Proposal of *Mycetocola* gen. nov. in the family *Microbacteriaceae* and three new species, *Mycetocola saprophilus* sp. nov., *Mycetocola tolaasinivorans* sp. nov. and *Mycetocola lacteus* sp. nov., isolated from cultivated mushroom, *Pleurotus ostreatus*

Takanori Tsukamoto,† Mariko Takeuchi, Osamu Shida, Hitoshi Murata and Akira Shirata

Author for correspondence: Takanori Tsukamoto. Tel: +81 45 211 7153. Fax: +81 45 211 0611. e-mail: taktak@air.linkelclub.or.jp

The taxonomic positions of 10 tolaasin-detoxifying bacteria, which were isolated from the cultivated mushroom *Pleurotus ostreatus*, were investigated. These strains are Gram-positive, obligately aerobic, non-sporulating and irregular rod-shaped bacteria. They have the following characteristics: the major menaquinone is MK-10, the DNA G+C content ranges from 64 to 65 mol%, the diamino acid in the cell wall is lysine and the muramic acid in the peptidoglycan is an acetyl type. The major fatty acids are anteiso-C_{15:0} and anteiso-C_{17:0}. On the basis of morphological, physiological and chemotaxonomic characteristics, together with DNA–DNA reassociation values and 16S rRNA gene sequence comparison data, the new genus *Mycetocola* gen. nov. is proposed for these bacteria in the family *Microbacteriaceae* and three new species are also proposed: *Mycetocola saprophilus* sp. nov. (type strain CM-01T = IFO 16274T = MAFF 211324T = NRRL B-24119T), *Mycetocola tolaasinivorans* sp. nov. (type strain CM-05T = IFO 16277T = MAFF 211325T = NRRL B-24120T) and *Mycetocola lacteus* sp. nov. (type strain CM-10T = IFO 16278T = MAFF 211326T = NRRL B-24121T). The type species of the genus is *Mycetocola saprophilus* sp. nov.

**Keywords:** *Mycetocola* gen. nov., *Mycetocola saprophilus* sp. nov., *Mycetocola tolaasinivorans* sp. nov., *Mycetocola lacteus* sp. nov.

**INTRODUCTION**

*Pseudomonas tolaasii* Paine produces pathogenic extracellular toxins, tolaasins (Nutkins et al., 1991; Shirata et al., 1995), and causes brown blotch disease in economically important cultivated mushrooms *Pleurotus ostreatus* Kummer and *Agaricus bisporus* Singer (Suyama & Fujii, 1993; Tolaas, 1915). In the course of the microbiological study of brown blotch disease, we isolated from *Pleurotus ostreatus* fruiting bodies some Gram-positive bacteria which detoxify the tolaasins and suppress the development of the disease (Tsukamoto et al., 1998). They were obligately aerobic, non-sporulating and irregular rod-shaped bacteria. The result of phylogenetic analysis of the 16S rRNA gene showed that the tolaasins-detoxifying bacteria belong to the family *Microbacteriaceae* and bacteriological analyses also supported this result.

1972). Frigoribacterium (Kämpfer et al., 2000), Leifsonia (Evtushenko et al., 2000), Leucobacter (Takeuchi et al., 1996), Microbacterium (Takeuchi & Hatano, 1998) and Rathayibacter (Zgurskaya et al., 1993). The bacteria we isolated from Pleurotus ostreatus contain lysine as the diamino acid and acetyl-type muramic acid in the peptidoglycan, MK-10 as the major menaquinone, a DNA G+C content of 63.9–65.2 mol% and the isolated bacteria cannot grow at 4°C. Species of the genus Frigoribacterium and some species of Microbacterium have lysine in the cell wall. However, the isolated bacteria are different from these organisms in that they possess a different menaquinone and have a different G+C content and growth temperature. Also, the results of phylogenetic analysis of the 16S rRNA gene revealed that the isolated bacteria form an independent cluster and that this cluster is isolated from any of the subclusters corresponding to the established genera within the family Microbacteriaceae.

This paper describes the unique characteristics of the strains isolated from rotting Pleurotus ostreatus fruiting bodies. The phylogenetic data show that they represent a new genus in the family Microbacteriaceae. Chemotaxonomic and physiological data support this conclusion. We propose a new genus, Mycetocola gen. nov., and three new species, Mycetocola saprophilus sp. nov., Mycetocola tolaasinivorans sp. nov. and Mycetocola lacteus sp. nov.

