Rarobacter faecitabidus gen. nov., sp. nov., a Yeast-Lysing Coryneform Bacterium

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Phenotypic and chemotaxonomic characteristics of four isolates of yeast-lysing bacteria isolated from wastewater treatment systems were examined. The isolates were nonsporeforming, gram-positive, facultative anaerobic, irregular rods that were motile by multitrichous flagella. The isolates had an absolute requirement for hemin or hemoprotein for aerobic growth. Under anaerobic conditions, the isolates did not need heme compounds, but needed carbon dioxide. The deoxyribonucleic acid (DNA) base composition was 65.7 to 66.1 mol% guanine plus cytosine. The amino acid composition of the cell wall peptidoglycan was d-alanine, l-alanine, d-glutamic acid, L-ornithine, and d-serine (1:1:2:1:1). The major fatty acid of whole cells was 12-methyltetradecanoic acid. The major isoprenoid quinone was menaquinone with nine isoprene units.

DNA-DNA hybridizations revealed clear separation of the isolates from known genera of the coryneform group. Therefore, Rarobacter faecitabidus gen. nov., sp. nov., is proposed for the isolates. The type strain is YLM-1 (JCM 6097).

In previous papers (5, 30) we reported the isolation of novel yeast-lysing bacteria from the wastewater treatment systems of alcoholic beverage factories. These bacteria adhered to and lysed viable cells of Saccharomyces, Hansenula, and Candida species. These bacteria hardly grew on nutrient agar but grew well on media containing extracts of viable yeast cells. Further, an essential factor for aerobic growth of the bacteria was hemin or hemoprotein.

This paper deals with the phenotypic characteristics, chemotaxonomic characteristics, deoxyribonucleic acid (DNA) base composition, and DNA-DNA hybridization of four yeast-lysing bacteria. Rarobacter faecitabidus gen. nov., sp. nov., is proposed for these strains, with strain YLM-1 (JCM 6097) as the type strain.

MATERIALS AND METHODS

Microorganisms and cultural conditions. Four strains of the yeast-lysing bacteria, YLM-1T (T, type strain), YLM-11, YLM-39, and YLM-139, were used. They were isolated from activated sludge of wastewater treatment systems of alcoholic beverage factories (YLM-1T, YLM-11, and YLM-139) and from the discharged water of an alcoholic beverage factory (YLM-39) (5, 30). They were maintained on YM-catalase agar, which contained (per liter) 5.74 g of K2HP04, 2.77 g of KH2P04, 15 g of glucose, 10 g of peptone, 20 mg of MgSO4·7H2O, and 0.3 g of FeCl3·6H2O.

For identifying the isolates, colony appearance was observed on YM-catalase agar and nutrient agar but grew well on media containing extracts of viable yeast cells. Further, an essential factor for aerobic growth of the bacteria was hemin or hemoprotein.

This paper deals with the phenotypic characteristics, chemotaxonomic characteristics, deoxyribonucleic acid (DNA) base composition, and DNA-DNA hybridization of four yeast-lysing bacteria. Rarobacter faecitabidus gen. nov., sp. nov., is proposed for these strains, with strain YLM-1 (JCM 6097) as the type strain.

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Morphological characteristics. The morphology of cells grown on YM-catalase agar and nutrient agar containing 60 mg of catalase per liter (nutrient-catalase agar) was investigated. To examine pleomorphism, 2% (wt/vol) sodium citrate was added to nutrient-catalase agar (28). Gram stain characteristics were examined by the method of Hucker and Conn (6). Motility was observed by the hanging-drop method, and flagellation was confirmed by transmission electron microscopy with a JEOL model 200CX microscope at 100 kV after negative staining with 1% (wt/vol) phosphotungstic acid. For thin-section electron micrographs, cells were fixed in 3% (wt/vol) glutaraldehyde–1% (wt/vol) OsO4, dehydrated, and embedded in Spurr resin.

Cultural characteristics. Colonial appearance was observed after incubation for 2 days at 30°C. YM-catalase agar was used for aerobic cultures, and nutrient agar was used in a disposable anaerobic system (Anaeromate; Nissui) for anaerobic cultures.

Physiological characteristics. Growth temperature, pH, and tolerance to NaCl were tested in nutrient-catalase broth for 3 days. Growth temperature was tested at pH 7, and effect of pH on growth was tested at 30°C. Tolerance to NaCl was tested at 30°C and pH 7. The heme requirement was examined by using nutrient agar. For studying vitamin requirements, the media of Keddie et al. (12) were used with 10 mg of hemin (Wako Pure Chemical Industries Ltd., Tokyo, Japan) per liter instead of catalase.

