones and polar lipids.


of cellular fatty acids. USFCC News 20, 16.

Schleifer, K. H. (1985). Analysis of the chemical composition and
primary structure of murein. Methods Microbiol 18, 123–156.

Schleifer, K. H. & Kandler, O. (1972). Peptidoglycan types of bacterial
477.


Stackebrandt, E. & Schumann, P. (2000). Description of
Boderiellaceae fam. nov., Dermacoccaceae fam. nov., Ratrobacceae
fam. nov. and Sanguibacteraeae fam. nov. and emendation of some
families of the order Micrococccineae. Int J Syst Evol Microbiol 50,
1279–1283.

Taxonomic dissection of the genus Micrococcus: Kocuria gen. nov.,
Nesterenkonia gen. nov., Kytorococcus gen. nov., Dermacoccus gen. nov., and
692.

identification of aerobic actinomycetes by thin-layer chromatography.

evolutionary genetics analysis (MEGA) software version 4.0. Mol Biol
Evol 24, 1596–1599.

structure and 16S rRNA gene sequence-based definition of higher
ranks of the class Actinobacteria, with the proposal of two new
suborders and four new families and emended descriptions of the