METHODOLOGICAL, PHYSIOLOGICAL AND BIOCHEMICAL CHARACTERISTICS. Cell morphology was determined by phase-contrast microscopy following growth on PS agar. One-day-old cells in PS broth medium were negatively stained with 20% phosphotungstic acid (pH 6.5) and were observed with a JEM-1010 transmission electron microscope (JEOL). Physiological and biochemical characteristics were examined as described by Nishiyama (1981) and Azegami et al. (1987). Dye’s medium C (Dye, 1962) and OY medium (Dye, 1968) were used as the basal media for acid production and utilization tests, respectively.

Chemical analyses. Cell walls were prepared from about 500 mg (dry wt) bacterial cells as described by Schleifer & Kandler (1972). Amino acids in the acid hydrolysate of the cell walls were identified by two-dimensional ascending chromatography on cellulose TLC plates (Tokyo Kasei) by the method of Harper & Davis (1979) and by HPLC as their phenylthiocarbamoyl derivatives with a model Shimadzu LC-6AD HPLC apparatus, according to the manufacturer’s instructions. Glycolate tests were performed by the method of Uchida et al. (1999). Cellular fatty acids were extracted from dried cells (50 mg) by acetic anhydride, purified (Minnikin et al., 1979) and analysed by GLC-MS with a GC/MS-QP5000 spectrometer (Shimadzu) combined with a CLASS-5000 MS Workstation computer system. GLC analyses were carried out using a GC-17A gas chromatograph (Shimadzu). A BPX70 capillary column (SGE) containing 70% cyanopropyl equivalent modified siloxane (50 μm × 0.25 mm) was used at 80°C for 2 min, 80–150°C at 15°C min⁻¹, 150–250°C at 8°C min⁻¹ and then 250°C for 5 min, with helium as carrier gas at a flow rate of 1.4 ml min⁻¹. Menaquinones were extracted from dry cells (200 mg) with chloroform/methanol (2:1, v/v), purified by silica gel TLC (Kieselgel 60F₂₅₄ plates; Merck) using hexane/diethyl ether (85:15, v/v) as solvent, extracted with acetone, dried under nitrogen stream and then analysed by HPLC with a Shimadzu model LC-5A instrument equipped with a Zorbax octadecyl silane column (150 × 4.6 mm).

DNA base composition and DNA relatedness. Isolation and purification of chromosomal DNA and estimation of G+C content were performed by the methods of Takagi et al. (1993). DNA relatedness values were determined as described by Ezaki et al. (1989).

Amplification and sequencing of the 16S rRNA gene. The 16S rRNA gene was amplified by PCR using prokaryotic 16S rRNA gene universal primers 27F (5′-AGAGTTTGATCMCTGGCTCAG-3′; position 8–27 in Escherichia coli) and 1492r (5′-TACGGYTACCTTGGTATCTAC-3′; 1513–

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**Table 1. Bacterial strains isolated from cultivated mushrooms and 16S rRNA gene accession numbers**

<table>
<thead>
<tr>
<th>Strain</th>
<th>Geographical origin of mushrooms</th>
<th>Proposed name</th>
<th>DDBJ accession no.</th>
</tr>
</thead>
<tbody>
<tr>
<td>CM-01⁰</td>
<td>Yamagata prefecture, Japan</td>
<td>Mycetocola saprophilus</td>
<td>AB012647</td>
</tr>
<tr>
<td>CM-02</td>
<td>Yamagata prefecture, Japan</td>
<td>Mycetocola saprophilus</td>
<td>AB012646</td>
</tr>
<tr>
<td>CM-20</td>
<td>Ibaraki prefecture, Japan</td>
<td>Mycetocola lacteus</td>
<td>AB012648</td>
</tr>
</tbody>
</table>

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The PCR products were purified by using a Sepharose
Cl-2B gel (Pharmacia). The sequencing reactions were
performed by using an ABI PRISM Big Dye Terminator
Cycle Sequencing Ready Reaction Kit (Applied Bio-
systems). Primers used for sequencing were 27f, 530f (5’-
GTGCCAGCMGCGCGG-3’; 515–530), 1114f (5’-GCA-
ACGAGCCGAAACC-3’; 1099–1114), 515r (5’-CCGGG-
CKGCTGGCAC-3’; 530–515), 1100r (5’-GGTTTGGTCG-
TCGTTG-3’; 1114–1100) and 1492r. All PCR reactions
were performed with a Perkin-Elmer Cetus model 9600
thermal cycler. Each extension product resulting from the
sequencing reaction was purified through a Centri-Sep spin
column (Applied Biosystems) and sequenced by using an
ABI model 377 automated DNA sequencer.

