Bacteroides oulorum sp. nov., a Nonpigmented Saccharolytic Species from the Oral Cavity

HAROUN N. SHAH,^{1*} MATTHEW D. COLLINS,² JUNKO WATABE,³ AND TOMOTARI MITSUOKA^{3,4}

Department of Oral Microbiology, London Hospital Medical College, London E1 2AD, United Kingdom¹; Department of Microbiology, National Institute for Research in Dairying, Shinfield, Reading RG2 9AT, United Kingdom²; The Institute of Physical and Chemical Research, Wako, Saitama 351, Japan³; and Department of Biomedical Science, Faculty of Agriculture, University of Tokyo, Bunkyo-ku, Tokyo 113, Japan⁴

Bacteroides oulorum, a new nonpigmented, saccharolytic species from oral cavities, is described. This species differs both biochemically and chemically from related taxa, such as *Bacteroides oralis*, *Bacteroides buccalis*, *Bacteroides denticola*, *Bacteroides veroralis*, and *Bacteroides pentosaceus*. The major fermentation products in glucose broth are acetate and succinate. In common with other members of the genus *Bacteroides*, all strains contain malate dehydrogenase and glutamate dehydrogenase, but they differ from some species, such as *Bacteroides fragilis*, in lacking glucose-6-phosphate dehydrogenase and 6-phosphogluconate dehydrogenase. The long-chain fatty acids are predominantly of the straight-chain saturated, iso- and anteiso-methyl branched types, with 12-methyltetradecanoic acid constituting the major acid. Strains of *B. oulorum* can be clearly distinguished from other oral *Bacteroides* species by the presence of major amounts of unsaturated menaquinones with 10 isoprene units. The deoxyribonucleic acid base composition of *B. oulorum* is 45 to 46 mol% guanine plus cytosine. The type strain is WPH 179 (= NCTC 11871).

Until recently, the taxonomy of nonpigmented saccharolytic oral *Bacteroides* has been unsatisfactory (5, 6, 19, 24). Chemotaxonomic techniques, such as deoxyribonucleic acid (DNA) base composition, DNA-DNA homology, enzymatic, and lipid analyses, have confirmed the heterogeneity of this large group of organisms and have led to the recognition of several new species, including *Bacteroides buccae*, *Bacteroides oris* (8), *Bacteroides buccalis*, *Bacteroides denticola*, *Bacteroides pentosaceus* (19), *Bacteroides capillus* (11), and *Bacteroides veroralis* (24). In the course of a systematic study of nonpigmented, saccharolytic *Bacteroides* strains from gingival plaque, three isolates were found to be phenotypically distinct from *Bacteroides oralis* and related species (Shah, Mitsuoka, Watabe, and Collins. Abstr. Br. Soc. Dent. Res. 1984, abstr. no. 237). In this paper we describe the results of a comparative biochemical and chemical study of these isolates and other oral *Bacteroides* species. Our results indicate that the three strains studied are members of the genus *Bacteroides* since they are gram-negative, obligately anaerobic, nonsporeforming rod-shaped organisms which produce major amounts of acetic and succinic acids as the end products of glucose metabolism. Furthermore, on the basis of biochemical, chemical, and genetic data these three strains represent a distinct species, for which the name *Bacteroides oulorum* sp. nov. is proposed.

MATERIALS AND METHODS

Strains. The test strains are listed in Table 1. *B. oulorum* WPH 179^T (T = type strain) was isolated from subgingival plaque by W. P. Holbrook, and strains RS14 and RS20 were isolated from the gingival crevices of two individuals (London Hospital, London, United Kingdom).

Physiological reactions and acid end product analysis. All strains were grown and maintained by weekly subculture on modified Eggerth-Gagnon agar (14), horse blood agar plates, or BM medium, as described previously (23). Physiological

reactions were determined with an API 20A anaerobic test kit (API, Montalieu-Varcien, France). The pH of each well was recorded with a micro pH electrode (Pye Unicam, Cambridge, United Kingdom) after 48 h of growth (10). Cells grown in BM or peptone-yeast extract-glucose medium were analyzed for their metabolic end products by gas-liquid chromatography as described previously (1, 2).

