Proposal of Two New Species in the Genus *Microbacterium*: *Microbacterium dextranolyticum* sp. nov. and *Microbacterium aurum* sp. nov.

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The taxonomic positions of *Flavobacterium* sp. strain IFO 14592^T (= M-73^T) (T = type strain), a dextran- α -1,2-debranching enzyme producer, and *Microbacterium* sp. strain IFO 15204^T (= H-5^T), an isolate obtained from corn steep liquor, were investigated; on the basis of the results of chemotaxonomic and phenetic studies and DNA-DNA similarity data, we propose that these bacteria should be classified in the genus *Microbacterium* as *Microbacterium dextranolyticum* sp. nov. and *Microbacterium aurum* sp. nov., respectively. The type strain of *M. dextranolyticum* is strain IFO 14592, and the type strain of *M. aurum* is strain IFO 15204.

The genus *Microbacterium* was proposed by Orla-Jensen (15), and its description was emended by Collins et al. (1). Four species have been described previously: *Microbacterium lacticum*, *Microbacterium imperiale*, *Microbacterium laevaniformans*, and *Microbacterium arborescens* (1, 5, 6).

During a taxonomic study of *Flavobacterium* strains in the Institute for Fermentation at Osaka (IFO) culture collection, we found that *Flavobacterium* sp. strain IFO 14592^T (= M-73^T) (T = type strain), a dextran- α -1,2-debranching enzyme producer (8, 13), and strain IFO 15204^T (= H-5^T), an isolate obtained from corn steep liquor, belong to the genus *Microbacterium* (21). To determine the taxonomic positions of these organisms, we examined their physiological and chemotaxonomic characteristics and compared these characteristics with those of previously described species of the genus *Microbacterium*.

In this paper we describe characterization of these two strains and propose that they are representatives of two new species of the genus *Microbacterium* on the basis of the results of chemotaxonomic, phenetic, and DNA-DNA hybridization studies.

MATERIALS AND METHODS

Bacterial strains and culture conditions. The bacterial strains which we studied are listed in Table 1. In addition to the type strains, reference strains of *M. lacticum* and *M. laevaniformans* were included. All strains were cultured at 28°C with aerobic shaking in a peptone-yeast extract medium supplemented with brain heart infusion (PY-BHI medium), which contained 1% peptone, 0.2% yeast extract, 0.2% Bacto brain heart infusion (Difco Laboratories), 0.2% NaCl, and 0.2% D-glucose (pH 7.2). Cells were harvested by centrifugation, washed with water, and then lyophilized.

Morphological and phenotypic characteristics. Cell morphology was determined by using cells grown on PY-BHI medium. Motility was determined with a light microscope by the hanging drop method. Unless otherwise indicated, all tests were carried out at 28°C. Catalase activity was determined by bubble formation in a 3% hydrogen peroxide solution. Oxidase activity was determined by the oxidation

of 1% tetramethyl-*p*-phenylenediamine on filter paper. Acid production from carbohydrates was studied in a medium containing 0.3% peptone, 0.25% NaCl, 0.003% bromocresol purple, and 0.5% carbohydrate (pH 7.2). Assimilation of organic acids was studied in a medium containing 0.5% organic acid (sodium salt), 0.02% D-glucose, 0.01% yeast extract, 0.01% peptone, 0.01% Bacto brain heart infusion, 0.01% K₂HPO₄, 0.5% NaCl, 2% agar, and 12 ppm of phenol red (pH 7.0). Nitrate reduction and hydrolysis of starch, gelatin, casein, and esculin were tested by the methods described by Cowan and Steel (2).

Peptidoglycan analysis. Cell walls were prepared from ca. 500 mg (dry weight) of cells by mechanical disruption with an ultrasonic oscillator and were purified as described by Schleifer and Kandler (18). The amino acid compositions of complete wall hydrolysates were determined with a model LC-6AD high-performance liquid chromatography (HPLC) apparatus (Shimadzu Co., Ltd., Kyoto, Japan) equipped with a Wakopak WS-PTC column (Wako Pure Chemical Industries, Ltd., Osaka, Japan) as phenylthiocarbamoyl derivatives according to the manufacturer's instructions (23). The amino acid compositions were determined by two-dimensional descending chromatography on cellulose thin-layer chromatography (TLC) plates (Tokyo Kasei Co., Ltd., Tokyo, Japan) by the method of Harper and Davis (4). The configurations of the amino acids were determined by measuring the amino acid contents of the hydrolysates before and after incubation with D- and L-amino acid oxidase (alanine and serine), L-lysine decarboxylase (lysine), or L-glutamic acid decarboxylase (glutamic acid), as described by Kandler and König (7).