Phylogenetic analysis and nucleotide sequence accession
numbers. The multiple alignment of sequences, calculation
of nucleotide substitution rates (Ksub values; Kimura, 1980),
construction of a neighbour-joining phylogenetic tree
(Saitou & Nei, 1987) and a bootstrap analysis with 1000
replicates for evaluation of phylogenetic tree topology
(Felsenstein, 1985) were carried out with the clustal w
multiple sequence alignment program (Thompson et al.,
1994). The 16S rRNA gene sequences determined in this
study have been deposited in the DDBJ database under the
accession numbers shown in Table 1.

RESULTS

Morphological, biochemical and physiological
characteristics

All of the strains were Gram-positive, non-sporulating,
non-motile, irregular rods, 0–2–4 µm wide and 2–0–3.5 µm long in
PS broth medium (Fig. 1). They were
aerobic and no growth was found under anaerobic
conditions. The strains formed smooth, yellowish-
white colonies on PS agar. The optimal temperature
for growth was 25 °C and the maximum temperature
for growth was 33 °C for all strains. No strain grew at
4 °C. Ten strains were divided into three groups. The
first group contains three strains, CM-01T, CM-02 and
CM-03, which did not hydrolyse Tween 80 and did not
produce acid from erythritol, but did produce acid
from melezitose and utilize citrate. The second group
contains one strain, CM-05T, which did not hydrolyse
Tween 80, did not produce acid from erythritol and
melezitose and did not utilize citrate. The third group
is composed of six strains, CM-10T, CM-14, CM-15,
CM-16, CM-20 and CM-21, which hydrolysed Tween
80, produced acid from erythritol and melezitose and
utilized citrate.

Chemotaxonomic characteristics

The amino acid composition of the cell walls of the
representative strains of each group was glutamic acid,
glycine, alanine, lysine and an unknown amino acid in
the molar ratio of 0:60:1:50:1:00:2:14:1:03 for strain
CM-01T, 2:11:2:06:1:00:1:74:0:94 for strain CM-05T
and 1:69:1:39:1:00:1:11:0:80 for strain CM-10T. De-
spite further analysis using two-dimensional paper
chromatography, the identification of the unknown
amino acid was unsuccessful. The glycan moiety of the
cell walls of all strains contained acetyl residues.
Cellular fatty acids of all the strains were composed
mainly of anteiso-C15:0, anteiso-C17:0 and iso-C16:0,
and the composition ratios were approximately 56, 39
and 5% in strains CM-01T, CM-02 and CM-03, 63, 33
and 4% in strain CM-05T and 51, 46 and 3% in strains
CM-10T, CM-14, CM-15, CM-16, CM-20 and CM-21,
respectively. These classifications agree with the results
derived from the biochemical and physiological tests
(see above). The menaquinones of strain CM-01T were
MK-10 (53%), MK-9 (23%), MK-11 (12%) and MK-
8 (8%), those of strain CM-05T were MK-10 (58%),
MK-9 (21%), MK-11 (14%) and MK-8 (4%), and
those of strain CM-10T were MK-10 (54%), MK-9
(21%), MK-11 (14%) and MK-8 (4%).

DNA relatedness

The levels of DNA relatedness were analysed and the
results are presented in Table 2. Three strains CM-01T,
CM-02 and CM-03 were related with 81–96% homol-
y and the levels among the other seven strains
ranged from 12 to 54%. Strain CM-05T did not show
a high level of DNA relatedness with any other strains
(18–28%). Six strains, CM-10T, CM-14, CM-15, CM-
16, CM-20 and CM-21, showed a high level of DNA
relatedness with each other (79–84%), but did not
show a high level of relatedness with the other four
strains (16–52%). On the basis of these results, the
three groups into which the 10 strains have been
divided can be classified at the species level.

