

**REVIEW ARTICLE**

Update on the Taxonomy of Clinically Important Anaerobic Bacteria

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임상적으로 중요한 무산소성 세균의 분류 업데이트

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Update**ABSTRACT**

The taxonomy of bacteria in the field of clinical microbiology is in a state of constant flux. A large-scale revamping of the classification and nomenclature of anaerobic bacteria has taken place over the past few decades, mainly due to advances in molecular techniques such as 16S rRNA and whole genome sequencing (WGS). New genera and species have been added, and existing genera and species have been reclassified or renamed. A major role of the clinical microbiological laboratories (CMLs) is the accurate identification (ID) and appropriate antimicrobial susceptibility testing (AST) for clinically important bacteria, and rapid reporting and communication of the same to the clinician. Taxonomic changes in anaerobic bacteria could potentially affect the choice of appropriate antimicrobial agents and the antimicrobial breakpoints to use. Furthermore, current taxonomy is important to prevent treatment failures of emerging pathogenic anaerobes with antimicrobial resistance. Therefore, CMLs should periodically update themselves on the changes in the taxonomy of anaerobic bacteria and suitably inform clinicians of these changes for optimum patient care. This article presents an update on the taxonomy of clinically important anaerobic bacteria, together with the previous names or synonyms. This taxonomy update can help guide antimicrobial therapy for anaerobic bacterial infections and prevent treatment failure and can be a useful tool for both CMLs and clinicians.

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INTRODUCTION

Anaerobic bacteria are considered as etiologic agents in a number of clinical diseases, including aspiration pneumonia, brain abscess, and intra-abdominal infections [1, 2]. As the number of immunocompromised patients has been increased, the clinical importance of anaerobic

bacterial infections has been extended [3]. The development of molecular technologies including 16S rDNA sequencing and genome sequencing has led to major changes among taxonomy of anaerobic bacteria, as well as aerobic bacteria, in the fields of clinical microbiology [4, 5]. Taxonomic changes potentially affect interpretation of susceptibility testing and reporting for anaerobes, and tracking of new names is important to work toward better improvement of patient treatment and disease management [6]. The Clinical and Laboratory Standards Institute (CLSI) provides the performance standards for AST stated with

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changed taxonomy in their updated guidelines, such as *Cutibacterium* (formerly *Propionibacterium*) *acnes* and *Clostridiodes* (formerly *Clostridium*) *difficile* [7]. According to CLSI guideline, clinical microbiological laboratory (CML) may not be necessary to perform the AST for all anaerobic bacteria isolated from culture, because their antimicrobial susceptibility patterns are often predictable. However, antimicrobial resistance in anaerobic infections has been associated with poor clinical outcome due to treatment failure. Recently, the importance of the treatment of *C. difficile* infection has increased in both hospitals and the community, as emerging pathogen with high virulence and resistance of fluoroquinolones [8]. Furthermore, CLSI has published the data of cumulative AST for anaerobes, relatively limited on anaerobic organisms in spite of the clinical importance in guiding empiric therapy. CMLs have problems on identification (ID) of new and unusual species, such as *Actinotignum schaalii*, a newly recognized uropathogen with resistance of trimethoprim-sulfamethoxazole and ciprofloxacin, and history of treatment failure [9]. This article presents update on taxonomy of clinically

important anaerobic bacteria with previous names or synonyms. Current taxonomy is important to perform the accurate organism identification, and antimicrobial susceptibility testing in the aspect of emerging pathogens. The taxonomy update can help guide patient management and prevent treatment failures in both CMLs and clinicians.

MAIN ISSUE

1. Anaerobic Gram-positive cocci and other anaerobic cocci

The anaerobic gram-positive cocci (AGPC) are part of the commensal flora of humans and are also associated with a variety of human infections [10]. AGPC belongs to the *Firmicutes* phylum, and the taxonomy of AGPC has undergone extensive changes of new genera and species (Table 1). Most clinical isolates of AGPC were described in the genus of *Peptococcus* and *Peptostreptococcus*. In 1983, four *Peptococcus* species (*P. asaccharolyticus*, *P. indolicus*, *P. prevotii* and *P. magnus*) were transferred to the genus

Table 1. Taxonomic changes of anaerobic gram-positive cocci isolated from humans

Phylum and genus	Species or subspecies	Previous name(s) or synonym	References
<i>Firmicutes</i>			
<i>Anaerococcus</i> *	<i>A. hydrogenalis</i>	<i>Peptostreptococcus hydrogenalis</i>	[14]
	<i>A. lactolyticus</i>	<i>Peptostreptococcus lactolyticus</i>	[14]
	<i>A. octavius</i>	<i>Peptostreptococcus octavius</i>	[14]
	<i>A. prevotii</i>	<i>Peptostreptococcus prevotii</i>	[14]
	<i>A. tetradus</i>	<i>Peptostreptococcus tetradus</i>	[14]
	<i>A. vaginalis</i>	<i>Peptostreptococcus vaginalis</i>	[14]
<i>Anaerosphaera</i> *	<i>A. aminiphila</i>	New species	[15]
<i>Atopobium</i> *	<i>A. parvulum</i>	<i>Streptococcus parvulus</i>	[17]
<i>Blautia</i> *	<i>B. producta</i>	<i>Peptostreptococcus productus</i> , <i>Ruminococcus productus</i>	[18]
<i>Fingoldia</i> *	<i>F. magna</i>	<i>Peptostreptococcus magnus</i>	[12]
<i>Gallicola</i> *	<i>G. barnesae</i>	<i>Peptostreptococcus barnesae</i>	[14]
<i>Murdochiella</i> *	<i>M. asaccharolytica</i>	New species	[16]
<i>Parvimonas</i> *	<i>P. micra</i>	<i>Peptostreptococcus micros</i> , <i>Micromonas micros</i>	[12, 13]
<i>Peptococcus</i>	<i>P. niger</i>		[11]
<i>Peptoniphilus</i> *	<i>P. asaccharolyticus</i>	<i>Peptostreptococcus asaccharolyticus</i>	[14]
	<i>P. harei</i>	<i>Peptostreptococcus harei</i>	[14]
	<i>P. indolicus</i>	<i>Peptostreptococcus indolicus</i>	[14]
	<i>P. ivorii</i>	<i>Peptostreptococcus ivorii</i>	[14]
	<i>P. lacrimalis</i>	<i>Peptostreptococcus lacrimalis</i>	[14]
<i>Peptostreptococcus</i>	<i>P. anaerobius</i>		[12]

*New genus.