Biochemical characteristics. Unless otherwise indicated, methods described in the Manual of Clinical Microbiology (14) were used for the tests. Catalase (60 mg/liter) was added to the test media. Nitrate reduction and denitrification were examined by using potassium nitrate broth. Utilization of inorganic nitrogen was tested by using yeast carbon base (Difco). An oxidation and fermentation test was conducted as described by Hugh and Leifson (7). The method of Yamada and Komagata (28) was employed to examine production of acid from carbohydrates and assimilation of organic acids. Production of gas was checked in 1% (wt/vol) peptone broth containing 1% (wt/vol) glucose. Hydrolysis of...
starch and casein was tested on nutrient agar plates containing 0.2% (wt/vol) soluble starch or 1% (wt/vol) casein. Hydrolysis of gelatin was tested on agar plates and stab cultures. Hydrolysis of cellulose was tested by disintegration of filter paper and depolymerization of carboxymethyl cellulose (23). Hemolysis was tested on sheep blood agar (Nissui). Acetoin production was tested by using MR-VP medium (Difco), and indole production was examined by using 1% (wt/vol) peptone broth and Kovac reagent. For production of hydrogen sulfide, triple sugar iron agar (Difco), Klöger iron agar (Difco), and lead acetate test paper were used. Extracellular deoxyribonuclease (DNase) was tested for 20 days, using DNase test agar (Difco); urease was tested for 6 days, using Christensen's urea agar (Difco), and oxidase was tested with oxidase test paper (Nissui). For the catalase test, hemin (10 mg/liter) instead of catalase was added to nutrient agar, and bubbling was observed after pouring 3% hydrogen peroxide on the colonies.

Isolation of DNA. DNA was isolated by the phenol method (16) with some modifications. A mixture of phenol and chloroform (1:1, vol/vol) was used instead of phenol to remove proteins, and 50 μg of ribonuclease A (Sigma) per ml was used for hydrolysis of ribonucleic acid.

Determination of DNA base composition. DNA base composition was determined by reversed-phase high-performance liquid chromatography (HPLC) after enzymatic hydrolysis of DNA into nucleosides (22).

Cell wall analysis. Cell walls were prepared as described by Yamada and Komagata (26) with some modifications. Freshly cultured cells were disrupted by a mechanical cell homogenizer (B. Braun, Melsungen AG, Federal Republic of Germany). The crude cell wall fraction was collected by centrifugation and purified by digestion with trypsin, pronase E (Protease Type XIV; Sigma) (1 mg of pronase E per ml of 50 mM phosphate buffer [pH 7.6] at 37°C for 5 h), and pepsin. After acid hydrolysis, amino acids were determined by an amino acid analyzer (model 835; Hitachi Ltd., Tokyo, Japan). The configuration of the amino acids was determined as described by Kandler and König (9). Sugars of purified cell walls were analyzed by paper chromatography (1). The acyl type of cell wall was determined by a colorimetric method (25). Detergents of cellular fatty acid composition. Fatty acid composition of whole cells was determined as described by Suzuki and Komagata (19).

Determination of quinone system. Isoprenoid quinones were extracted from lyophilized cells with chloroform-methanol (2:1, vol/vol) and purified by thin-layer chromatography. The purified quinones were analyzed by HPLC (21). The abbreviations used for menaquinones are in the form MK-<i>n</i>(<i>H</i><sub><i>m</i><sup>x</sup>)), with <i>n</i> indicating the number of isoprene units in the side chain and <i>m</i> indicating the number of hydrogen atoms saturating the isoprenoid chain.

DNA-DNA hybridization. DNA-DNA relatedness values were determined by the membrane filter method (11). DNA of strain YLM-<i>T</i> was labeled by the nick translation method, using kits TRK.625 and TRK.5000 (Amersham International, Buckinghamshire, United Kingdom). A DNA filter of <i>P.</i> <i>aeruginosa</i> KS 0025<sup>T</sup> was used as the negative control.

RESULTS

Morphological characteristics. Cells of the four isolates were irregular rods (0.2 to 0.3 by 0.8 to 1.0 μm) and were pleomorphic, especially on the sodium citrate supplemented medium. Branching of cells was not observed. V-forms were observed. They were gram positive, but were gram variable in old cultures and not acid fast. Cells were motile and had multitrichous flagella. No spores were observed, and the cell cultures did not survive when heated at 80°C for 10 min. A thin-section electron micrograph showed a cell wall typical of gram-positive bacteria (Fig. 1).

