NOTES

Proposal To Restrict the Genus *Bacteroides* (Castellani and Chalmers) to *Bacteroides fragilis* and Closely Related Species

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The genus *Bacteroides* (Castellani and Chalmers) as presently constituted is phenotypically and phylogenetically extremely heterogeneous. However, biochemical, chemical, and molecular biological data indicate that *Bacteroides fragilis* (the type species) and related species form a coherent taxonomic group. Therefore, we formally propose that the genus *Bacteroides* be restricted to the *B. fragilis* group of species, and the description of the genus is emended accordingly.

It is now well recognized that the taxonomy of the genus *Bacteroides* is unsatisfactory and that the genus is in need of revision (see reference 5 for a review). As defined in *Bergey's Manual of Systematic Bacteriology* (8), the genus comprises a heterogeneous collection of obligately anaerobic, gram-negative, nonsporing, rod-shaped bacteria. More than 50 species are currently recognized on the Approved Lists of Bacterial Names (15). These species exhibit a variety of cellular morphologies and are biochemically and physiologically extremely heterogeneous (2, 16, 19, 26).

The application of biochemical, chemical, and, more recently, molecular biological techniques has done much to clarify the inter- and intragenic structure of *Bacteroides*. On the basis of biochemical and chemical criteria there is now good evidence that the genus should be restricted to the type species, *Bacteroides fragilis*, and closely related organisms (5). These closely related organisms include *Bacteroides caccae*, *Bacteroides distasonis*, *Bacteroides eggerthii*, *Bacteroides merdae*, *Bacteroides ovatus*, *Bacteroides stercoris*, *Bacteroides thetaiotaomicron*, *Bacteroides uniformis*, and *Bacteroides vulgatus*. The organisms of the "*B. fragilis* group" have a relatively narrow guanine-plus-cytosine range (ca. 40 to 48 mol%) and are biochemically homogeneous (8, 10, 22). *B. fragilis* and related species are saccharolytic and produce acetic and succinic acids as major metabolic end products of glucose metabolism (8). They differ significantly from other *Bacteroides* species in possessing enzymes of the hexose monophosphate shunt-pentose phosphate pathway (5, 22). *B. fragilis* and related species also possess sphingolipids, predominantly methyl branched long-chain fatty acids, and menaquinones as the sole respiratory quinones (5, 22). On the basis of these criteria several species have now been excluded from the genus and have been given separate generic status. Examples include *Anaerorhabdus* for *Bacteroides furcosus* (23); *Megamonas* for *Bacteroides hypermegas* (20); *Mitsuokella* for *Bacteroides multiacidus* (21); *Porphyromonas* for *Bacteroides asaccharolyticus*, *Bacteroides endodontalis*, and *Bacteroides gingivalis* (24); *Rikenella* for *Bacteroides microfus* (6); *Sebalidella* for *Bacteroides termiditis* (3); and *Tissierella* for *Bacteroides praeacutus* (4). Ribosomal ribo-

nucleic acid studies have also revealed considerable heterogeneity within the genus *Bacteroides* (11, 17, 18, 25). For example, 16S ribosomal ribonucleic acid cataloging studies have led to the reclassification of *Bacteroides amylophilus* in a new genus, *Ruminobacter* (25). Ribosomal ribonucleic acid-deoxyribonucleic acid homology studies (11) have also demonstrated that *B. fragilis* and related species form a phylogenetically coherent group distinct from other *Bacteroides* species, consistent with chemotaxonomic evidence (5, 22).

We have suggested on several occasions that the genus *Bacteroides* should be confined to the *B. fragilis* group of species (3–5, 24). However, despite the overwhelming phenotypic and phylogenetic evidence, workers have described a number of new species which bear little resemblance to *B. fragilis* and related species (e.g., *Bacteroides forsythus* [26] and *Bacteroides galacturonicus* and *Bacteroides pectinophilus* [9]). Thus, there is an urgent need to tighten the circumscription of the genus *Bacteroides* to prevent its continuing use as a repository for a varied collection of obligately anaerobic, gram-negative, nonsporing, rod-shaped bacteria. Therefore, we formally propose that the genus *Bacteroides* be restricted to *B. fragilis* and closely related species and emend the description of the genus accordingly.

Emended description of the genus *Bacteroides* (Castellani and Chalmers). Gram-negative, obligately anaerobic, non-sporeforming, nonmotile, rod-shaped cells. Cells are approximately 0.5 to 1.3 by 1.6 to 11 μ m. Chemoorganotrophic. Saccharoclastic. Major end products of glucose metabolism are acetic and succinic acids; lower levels of other acids may be produced. Weakly proteolytic. Grows but not always stimulated in the presence of 20% bile. Esculin is hydrolyzed. Nitrate is not reduced to nitrite. Indole variable. Malate dehydrogenase, glutamate dehydrogenase, glucose-6-phosphate dehydrogenase, and 6-phosphogluconate dehydrogenase are present. Cell wall peptidoglycan contains meso-diaminopimelic acid as the diamino acid. The principal respiratory quinones are menaquinones with 10 isoprene units or 11 isoprene units or both. Sphingolipids are produced. Both nonhydroxylated and 3-hydroxylated long-chain fatty acids are present. The nonhydroxylated acids are predominantly of the straight-chain saturated, anteiso- and iso-methyl branched-chain types. The deoxyribonucleic acid