Peptostreptococcus leaving *Peptococcus niger* as the single species in the genus *Peptococcus* [11]. Since 1998, the genus *Peptostreptococcus* has been divided into several novel genera. *Peptostreptococcus magnus* and *P. micros* were transferred to two new genera, *Finegoldia* and *Micromonas*, respectively [12]. The genus *Micromonas* has more recently been replaced by *Parvimonas* [13]. For the remained peptostreptococci, three new genera were proposed; *Peptoniphilus*, *Anaerococcus* and *Gallicola* [14]. In addition, two novel genera have been proposed; *Anaerosphaera*, with the type species *A. aminiphila*, most closely related to species of the genus *Peptoniphilus* [15] and *Murdochiella*, with the type species *M. asaccharolytica*, most closely related to *Parvimonas micra* and *Finegoldia magna* [16]. Among the other AGPC, *Streptococcus parvulus* has been changed to the genus *Atopobium*, as *A. parvulum* [17]; *Ruminococcus productus* (formerly *Peptostreptococcus productus*) was reclassified in a new genus *Blautia*, as *B. product* [18].

The anaerobic gram-negative cocci (AGNC), including the genera *Veillonella*, *Acidaminococcus*, *Megasphaera*, *Anaeroglobus*, and *Negativicoccus*, which was the recently described, have been classified in a single family, the *Acidaminococcaceae* [19]. Of the genus of *Veillonella*, *V. dispar*, *V. parvula* and *V. atypica*, have so far been isolated from human flora. Currently, the species *V. alcalescens* was abolished [20].

2. Anaerobic Gram-positive rods

The anaerobic gram-positive rods (AGPR) are widely distributed among the phylum *Actinobacteria* and *Firmicutes*. More recently, taxonomic reclassification of AGPR has undergone changes of new genera within these two phyla (Table 2).

1) Phylum *Actinobacteria*

The genera *Actinomyces*, *Actinobaculum*, *Actinotignum*, *Mobiluncus*, and *Varibaculum* belong to the family *Actinomycetaceae*. Important taxonomic reclassification has occurred within the genus *Actinomyces*, such

that *A. naeslundii* has been reclassified within the genus *Actinomyces*, which is previously considered “*A. naeslundii* genospecies 1”, and *Actinomyces oris* and *A. johnsonii* have been represented as novel species [21]. *Actinobaculum schaalii* and *A. urinale* of the genus *Actinobaculum* have been reclassified into the novel genus *Actinotignum* and *Actinotignum sanguinis* has been described as a novel species [22]. Recently, *Actinotignum schaalii* is recognized as an uropathogen with resistance of antimicrobials, but other *Actinotignum* species are less associated with human infections [9]. *Actinobaculum massiliense* and *A. suis* (previously named *Actinomyces massiliae* and *A. suis* are remained in the genus *Actinobaculum* [23, 24].

The genus *Propionibacterium* contains bacteria isolated from human sources and dairy products. Recently, important taxonomic reclassification has occurred in the cutaneous species of the genus. *P. acnes*, *P. granulosum*, *P. avidum*, and *P. humersii* have been reclassified into the novel genus *Cutibacterium*. *P. propionicum* has been reclassified as *Pseudopropionibacterium propionicum* [25]. *Bifidobacterium* and the closely related genera *Alloscardovia* [26], *Parascardovia*, and *Scardovia* [27] belong to the family *Bifidobacteriaceae*. There are currently 50 *Bifidobacterium* species, of which 11 species have been isolated from the human gut and oral cavity. *B. logum* including the former species *B. infantis* and *B. suis* is reclassified as three subspecies [28].

The genus *Atopobium* was proposed for *Lactobacillus minutus*, *Lactobacillus rimae* and *Streptococcus parvulus*, reclassified as *A. minutus*, *A. rimae* and *A. parvulum* [17]. The genus *Collinsella* has been proposed for *Eubacterium aerofaciens* with one species, *Collinsella aerofaciens* [29]. Other genus *Eggerthella* includes *E. lenta* and *E. sinensis*, and *E. hongkongensis* is now reclassified as the only member of the novel genus *Paraeggerthella* [30].