The peptidoglycan structure was determined by the method of Schleifer and Kandler (18). Partial acid hydrolysates were examined by two-dimensional TLC, and peptides were identified on the basis of their chromatographic mobilities and staining characteristics (18). The N-terminal amino acid of the interpeptide bridge was determined by dinitrophenylation of the undegraded peptidoglycan (18).

Cell wall sugar analysis. Cell walls were hydrolyzed with 2 N HCl at 100°C for 2 h, dried in vacuo, and then analyzed by the method of Mikami and Ishida (10) by using an HPLC apparatus (model LC-5A; Shimadzu Co., Ltd.) equipped with a Shim-pack ISA 07/S2504 column (250 by 4 mm) and a Shimadzu model RE-530 spectrofluorometer (20).

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TABLE 1. Bacterial strains used

Species	Strain (IFO no.)	Other designation(s) ^a	Reference and/or source	Proposed reclassification
<i>M. lacticum</i>	14135 ^T	ATCC 8180 ^T		
<i>M. lacticum</i>	14137	ATCC 8181		
<i>M. lacticum</i>	14138	ATCC 49094		
<i>M. laevaniformans</i>	14471 ^T	ATCC 15953 ^T		
<i>M. laevaniformans</i>	15234	NCFB 2288, ATCC 49090	14	<i>Aureobacterium</i> sp.
<i>M. laevaniformans</i>	15235	NCFB 2289, ATCC 49091	14	<i>Aureobacterium</i> sp.
<i>M. imperiale</i>	12610 ^T	ATCC 8365 ^T		
<i>M. arborescens</i>	3750 ^T	ATCC 4358 ^T		
<i>Flavobacterium</i> sp.	14592 ^T	M-73 ^T	Soil (8, 13)	<i>M. dextranolyticum</i> sp. nov.
<i>Microbacterium</i> sp.	15204 ^T	H-5 ^T	Corn steep liquor (this study)	<i>M. aurum</i> sp. nov.

^a ATCC, American Type Culture Collection, Rockville, Md.; NCFB, National Collection of Food Bacteria, AFRC Institute of Food Research Reading Laboratory, Shinfield, Reading, England.

Glycolyl analysis. Glycolate tests were performed by using the method described by Uchida and Aida (22).

Analysis of cellular fatty acids. Fatty acids were extracted from dry cells (50 mg) by acid methanolysis and were examined by using a model GC-9A gas-liquid chromatography apparatus (Shimadzu Co., Ltd.) equipped with a glass column (0.2 cm by 5 m) containing 10% diethyleneglycol succinate on Chromosorb W at 180°C (19).

Analysis of polar lipids. Free lipids were extracted from dry cells (100 mg), purified by the method of Minnikin et al. (12), and examined by two-dimensional TLC, using Kiesel-gel 60 F₂₅₄ plates. Lipids were visualized by spraying the plates with 10% molybdophosphoric acid in ethanol, followed by heating at 140°C for 10 min. The following specific spray reagents were also used: α -naphthol for sugars and ninhydrin for amino groups.

Analysis of mycolic acids. Mycolic acids were analyzed by the method of Minnikin et al. (11).

Analysis of isoprenoid quinones. Menaquinones were extracted from dry cells (200 mg) with chloroform-methanol (2:1, vol/vol), purified by TLC (using benzene as the solvent), extracted with diethyl ether, dried under a nitrogen stream, and then analyzed by HPLC by using a Shimadzu model LC-5A instrument equipped with a Zorbax octyldecyl silane column (4.6 by 150 mm).