*Fig. 1. Electron micrograph of negatively stained cells of Mycetocola saprophilus, showing pleomorphic, rod-shaped cells
with mesosomes. Cells are 0.2–0.4 µm wide and 2.0–3.5 µm long.*
Table 2. DNA base composition and DNA relatedness of the strains

<table>
<thead>
<tr>
<th>Strain</th>
<th>G + C content (mol%)</th>
<th>DNA relatedness (%) with:</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>CM-01&lt;sup&gt;T&lt;/sup&gt;</td>
</tr>
<tr>
<td>CM-01&lt;sup&gt;T&lt;/sup&gt;</td>
<td>65.2</td>
<td>100</td>
</tr>
<tr>
<td>CM-02</td>
<td>65.2</td>
<td>81</td>
</tr>
<tr>
<td>CM-03</td>
<td>65.2</td>
<td>96</td>
</tr>
<tr>
<td>CM-05&lt;sup&gt;T&lt;/sup&gt;</td>
<td>65.1</td>
<td>12</td>
</tr>
<tr>
<td>CM-10&lt;sup&gt;T&lt;/sup&gt;</td>
<td>63.9</td>
<td>42</td>
</tr>
<tr>
<td>CM-14</td>
<td>64.6</td>
<td>46</td>
</tr>
<tr>
<td>CM-15</td>
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<tr>
<td>CM-16</td>
<td>64.6</td>
<td>46</td>
</tr>
<tr>
<td>CM-20</td>
<td>64.6</td>
<td>54</td>
</tr>
<tr>
<td>CM-21</td>
<td>64.7</td>
<td>47</td>
</tr>
</tbody>
</table>

Phylogenetic analysis of 16S rRNA gene

Almost complete 16S rRNA gene sequences of 1444 or 1445 bases of the 10 strains were determined. Strains CM-01<sup>T</sup>, CM-02 and CM-03 had identical 16S rRNA gene sequences as did strains CM-10<sup>T</sup>, CM-14, CM-15, CM-16, CM-20 and CM-21. The phylogenetic tree based on calculated $K_{\text{nuc}}$ values clearly shows that the representative strains CM-01<sup>T</sup>, CM-05<sup>T</sup> and CM-10<sup>T</sup> formed an independent cluster at the base of the Microbacterium cluster in the family Microbacteriaceae with a 100% bootstrap confidence level (Fig. 2).

DISCUSSION

We isolated from rotting <i>Pleurotus ostreatus</i> fruiting bodies 10 micro-organisms that markedly reduce the level of extracellular toxins, tolaasins, produced by <i>Pseudomonas tolaasii</i>, the most destructive pathogen of cultivated mushrooms. They were saprophytic, but not parasitic nor pathogenic to <i>Pleurotus ostreatus</i> (Tsukamoto et al., 1998). To clarify the taxonomic positions of these bacteria, we examined their morphological, physiological and chemotaxonomic characteristics, together with DNA–DNA reassociation values and 16S rRNA gene sequence comparisons. The strains are Gram-positive, obligately aerobic, non-sporulating and irregular rod-shaped bacteria with high G + C contents (64–65 mol%) and they also have the following characteristics: the
The 10 strains in the genus *Mycetocola* can be divided into three species according to the results of DNA–DNA hybridization tests (Table 2). This conclusion was supported by the results of phenotypic characterization, hydrolysis of Tween 80, acid production from erythritol or melezitose, utilization of citrate and patterns of cellular fatty acids. 16S rRNA gene sequence analysis of the representative strains of these three groups reinforced their status as novel species in the genus *Mycetocola*. On the basis of these physiological and chemotaxonomic characteristics, and the result of phylogenetic analysis together with DNA–DNA reassociation, we propose the new species *Mycetocola saprophilus* sp. nov., *Mycetocola tolaasini-vorans* sp. nov., and *Mycetocola lacteus* sp. nov. The type species of the genus is *Mycetocola saprophilus*.

**Description of Mycetocola gen. nov.**

*Mycetocola* (my.ce.to.co.la. L. n. *myceto* fungus; Gr. adj. *-cola* inhabitant; M.L. masc. n. *mycetocola* fungus-dweller).