Table 2. Taxonomic changes of anaerobic gram-positive rods isolated from humans

Phylum and genus	Species or subspecies	Previous name(s) or synonym	References
<i>Actinobacteria</i>			
<i>Actinobaculum</i> *	<i>A. massiliense</i>	<i>Actinomyces massiliae</i>	[23]
	<i>A. suis</i>	<i>Actinomyces suis</i>	[24]
<i>Actinomyces</i>	<i>A. johnsonii</i>	New species, <i>A. naeslundii</i> genospecies WVA 963	[21]
	<i>A. naeslundii</i>	<i>A. naeslundii</i> genospecies 1	[21]
	<i>A. oris</i>	New species, <i>A. naeslundii</i> genospecies 2	[21]
<i>Actinotignum</i> *	<i>A. sanguinis</i>	New species	[22]
	<i>A. schaalii</i>	<i>Actinobaculum schaalii</i>	[22]
	<i>A. urinale</i>	<i>Actinobaculum urinale</i>	[22]
<i>Alloscardovia</i> *	<i>A. omnicoles</i>	New species	[26]
<i>Bifidobacterium</i>	<i>B. logum</i> subspecies <i>infantis</i>	New subspecies, <i>B. infantis</i>	[28]
	<i>B. logum</i> subspecies <i>longum</i>	New subspecies, <i>B. logum</i>	[28]
	<i>B. logum</i> subspecies <i>suis</i>	New subspecies, <i>B. suis</i>	[28]
<i>Collinsella</i> *	<i>C. aerofaciens</i>	<i>Eubacterium aerofaciens</i>	[29]
<i>Cutibacterium</i> *	<i>C. acnes</i>	<i>Propionibacterium acnes</i>	[25]
	<i>C. avidum</i>	<i>Propionibacterium avidum</i>	[25]
	<i>C. granulorum</i>	<i>Propionibacterium granulorum</i>	[25]
	<i>C. humersii</i>	<i>Propionibacterium humersii</i>	[25]
<i>Paraeggerthella</i> *	<i>P. hongkongensis</i>	<i>Eggerthella hongkongensis</i>	[30]
<i>Parascardovia</i> *	<i>P. denticola</i>	<i>Bifidobacterium denticolens</i>	[27]
<i>Pseudopropionibacterium</i> *	<i>P. propionicum</i>	<i>Propionibacterium propionicum</i>	[25]
<i>Scardovia</i> *	<i>S. inopinata</i>	<i>Bifidobacterium inopinatum</i>	[27]
<i>Firmicutes</i>			
<i>Anaerostipes</i> *	<i>A. hadrus</i>	<i>Eubacterium hadrum</i>	[32]
<i>Atopobium</i>	<i>A. minutus</i>	<i>Lactobacillus minutus</i>	[17]
	<i>A. rimae</i>	<i>Lactobacillus rimae</i>	[17]
<i>Clostridioides</i> *	<i>C. difficile</i>	<i>Clostridium difficile</i>	[34]
<i>Clostridium</i>	<i>C. maximum</i>	<i>Sarcina maxima</i>	[31]
	<i>C. moniliforme</i>	<i>Eubacterium moniliforme</i>	[31]
	<i>C. tarantellae</i>	<i>Eubacterium tarantellae</i>	[31]
	<i>C. ventriculi</i>	<i>Sarcina ventriculi</i>	[31]
<i>Dorea</i>	<i>D. formicigenerans</i>	<i>Eubacterium formicigenerans</i>	[33]
<i>Eubacterium</i>	<i>E. sulci</i>	<i>Fusobacterium sulci</i>	[55]
<i>Filifactor</i>	<i>F. alocis</i>	<i>Fusobacterium alocis</i>	[55]
<i>Hathewayia</i> *	<i>H. histolytica</i>	<i>Clostridium histolyticum</i>	[31]
	<i>H. limosa</i>	<i>Clostridium limosum</i>	[31]
	<i>H. proteolytica</i>	<i>Clostridium proteolyticum</i>	[31]
<i>Hungatella</i> *	<i>H. hathewayi</i>	<i>Clostridium hathewayi</i>	[37]
<i>Paeniclostridium</i> *	<i>P. sordellii</i>	<i>Clostridium sordellii</i>	[36]
<i>Paraclostridium</i> *	<i>P. bifementans</i>	<i>Clostridium bifementans</i>	[36]
<i>Terrisporobacte</i> *	<i>T. glycolicus</i>	<i>Clostridium glycolicum</i>	[35]

*New genus.

2) Phylum Firmicutes

The genus *Lactobacillus* belongs to the order *Lactobacillales* and family *Lactobacillaceae*. Although numerous others have been assigned to other genera, the phylogenetic relationship between the diverse species is complicated and poorly defined not yet.

The genus *Eubacterium* is phylogenetically diverse, and many *Eubacterium* species, which have been assigned to other genera, are now widely distributed

within the phylum *Firmicutes*. *Eubacterium moniliforme* and *E. tarantellae* was reclassified to the genus *Clostridium* as *C. moniliforme* and *C. tarantellae*, and additionally *Sarcina maxima* and *S. ventriculi* was reclassified as *Clostridium maximum* and *C. ventriculi* [31]. The family *Lachnospiraceae* includes a number of former members of the genus *Eubacterium*. *Eubacterium hadrum* was reclassified as *Anaerostipes hadrus*, *E. formicigenerans* as *Dorea formicigenerans* [32, 33].

Among the genus *Clostridium*, *Clostridium difficile* and *C. mangenotii* were reclassified to the new genus *Clostridioides*, as *Clostridioides difficile* and *Clostridioides mangenotii* [34]. *C. glycolicum* was reclassified to the new genus *Terrisporobacte*, also changed to *T. glycolicus* [35]; *C. bifementans*, and *C. sordellii* were reclassified to the new genus *Paracllostridium* and *Paeniclostridium*, respectively [36]; *C. hathewayi* was reclassified to *Hungatella hathewayi* [37]; *Clostridium histolyticum*, *C. limosum* and *C. proteolyticum* were reclassified to the new genus *Hathewayia* as *H. histolytica*, *H. limosa* and *H. proteolytica* [31].

3. Anaerobic Gram-negative rods

Most of anaerobic gram-negative rods (AGNR) belong to the phylum *Bacteroidetes*, including the families *Bacteroidaceae*, *Porphyromonadaceae*, *Prevotellaceae*, and *Rikenellaceae*, and to the phylum *Fusobacteria* including the families *Fusobacteriaceae* and *Leptotrichiaceae*. The taxonomic changes have occurred within the phylum *Bacteroidetes*, especially those of the genus *Bacteroides*; new species have been described and some species have been transferred to other genera, since 2006 (Table 3).

1) *Bacteroides* and *Parabacteroides*

The genus *Bacteroides*, consisting of saccharolytic, bile-resistant, and nonpigmented species, is limited to species within the *Bacteroides fragilis* group, which now more than 20 species. The other species within the *B. fragilis* group are more resistant to many antimicrobials than *B. fragilis* and exclusion of the more resistant species in a published data of susceptibility may provide misleading results [38]. Some former *Bacteroides* species have been reclassified in the genus *Prevotella* and *Porphyromonas* [39, 40]. The genus *ParaBacteroides* consists of three former *Bacteroides* species, which are *P. distasonis*, *P. goldsteinii*, and *P. merdae*, and in addition, *P. gordonii* and *P. johnsonii* [41-43]. The latest new species is *P. chongii*, isolated from blood of a patient with peritonitis [44].