DNA base composition. DNA was obtained by the method of Saito and Miura (16). The G+C content of DNA was

determined by the method of Mesbah et al. (9) after treatment with P₁ nuclease and alkaline phosphatase and by HPLC by using a model LC-6AD instrument (Shimadzu Co., Ltd.) equipped with a Cosmosil 5C₁₈-AR column (4.6 by 150 mm; Nacalai Tesque, Inc., Tokyo, Japan).

DNA-DNA hybridization. DNA-DNA hybridization was carried out fluorometrically in microdilution wells by using biotinylated DNA (3).

RESULTS AND DISCUSSION

Morphological, physiological, and biochemical characteristics. Both strains were gram-positive, nonmotile rods, and the cells were arranged in V formations. Colonies on PY-BHI agar were yellow. Strain IFO 14592^T exhibited good growth aerobically on nutrient agar and produced acid from many carbohydrates. Strain IFO 15204^T grew poorly on nutrient agar and produced acid only from D-galactose, sucrose, trehalose, raffinose, and inulin.

Chemotaxonomic characteristics. The chemotaxonomic characteristics of the two strains are summarized in Table 2. The amino acid analysis and determination of the configurations of the amino acids in the cell wall hydrolysates revealed the presence of D-alanine, D-glutamic acid plus hydroxyglutamic acid, glycine, and L-lysine (molar ratio, ca. 1:1:2:2) in strain IFO 14592^T and D-alanine, D-glutamic acid plus hydroxyglutamic acid, L-homoserine, D-lysine, and

TABLE 2. Chemotaxonomic characteristics of *Microbacterium* strains^a

Species	Strain (IFO no.)	G+C content (mol%)	Menaquinone(s)	Peptidoglycan type	Amino acid(s) in cell wall ^b	Cell wall sugars ^c
<i>M. lacticum</i>	14135 ^T	70.0	MK-11, MK-12	B1 α	L-Lys	Rha, Man, Gal
<i>M. lacticum</i>	14137	69.0	MK-11, MK-12	B1 α	L-Lys	Rha, (Man), Gal
<i>M. lacticum</i>	14138	69.8	MK-11, MK-12	B1 α	L-Lys	Rha, Man, Gal
<i>M. laevaniformans</i>	14471 ^T	70.5	MK-11, MK-12	B1 α	L-Lys	Rha, Man, Gal, Xyl
<i>M. laevaniformans</i>	15234	70.3	MK-12	B2 β	L-Hsr, D-Orn	Rha, Fuc, Gal
<i>M. laevaniformans</i>	15235	70.1	MK-12	B2 β	L-Hsr, D-Orn	Rha, Fuc, Gal
<i>M. imperiale</i>	12610 ^T	71.2	MK-11, MK-12	B1 β	L-Hsr, D-Lys	Rha, Man, Gal
<i>M. arborescens</i>	3750 ^T	71.0	MK-11, MK-12	B1 β	L-Hsr, D-Lys	6dTal, Man, Gal
<i>M. dextranolyticum</i>	14592 ^T	68.3	MK-11, MK-12	B1 α	L-Lys	6dTal, Man, Gal
<i>M. aurum</i>	15204 ^T	69.2	MK-11, MK-12	B1 β	L-Hsr, D-Lys	Fuc, Gal, Glc

^a The data for the type strains of previously described species are from reference 1. All strains contained 12-methyltetradecanoic acid, 14-methylpentadecanoic acid, and 14-methylhexadecanoic acid as major cellular fatty acids. All strains contained the following polar lipids: diphosphatidylglycerol, phosphatidylglycerol, and glycolipid. None of the strains contained mycolic acid, and all strains contained cell wall glycolyl groups.

^b L-Lys, L-lysine; L-Hsr, L-homoserine; D-Orn, D-ornithine; D-Lys, D-lysine. In addition, all of the strains contained glycine, alanine, and glutamate plus 3-hydroxyglutamate.

^c Rha, rhamnose; Gal, galactose; Glc, glucose; Man, mannose; 6dTal, 6-deoxytalose; Xyl, xylose; Fuc, fucose. Parentheses indicate that a trace amount is present.

