Auritidibacter ignavus gen. nov., sp. nov., of the family *Micrococcaceae* isolated from an ear swab of a man with otitis externa, transfer of the members of the family *Yaniellaceae* Li *et al.* 2008 to the family *Micrococcaceae* and emended description of the suborder *Micrococcineae*

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A Gram-reaction-positive, aerobic, catalase-positive, non-spore-forming, rod-shaped bacterium designated IMMIB L-1656^T was isolated from an ear swab of a man and characterized using a polyphasic approach. 16S rRNA gene sequence analysis indicated that strain IMMIB L-1656^T is related to members of the family *Micrococcaceae* (<95.1 % sequence similarity). Analysis using different phylogenetic algorithms consistently grouped strain IMMIB L-1656^T with members of the genus *Yaniella*. The organism possessed a cell-wall murein based on L-lysine (variation A4 α , type L-Lys–Gly–L-Glu), MK-10 as the predominant menaquinone and long-chain cellular fatty acids of straight-chain and branched-chain saturated types (with iso-C_{15:0} and anteiso-C_{17:0} predominating). The polar lipids included diphosphatidylglycerol, phosphatidylglycerol and phosphatidylinositol in addition to unknown glycolipids. The DNA G + C content was 59.7 mol%. Based on its distinctive genotypic and phenotypic characteristics, strain IMMIB L-1656^T represents a novel species in a novel genus, for which the name *Auritidibacter ignavus* gen. nov., sp. nov. is proposed. We also propose that members of the family *Yaniellaceae* be transferred to the family *Micrococcaceae* with amendments to the description of the suborder *Micrococcineae*. The type strain of *Auritidibacter ignavus* is IMMIB L-1656^T (=DSM 45359^T =CCUG 57943^T).

The taxonomy of the broad group of Gram-positive, catalase-positive, coccus- to rod-shaped organisms that belong phylogenetically to the actinomycete group has undergone major changes during the past 20 years (Stackebrandt *et al.*, 1980, 1995, 1997). The most significant change has been the rapid growth in the number of recognized genera. Some of the newly described genera have arisen through taxonomic revision of existing genera, e.g. *Kocuria*, *Nesterenkonia*, *Kytococcus* and *Dermacoccus* from the genus *Micrococcus* (Stackebrandt *et al.* 1995) and

Citricoccus from the genus *Kocuria* (Altenburger *et al.*, 2002). However, a large majority of genera have been newly defined due to the utility of 16S rRNA gene sequencing and database searches, resulting in improved knowledge of the phylogeny of these organisms (Stackebrandt *et al.*, 1997; Stackebrandt & Schumann, 2000; Li *et al.*, 2004; Zhi *et al.*, 2009). During the course of characterization of bacterial isolates encountered in clinical specimens, we isolated a novel strain with an uncertain taxonomic affiliation. In this paper, we report the results of a polyphasic taxonomic study, which suggest that strain IMMIB L-1656^T represents novel species of a novel genus, for which the name *Auritidibacter ignavus* gen. nov., sp. nov. is proposed.

Strain IMMIB L-1656^T was isolated from an ear swab of a 28-year-old man with fulminant otitis externa by plating

The GenBank/EMBL/DDBJ accession number for the 16S rRNA sequence of strain IMMIB L-1656^T is FN554542.