2) *Prevotella* and *Porphyromonas*

The genus *Prevotella* consists of moderately saccharolytic, bile-sensitive, predominantly oral species of formerly classified in the genus *Bacteroides* [39]. Novel *Prevotella* species, *P. micans* and *P. nanceiensis*, have been isolated not only from the oral cavity, but also from other sites of the body [45, 46]. The nonpigmented former *Mitsuokella dentalis* and *Hallella seregens*, which are associated with endodontic and other oral infections, have been reclassified as *Prevotella dentalis* [47].

The genus *Porphyromonas* consists of asaccharolytic, pigmented species of formerly classified in the genus *Bacteroides* [40]. Among *Porphyromonas* species which are frequently detected in humans, *P. gingivalis* and *P. endodontalis* (formerly *Bacteroides gingivalis* and *B. endodontalis*) are closely related to the acute symptoms in endodontic infections [48]. The newly described species of human origin are *P. pasteri*, isolated from human saliva [49], and *P. pogonae* isolated from clinical specimens [50].

3) *Fusobacterium*

Based on the 16S-23S rDNA internal transcribed spacer regions (ITS), *Fusobacterium* species were composed of three phylogenetic clusters: the first cluster (all nonoral) included *F. mortiferum*, *F. varium*, and *F. ulcerans*; the second cluster (all oral) contained *F. nucleatum* subspecies, *F. naviforme*, *F. simiae*, and *F. periodonticum*; the third cluster (all invasive potential) included *F. necrophorum* subspecies and *F. gonidiaformans* [51]. *F. nucleatum*, the most commonly encountered in oral infection, is very heterogenous and currently classified as four subspecies including subsp. *nucleatum*, *polymorph*, *vincentii*, and *animalis*. *F. nucleatum* subspecies *fusiform* is a later synonym of subspecies *vincentii* [52]. In more recent, analyses using the genome sequences strongly suggest that four *F. nucleatum* subspecies should be reclassified as *Fusobacterium* species [53]. *Fusobacterium equinum*, a new species that is phenotypically similar to *F. necrophorum*, has been described from the normal oral cavity

Table 3. Taxonomic changes of anaerobic gram-negative rods isolated from humans

Phylum and genus	Species or subspecies	Previous name(s) or synonym	References
<i>Bacteroidetes</i>			
<i>Bacteroides</i>	<i>B. fragilis</i> group		[38]
<i>Parabacteroides</i>	<i>P. chongii</i>	New species	[44]
	<i>P. distasonis</i>	<i>Bacteroides distasonis</i>	[41]
	<i>P. godonii</i>	New species	[42]
	<i>P. goldsteinii</i>	<i>Bacteroides goldsteinii</i>	[41]
	<i>P. johnsonii</i>	New species	[43]
	<i>P. merdae</i>	<i>Bacteroides merdae</i>	[41]
<i>Porphyromonas</i>	<i>P. asaccharolytica</i>	<i>Bacteroides asaccharolyticus</i>	[40]
		<i>Bacteroides melaninogenica</i> subspecies <i>asaccharolytica</i>	[40]
	<i>P. endodontalis</i>	<i>Bacteroides endodontalis</i>	[40]
	<i>P. gingivalis</i>	<i>Bacteroides gingivalis</i>	[40]
	<i>P. pasteri</i>	New species	[49]
	<i>P. pogonae</i>	New species	[50]
<i>Prevotella</i>	<i>P. bivia</i>	<i>Bacteroides bivia</i>	[39]
	<i>P. buccae</i>	<i>Bacteroides buccae</i> , <i>Bacteroides ruminicola</i> subspecies <i>brevis</i>	[39]
		<i>Bacteroides capillus</i> , <i>Bacteroides pentosaceus</i>	
	<i>P. buccalis</i>	<i>Bacteroides buccalis</i>	[39]
	<i>P. corporis</i>	<i>Bacteroides corporis</i>	[39]
	<i>P. dentalis</i>	<i>Mitsuokella dentalis</i> , <i>Hallella seregens</i>	[47]
	<i>P. denticola</i>	<i>Bacteroides denticola</i>	[39]
	<i>P. disiens</i>	<i>Bacteroides disiens</i>	[39]
	<i>P. heparinolytica</i>	<i>Bacteroides heparinolyticus</i> , related to <i>B. fragilis</i> group	[39]
	<i>P. intermedia</i>	<i>Bacteroides intermedius</i>	[39]
		<i>Bacteroides melaninogenica</i> subspecies <i>intermedius</i>	
	<i>P. micans</i>	New species	[45]
	<i>P. loescheii</i>	<i>Bacteroides loescheii</i>	[39]
	<i>P. melaninogenica</i>	<i>Bacteroides melaninogenica</i>	[39]
		<i>Bacteroides melaninogenica</i> subspecies <i>melaninogenicus</i>	
	<i>P. nanceiensis</i>	New species	[46]
	<i>P. oralis</i>	<i>Bacteroides oralis</i>	[39]
	<i>P. oris</i>	<i>Bacteroides oris</i> , <i>Bacteroides ruminicola</i> subspecies <i>brevis</i>	[39]
	<i>P. oulorum</i>	<i>Bacteroides oulorum</i> , <i>Prevotella oulora</i>	[39]
	<i>P. veroalis</i>	<i>Bacteroides veroalis</i>	[39]
	<i>P. zooglyphiformans</i>	<i>Bacteroides zooglyphiformans</i> , related to <i>B. fragilis</i> group	[39]
<i>Fusobacteria</i>			
<i>Fusobacterium</i>	<i>F. equinum</i>	New species	[54]
	<i>F. nucleatum</i> subspecies <i>animalis</i>		[52]
	<i>F. nucleatum</i> subspecies <i>nucleatum</i>		[52]
	<i>F. nucleatum</i> subspecies <i>polymorphum</i>		[52]
	<i>F. nucleatum</i> subspecies <i>vincentii</i>	Later synonym of <i>F. nucleatum</i> subspecies <i>fusiform</i>	[52]
	<i>F. pseudoperiodonticum</i>	New species	[56]
<i>Dialister</i>	<i>D. invisus</i>	New species	[57]
	<i>D. pneumosintes</i>	<i>Bacteroides pneumosintes</i>	[57]
<i>Selenomonas*</i>	<i>S. sputigena</i>		[58]
<i>Proteobacteria</i>			
<i>Bilophila*</i>	<i>B. wadsworthia</i>	New species	[60]
<i>Sutterella*</i>	<i>S. wadsworthensis</i>	<i>Campylobacter gracilis</i> , <i>Bacteroides gracilis</i>	[59]

*New genus.