Dehydrogenase activity and electrophoresis. Malate dehydrogenase and glutamate dehydrogenase activities were measured in cell-free extracts of all strains by a spectrophotometric method (21), and the relative electrophoretic mobilities of these enzymes were determined both on Cellolog strips (Reeve Angel Scientific Ltd.) (22) and by polyacrylamide gel electrophoresis (15, 16, 24). Glucose-6-phosphate dehydrogenase and 6-phosphogluconate dehydrogenase activities were tested by a spectrophotometric method similar to the method described above (22).

Extractions and analysis of fatty acid methyl esters. Dry cells (50 mg) were degraded by acid methanolysis and examined by thin-layer chromatography and gas-liquid chromatography as described previously (4).

Analysis of isoprenoid quinones. Isoprenoid quinones were extracted from dry cells (100 mg) as described previously (3). Purified quinones were analyzed by reverse-phase partition high-performance liquid chromatography, using a chromatograph (Laboratory Data Control) fitted with a Spherisorb ODS (5 μ) column and methanol-1-chlorobutane (100:20, vol/vol) as the eluent (1.5 ml/min). Quinones were monitored at 270 nm, and quantitation was achieved by using a model 308 computer integrator (Laboratory Data Control). Mass spectra of the quinones were recorded with a model AE1 MS9 instrument by using a direct insertion probe, an ionizing voltage of 70 eV, and a temperature range of 180 to 220°C.

DNA base composition. DNA was isolated and purified by previously described methods (12, 17). The guanine-plus-cytosine (G+C) contents of DNA preparations were estimated by thermal denaturation (13), using either an auto-

* Corresponding author.

TABLE 1. Physiological and biochemical characteristics of *B. oulorum* and related taxa

Strain(s) ^a	Acid produced ^b from:							
	Arabi- nose	Cello- biose	Glyc- erol	Meli- biose	Rham- nose	Salic- in	Xylan	Xylose
<i>B. denticola</i> NCDO 2352 ^T and 1221	-	-	+	-	-	-	-	-
<i>B. buccalis</i> NCDO 2354 ^T and VPI 8906D	-	+	-	+	-	+	-	-
<i>B. oralis</i> ATCC 33269 ^T	-	+	-	+	-	+	-	-
<i>B. veroralis</i> ATCC 33779 ^T	-	+	-	w+	-	-	+	-
<i>B. pentosaceus</i> NCDO 2353 ^T , J1, and WPH 61	+	+	-	+	+	+	+	+
<i>B. oulorum</i> WPH 179 ^T , RS14, and RS20	-	-	-	w+	-	-	-	-

^a All strains produced acid from glucose, lactose, maltose, mannose, raffinose, and sucrose. All strains failed to produce acid from mannitol, melezitose, sorbitol, and trehalose. All strains hydrolyzed esculin and were indole negative. All strains failed to hydrolyze gelatin. Information in part from references 7, 19, and 24.

^b +, Positive reaction; -, negative reaction; w+, weak reaction.

matic recording spectrophotometer (Komatsu Electronics, Tokyo, Japan) or a model 240 spectrophotometer (Gilford Instrument Laboratories, Inc., Oberlin, Ohio) equipped with a Gilford model 2527 thermoprogrammer at heating rates of 0.5 and 1°C/min; calf thymus DNA or *Escherichia coli* strain B DNA was used as a reference.

DNA-DNA reassociation. DNA-DNA reassociation experiments were performed as described previously by using the S1 nuclease procedure (9, 21, 24). S1 nuclease digestion was performed with 0.5 U of S1 nuclease (Seikagaku, Kogyo Co., Tokyo, Japan). After incubation for 15 min at 37°C, an equal volume of 10% trichloroacetic acid was added to each tube. The tubes were cooled to 4°C for at least 1 h, and the precipitates were collected on nitrocellulose membrane filters (type HA; Millipore Corp., Bedford, Mass.). The membranes were dried, and the radioactivity was measured.