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

on Columbia agar supplemented with 5% sheep's blood (BD). Motility was observed by the hanging-drop technique using cells in the exponential growth phase in BHI broth (BD). Cell morphology was observed using a transmission electron microscope (Philips CM-10) and cultures grown in BHI broth at 35 °C for 17–140 h. Negative staining of cells was performed with 1% phosphotungstic acid. Growth was tested on DST agar (Oxoid), BHI agar (BD), Columbia agar supplemented with 5% sheep's blood and TSA agar (Oxoid). Growth at 5, 10, 22, 30, 37 and 42 °C was determined on Columbia agar and tolerance of 0, 2, 4, 6, 8, 10, 12 and 14% NaCl was determined in nutrient broth. The range and optimum pH for growth was determined by incubation in BHI broth at pH 4, 5, 6, 7.4, 8 and 9. Test medium at low pH was obtained by adding hydrochloric acid (6 M) and medium at pH >7.4 was obtained by the addition of sodium hydroxide (1 M). Oxidase activity was determined using the DrySlide oxidase test (BBL System; BD). The presence of catalase was assessed using 3% H₂O₂. The unidentified isolate was characterized biochemically using the API Coryne and API ZYM systems according to the manufacturer's instructions (bioMérieux). Hydrolysis of adenine, casein, elastin, guanine, hypoxanthine, testosterone, tyrosine and xanthine was investigated by using methods described previously (Gordon, 1966, 1967; Gordon & Mihm, 1957). DNase test agar (Difco) was used for the DNase assay. Starch hydrolysis was assessed by using the method of Barrow & Feltham (1993). The CAMP (Christie–Atkins–Munch–Petersen) test was carried out with *Staphylococcus aureus* CECT 4013 by using conventional procedures (Facklam & Elliot, 1995). Tests to determine carbon source utilization were performed as described previously (Yassin *et al.*, 1995). Resistance to antibiotics was investigated by using the method of Bauer *et al.* (1966).

Whole-cell sugars were determined by using the method of Lechevalier (1968). Fatty acid methyl ester analysis was performed according to methods described previously (Minnikin *et al.*, 1980; Yassin *et al.*, 2007). Isoprenoid quinones were extracted and purified according to Collins *et al.* (1977). Mass spectral analyses of the quinones were recorded as described by Yassin & Hupfer (2006) in positive ion mode on a Q-TOF 2 mass spectrometer (Micromass) equipped with a nanospray source. Phospholipids were extracted, purified and identified using two-dimensional TLC as described previously by Yassin *et al.* (1993). The DNA G+C content was determined by HPLC according to Mesbah *et al.* (1989). The peptidoglycan was isolated after cells were disrupted by shaking with glass beads and digested with trypsin according to the method of Schleifer (1985). Amino acids and peptides in cell-wall hydrolysates were analysed by two-dimensional TLC on cellulose plates by using previously described solvent systems (Schleifer, 1985). The identity of amino acids was confirmed and the molar ratio of *N*-heptafluorobutyl amino acid isobutyl esters was estimated by GC (14A; Shimadzu) and GC–MS (320-MS; Varian) (MacKenzie, 1987; Groth *et al.*, 1996).

The 16S rRNA gene of the isolate was amplified by PCR, using procedures described previously (Rainey *et al.*, 1996), and sequenced directly using a *Taq* Dye-Deoxy terminator cycle sequencing kit (Applied Biosystems) and an automatic DNA sequencer (310; Applied Biosystems). The closest known relatives of the novel isolate were determined by performing database searches. The 16S rRNA gene sequence of strain IMMIB L-1656^T and closely related sequences were retrieved from GenBank, added to the ARB database (Ludwig *et al.*, 2004) and aligned using the appropriate tool from the ARB software package. The resulting alignment was corrected manually and phylogenetic trees were reconstructed using maximum-parsimony (Fitch, 1971), neighbour-joining (Saitou & Nei, 1987) and maximum-likelihood (Felsenstein, 1981) methods. The evolutionary distance matrix for the neighbour-joining method was calculated using the correction of Jukes & Cantor (1969). The topology of the neighbour-joining tree was evaluated using bootstrap analysis (Felsenstein, 1985) based on 1000 resamplings.