[54]. The *Fusobacterium alocis* and *F. sulci*, belonged to Clostridium cluster XI, have been reclassified as *Filifactor alocis* and *Eubacterium sulci*, respectively [55]. The latest proposed new species is *F. pseudope-*

riodonticum isolated from oral cavity based on the whole-genome analysis, most closely related to *F. periodonticum* [56].

4) Other anaerobic gram-negative rods

Among the genus *Dialister*, *D. invisus* and *D. pneumosintes* (formerly *Bacteroides pneumosintes*) isolated from the oral cavity [57]. *Selenomonas sputigena* of the genus *Selemonas*, as type species, is found in specimens from oral infections [58]. *Sutterella wadsworthensis*, new species of the genus *Sutterella*, formerly *Campylobacter gracilis* (*Bacteroides gracilis*), has been isolated from clinical specimens [59]. The genus *Bilophila* in the family *Desulfovibrionaceae* includes one human species, *Bilophila wadsworthia*, which is an important pathogen in humans [60].

CONCLUSION

Anaerobic bacteria are part of the commensal microbiota of humans in multiple sites of the body as opportunistic pathogens in many infections. The anaerobic taxonomy has undergone considerable changes over the years, mainly due to the increased widespread use of molecular technologies, including 16S rRNA sequencing and WGS. Existing genera and species have been reclassified or renamed and new genera and species have been added, resulting in changes of taxonomy. A subset of these changes is relevant to the field of anaerobic clinical microbiology, particularly in the context of accurate ID and appropriate AST, and epidemiology of emerging infections. The taxonomic updates are necessary to keep track of new names to aim at better description and recognition of the bacterium-disease associations. As the large percentage of the new species described are based on a single isolate of a new species, which was recovered from stool of a healthy person, taxonomic updates are necessary to determine the clinical importance. Furthermore, Current taxonomy is important to work toward better improvement of patient treatment and disease management, because antimicrobial resistance and misidentification of emerging pathogenic anaerobes, such as *A. schaalii* and *Cutibacterium difficile*, can be caused the inappropriate empiric therapy. Therefore,

CML should periodically update the taxonomic changes of anaerobic bacteria and properly inform clinicians of these changes. This article presents taxonomic changes of clinically important anaerobic bacteria. The update on taxonomy of anaerobic bacteria can help both CML and clinician guide empiric therapy for patient care and prevent treatment failure.

요약

임상미생물학 분야에서 세균의 분류는 끊임없이 변화하는 상태에 있다. 무산소성 세균의 대규모 분류와 명명법은 지난 수십 년 동안 발생되었는데, 주로 16S rRNA 염기서열 분석 및 전체 게놈 염기서열(WGS) 분석과 같은 분자 기술의 발전 때문이다. 새로운 균속과 균종이 추가되었고, 기존 균종과 균속은 재분류되었거나 재명명되었다. 임상미생물검사실의 주요 역할은 임상적으로 중요한 세균의 정확한 동정 및 적절한 감수성 시험, 그리고 신속한 보고 및 임상과의 의사 소통이다. 무산소성 세균의 분류학적 변화는 진단적으로 적절한 보고 항균제의 선택과 항균제 감수성 해석 기준의 적용에 잠정적으로 영향을 미칠 수 있다. 이는 신형 병원성 무산소성 세균의 항균제 내성 및 잘못된 동정은 환자 치료에 있어서 부적절한 경험적 치료를 유발할 수 있기 때문이다. 따라서, 임상미생물검사실은 주기적으로 무산소성 세균의 분류학적 변경 사항을 업데이트하고, 임상에게 이러한 변경 사항을 적절하게 알려야 한다. 이 논문에서는 임상적으로 중요한 무산소성 세균의 분류에 관한 업데이트를 제시하였고, 이전의 균명 또는 동의어를 함께 기술하였다. 무산소성 세균의 분류 업데이트는 무산소성 세균 감염에 대한 항균제 요법을 안내하고, 치료 실패를 예방하는데 임상미생물검사실과 임상 모두에게 도움이 될 수 있다.

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REFERENCES

1. Jousimies-Somer H, Summanen P, Citron DM, Baron EJ, Wexler HM, Finegold SM. Wadsworth-KTL Anaerobic Bacteriology Manual. 6th ed. Belmont: Star Publishing Co; 2002.
2. Nagy E. Anaerobic infections: update on treatment considerations. *Drugs*. 2010 May 7;70(7):841-58. <https://doi.org/10.2165/>