Cells are Gram-positive, obligately aerobic, irregular rods, 0.2–0.4 × 2.0–3.5 μm. Endospores are not produced. Non-motile. Colonies are circular, convex, smooth and yellowish-white on PS agar. Growth optimal at 25 °C, but no growth above 33 °C nor at 4 °C in PS broth medium. Catalase is produced, but oxidase is not produced. The following tests are positive: aesculin hydrolysis, growth in peptone water, acid production from D- cellubiose, dextrin, D-fructose, D-galactose, D-glucose, glycerol, lactose, maltose, D-mannitol, D-mannose, melibiose, D-ribose, salicin, D-sorbitol, sucrose, trehalose and D-xylose, and utilization of fumarate. The following tests are negative: reduction of nitrate or nitrite, nitrate respiration, liquefaction of gelatin, Voges–Proskauer reaction, methyl red reaction, lecithinase, tyrosinase, urease, hydrolysis of arbutin, arginine and casein, production of diffusible and fluorescent pigment, hydrogen sulfide, indole, 3-ketolactose, 2-ketogluconate and levan from sucrose, growth in Corn’s solution, Fermi’s solution and Uschinsky’s solution, utilization of asparagine as sole source of carbon and nitrogen, maceration of potato tubers, hypersensitive reaction in tobacco leaves, acid production from D-arabinose, L-arabinose,
peptone water, acid production from tests are positive: aesculin hydrolysis, growth in 33 °C. Motile. Smooth, yellowish-white colonies are found on dextrin, *Pleurotus ostreatus* saprophilus family *Microbacteriaceae*. Type species is *Mycetocola saprophilus*. Isolated from cultivated mushroom *Pleurotus ostreatus*.

**Description of Mycetocola saprophilus sp. nov.**

*Mycetocola saprophilus* (sa.pro.ph’il.us. Gr. adj. sapros putrid; Gr. adj. philus loving; M.L. adj. saprophilus putrid-loving).

Cells are Gram-positive, obligately aerobic, irregular rods, 0·2–0·4 × 2·0–3·5 μm, non-sporulating and non-motile. Smooth, yellowish-white colonies are found on PS agar. The maximum temperature for growth is 33 °C and the optimal temperature for growth is 25 °C, but no growth at 4 °C in PS broth medium. Catalase is produced, but oxidase is not produced. The following tests are positive: aesculin hydrolysis, growth in peptone water, acid production from d-cellobiose, dextrin, d-fructose, d-galactose, d-glucose, glycerol, lactose, maltose, d-mannitol, d-mannose, melezitose, melibiose, d-ribose, salicin, d-sorbitol, sucrose, trehalose and d-xylene, utilization of citrate and fumarate, and detoxification of tolaasins produced by *Pseudomonas tolaasii*. The following tests are negative: reduction of nitrate or nitrite, nitrate respiration, liquefaction of gelatin, Voges–Proskauer reaction, methyl red reaction, lecinthinase, tyrosinase, urease, hydrolysis of arbutin, arginine, casein and Tween 80, production of diffusible and fluorescent pigment, hydrogen sulfide, indole, 3-ketolactose, 2-ketogluconate and levans from sucrose, growth in Corn’s solution, Fermi’s solution and Ushinsky’s solution, utilization of asparagine as sole source of carbon and nitrogen, maceration of potato tubers, hypersensitive reaction in tobacco leaves, acid production from d-arabinose, l-arabinose, d-dulcitol, erythritol, m-inositol, inulin, melezitose, d-rhamnose, l-rhamnose and starch, and utilization of benzoate, butyrate, citrate, m-hydroxybenzoate, malonate, oxalate, propionate, d- and l-tartarate. Cell wall peptidoglycan contains lysine as a diamino acid and the muramic acid of the cell wall is an acetyl type. The major isoprenoid quinone is menaquinone MK-10 and small amounts of MK-9 and MK-11 are present. The major fatty acids are anteiso-C_{15:0} and anteiso-C_{17:0}. The G + C content is 65·2 mol %. Forms an independent phylogenetic cluster at the base of the *Microbacterium* cluster in the family *Microbacteriaceae*. Type strain is *Mycetocola saprophilus* CM-01T (=IFO 16274T = MAFF 211324T = NRRL B-24119T).

**Description of Mycetocola tolaasinivorans sp. nov.**

*Mycetocola tolaasinivorans* (to.laa.si.ni.vo’rans. N.L. neut. n. tolaasium tolaasin, type of toxin produced by *Pseudomonas tolaasii*; L. part. adj. vorans devouring, decomposing; N.L. part. adj. tolaasinivorans tolaasin-decomposing).

