Reclassification of *Bacteroides levii* (Holdeman, Cato, and Moore) in the Genus *Porphyromonas*, as *Porphyromonas levii* comb. nov.

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The genus *Bacteroides* was recently redefined to include only the type species *Bacteroides fragilis* and closely related taxa. Most other species that were previously designated *Bacteroides* have been reclassified in new genera. The taxonomic position of *Bacteroides levii* (Holdeman, Cato, and Moore) has remained incertae sedis. On the basis of biochemical, chemical and comparative 16S rRNA sequence analyses, this species shares a high degree of similarity with members of the genus *Porphyromonas*. We therefore formally propose that *Bacteroides levii* (Holdeman, Cato, and Moore) be reclassified in the genus *Porphyromonas*, as *Porphyromonas levii* comb. nov.

The taxonomy of the genus *Bacteroides* has undergone major revision in the past few years (25, 26). The genus as described in *Bergey's Manual of Systematic Bacteriology* (8) comprises an ill-defined association of obligately anaerobic, gram-negative, nonsporing, rod-shaped bacteria. Extensive chemotaxonomic (e.g., porphyrin characterization [31], multilocus enzyme electrophoresis [37], lipid analyses [1, 27]) and genotypic (e.g., DNA base composition [30, 36, 38]) studies performed in the late 1970s through the 1980s revealed marked heterogeneity within the genus. On the basis of these studies Shah and Collins (33–35) proposed that the genus *Bacteroides* be divided into three major groups: (i) a redefined genus *Bacteroides*, restricted to members of the *B. fragilis* group; (ii) genus *Prevotella*, consisting of moderately saccharolytic, bile-sensitive, predominantly oral species, such as *P. melaninogenica*; and (iii) genus *Porphyromonas*, for the pigmented species *P. asaccharolytica* and close relatives. A number of predominantly monospecific genera (e.g., *Anaerorhabdus* [32], *Catonella* [21], *Dialister* [21], *Fibrobacter* [20], *Hallella* [21], *Johnsonella* [21], *Megamonas* [28], *Mitsuokella* [29], *Oribaculum* [21], *Rikenella* [4], *Ruminobacter* [40], *Sebaldella* [31], and *Tissierella* [3]) have been described for some of the species that do not conform to the description of these three genera. The species *B. levii* (formerly *B. melaninogenicus* subspecies *levii*) (10, 11) was excluded from the genus *Bacteroides* as redefined by Shah and Collins (34), and its taxonomic position is currently incertae sedis.

B. levii resembles *Porphyromonas* species in forming pigmented colonies on blood agar and possessing similar dehydrogenase profiles (30). However, unlike the majority of porphyromonad species, *B. levii* is weakly saccharolytic (8). Because of the placement of "saccharolytic pigmented" species in the genus *Prevotella* and "non-fermentative pigmented" species in the genus *Porphyromonas*, the taxonomic position of the weakly saccharolytic *B. levii* has thus remained unresolved. Recently several new asaccharolytic pigmented species such as *P. circumdentaria* (18), *P. cangingivalis*, *P. cansulci* (2), *P. gingivicanis*, and *P. crevioricanis* (7) and the weakly saccharolytic

P. macacae (syn. *P. salivosa*) (17) were assigned to the genus *Porphyromonas*. The mol% G+C range of the resulting enlarged genus *Porphyromonas* is now approximately 40 to 55% and species characteristically produce complex metabolic end product profiles that include acetic, propionic, butyric, isovaleric, phenylacetic, or succinic acids. *B. levii* (46 to 48 mol% G+C) produces significant levels of *n*-butyric and acetic acids and in this respect is compatible with some members of the genus *Porphyromonas* (Table 1). The highly distinctive feature of 13-methyl-tetradecanoic acid (*i*-C_{15:0}) as a major long-chain cellular fatty acid of porphyromonads is also produced by *B. levii* (Table 1). By contrast, *Bacteroides* and *Prevotella* species possess 12-methyl tetradecanoic acid (*ai*-C_{15:0}) as their major long-chain cellular fatty acid (1, 34, 35) and produce a simpler metabolic end product profile of mainly acetic and succinic acids.

Recently, 16S rRNA gene sequencing has confirmed the validity of restricting the genus *Bacteroides* to the *B. fragilis* group of species (2, 22–24) and in the main support the taxonomic restructuring proposed by Shah and Collins (33–35). In particular, these studies show that *Prevotella* and *Porphyromonas* are phylogenetically distinct and that the weakly saccharolytic pigmented species *B. levii* is also a member of the genus *Porphyromonas* (Fig. 1). Thus on the basis of the phylogenetic evidence and the phenotypic distinctiveness of *B. levii*, we formally propose the reclassification of this species in the genus *Porphyromonas*. Since *B. levii* is weakly saccharolytic, and all *Porphyromonas* species produce malate and glutamate dehydrogenases but some species (mainly of animal origin) additionally possess glucose-6-phosphate and 6-phosphogluconate dehydrogenases, we further propose that the description of the genus *Porphyromonas* be amended accordingly.