FIG. 1. Proposed structure of the peptidoglycan of *M. aurum* IFO 15204^T. Abbreviations: Gly, glycine; D-Glu, D-glutamic acid; Hyg, 3-hydroxyglutamic acid; L-Hsr, L-homoserine; D-Ala, D-alanine; L-Lys, L-lysine; GlcNAc, N-acetylglucosamine; MurNAc, N-acetylmuramic acid. The interpeptide bridge is enclosed by a dashed line.

glycine (molar ratio, ca. 1:1:1:2:1) in strain IFO 15204^T. Homoserine was not present in strain IFO 14592^T.

The peptidoglycan studies of Schleifer (17) and Schleifer and Kandler (18) showed that the species included in the genus *Microbacterium* contain the B1 α and B1 β types of peptidoglycan. An analysis of the amino acid compositions of their cell walls suggested that strains IFO 14592^T and IFO 15204^T contain the B1 α and B1 β peptidoglycan types, respectively. An examination of the primary structures indicated that the peptidoglycan in strain IFO 14592^T is the usual B1 α type (data not shown), but that the peptidoglycan in strain IFO 15204^T is B1 β type (Fig. 1), except that the structure of the interpeptide bridge is slightly different from the structures of the interpeptide bridges in the previously described species *M. imperiale* (18) and *M. arborescens* (data not shown) because these two species contain 2 mol of glycine residues in the interbridge unit, whereas strain IFO 15204^T contains only 1 mol. Both strain IFO 14592^T and strain IFO 15204^T possess high levels of glycolate in the glycan moiety of the cell walls, which suggests that muramic acid occurs in the N-glycolyl form rather than the more common N-acetyl form. Mycolic acids are not present in these strains. The cell wall sugars 6-deoxytalose, galactose, and glucose were detected in strain IFO 14592^T, and fucose, galactose, and glucose were detected in strain IFO 15204^T. The two strains had very similar fatty acid profiles, composed primarily of anteiso-methyl branched acids, anteiso-C_{15:0}, and anteiso-C_{17:0}, and both possessed long unsaturated menaquinones (11 and 12 isoprene units). In the two-dimensional TLC analysis of the polar lipids, diphosphatidylglycerol, phosphatidylglycerol, and an unidentified glycolipid were detected in the extracts of both strains. The DNA base compositions of strains IFO 14592^T and IFO 15204^T were 68.3 and 69.2 mol%, respectively.

On the basis of the chemotaxonomic characteristics described above, both strains were identified as members of the genus *Microbacterium* and could be differentiated from members of the genera *Curtobacterium* and *Aureobacterium* and all other coryneform genera described previously (Table 3).

A chemotaxonomic study of the reference strains of *M. laevaniformans*, IFO 15234 (= NCFB 2288) and IFO 15235 (= NCFB 2289), revealed that they have DNA G+C con-

tents and cellular fatty acid compositions similar to those of other species of the genus *Microbacterium*, but differ in their menaquinone compositions and the amino acid compositions of their peptidoglycans (Table 2). These findings indicate that these organisms should be excluded from the genus *Microbacterium* and should probably be assigned to the genus *Aureobacterium*.

DNA-DNA relatedness. As shown in Table 4, the levels of DNA-DNA similarity between strains IFO 14592^T and IFO 15204^T and the type strains of the previously described species of the genus *Microbacterium* were low.

Phenotypic differentiation. The results described above indicate that each of the new strains constitutes a separate taxon. Differential characteristics of these strains and the four previously described species of the genus *Microbacterium* are summarized in Table 5.

The description of the genus *Microbacterium* was emended by Collins et al. (1). The members of this genus are characterized by the presence of L-lysine (and L-homoserine) in the cell walls (B1 α or B1 β type of peptidoglycan), by the presence of a glycine in the interpeptide bridge, by the presence of N-glycolyl residues in the cell walls, by having isoprenoid menaquinones with 11 and 12 isoprene units, by G+C values of 66 to 69 mol%, and by slow and weak acid production from sugars. On the basis of biochemical and chemical criteria, strains IFO 14592^T and IFO 15204^T can be distinguished readily from all previously described species of the genus *Microbacterium* and in our opinion warrant status as new taxa; therefore, we propose that these organisms should be classified as new species in the genus *Microbacterium*, *Microbacterium dextranolyticum* sp. nov. and *Microbacterium aurum* sp. nov., respectively.