- 11534490-000000000-00000
3. Park Y, Lee Y, Kim M, Choi JY, Yong D, Jeong SH, et al. Recent trends of anaerobic bacteria isolated from clinical specimens and clinical characteristics of anaerobic bacteremia. *Infect Chemother.* 2009;41:216-223.
 4. Janda JM. Taxonomic update on proposed nomenclature and classification changes for bacteria of medical importance, 2015. *Diagn Microbiol Infect Dis.* 2016;86:123-127. <https://doi.org/10.1016/j.diagmicrobio.2016.06.021>
 5. Ramasamy D, Mishra AK, Lagier JC, Padhmanabhan R, Rossi M, Sentaosa E, et al. A polyphasic strategy incorporating genomic data for the taxonomic description of novel bacterial species. *Int J Syst Evol Microbiol.* 2014;64:384-391. <https://doi.org/10.1099/ijs.0.057091-0>
 6. Munson E. Moving targets of bacterial taxonomy revision: what are they and why should we care?. *Clin Microbiol Newsl.* 2020;42:111-120. <https://doi.org/10.1016/j.clinmicnews.2020.06.002>
 7. Clinical and Laboratory Standards Institute. Performance standards for antimicrobial susceptibility testing; 28th ed, M100. Wayne: Clinical and Laboratory Standards Institute; 2018.
 8. Kuijper EJ, Barbut F, Brazier JS, Kleinkauf N, Eckmanns T, Lambert ML, et al. Update of *Clostridium difficile* infection due to PCR ribotype 027 in Europe, 2008. *Euro Surveill.* 2008;13:18942.
 9. Lotte R, Lotte L, Ruimy R. *Actinotignum schaalii* (formerly *Actinobaculum schaalii*): a newly recognized pathogen-review of the literature. *Clin Microbiol Infect.* 2016;22:28-36. <https://doi.org/10.1016/j.cmi.2015.10.038>
 10. Murdoch DA. Gram-positive anaerobic cocci. *Clin Microbiol Rev.* 1998;11:81-120. <https://doi.org/10.1128/CMR.11.1.81>
 11. Ezaki T, Yamamoto N, Ninomiya K, Suzuki S, Yauuchi E. Transfer of *Peptococcus indolicus*, *Peptococcus asaccharolyticus*, *Peptococcus prevotii* and *Peptococcus magnus* to the genus *Peptostreptococcus* and proposal of *Peptostreptococcus tetradius* sp. nov. *Int J Syst Bacteriol.* 1983;33:683-698. <https://doi.org/10.1099/00207713-33-4-683>
 12. Murdoch DA, Shah HN. Reclassification of *Peptostreptococcus magnus* (Prevot 1933) Holdeman and Moore 1972 as *Fingoldia magna* comb. nov. and *Peptostreptococcus micros* (Prevot 1933) Smith 1957 as *Micromonas micros* comb. nov. *Anaerobe.* 1999;5:555-559. <https://doi.org/10.1006/anae.1999.0197>
 13. Tindall BJ, Euzéby JP. Proposal of *Parvimonas* gen. nov. and *Quatronicoccus* gen. nov. as replacements for the illegitimate, prokaryotic, generic names *Micromonas* Murdoch and Shah 2000 and *Quadricoccus* Maszenan et al. 2002, respectively. *Int J Syst Evol Microbiol.* 2006;56:2711-2713. <https://doi.org/10.1099/ijs.0.64338-0>
 14. Ezaki T, Kawamura Y, Li N, Li ZY, Zhao L, Shu S. Proposal of the genera *Anaerococcus* gen. nov., *Peptoniphilus* gen. nov. and *Gallicola* gen. nov. for members of the genus *Peptostreptococcus*. *Int J Syst Evol Microbiol.* 2001;51:1521-1528. <https://doi.org/10.1099/00207713-51-4-1521>
 15. Ueki A, Abe K, Suzuki D, Kaku N, Watanabe K, Ueki K. *Anaerospaera aminiphila* gen. nov., sp. nov., a glutamate-degrading, Gram-positive anaerobic coccus isolated from a methanogenic reactor treating cattle waste. *Int J Syst Evol Microbiol.* 2009;59:3161-3167. <https://doi.org/10.1099/ijs.0.011858-0>
 16. Ulger-Toprak N, Liu C, Summanen PH, Finegold SM. *Murdochiella asaccharolytica* gen. nov., sp. nov., a Gram-stain-positive, anaerobic coccus isolated from human wound specimens. *Int J Syst Evol Microbiol.* 2010;60:1013-1016. <https://doi.org/10.1099/ijs.0.015909-0>
 17. Collins MD, Wallbanks S. Comparative sequence analyses of the 16S rRNA genes of *Lactobacillus minutus*, *Lactobacillus rimae* and *Streptococcus parvulus*: proposal for the creation of a new genus *Atopobium* FEMS Microbiol Lett. 1992;74:235-240. <https://doi.org/10.1111/j.1574-6968.1992.tb05372.x>
 18. Liu C, Finegold SM, Song Y, Lawson PA. Reclassification of *Clostridium coccooides*, *Ruminococcus hansenii*, *Ruminococcus hydrogenotrophicus*, *Ruminococcus luti*, *Ruminococcus productus* and *Ruminococcus schinkii* as *Blautia coccooides* gen. nov., comb. nov., *Blautia hansenii* comb. nov., *Blautia hydrogenotrophica* comb. nov., *Blautia luti* comb. nov., *Blautia producta* comb. nov., *Blautia schinkii* comb. nov. and description of *Blautia wexlerae* sp. nov., isolated from human faeces. *Int J Syst Evol Microbiol.* 2008;58:1896-1902. <https://doi.org/10.1099/ijs.0.65208-0>
 19. Marchandin H, Teyssier C, Campos J, Jean-Pierre H, Roger F, Gay B, et al. *Negativicoccus succinicivorans* gen. nov., sp. nov., isolated from human clinical samples, emended description of the family *Veillonellaceae* and description of *Negativicutes* classis nov. in the bacterial phylum Firmicutes. *Int J Syst Evol Microbiol.* 2010;60:1271-1279. <https://doi.org/10.1099/ijs.0.013102-0>
 20. Marchandin H, Teyssier C, Siméon de Buochberg M, Jean-Pierre H, Carriere C, Jumas-Bilak E. Intra-chromosomal heterogeneity between the four 16S rRNA gene copies in the genus *Veillonella*: implications for phylogeny and taxonomy. *Microbiology (Reading).* 2003;149:1493-1501. <https://doi.org/10.1099/mic.0.26132-0>
 21. Henssge U, Do T, Radford DR, Gilbert SC, Clark D, Beighton D. Emended description of *Actinomyces naeslundii* and descriptions of *Actinomyces oris* sp. nov. and *Actinomyces johnsonii* sp. nov., previously identified as *Actinomyces naeslundii* genospecies 1, 2 and WVA 963. *Int J Syst Evol Microbiol.* 2009;59:509-516. <https://doi.org/10.1099/ijs.0.000950-0>
 22. Yassin AF, Spröer C, Pukall R, Sylvester M, Siering C, Schumann P. Dissection of the genus *Actinobaculum*: Reclassification of *Actinobaculum schaalii* Lawson et al. 1997 and *Actinobaculum urinale* Hall et al. 2003 as *Actinotignum schaalii* gen. nov., comb. nov. and *Actinotignum urinale* comb. nov., description of *Actinotignum sanguinis* sp. nov. and emended descriptions of the genus *Actinobaculum* and *Actinobaculum suis*: and re-examination of the culture deposited as *Actinobaculum massiliense* CCUG 47753T (= DSM 19118T), revealing that it does not represent a strain of this species. *Int J Syst Evol Microbiol.* 2015;65:615-624. <https://doi.org/10.1099/ijs.0.069294-0>
 23. Greub G, Raoult D. "*Actinobaculum massiliae*," a new species causing chronic urinary tract infection. *J Clin Microbiol.* 2002;40:3938-3941. <https://doi.org/10.1128/JCM.40.11.3938-3941.2002>
 24. Lawson PA, Falsen E, Akervall E, Vandamme P, Collins MD. Characterization of some *Actinomyces*-like isolates from human clinical specimens: reclassification of *Actinomyces suis* (Soltys and Spratling) as *Actinobaculum suis* comb. nov. and description of *Actinobaculum schaalii* sp. nov. *Int J Syst Bacteriol.* 1997;47:899-903. <https://doi.org/10.1099/00207713-47-3-899>