Cultural characteristics. Colonies grown aerobically on YM-catalase agar were about 1 to 2 mm in diameter, pale yellow, opaque, circular, convex, entire, and smooth. The strains grew more weakly under anaerobic rather than aerobic conditions. Colonies grown anaerobically on YM
aglar in an atmosphere containing carbon dioxide were about 0.5 to 1 mm in diameter, beige, translucent, circular, flat, entire, and smooth. Water-soluble pigments were not produced.

Physiological and biochemical characteristics. The isolates grew at 20 to 39°C, but did not grow below 15 or above 41°C. The optimal temperature was 30°C. They grew well at pH 6 to 8 but did not grow below pH 5 or above pH 9. They grew at 20 to 39°C, but did not grow below 15 or above 41°C. The four strains showed more than 50% DNA complementarity to strain YLM-1T, while the other coryneform bacteria showed less than 5% complementarity to strain YLM-1T.

DISCUSSION

The four isolates were nonsporeforming, gram-positive, non-acid-fast, irregular rods and showed V-forms. These characteristics showed that these isolates belong to the coryneform group of bacteria (15).

It has been reported that some gram-positive bacteria have the ability to lyse yeast cells (10, 13) and fungus cells (20). These bacteria satisfy the characteristics of the genus Oerskovia (2, 13), possibly O. xanthineolytica. Our isolates are quite different from Oerskovia strains not only in their morphological characteristics, but also in their chemotaxonomic features, especially in their isoprenoid quinone and diaminopimelic acid in peptidoglycan.

Table 3 shows the amino acid compositions of the peptidoglycan of the isolates and some other coryneform bacteria. Based on the amino acid composition, the peptidoglycan type of our isolates may be group A of Schleifer and Kandler (17). The genera of coryneform bacteria whose cell walls are acetyl. The major fatty acid of whole cells was 12-methyltetradecanoic acid (anteiso-C₁₂₅₅) (about 50% of the total acid) (Table 2). The major isoprenoid quinone was MK-9 (more than 90%); small amounts of MK-8 and MK-7 were detected.

DNA-DNA hybridization. Table 1 shows DNA-DNA relatedness among the strains and several coryneform bacteria. The four strains showed more than 50% DNA complementarity to strain YLM-1T, while the other coryneform bacteria showed less than 5% complementarity to strain YLM-1T.

TABLE 1. G+C contents of DNA and DNA-DNA hybridization of isolates and some coryneform and related bacteria

<table>
<thead>
<tr>
<th>Strain designation</th>
<th>G+C content mol%</th>
<th>% DNA complementarity with [3H]DNA of YLM-1T</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Rarobacter faecitabidus</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>YLM-1T</td>
<td>66.1</td>
<td>100</td>
</tr>
<tr>
<td>YLM-11</td>
<td>65.8</td>
<td>54</td>
</tr>
<tr>
<td>YLM-39</td>
<td>65.7</td>
<td>62</td>
</tr>
<tr>
<td>YLM-113</td>
<td>65.8</td>
<td>73</td>
</tr>
<tr>
<td><strong>Curtobacterium citreum JCM 1345T</strong></td>
<td>71.5</td>
<td>2</td>
</tr>
<tr>
<td><strong>Aureobacterium testaceum JCM 1353T</strong></td>
<td>65.1</td>
<td>2</td>
</tr>
<tr>
<td><strong>Cellulomonas fimii JCM 1341T</strong></td>
<td>74.0</td>
<td>4</td>
</tr>
<tr>
<td><strong>Cellulomonas flavigena JCM 1489T</strong></td>
<td>72.7*</td>
<td>4</td>
</tr>
<tr>
<td><strong>Oerskovia turbata JCM 3160T</strong></td>
<td>72.1</td>
<td>4</td>
</tr>
<tr>
<td><strong>Oerskovia xanthineolytica JCM 3164T</strong></td>
<td>74.3</td>
<td>3</td>
</tr>
</tbody>
</table>

* Data from reference 27.