RESULTS AND DISCUSSION

The results of the biochemical tests are shown in Table 1. These results confirmed the close biochemical relatedness of the taxa tested. *B. oulorum* most closely resembled *B. denticola* but could be distinguished from the latter by its inability to ferment glycerol. *B. oulorum* also differed from *B. denticola* in weakly fermenting melibiose. *B. buccalis* and *B. oralis* were readily distinguished from *B. oulorum* in fermenting cellobiose and salicin, whereas *B. pentosaceus* differed from all of the other species examined in fermenting the pentose sugars arabinose and xylose (Table 1).

All of the strains examined produced major levels of acetic

and succinic acids from peptone-yeast extract-glucose or BM medium. In addition, the strains of *B. buccalis* produced isovaleric acid, as reported previously (24). All taxa produced high levels of malate dehydrogenase and glutamate dehydrogenase (>200 nmol of coenzyme reduced per mg of protein per min). However, characteristic electrophoretic mobilities of these enzymes permitted the rapid delineation of most of the species (Table 2) (22, 24). For example, the malate dehydrogenase mobilities of *B. oulorum* strains were similar and could be readily distinguished from the malate dehydrogenase mobilities of the other species examined (Table 2).

Strains of *B. oulorum* contained both non-hydroxylated and 3-hydroxylated long-chain fatty acids. The non-hydroxylated fatty acids were primarily of the straight-chain saturated, iso- and anteiso-methyl branched-chain types, with 12-methyltetradecanoic (anteiso-C_{15:0}) acid constituting the major component (Table 3). The 3-hydroxy acids were composed of straight-chain saturated and iso-methyl branched types, with 3-hydroxy-hexadecanoic (3-OH-C_{16:0}) and 3-hydroxy-15-methylhexadecanoic (3-OH-iso-C_{17:0}) acids predominating. The long-chain fatty acid composition of *B. oulorum* is consistent with that of other *Bacteroides* species (20) but does not delineate clearly the former from other oral *Bacteroides* species (viz., *B. buccalis*, *B. denticola*, *B. oralis*, and *B. pentosaceus*).

All of the test strains possessed menaquinones (vitamin K₂) as their sole respiratory quinones. The quantitative menaquinone profiles are shown in Table 4. Strains of *B. oulorum* were readily distinguished from all of the other oral *Bacteroides* species examined because they possessed unsaturated menaquinones with 10 isoprene units (MK-10) as the major component (ca. 80%) (Table 4). *B. oralis* contained MK-13, *B. buccalis* contained MK-13 and MK-12, *B. denticola* contained MK-11 and MK-12, *B. pentosaceus* con-

TABLE 2. Electrophoretic mobilities of malate dehydrogenase and glutamate dehydrogenase and major end products of metabolism of *B. oulorum* and related taxa

Strain	Relative mobility in Cellogel (cm) ^a		Major acid end products ^b
	Malate dehydrogenase	Glutamate dehydrogenase ^c	
<i>B. buccalis</i>			
NCDO 2354 ^T	5.3	4.2	A,S, iV
VPI 8906D	5.3	4.1	A,S, iV
<i>B. oulorum</i>			
WPH 179 ^T	3.0	NT ^d	A,S
RS14	2.9	NT	A,S
RS20	3.1	NT	A,S
<i>B. denticola</i>			
NCDO 2352 ^T	4.2	3.4	A,S
1221	4.1	3.4	A,S
<i>B. oralis</i> ATCC 33269 ^T	4.1	5.2	A,S
<i>B. pentosaceus</i>			
NCDO 2353 ^T	3.9	4.8	A,S
J1	3.9	4.7	A,S
WPH 61	3.7	4.8	A,S
<i>B. veroralis</i> ATCC 33779 ^T	5.1	4.1	A,S

^a All mobilities were measured relative to the enzyme of *Bacteroides intermedius* strain T588.

^b A, Acetic acid; S, succinic acid; iV, isovaleric acid. Information in part from references 7, 19, and 24.

^c Glutamate dehydrogenase is nicotinamide adenine dinucleotide dependent (22).

^d NT, Not tested.