To investigate the phylogenetic affinities of strain IMMIB L-1656^T, the almost-complete 16S rRNA gene sequence of the strain (1466 nt) was determined in this study. Sequence database searches (BLAST) indicated that strain IMMIB L-1656^T was most closely related to genera of the family *Micrococcaceae*. Similarity values of the 16S rRNA gene sequences calculated for strain IMMIB L-1656^T indicated that the closest type strains of species with validly published names were *Kocuria rosea* DSM 20447^T (95.1%), *Yaniella flava* YIM 70178^T (94.8%), *Yaniella halotolerans* YIM 70085^T (94%), *Citricoccus muralis* 4-0^T (94%), *Arthrobacter globiformis* DSM 20124^T (93.9%), *Micrococcus luteus* DSM 20030^T (93.9%) and *Zhihengliuella halotolerans* YIM 70185^T (93.9%). The 16S rRNA gene sequence similarities between strain IMMIB L-1656^T and other members of the suborder *Micrococcineae* were less than 90%. A tree constructed using the neighbour-joining method showing the nearest phylogenetic relatives of strain IMMIB L-1656^T is shown in Fig. 1. Phylogenetically, strain IMMIB L-1656^T formed a distinct subline within a broad range of taxa including species of the genera *Acaricomes*, *Arthrobacter*, *Citricoccus*, *Micrococcus*, *Nesterenkonia*, *Renibacterium*, *Rothia* and *Zhihengliuella*. In particular, the bacterium forms an association with the genus *Yaniella*. Although the association of strain IMMIB L-1656^T with *Yaniella* was supported by a bootstrap resampling value of 86%, it exhibited 5.5–6.4% sequence divergence from members of this genus, thereby demonstrating that it is only distantly related to *Yaniella*.

It is important to point out that the 16S rRNA gene sequence of strain IMMIB L-1656^T contained most of the signature nucleotides that have been defined for the suborder *Micrococcineae* (Zhi *et al.*, 2009), the exception being a uracil (U) residue instead of an adenine (A) residue at position 986 and a guanine (G) residue instead of A at position 987. In addition, strain IMMIB L-1656^T possesses a set of signature nucleotides that places it in a novel

Fig. 1. Neighbour-joining tree based on 16S rRNA gene sequences showing the position of strain IMMIB L-1656^T within the radiation of species of the family Micrococcaceae. Numbers at nodes indicate levels of bootstrap support >70% based on neighbour-joining analysis of 1000 resampled datasets. Bar, 1% sequence divergence.

phylogenetic lineage. These are nucleotides at positions 400 (U), 671 (U), 986 (U), 987 (G), 1120 (U) and 1408 (G). Thus, in view of the low level of 16S rRNA gene sequence similarity between strain IMMIB L-1656^T and other taxa of the suborder Micrococcineae (<94.5% similarity) and taking into account the diagnostic signature nucleotides from the 16S rRNA, strain IMMIB L-1656^T should be classified as a novel species of a novel genus. Moreover, we observed that, in the 16S rRNA secondary structure of all members of the Micrococcineae, the nucleotide U at position 598 paired with A at position 642, which was inconsistent with the pairing 598:640 (U–G) previously published by Zhi *et al.* (2009). Accordingly, an emended description of the suborder Micrococcineae is proposed.

Finally, we examined the pattern of signature nucleotides that has previously been defined for the family Yaniellaceae (Zhi *et al.*, 2009). The following corrections should be noted: C instead of A at position 131, A instead of C at position 196, A instead of U at position 444, C instead of U at position 843 and C instead of G at position 1109. These indicate that the pattern of signature nucleotides should be 131:231 (C–G), 196 (A), 342:347 (C–G), 444:490 (A–U), 580:761 (C–G), 602:636 (C–G), 670:736 (A–U), 822:878 (G–C), 823:877 (G–C), 826:874 (C–G), 827 (U), 843 (C), 950:1231 (U–A), 1047:1210 (G–C), 1109 (C), 1145 (G), 1309:1328 (G–C), 1361 (G), 1383 (C). Surprisingly, this pattern (except for position 196) corresponded to the

pattern defined for the family Micrococcaceae by Zhi *et al.* (2009). This evidence clearly precludes the genus Yaniella from being in a separate family within the suborder Micrococcineae and confirms the incorporation of the members of the Yaniellaceae in the family Micrococcaceae. For the comprehensive characterization of new members of the suborder Micrococcineae, the proposed minimal standards suggested by Schumann *et al.* (2009) should be considered.