Description of *Porphyromonas levii* (Holdeman, Cato, and Moore) comb. nov. The description below is based on previous studies (6–19, 27, 37, 41) and our own observations:

Gram-negative, obligately anaerobic, nonsporeforming, non-motile rods or coccobacilli. Cells in broth are 0.5 to 1 by 2 to 5 µm. Cells from solid media are coccobacilli or short rods. Colonies on blood agar plates are smooth, shiny, convex, and 1 to 2 mm in diameter and darken from the edge of the colony toward the center between 4 and 8 days. Protoheme is the major porphyrin produced, but traces of protoporphyrin also occur. Succinate stimulates growth and can replace the requirement for protohaem. Few sugars such as glucose and

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TABLE 1. Salient features of current members of the genus *Porphyromonas* and identification of *P. levii* from among these species^a

<i>Porphyromonas</i> species	Mol% G+C	G6PDH and 6PGDH ^b	Major acid end products ^c	Major cellular fatty acids (%) ^d	Important phenotypic tests
<i>P. asaccharolytica</i> ^T	52–54	—	A, P, B, iB, iV	<i>i</i> -C _{15:0} (60–87)	α-Fucosidase
<i>P. cangingivalis</i>	55	+	A, B	<i>i</i> -C _{15:0} (32), <i>ai</i> -C _{15:0} (12)	Catalase
<i>P. canoris</i>	49–51	+	A, P, iV, S	<i>i</i> -C _{15:0} (37), 3-OH, <i>i</i> -C _{17:0} (12)	Chymotrypsin, β-galactosidase, <i>N</i> -acetyl-β-glucosaminidase
<i>P. cansulci</i>	49–51	—	A, P, B, iV, S	<i>i</i> -C _{15:0} (49), C _{16:0} (12)	Catalase
<i>P. circumdentaria</i>	40–42	—	A, B, iV, S	<i>i</i> -C _{15:0} (56), C _{16:0} (11)	Catalase
<i>P. crevioricanis</i>	44–45	—	A, P, iV(S)	ND	HA ^e activity
<i>P. endodontalis</i>	49–51	—	A, B	<i>i</i> -C _{15:0} (30–43) 3-OH, <i>i</i> -C _{17:0} (20–30)	Indole produced; negative (most tests) UV fluorescence colonies on blood agar
<i>P. gingivalis</i>	47–50	—	A, B, iV, Pa	<i>i</i> -C _{15:0} (16–56) <i>ai</i> -C _{15:0} (5–21), 3-OH, <i>i</i> -C _{17:0} (30–34)	HA activity Cysteine proteinase
<i>P. gingivicanis</i>	41–42	—	A, B, iV	ND	
<i>P. levii</i>	46–48	V	A, B	<i>i</i> -C _{15:0} (22–32), <i>ai</i> -C _{15:0} (7–35)	Acid from: glucose and lactose, gelatin (liquified)
<i>P. macacae</i>	42–45	V	PA, B, iV, S, Pa	<i>i</i> -C _{15:0} (13–42), <i>ai</i> -C _{15:0} (25–30)	Acid from glucose, lactose and mannose; lipase, proteinase, α-galactosidase

^a Data compiled from references 1, 4, 7–11, 19, 27, 30, 39, and 41.^b G6PDH, glucose-6-phosphate dehydrogenase; 6PGDH, 6-phosphogluconate dehydrogenase; V, present in some strains.^c Acid end products (concentrations >10² M are considered significant): A, acetic; P, propionic; nB, *n*-butyric; iV, isovaleric; S, succinic acids; Pa, phenylacetic acid. Acids in parenthesis are present in some strains as major acid end products.^d *i*-C_{15:0}, 13-methyl-tetradecanoic acid; *ai*-C_{15:0}, 12-methyl-tetradecanoic acid; 3-OH-*i*-C_{17:0}, 3-hydroxy-15-methylhexadecanoic acid; ND, not determined.^e HA, hemagglutinin.

lactose are weakly fermented. Most other commonly occurring sugars such as arabinose, cellobiose, maltose, melezitose, melibiose, raffinose, rhamnose, ribose, salicin, sucrose, trehalose, and xylose are not fermented. Growth is markedly af-

fected by the presence of protein hydrolysates such as trypticase, proteose peptone, and yeast extract. Some amino acids such as asparagine, tryptophan, and phenylalanine and glutamine are utilized.

Major fermentation products from BM or PYG medium are *n*-butyric and acetic acids; lower levels of propionic, isobutyric, isovaleric, and succinic acids are also produced. Indole is not produced. Nitrate is not reduced to nitrite. Starch and esculin are not hydrolyzed. Malate and glutamate dehydrogenases are present; some strains possess glucose-6-phosphate and 6-phosphogluconate dehydrogenase.

The principal respiratory quinones are menaquinones. Both nonhydroxylated and 3-hydroxylated fatty acids are present. The nonhydroxylated fatty acids are composed of predominantly *iso*-methyl branched types, with *i*-C_{15:0} acid predominating.

The DNA base compositions ranges between 46 and 48 mol% G+C.

The type strain is strain ATCC 29147.

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FIG. 1. Unrooted phylogenetic tree based on 16S rRNA sequences showing the placement of *B. levii* within the genus *Porphyromonas*.

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