TABLE 4. Menaquinone compositions of *B. oulorum* and related taxa

Strain	% Composition of the following menaquinone prenolols: ^a					
	MK-9	MK-10	MK-11	MK-12	MK-13	MK-14
<i>B. oulorum</i>						
WPH 179 ^T	3.5	80.0	16.5	— ^b	—	—
RS14	3.5	82.5	14.0	—	—	—
RS20	4.0	78.0	18.0	—	—	—
<i>B. denticola</i> NCDO 2426 ^T	0.5	8.5	61.0	28.0	2.0	—
<i>B. oralis</i> ATCC 33269 ^T	—	—	4.0	10.0	68.0	18.0
<i>B. pentosaceus</i> NCDO 2353 ^T	—	—	8.5	44.0	45.0	2.5
J1	—	—	6.5	44.5	46.5	2.5
<i>B. veroralis</i> ATCC 33779 ^T	1.0	35.0	60.0	4.0	—	—

^a The *m/z* values of M⁺ for the menaquinone prenolols were as follows: MK-9, 784; MK-10, 852; MK-11, 920; MK-12, 988; MK-13, 1,056; and MK-14, 1,124.

^b —, Not present.

tained MK-12, and *B. veroralis* contained MK-11 and MK-10 (Table 4). The presence of "species-specific" fingerprints in the taxa described above further emphasize the value of menaquinone analyses in the taxonomy of the genus *Bacteroides* (18, 20).

The DNA base compositions of the test strains and the results of DNA-DNA hybridization experiments are shown in Table 5. *B. oulorum* strains possessed a G+C content of 45.1 to 46.0 mol%. These data clearly distinguish *B. oulorum* from *B. denticola* and *B. pentosaceus*, which possess a significantly higher G+C range, 50 to 52 mol% (Table 5). However, the G+C content of *B. oulorum* is similar to that of *B. buccalis* (45 to 46 mol%) and that of *B. oralis* (44 mol%) (Table 5). The three strains of *B. oulorum* formed a single DNA homology group (95 to 103% homology) quite distinct from representatives of the other species examined (<30% homology) (Table 5). These genetic data, in conjunction with biochemical, enzymatic, and menaquinone differences, clearly indicate that *B. oulorum* is a distinct species. A full description of *B. oulorum* (*ou.lor.um*. Gr. n. *oula* the gums; N.L. gen. pl. n. *oulorum* of the gums) is given below.

Description of *Bacteroides oulorum* sp. nov. (i) **Cellular characteristics.** Nonmotile, nonsporeforming, gram-negative rods approximately 0.5 µm wide by 1.0 to 1.5 µm long. Gram stains reveal short rods, which may occur singly, in pairs, or in chains of rods (24).

(ii) **Colonies.** After 2 days of incubation on Eggerth-Gagnon agar, colonies are approximately 1.0 mm in diameter, circular, entire, convex, translucent, smooth, and shiny (24). Similar colonial morphology occurs on blood agar plates, but the colonies are low, convex, and opaque.

(iii) **Cultural characteristics.** Obligately anaerobic. Cells grow well in either prerduced peptone-yeast extract-glucose or BM medium supplemented with hemin and menadione (23). The terminal pH in glucose-containing broth media is 5.0; the terminal pH in media without glucose is pH 6.2.

(iv) **Biochemical and chemical characteristics.** Acid is produced from glucose, fructose, glycogen, inulin, lactose, maltose, mannose, raffinose, starch, and sucrose. Acid is not produced from arabinose, cellobiose, glycerol, mannitol, melezitose, rhamnose, salicin, sorbitol, trehalose, xylan, and xylose. Esculin is hydrolyzed. Gelatin is not hydrolyzed. Indole negative. Major end products of metabolism