The chemotaxonomic data are consistent with the results of the phylogenetic analyses and support the conclusion that strain IMMIB L-1656^T should be classified within a novel genus of the suborder Micrococcineae (Table 1). Cell-wall analysis revealed that strain IMMIB L-1656^T contained no characteristic cell-wall sugars. Peptidoglycan hydrolysates (4 M HCl, 100 °C, 16 h) contained lysine, alanine, glycine and glutamic acid in an approximate molar ratio of 1.0:2.3:1.3:2.9. The peptides L-Ala–D-Glu/D-Ala–L-Glu, L-Lys–D-Ala, L-Lys–Gly, D-Ala–L-Lys–Gly and Gly–Glu were detected in the partial hydrolysate of the peptidoglycan (4 M HCl, 100 °C, 0.75 h). Dinitrophenylation, performed according to Schleifer (1985), revealed that glutamic acid represented the N terminus of the interpeptide bridge. Traces of dinitrophenylated glycine were also found. From the available data, it can be concluded that the peptidoglycan of strain IMMIB L-1656^T represents type A4α L-Lys–Gly–L-Glu (Schleifer & Kandler, 1972; A11.56

Table 1. Chemotaxonomic characteristics of isolate IMMIB L-1656^T, representative genera of the family *Micrococcaceae* and the genera *Yaniella* and *Zhihengliuella*

Data compiled from Stackebrandt *et al.* (1995) and Schumann *et al.* (2009). MCA, monocarboxylic amino acid; var., variable amino acid composition in the interpeptide bridge; DAP, diaminopimelic acid; DMDG, dimannosyldiacylglycerol; DPG, diphosphatidylglycerol; PG, phosphatidylglycerol; PI, phosphatidylinositol; PL, unidentified phospholipid(s); GL, unidentified glycolipid(s); S, saturated fatty acids; U, unsaturated fatty acids; A, anteiso-branched fatty acids; I, iso-branched-chain fatty acids; ND, no data available.

Taxon	Morphology	Motility	Peptidoglycan type	Peptidoglycan variation	Major menaquinone(s)	Fatty acids	Polar lipids	DNA G + C content (mol%)
Strain IMMIB L-1656 ^T	Rod-coccus cycle	+/-	L-Lys-Gly-L-Glu	A4 α	9, 10, 11	S, U, A, I	DPG, PG, PI, PL, GL	59.7
<i>Acaricomes phytoseiuli</i>	Rods	ND	L-Lys-L-Ala ₃	A3 α	10(H ₂)	S, A, I	DPG, PG, PI	57.7
<i>Arthrobacter globiformis</i> group	Rod-coccus cycle	+/-	L-Lys-MCA _{var.}	A3 α	8(H ₂), 9(H ₂), 10(H ₂)	S, A, I	DPG, PG, PI, DMDG	61-69
<i>Arthrobacter nicotianae</i> group	Rod-coccus cycle	+/-	L-Lys-Ala-Glu, L-Lys-Ser-Glu, L-Lys-Glu, L-Lys-Asp		8, 9, 10	S, A, I	DPG, PG, PI, DMDG	58-66
<i>Citricoccus</i>	Coccoid	-	L-Lys-Gly-Glu	A4 α	7(H ₂), 8(H ₂), 9(H ₂)	S, A, I	DPG, PG, PI, GL	63-68
<i>Kocuria</i>	Coccoid	-	L-Lys-L-Ala ₃₋₄	A3 α	7(H ₂), 8(H ₂), 9(H ₂)	S, A, I	DPG, PG, PI, GL	66-75
<i>Micrococcus</i>	Coccoid	-	L-Lys-peptide subunit		8, 8(H ₂)	S, A, I	DPG, PG, PI, GL	69-74
<i>Nesterenkonia</i>	Coccoid	-	L-Lys-Gly-Glu, L-Lys-Gly-Asp, L-Lys-Glu	A4 α	8, 9	S, A, I	DPG, PG, PI, GL	64-72
<i>Renibacterium</i>	Rods	-	L-Lys-Ala-Gly		9, 10	A	DPG, GL	52-54
<i>Rothia</i>	Rods	-	L-Lys-Glu-L-Ala, L-Lys-L-Ala ₃ , L-Lys-Ser, L-Lys-L-Gly, L-Lys-L-Ala	A3 α	6(H ₂), 7	S, A, I	DPG, PG	49-60
<i>Terrabacter</i>	Rod-coccus cycle	+/-	LL-DAP	A3 γ	8(H ₄)	S, A, I	DPG, PE, PI	69.8-73.4
<i>Yaniella</i>	Coccoid	-	L-Lys-Gly-L-Glu	A4 α	8, 9	S, A, I	DPG, PG, PI, GL	53.5
<i>Zhihengliuella</i>	Rods	-	L-Lys-L-Ala-L-Glu	A4 α	8, 9, 10	S, A, I	DPG, PG, PI, GL	66.5