25. Scholz CFP, Kilian M. The natural history of cutaneous propionibacteria, and reclassification of selected species within the genus *Propionibacterium* to the proposed novel genera *Acidipropionibacterium* gen. nov., *Cutibacterium* gen. nov. and *Pseudopropionibacterium* gen. nov. Int J Syst Evol Microbiol. 2016;66:4422-4432. <https://doi.org/10.1099/ijsem.0.001367>
26. Huys G, Vancanneyt M, D'Haene K, Falsen E, Wauters G, Vandamme P. *Alloscardovia omnicoles* gen. nov., sp. nov., from human clinical samples. Int J Syst Evol Microbiol. 2007;57:1442-1446. <https://doi.org/10.1099/ijms.0.64812-0>
27. Jian W, Dong X. Transfer of *Bifidobacterium inopinatum* and *Bifidobacterium denticolens* to *Scardovia inopinata* gen. nov., comb. nov., and *Parascardovia denticolens* gen. nov., comb. nov., respectively. Int J Syst Evol Microbiol. 2002;52:809-812. <https://doi.org/10.1099/00207713-52-3-809>
28. Mattarelli P, Bonaparte C, Pot B, Biavati B. Proposal to reclassify the three biotypes of *Bifidobacterium longum* as three subspecies: *Bifidobacterium longum* subsp. *longum* subsp. nov., *Bifidobacterium longum* subsp. *infantis* comb. nov. and *Bifidobacterium longum* subsp. *suis* comb. nov. Int J Syst Evol Microbiol. 2008;58:767-772. <https://doi.org/10.1099/ijms.0.65319-0>
29. Kageyama A, Benno Y, Nakase T. Phylogenetic and phenotypic evidence for the transfer of *Eubacterium aerofaciens* to the genus *Collinsella* as *Collinsella aerofaciens* gen. nov., comb. nov. Int J Syst Bacteriol. 1999;49:557-565. <https://doi.org/10.1099/00207713-49-2-557>
30. Würdemann D, Tindall BJ, Pukall R, Lünsdorf H, Strömpl C, Namuth T, et al. *Gordonibacter pamelaiae* gen. nov., sp. nov., a new member of the *Coriobacteriaceae* isolated from a patient with Crohn's disease, and reclassification of *Eggerthella hongkongensis* Lau et al. 2006 as *Paraeggerthella hongkongensis* gen. nov., comb. nov. Int J Syst Evol Microbiol. 2009;59:1405-1415. <https://doi.org/10.1099/ijms.0.005900-0>
31. Lawson PA, Rainey FA. Proposal to restrict the genus *Clostridium* *Prazmowski* to *Clostridium butyricum* and related species. Int J Syst Evol Microbiol. 2016;66:1009-1016. <https://doi.org/10.1099/ijsem.0.000824>
32. Allen-Vercoe E, Daigneault M, White A, Panaccione R, Duncan SH, Flint HJ, et al. *Anaerostipes hadrus* comb. nov., a dominant species within the human colonic microbiota: reclassification of *Eubacterium hadrum* Moore et al. 1976. Anaerobe. 2012;18(5):523-529. <https://doi.org/10.1016/j.anaerobe.2012.09.002>
33. Taras D, Simmering R, Collins MD, Lawson PA, Blaut M. Reclassification of *Eubacterium formicigenerans* Holdeman and Moore 1974 as *Dorea formicigenerans* gen. nov., comb. nov., and description of *Dorea longicatena* sp. nov., isolated from human faeces. Int J Syst Evol Microbiol. 2002;52:423-428. <https://doi.org/10.1099/00207713-52-2-423>
34. Lawson PA, Citron DM, Tyrrell KL, Finegold SM. Reclassification of *Clostridium difficile* as *Clostridioides difficile* (Hall and O'Toole 1935) Prévot 1938. Anaerobe. 2016;40:95-99. <https://doi.org/10.1016/j.anaerobe.2016.06.008>
35. Gerritsen J, Fuentes S, Grievink W, van Niftrik L, Tindall BJ, Timmerman HM, et al. Characterization of *Romboutsia ilealis* gen. nov., sp. nov., isolated from the gastro-intestinal tract of a rat, and proposal for the reclassification of five closely related members of the genus *Clostridium* into the genera *Romboutsia* gen. nov., *Intestinibacter* gen. nov., *Terrisporobacter* gen. nov. and *Asaccharospora* gen. nov. Int J Syst Evol Microbiol. 2014;64:1600-1616. <https://doi.org/10.1099/ijms.0.059543-0>
36. Sasi Jyothsna TS, Tushar L, Sasikala C, Ramana CV. *Paraclostridium benzoelyticum* gen. nov., sp. nov., isolated from marine sediment and reclassification of *Clostridium bifermentans* as *Paraclostridium bifermentans* comb. nov. Proposal of a new genus *Paeniclostridium* gen. nov. to accommodate *Clostridium sor-dellii* and *Clostridium ghonii*. Int J Syst Evol Microbiol. 2016;66:1268-1274. <https://doi.org/10.1099/ijsem.0.000874>
37. Kaur S, Yawar M, Kumar PA, Suresh K. *Hungatella effluvii* gen. nov., sp. nov., an obligately anaerobic bacterium isolated from an effluent treatment plant, and reclassification of *Clostridium hathewayi* as *Hungatella hathewayi* gen. nov., comb. nov. Int J Syst Evol Microbiol. 2014;64:710-718. <https://doi.org/10.1099/ijms.0.056986-0>
38. Wexler HM. *Bacteroides*: the good, the bad, and the nitty-gritty. Clin Microbiol Rev. 2007;20:593-621. <https://doi.org/10.1128/CMR.00008-07>
39. Shah HN, Collins DM. *Prevotella*, a new genus to include *Bacteroides melaninogenicus* and related species formerly classified in the genus *Bacteroides*. Int J Syst Bacteriol. 1990;40:205-208. <https://doi.org/10.1099/00207713-40-2-205>
40. Shah HN, Collins MD. Proposal for reclassification of *Bacteroides asaccharolyticus*, *Bacteroides gingivalis*, and *Bacteroides endodontalis* in a new genus, *Porphyromonas*. Int J Syst Bacteriol. 1988;38:128-131. <https://doi.org/10.1099/00207713-38-1-128>
41. Sakamoto M, Benno Y. Reclassification of *Bacteroides distasonis*, *Bacteroides goldsteinii* and *Bacteroides merdae* as *ParaBacteroides distasonis* gen. nov., comb. nov., *ParaBacteroides goldsteinii* comb. nov. and *ParaBacteroides merdae* comb. nov. Int J Syst Evol Microbiol. 2006;56:1599-1605. <https://doi.org/10.1099/ijms.0.64192-0>
42. Sakamoto M, Suzuki N, Matsunaga N, Koshihara K, Seki M, Komiya H, et al. *ParaBacteroides gordonii* sp. nov., isolated from human blood cultures. Int J Syst Evol Microbiol. 2009;59:2843-2847. <https://doi.org/10.1099/ijms.0.010611-0>
43. Sakamoto M, Kitahara M, Benno Y. *ParaBacteroides johnsonii* sp. nov., isolated from human faeces. Int J Syst Evol Microbiol. 2007;57:293-296. <https://doi.org/10.1099/ijms.0.010611-0>
44. Kim H, Im WT, Kim M, Kim D, Seo YH, Yong D, et al. *ParaBacteroides chongii* sp. nov., isolated from blood of a patient with peritonitis. J Microbiol. 2018;56:722-726. <http://www.springerlink.com/content/120956>.
45. Downes J, Liu M, Kononen E, Wade WG. *Prevotella micans* sp. nov., isolated from the human oral cavity. Int J Syst Evol Microbiol. 2009;59:771-774. <https://doi.org/10.1099/ijms.0.002337-0>
46. Alauzet C, Mory F, Carlier JP, Marchandin H, Jumas-Bilak E, Lozniewski A. *Prevotella nanceiensis* sp. nov., isolated from human clinical samples. Int J Syst Evol Microbiol. 2007;57:2216-2220. <https://doi.org/10.1099/ijms.0.65173-0>
47. Willems A, Collins MD. 16S rRNA gene similarities indicate that *Hallella sergens* (Moore and Moore) and *Mitsuokella dentalis* (Haapsalo et al.) are genealogically highly related and are members of the genus *Prevotella*: emended description of the genus *Prevotella* (Shah and Collins) and description of *Prevotella dentalis* comb. Nov. Int J Syst Bacteriol. 1995;45:832-826. <https://doi.org/10.1099/00207713-45-3-832>