TABLE 3. Long-chain fatty acid compositions of *B. oulorum* and *B. oralis*

Strain	Fatty acid composition (%) ^a																								
	C _{11:0}	ai-C _{13:0}	i-C _{14:0}	C _{14:0}	i-C _{15:0}	ai-C _{15:0}	C _{15:0}	i-C _{16:0}	C _{16:1}	C _{16:0}	i-C _{17:0}	ai-C _{17:0}	C _{17:0}	C _{18:1} (ω9)	C _{18:0}	3-OH-i-C _{13:0}	3-OH-C _{14:0}	3-OH-i-C _{15:0}	3-OH-C _{15:0}	3-OH-i-C _{16:0}	3-OH-C _{16:0}	3-OH-i-C _{17:0}	3-OH-C _{17:0}	3-OH-i-C _{18:0}	3-OH-C _{18:0}
<i>B. oulorum</i>																									
WPH 179 ^T	0.8	1.4	0.9	15.5	37.0	0.8	3.4	tr		6.3	11.8	6.3	0.2	0.8	4.5										
RS14	0.1	0.6	1.3	0.8	15.3	35.1	0.8	3.4	0.4	6.3	12.0	6.9	0.2	0.7	5.2										
RS20		0.7	1.5	0.7	13.5	38.0	1.0	2.2	0.2	5.5	11.6	7.0	0.1	1.5	5.0										
<i>B. oralis</i>		tr	2.9	1.9	2.3	26.4	1.0	4.3	5.9	27.0	2.5	4.2	0.4	8.9	3.9	0.2	0.1	0.6							
ATCC 33269																									

^a Abbreviations for fatty acids are illustrated by the following examples: C_{18:0}, straight-chain saturated octadecanoic acid; C_{18:1}, monounsaturated octadecenoic acid; ai-C_{15:0}, anteiso-methyl branched 12-methyltetradecanoic acid; i-C_{15:0}, iso-methyl branched 13-methyltetradecanoic acid; 3-OH-C_{16:0}, 3-hydroxy-hexadecanoic acid.

TABLE 5. DNA base compositions and DNA-DNA homologies

Strain	G+C content of DNA (mol%) ^a	% DNA homology to:					
		<i>B. denticola</i> NCDO 2352 ^T	<i>B. buccalis</i> VPI 8906D	<i>B. oralis</i> ATCC 33269 ^T	<i>B. veroralis</i> ATCC 33779 ^T	<i>B. pentosaceus</i> NCDO 2353 ^T	<i>B. oulorum</i> WPH 179 ^T
<i>B. denticola</i> NCDO 2352 ^T 1221	50–51	89–100	20–38	10–35	10–32	16–32	20–26
<i>B. buccalis</i> VPI 8906D NCDO 2354 ^T	45–46	11–15	88–100	26–38	14	29–34	21–34
<i>B. oralis</i> ATCC 33269 ^T	44	29	16	100	30	24	21
<i>B. veroralis</i> ATCC 33779 ^T	42	NT ^b	35	33	100	NT	21
<i>B. pentosaceus</i> NCDO 2353 ^T J1	51–52	10–26	11–25	0–23	NT	72–100	20
WPH 61							
<i>B. oulorum</i> WPH 179 ^T	45.1	25	31	20	31	21	95–103
RS14	46.0	NT	NT	NT	NT	NT	95–103
RS20	45.7	NT	NT	NT	NT	NT	95–103

^a Information in part from references 7, 19, and 24.^b NT, Not tested.

are acetate and succinate. Malate dehydrogenase and glutamate dehydrogenase are present, whereas glucose-6-phosphate dehydrogenase and 6-phosphogluconate dehydrogenase are absent.

Sphingolipids are present. Possesses both non-hydroxylated long-chain fatty acids (ca. 90%) and 3-hydroxy long-chain fatty acids (ca. 10%). The non-hydroxylated acids are primarily of the straight-chain saturated, iso- and anteiso-methyl branched types, with 12-methyltetradecanoic acid constituting the major component. The 3-hydroxy acids are of the straight-chain saturated and iso-methyl branched types, with 3-hydroxy-hexadecanoic and 3-hydroxy-15-methylhexadecanoic acids the predominant components. The major respiratory quinones are menaquinones with 10 isoprene units (MK-10). The G+C content of the DNA ranges from 45 to 46 mol%, as determined by the melting temperature method.

(v) **Source.** Isolated from gingival crevices.

(vi) **Type strain.** The type strain is WPH 179 (= NCTC 11871).

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