according to http://www.dsmz.de/microorganisms/main.php?content_id=35). Mycolic acids were not detected in whole-cell acid methanolysates. Analysis of the non-hydroxylated fatty acids of strain IMMIB L-1656^T revealed the presence of straight-chain saturated fatty acids C_{14:0} (0.5 % of total fatty acids), C_{15:0} (0.1 %), C_{16:0} (5.5 %) and C_{18:0} (0.3 %), branched-chain fatty acids i-C_{14:0} (0.5 %), iso-C_{15:0} (27.5 %), anteiso-C_{15:0} (16.4 %), iso-C_{16:0} (18.0 %), iso-C_{17:0} (2.6 %) and anteiso-C_{17:0} (28.4 %) and the monounsaturated fatty acid C_{18:1} ω 9c (0.1 %). The phospholipids included diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol and one additional unknown phospholipid (Supplementary Fig. S1a, available in IJSEM Online), i.e. phospholipid type PI according to Lechevalier *et al.* (1977). In addition, an unknown glycolipid spot was identified by TLC (Supplementary Fig. S1b). MS analysis showed that the respiratory quinones consisted of

unsaturated menaquinones MK-9, MK-10 and MK-11, with MK-10 as the predominant component. The DNA G + C content was 59.7 mol%. This chemical profile serves to distinguish strain IMMIB L-1656^T from members of all other genera of the suborder *Micrococcineae*.

Strain IMMIB L-1656^T was aerobic, catalase-positive and oxidase-negative. Colonies were cream coloured on DST agar (Supplementary Fig. S2), Columbia agar supplemented with 5 % sheep's blood, BHI agar and TSA. Strain IMMIB L-1656^T had a rod-coccus cycle. The cells were cocci in the stationary growth phase, rods in 11-hour-old cultures, predominantly short rods or oval-shaped after 60 h and had a coccoid shape again after 108 h (Supplementary Fig. S3). Cells were Gram-reaction-positive, motile and grew at 10-37 °C. The Voges-Proskauer reaction was positive. Nitrate reduction was negative. Tests for alkaline phosphatase, ester

lipase C8, naphthol-AS-BI-phosphohydrolase, α -glucosidase and pyrazinamidase activities were positive. The cells were sensitive to the following antimicrobial agents (μ g per disc):

ampicillin (10), cefazolin (30), clindamycin (2), oxacillin (5), penicillin (10) and vancomycin (30). A battery of phenotypic and biochemical tests was performed on strain

Table 2. Differential biochemical characteristics of isolate IMMIB L-1656^T and phylogenetically related representatives of genera of the family *Micrococcaceae*

Strains: 1, IMMIB L-1656^T (data from this study); 2, *Arthrobacter globiformis* DSM 20124^T (Mages *et al.*, 2008; Funke *et al.*, 1996); 3, *Citricoccus muralis* DSM 14442^T (Altenburger *et al.*, 2002; Li *et al.*, 2005); 4, *Kocuria rosea* DSM 20447^T (Stackebrandt *et al.*, 1995); 5, *Micrococcus luteus* DSM 20030^T (Wieser *et al.*, 2002); 6, *Nesterenkonia halobia* DSM 20541^T (Stackebrandt *et al.*, 1995); 7, *Rothia dentocariosa* ATCC 17931^T (Georg & Brown, 1967; Gerencser & Bowden, 1986; Daneshvar *et al.*, 2004); 8, *Yaniella flava* YIM 70178^T (Li *et al.*, 2005, 2008); 9, *Yaniella halotolerans* YIM 70085^T (Li *et al.*, 2004, 2008); 10, *Zhihengliuella halotolerans* YIM 70185^T (Zhang *et al.*, 2007). ND, Not determined/no data available; v, variable.