TABLE 2. Cellular fatty acid compositions

<table>
<thead>
<tr>
<th>Strain</th>
<th>Fatty acid composition (%)a</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>a-13</td>
</tr>
<tr>
<td>YLM-1T</td>
<td>1</td>
</tr>
<tr>
<td>YLM-11</td>
<td>Tr</td>
</tr>
<tr>
<td>YLM-39</td>
<td>Tr</td>
</tr>
<tr>
<td>YLM-113</td>
<td>1</td>
</tr>
</tbody>
</table>

a Abbreviations for fatty acids are as follows: a-13, anteiso-branched tridecanoic acid; i-14, iso-branched tetradecanoic acid; and n-13, straight-chain tridecanoic acid.

b Less than 0.5%.
genus *Cellulomonas* have peptidoglycan of group A. However, there are no strains of the genus *Cellulomonas* which have the same amino acid composition as that of our isolates. Furthermore, the major isoprenoid quinone of the isolates is different from that of strains of the genus *Cellulomonas* (Table 4). On the basis of chemotaxonomic characteristics, there is no a suitable genus for the isolates among coryneform and related bacteria (Table 4). The results of DNA-DNA hybridization revealed that they formed an independent cluster within the coryneform group.

The isolates produced acid from limited kinds of sugars and sugar alcohols and did not assimilate the organic acids tested. These characteristics differ from those of the genera *Cellulomonas* and *Curtobacterium* (29). The isolates require heme compounds besides vitamins for aerobic growth and lyse viable yeast cells. These are distinctive characteristics of the isolates from the other coryneform bacteria.

Therefore, we propose a new genus, *Rarobacter*, and a new species, *Rarobacter faecitabidus*, for the isolates.

**Description of Rarobacter gen. nov.** The characteristics of Rarobacter (Ra.ro bac'ter. L. adj. rarus, curious; M. L. masc. n. bact' er, masculine form from Gr. neut. n. bac'tron, a rod; M. L. masc. n. Rarobacter, curious rod) are as follows. Cells are irregular rods, 0.2 to 0.3 by 0.8 to 1.0 μm. Gram positive, but readily decolorized. Not acid fast. Motile by multitrichous flagella. Endospores are not produced. Che-moorganotrophs. Optimal temperature is 30°C, and optimal pH is 6 to 8 for growth. Nitrate is not reduced to nitrite. Ammonium salt is utilized as nitrogen source, but nitrate is not utilized. Acid is produced aerobically and anaerobically from d-glucose and d-mannose, but not from L-arabinose or L-rhamnose. Organic acids studied thus far are not assimilated (see above). Starch, casein, and gelatin are hydrolyzed, but cellulose is not hydrolyzed. Acetoin and indole are not produced. Oxidase positive. DNA base composition ranges from 65.7 to 66.1 mol% G+C. Diamino acid of cell wall is L-ornithine. Cell wall acyl type is acetyl. Major cellular fatty acid is anteiso-C₁₅. Major isoprenoid quinone is MK-9. Type species is *Rarobacter faecitabidus*.

**Description of Rarobacter faecitabidus sp. nov.** In addition to the characteristics given for the genus, the characteristics of *Rarobacter faecitabidus* (fae.ci.ta'bi.dus. L. fem. n. faex, dregs; L. adj. tabidus, dissolving; M. L. masc. adj. faec.i.ta-bidus, dreg dissolving) are as follows. Facultative anaerobic. Requires hemin or hemoproteins besides biotin and thiamine as growth factors in the aerobic condition. Requires carbon dioxide but not hemin or hemoproteins for anaerobic growth. Colonies on nutrient-catalase agar are pale yellow, opaque, circular, convex, entire, and smooth. Acid is produced aerobically and anaerobically from d-glucose, d-fructose, d-mannose, maltose, celllobiose, dextrin, arabinin, and salicin, but not from L-arabinose, L-rhamnose, d-galactose, L-sorbosae, lactose, trehalose, raffinose, inulin, glycerol, erythritol, adonitol, mannotol, dulcitol, d-sorbitol, inositol, esculin, or α-methyl-D-glucoside. Hydrogen sulfide is not produced. DNase and urease negative. Catalase positive. DNA base composition is 65.7 to 66.1 mol% G+C (determined by the HPLC method). Amino acid composition of cell wall peptidoglycan is D-Ala, L-Ala, D-Glu, L-Orn, and D-Ser (1:1:2:11). Adheres to viable yeast cells of the genera *Saccharomyces* and *Hansenula*, agglutinates with them, and lyses them. Type strain is YLM-1 (JCM 6097). The description of the type strain is the same as that of the species. DNA base composition of the type strain is 66.1 mol% G+C.

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**LITERATURE CITED**