Description of *Microbacterium dextranolyticum* sp. nov. *Microbacterium dextranolyticum* (dex.tra.no.ly'ti.cum. Engl. n. *dextran*, polysaccharide produced by bacteria; Gr. adj. *lyticum*, dissolving; *dextranolyticum*, dextran dissolving). Good growth occurs on solid media in air; colonies are 2 to 4 mm in diameter, circular, low convex with entire margins, opaque, and moist. A yellow pigment is produced. In young cultures, small, slender rods are formed. Many cells are arranged at angles, forming V shapes; primary branching is uncommon. In older cultures rods are shorter, but a marked rod-coccus growth cycle does not occur. Gram-positive rods that are not acid fast and not motile. Endospores are not formed. The optimum growth temperature is ca. 30°C. Good aerobic growth. Acid is produced weakly from glucose, mannose, fructose, maltose, cellobiose, mannitol, xylose, L-arabinose, galactose, sucrose, lactose, trehalose, raffinose, inulin, arbutin, esculin, ethanol, butanol, melibiose, and melezitose, but not from ribose, D-arabinose, L-sorbose, xylitol, erythritol, adonitol, dulcitol, sorbitol, inositol, methanol, α -methyl-D-glucoside, L-rhamnose, starch, glycerol, and salicin. Pyruvate, fumarate, and succinate are assimilated, but acetate, lactate, malate, α -ketoglutarate, maleate, formate, butyrate, oxalate, pimelate, glycolate, glyoxylate, gluconate, propionate, and hippurate are not assimilated. Esculin, Tween 20, Tween 40, Tween 60, and Tween 80 are hydrolyzed, but gelatin and starch are not hydrolyzed. Urease negative. H₂S is produced. Voges-Proskauer reaction positive. Arginine is not decarboxylated.

The cell wall peptidoglycan contains L-lysine as the di-amino acid (variation B1 α). The glycan moiety of the cell wall contains glycolyl and acetyl residues. The cell wall sugars are rhamnose, 6-deoxytalose, galactose, and glucose. Mycolic acid is not present. The nonhydroxylated fatty acids are primarily anteiso- and iso-methyl branched acids. The

TABLE 3. Distinguishing chemotaxonomic features of coryneform taxa

Taxon	Wall di-amino acid ^a	Murein type ^b	G+C content (mol%)	Mycolic acids	Fatty acid types ^{c,d}	Major menaquinone(s)	Polar lipids ^{d,e}
<i>Agromyces</i>	L-DAB	B2 γ	71–76	–	S, A, I	MK-11, MK-12, MK-13	DPG, PG, GL
<i>Arcanobacterium</i>	Lys	A	48–52	–	S, U	MK-9(H ₄)	ND
<i>Arthrobacter</i> (globiformis group)	L-Lys	A3 α	59–69	–	S, A, I	MK-9(H ₂)	DPG, PG, (PI), GL
<i>Arthrobacter</i> (nicotianae group)	L-Lys	A4 α	59–69	–	S, A, I	MK-8, MK-9	DPG, PG, (PI), GL
<i>Aureobacterium</i>	D-Orn	B2 β	67–70	–	S, A, I	MK-11, MK-12, MK-13, MK-14	DPG, PG, GL
<i>Brachybacterium</i>	meso-DAP	A4 γ	68–72	–	S, A, I	MK-7	DPG, PG, GL
<i>Brevibacterium</i>	meso-DAP	A1 γ	60–67	–	S, A, I	MK-8(H ₂), MK-7(H ₂)	DPG, PG, (PI), GL
<i>Cellulomonas</i>	L-Orn	A4 β , A4 α	71–76	–	S, A, I	MK-9(H ₄)	DPG, PI, PGL
<i>Corynebacterium</i>	meso-DAP	A1 γ	51–65	+	S, U, (T)	MK-9(H ₂), MK-8(H ₂)	DPG, PI, PIDM, (PG), (GL)
<i>Clavibacter</i>	L-DAB	B2 γ	67–78	–	S, A, I	MK-10, MK-9	DPG, PG, GL
<i>Curtobacterium</i>	D-Orn	B2 β	68–75	–	S, A, I	MK-9	DPG, PG, GLs
<i>Exiguobacterium</i>	Lys	A	53–56	–	S, A, I, U	MK-7	DPG, PG, PE
<i>Jonesia</i>	Lys	A	58–59	–	S, A, I	MK-9	DPG, PI, PGL
<i>Microbacterium</i>	L-Lys	B1 α , B1 β	69–75	–	S, A, I	MK-11, MK-12	DPG, PG, GL, (PGL)
<i>Nocardioideis</i>	LL-DAP	A3 γ	69–72	–	S, A, I, U, T, 2-OH	MK-8(H ₄), MK-9(H ₄)	DPG, PG, OH-PG
<i>Terrabacter</i>	LL-DAP	A3 γ	69–72	–	S, A, I, U	MK-8(H ₄)	DPG, PE, PL, PGL
<i>Aeromicrobium</i>	LL-DAP	A3 γ	70	–	S, U, T	None	ND
<i>Rarobacter</i>	L-Orn	A	65–66	–	S, A, I	MK-9	ND
<i>Renibacterium</i>	L-Lys	A3 α	52–54	–	S, A, I	MK-9, MK-10	DPG, GL
<i>Rubrobacter</i>	L-Lys	A3 α	68	–	12-H, A, 2-OH	MK-8	DPG, PG, PL, PGL, GL