Characteristic	1	2	3	4	5	6	7	8	9	10
Morphology*	R, C	R, C	C	C	C	C	BF, R, C	C	C	R
Rod-coccus cycle	+	+	—	—	—	—	—	—	—	—
Motility	+	—	—	—	—	—	—	—	—	—
pH tolerance	7.4–9	ND	6–10	ND	7–10	6–10	5.4–8.8	6–9	6.5–8.5	8–9
Growth temperature (°C)	10–37	ND	4–28	25–37	>45	20–40	35–37	ND	10–40	28.30
NaCl tolerance (%)	0–12	0–5	0–10	0–7.5	0–10	5–>23	0–4	0.5–25	0–25	0–10
Production of:										
Arginine dihydrolase	—	ND	—	—	ND	+	ND	+	+	+
α -Glucosidase	+	+	+	ND	+	+	+	ND	ND	—
β -Glucosidase	—	ND	—	ND	ND	+	—	—	+	+
α -Galactosidase	—	—	—	ND	—	—	—	—	—	+
β -Galactosidase	—	+	—	—	ND	+	—	+	—	—
Lysine decarboxylase	ND	ND	ND	ND	ND	+	ND	+	+	+
Lipase	+	—	+	ND	ND	ND	—	+	+	+
α -Mannosidase	—	+	ND	ND	ND	ND	—	ND	ND	ND
Aesculin hydrolysis	—	—	+	—	ND	+	+	ND	ND	ND
Casein hydrolysis	—	+	—	ND	—	ND	—	ND	ND	ND
Gelatin liquefaction	—	ND	+	—	ND	—	+	—	—	—
Starch hydrolysis	+	+	—	V	—	+	—	—	—	+
Nitrate reduction	—	—	—	+	—	—	+	—	—	—
Urease	—	—	+	—	+	—	—	—	+	—
Acetoin formation	+	ND	—	—	—	+	+	—	—	—
Acid production from:										
L-Arabinose	—	ND	ND	ND	—	ND	V	ND	ND	+
D-Glucose	—	—	—	V	ND	+	+	+	+	+
D-Fructose	ND	ND	ND	ND	+	ND	+	+	+	ND
Maltose	—	—	ND	ND	ND	+	+	+	+	+
Sucrose	—	—	—	ND	ND	+	+	—	+	+
Trehalose	—	ND	—	ND	+	—	ND	ND	ND	+
Utilization of:										
L-Arabinose	—	+	—	ND	—	+	ND	—	+	ND
Cellobiose	—	—	—	ND	—	ND	ND	+	+	ND
D-Glucose	—	+	+	V	+	ND	ND	+	+	ND
D-Galactose	—	+	—	—	—	ND	ND	+	+	ND
Lactose	—	—	+	—	ND	ND	ND	+	+	ND
Maltose	—	+	+	ND	—	ND	ND	+	+	ND
D-Mannose	—	ND	+	—	+	—	ND	+	+	ND
D-Mannitol	—	+	—	ND	—	ND	ND	—	+	ND
Starch	ND	ND	+	ND	ND	ND	ND	+	+	+
Sucrose	—	ND	+	ND	+	—	ND	—	+	ND
D-Xylose	—	—	—	+	—	+	ND	ND	ND	ND

*BF, branched filaments; R, rods; C, cocci.

IMMIB L-1656^T, the results of which appear in the genus and species descriptions and in Table 2.

This polyphasic taxonomic study warrants the conclusion that strain IMMIB L-1656^T represents a novel species of a novel genus within the suborder *Micrococcineae*. The uniqueness of the 16S rRNA gene signature nucleotides, the formation of a distinct phylogenetic branch and several phenotypic characteristics (Table 2) differentiate strain IMMIB L-1656^T from other related genera of the family *Micrococcaceae* and justify its classification in a new genus and species, for which the name *Auritidibacter ignavus* gen. nov., sp. nov. is proposed.

Description of *Auritidibacter* gen. nov.