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TABLE 1. Outline of the current taxonomic positions of *Bacteroides* species and related taxa

Species	Taxonomic status and/or comment	Reference(s)
Species currently designated <i>Bacteroides</i>		
<i>B. caccae</i> , <i>B. distasonis</i> , <i>B. eggerthii</i> , <i>B. fragilis</i> , <i>B. merdae</i> , <i>B. ovatus</i> , <i>B. stercoris</i> , <i>B.</i> <i>thetaiotaomicron</i> , <i>B. uniformis</i> , <i>B. vulgatus</i>	<i>Bacteroides</i> (emended definition)	
<i>B. bivius</i> , <i>B. buccae</i> , <i>B. buccalis</i> , <i>B. corporis</i> , <i>B. denticola</i> , <i>B. disiens</i> , <i>B. intermedius</i> , <i>B. heparinolyticus</i> , <i>B. loescheii</i> , <i>B.</i> <i>melaninogenicus</i> , <i>B. oralis</i> , <i>B. oris</i> , <i>B. oulorum</i> , <i>B. ruminicola</i> , <i>B. veroralis</i> , <i>B. zoogloeiformans</i>	<i>B. melaninogenicus</i> - <i>B. oralis</i> group; worthy of separate generic status	5, 15, 22
<i>B. levii</i> , <i>B. macacae</i> , <i>B. salivus</i>	Not <i>Bacteroides</i> ; possibly related to <i>Porphyromonas</i>	5, 13, 22
<i>B. ureolyticus</i> , <i>B. gracilis</i>	Not <i>Bacteroides</i> ; possibly related to <i>Campylobacter</i> or <i>Wolinella</i>	17
<i>B. capillosus</i>	Not <i>Bacteroides</i> ; generic position uncertain	5, 22
<i>B. cellulosolvens</i>	Not <i>Bacteroides</i> ; generic position uncertain	16
<i>B. coagulans</i>	Not <i>Bacteroides</i> ; generic position uncertain	5, 22
<i>B. forsythus</i>	Not <i>Bacteroides</i> ; generic position uncertain	26
<i>B. galacturonicus</i>	Not <i>Bacteroides</i> ; generic position uncertain	9
<i>B. helcogenes</i>	Not <i>Bacteroides</i> ; generic position uncertain	1
<i>B. nodosus</i>	Not <i>Bacteroides</i> ; generic position uncertain	5, 22
<i>B. pectinophilus</i>	Not <i>Bacteroides</i> ; generic position uncertain	9
<i>B. pneumosintes</i>	Not <i>Bacteroides</i> ; generic position uncertain	5, 22
<i>B. polypragmatus</i>	Not <i>Bacteroides</i> ; generic position uncertain	15
<i>B. putredinis</i>	Not <i>Bacteroides</i> ; generic position uncertain	5, 7, 22
<i>B. pyogenes</i>	Not <i>Bacteroides</i> ; generic position uncertain	1
<i>B. splanchnicus</i>	Not <i>Bacteroides</i> ; generic position uncertain	7, 22
<i>B. suis</i>	Not <i>Bacteroides</i> ; generic position uncertain	1
<i>B. tectum</i>	Not <i>Bacteroides</i> ; generic position uncertain	12
<i>B. xylanolyticus</i>	Not <i>Bacteroides</i> ; generic position uncertain	19
New genera for reclassified species		
<i>Anaerorhabdus</i>	Formerly <i>B. furcosus</i>	23
<i>Fibrobacter</i>	Formerly <i>B. succinogenes</i>	14
<i>Megamonas</i>	Formerly <i>B. hypermegas</i>	20
<i>Mitsuokella</i>	Formerly <i>B. multiacidus</i>	21
<i>Porphyromonas</i>	Formerly <i>B. asaccharolyticus</i> , <i>B. endodontalis</i> , and <i>B. gingivalis</i>	5, 22, 24
<i>Rikenella</i>	Formerly <i>B. microfus</i>	6
<i>Ruminobacter</i>	Formerly <i>B. amylophilus</i>	25
<i>Sebaldella</i>	Formerly <i>B. termiditis</i>	3
<i>Tissierella</i>	Formerly <i>B. praeacutus</i>	4

base composition ranges between 39 and 48 mol% guanine plus cytosine.

The type species is *B. fragilis*. Other currently described species which conform to the emended description include *B. caccae*, *B. distasonis*, *B. eggerthii*, *B. merdae*, *B. ovatus*, *B. stercoris*, *B. thetaiotaomicron*, *B. uniformis*, and *B. vulgatus*. *Bacteroides splanchnicus* shares a number of characteristics with *B. fragilis* and related species and is often regarded as a member of this group. However, *B. splanchnicus* differs from *B. fragilis* and related species in a number of important biochemical and chemical characteristics and should not be considered a member of the redefined genus (5). Ribosomal ribonucleic acid-deoxyribonucleic acid homology studies also have demonstrated that *B. splanchnicus* is phylogenetically distinct from *B. fragilis* and related species (11). Other validly described *Bacteroides* species which do not conform to the emended generic description and require further study and reclassification are listed in Table 1.

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