^a L-DAB, L-diaminobutyric acid; Lys, lysine; L-Lys, L-lysine; D-Orn, D-orithine; L-Orn, L-orithine; meso-DAP, meso-diaminopimelic acid; LL-DAP, LL-diaminopimelic acid.

^b Murein type as described by Schleifer and Kandler (18).

^c S, straight-chain saturated; A, anteiso-methyl branched; I, iso-methyl branched; U, monounsaturated; T, tuberculostearic acid; 12-H, 12-methylhexadecanoic acid; 2-OH, 2-hydroxylated fatty acids.

^d Parentheses indicate that a compound may or may not be present.

^e DPG, diphosphatidylglycerol; PG, phosphatidylglycerol; GL, glycolipid; PI, phosphatidylinositol; PGL, phosphoglycolipid; PIDM, phosphatidylinositol dimannoside; GLs, glycolipids; PE, phosphatidylethanolamine; OH-PG, 2-hydroxy fatty acid containing phosphatidylglycerol; PL, phospholipid; ND, not determined.

major fatty acids are anteiso-C_{15:0} and iso-C_{16:0}. Unsaturated menaquinones with 11 and 12 isoprene units are present. The polar lipids are diphosphatidylglycerol, phosphatidylglycerol, and dimannosyldiacylglycerol; an unknown monoglycosyldiacylglycerol and phosphoglycolipid are also present. The DNA base composition is 68.3 mol% G+C. Source: isolated from soil (8, 13).

The type strain is IFO 14592.

Description of *Microbacterium aurum* sp. nov. *Microbacterium aurum* (au'rum. L.n. *aurum*, gold). Good growth occurs on solid media in air; colonies are 1 to 2 mm in diameter, circular, low convex with entire margins, opaque, and moist. A golden yellow pigment is produced. In young cultures,

small, slender rods are formed. Many cells are arranged at angles, forming V shapes; primary branching is uncommon. In older cultures rods are shorter, but a marked rod-coccus growth cycle does not occur. Gram-positive rods that are not acid fast and not motile. Endospores are not formed. The optimum growth temperature is ca. 30°C. Acid is produced weakly from glucose, mannose, fructose, maltose, cellobiose, mannitol, galactose, L-rhamnose, sucrose, trehalose, raffinose, starch, and inulin, but not from D-xylose, L-arabinose, D-arabinose, glycerol, arbutin, esculin, salicin, ethanol, butanol, melibiose, melezitose, ribose, L-sorbose, xylitol, erythritol, adonitol, dulcitol, sorbitol, inositol, methanol, and α -methyl-D-glucoside. Acetate, α -ketoglutarate, and succinate are assimilated, but pyruvate, lactate, malate, maleate, formate, butyrate, oxalate, pimelate, glycolate, glyoxylate, gluconate, propionate, and hippurate are not assimilated. Esculin, starch, and Tween 60 are hydrolyzed, but Tween 20, Tween 40, Tween 80, and gelatin are not hydrolyzed. Urease negative. H₂S is produced. Voges-Proskauer reaction negative. Arginine is not decarboxylated.