Auritidibacter (Au.ri.ti.di.bac'ter. L. n. *auris*, -is the ear; L. suff. -itis, -itidis, suffix used for inflammation; N.L. masc. n. *bacter* a rod; N.L. masc. n. *Auritidibacter* rod-shaped bacterium causing inflammation of the ear, also referring to the source of isolation).

Cells are Gram-reaction-positive, motile, non-spore-forming and have a rod-coccus cycle. Aerobic and catalase-positive. Grow at 10–37 °C. The peptidoglycan type is type L-Lys-Gly-L-Glu, variation A4α. No characteristic cell-wall sugars are detected in whole-cell hydrolysates. The major long-chain cellular fatty acids are a mixture of straight-chain saturated, iso- and anteiso-methyl-branched acids. The predominant respiratory menaquinone is MK-10. The polar lipids are diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol and an unknown phospholipid (phospholipid type PI according to Lechevalier *et al.*, 1977). The DNA G+C content of the type strain of the type species is 59.7 mol%. The pattern of the 16S rRNA gene signature nucleotides consists of nucleotides at positions 400 (U), 671 (U), 986 (U), 987 (G), 1120 (U) and 1408 (G). The pattern of signature nucleotides must be considered tentative and should be updated as the number of sequences in this lineage increases. The type species is *Auritidibacter ignavus*.

Description of *Auritidibacter ignavus* sp. nov.

Auritidibacter ignavus (ig.na'vus. L. masc. adj. *ignavus* inactive).

In addition to properties described for the genus, the species shows the following characteristics. Cocci are 0.3–1 µm in diameter. Rods are 0.4–0.5 µm wide and 2.1–2.5 µm long. Colonies are cream-coloured, smooth and have an entire margin. Growth occurs on BHI agar, DST agar, Columbia agar supplemented with 5% sheep's blood and TSA agar. CAMP-reaction-negative with *S. aureus*. Tolerates 0–12% NaCl. Grows at pH 7.4–9.0 (optimum at pH 9.0) but not at pH 4–6. Nitrate reduction is negative. Acetoin production is positive. Hydrolyses DNA and starch (3 days of incubation). Tyrosine is weakly hydrolysed. Adenine, casein, elastin, aesculin, gelatin, guanine, hippurate, hypoxanthine, keratin, testosterone, xanthine and urea are not

hydrolysed. Acetate, adipate, adonitol, L-arabinose, isoamyl alcohol, 2,3-butanediol, cellobiose, citrate, *meso*-erythritol, D-galactose, D-glucose, D-gluconate, *m*-hydroxybenzoate, *p*-hydroxybenzoate, *myo*-inositol, L-lactate, lactose, maltose, D-mannitol, melezitose, 1,2-propanediol, raffinose, L-rhamnose, D-sorbitol, sucrose, trehalose and D-xylose are not assimilated. Acetamide, L-alanine, gelatin, L-proline and L-serine are not utilized as simultaneous sources of carbon and nitrogen. Activity is detected for alkaline phosphatase, ester lipase C8, naphthol-AS-BI-phosphohydrolase, α-glucosidase and pyrazinamidase. No activity is detected for acid phosphatase, arginine dihydrolase, esterase C4, β-glucosidase, α-galactosidase, β-galactosidase, β-glucuronidase, *N*-acetyl-β-glucosaminidase, lipase C14, α-mannosidase, α-fucosidase, α-chymotrypsin, trypsin, cystine arylamidase, leucine arylamidase, pyrrolidonyl arylamidase and valine arylamidase. The major fatty acids are iso-C_{15:0} and anteiso-C_{17:0}.

The type strain, IMMIB L-1656^T (=DSM 45359^T =CCUG 57943^T), was isolated from an ear swab of a 28-year-old man with fulminant otitis externa.

Emended description of the suborder *Micrococcineae* Stackebrandt *et al.* 1997 emend. Zhi *et al.* 2009

The description of the suborder *Micrococcineae* is as given by Stackebrandt *et al.* (1997) and emended previously by Zhi *et al.* (2009) with the following amendments. The pattern of 16S rRNA gene signature nucleotides consists of nucleotides at positions 127:234 (A–U), 598:642 (U–A), 657:749 (U–A), 953:1228 (G–C) and 1362 (A).

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