Cells are Gram-positive, obligately aerobic, irregular rods, 0·2–0·4 × 2·0–3·5 μm, non-sporulating and non-motile. Smooth, yellowish-white colonies are found on PS agar. The maximum temperature for growth is 33 °C and the optimal temperature for growth is 25 °C, but no growth at 4 °C in PS broth medium. Catalase is produced, but oxidase is not produced. The following tests are positive: aesculin hydrolysis, growth in peptone water, acid production from d-cellobiose, dextrin, d-fructose, d-galactose, d-glucose, glycerol, lactose, maltose, d-mannitol, d-mannose, melezitose, d-ribose, salicin, d-sorbitol, sucrose, trehalose and d-xylene, utilization of fumarate, and detoxification of tolaasins produced by *Pseudomonas tolaasii*. The following tests are negative: reduction of nitrate or nitrite, nitrate respiration, liquefaction of gelatin, Voges–Proskauer reaction, methyl red reaction, lecinthinase, tyrosinase, urease, hydrolysis of arbutin, arginine, casein and Tween 80, production of diffusible and fluorescent pigment, hydrogen sulfide, indole, 3-ketolactose, 2-ketogluconate and levans from sucrose, growth in Corn’s solution, Fermi’s solution and Ushinsky’s solution, utilization of asparagine as sole source of carbon and nitrogen, maceration of potato tubers, hypersensitive reaction in tobacco leaves, acid production from d-arabinose, l-arabinose, d-dulcitol, erythritol, m-inositol, inulin, melezitose, d-rhamnose, l-rhamnose and starch, and utilization of benzoate, butyrate, citrate, m-hydroxybenzoate, malonate, oxalate, propionate, d- and l-tartarate. Cell wall peptidoglycan contains lysine as a diamino acid and the muramic acid of the cell wall is an acetyl type. The major isoprenoid quinone is menaquinone MK-10 and small amounts of MK-9 and MK-11 are present. The major fatty acids are anteiso-C_{15:0} and anteiso-C_{17:0}. The G + C content is 65·2 mol %. Forms an independent phylogenetic cluster at the base of the *Microbacterium* cluster in the family *Microbacteriaceae*. Type strain is *Mycetocola tolaasinivorans* CM-05T (=IFO 16277T = MAFF 211325T = NRRL B-24120T = strain 9405T, described in Tsukamoto et al., 1998).

**Description of Mycetocola lacteus sp. nov.**

*Mycetocola lacteus* (lac.te’us. L. adj. lacteus milky).

Cells are Gram-positive, obligately aerobic, irregular rods, 0·2–0·4 × 2·0–3·5 μm, non-sporulating and non-motile. Smooth, yellowish-white colonies are found on PS agar. The maximum temperature for growth is 33 °C and the optimal temperature for growth is 25 °C, but no growth at 4 °C in PS broth medium. Catalase is produced, but oxidase is not produced. The following tests are positive: aesculin hydrolysis and Tween 80, growth in peptone water, acid production from d-
cellobiose, dextrin, erythritol, d-fructose, d-galactose, d-glucose, glycerol, lactose, maltose, d-mannitol, d-mannose, melezitose, melibiose, d-ribose, salicin, d-sorbitol, sucrose, trehalose and d-xylene, utilization of citrate and fumarate, and detoxification of tolaasins produced by *Pseudomonas tolaasii*. The following tests are negative: reduction of nitrate or nitrite, nitrate respiration, liquefaction of gelatin, Voges–Proskauer reaction, methyl red reaction, lecithinase, tyrosinase, urease, hydrolysis of arbutin, arginine and casein, production of diffusible and fluorescent pigment, hydrogen sulfide, indole, 3-ketolactose, 2-ketogluconate and levan from sucrose, growth in Corn’s solution, Fermi’s solution and Uschinsky’s solution, utilization of asparagine as sole source of carbon and nitrogen, maceration of potato tubers, hypersensitive reaction in tobacco leaves, acid production from d-arabinose, l-arabinose, d-ribose, m-inositol, inulin, d-raffinose, l-rhamnose and starch, and utilization of benzoate, butyrate, m-hydroxybenzoate, malonate, oxalate, propionate, d- and l-tartarate. Cell wall peptidoglycan contains lysine as a diamino acid and the mureamic acid of the cell wall is an acetyl type. The major isoprenoid quinone is menaquinone MK-10 and small amounts of MK-9 and MK-11 are present. The major fatty acids are anteiso-C15:0 and anteiso-C17:0. The G+C content is 63.9–64.7 mol%. Isolated from cultivated mushroom *Pleurotus ostreatus*. Type strain is CM-10T (=IFO 16278T = MAFF 211326T = NRRL B-24121T).

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