The cell wall peptidoglycan contains lysine as the diamino acid (variation B1 β). The glycan moiety of the wall contains glycolyl and acetyl residues. The cell wall sugars are fucose, galactose, and glucose. Mycolic acid is not present. The nonhydroxylated fatty acids are primarily anteiso- and iso-methyl branched acids. The major fatty acids are anteiso-C_{15:0}, anteiso-C_{17:0}, and iso-C_{16:0}. Unsaturated menaquinones with 11 and 12 isoprene units are present. The polar

TABLE 4. Levels of DNA-DNA similarity among strains of the genus *Microbacterium*

Unlabeled DNA from:	% Similarity to labeled DNA from:				
	IFO 14135 ^T	IFO 12610 ^T	IFO 3750 ^T	IFO 14592 ^T	IFO 15204 ^T
<i>M. lacticum</i> IFO 14135 ^T	100	9	5	15	18
<i>M. laevaniformans</i> IFO 14471 ^T	4	7	8	14	24
<i>M. imperiale</i> IFO 12610 ^T	10	100	32	19	30
<i>M. arborescens</i> IFO 3750 ^T	11	29	100	18	26
<i>M. dextranolyticum</i> IFO 14592 ^T	7	7	15	100	43
<i>M. aurum</i> IFO 15204 ^T	ND ^a	7	13	8	100

^a ND, not determined.

TABLE 5. Differential characteristics of *Microbacterium* species^a

Characteristic	<i>M. lacticum</i> IFO 14135 ^T	<i>M. laevaniformans</i> IFO 14471 ^T	<i>M. dextranolyticum</i> IFO 14592 ^T	<i>M. imperiale</i> IFO 12610 ^T	<i>M. arborescens</i> IFO 3750 ^T	<i>M. aurum</i> IFO 15204 ^T
Color of colonies	Yellow	Yellow	Yellow	Orange	Orange	Yellow
Motility	—	—	—	+	+	—
Growth on nutrient agar	Good	Good	Good	Poor	Poor	Poor
Growth at 37°C	—	+	—	+	—	+
Hydrolysis of:						
Gelatin	—	+	—	—	+	+
Starch	+	+	—	+	—	+
Tween 20	—	—	+	—	—	—
Tween 40	—	—	+	—	—	—
Tween 60	—	—	+	—	—	w
Tween 80	—	—	+	—	—	—
H ₂ S formation	—	+	+	+	+	+
Voges-Proskauer reaction	—	+	+	—	—	—
Decarboxylation of arginine	—	+	—	—	—	—
Acid produced from:						
D-Xylose	—	—	+	+	+	—
L-Arabinose	—	—	+	+	+	—
Sucrose	—	+	+	+	+	+
Trehalose	—	+	+	+	w	+
Raffinose	—	+	+	+	—	+
Melezitose	—	—	+	—	+	—
Inulin	—	—	+	—	—	+
Assimilation of:						
Acetate	+	+	—	+	+	+
Lactate	+	+	—	+	—	—
Malate	+	+	—	+	—	—
Fumarate	+	+	+	+	+	—
Propionate	+	+	—	—	—	—
Polar lipids						
Phosphoglycolipid	+	—	+	—	—	—
Glycolipid(s)	Multiple	Multiple	Multiple	Single	Single	Single
6-Deoxyhexose in cell walls	Rhamnose	Rhamnose	6-Deoxytalose	Rhamnose	6-Deoxytalose	Fucose
Peptidoglycan type	B1α	B1α	B1α	B1β	B1β	B1β

^a +, positive; —, negative; w, weak.

lipids are diphosphatidylglycerol, phosphatidylglycerol, and dimannosyldiacylglycerol. The DNA base composition is 69.2 mol% G+C. Source: isolated from commercially available corn steep liquor.

The type strain is IFO 15204.

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