- i.org/10.1099/00207713-45-4-832
48. Haapasalo M. Black-pigmented gram-negative anaerobes in endodontic infections. *FEMS Immunol Med Microbiol.* 1993;6:213-217. <https://doi.org/10.1111/j.1574-695X.1993.tb00329.x>
 49. Sakamoto M, Li D, Shibata Y, Takeshita T, Yamashita Y, Ohkuma M. *Porphyromonas pasteri* sp. nov., isolated from human saliva. *Int J Syst Evol Microbiol.* 2015;65:2511-2515. <https://doi.org/10.1099/ijs.0.000294>
 50. Kawamura Y, Kuwabara S, Kania SA, Kato H, Hamagishi M, Fujiwara N, et al. *Porphyromonas pogonae* sp. nov., an anaerobic but low concentration oxygen adapted coccobacillus isolated from lizards (*Pogona vitticeps*) or human clinical specimens, and emended description of the genus *Porphyromonas* Shah and Collins 1988. *Syst Appl Microbiol.* 2015;38:104-109. <https://doi.org/10.1016/j.syapm.2014.11.004>
 51. Conrads G, Claros MC, Citron DM, Tyrrell KL, Merriam V, Goldstein EJC. 16S-23S rDNA internal transcribed spacer sequences for analysis of the phylogenetic relationships among species of the genus *Fusobacterium*. *Int J Syst Evol Microbiol.* 2002;52:493-499. <https://doi.org/10.1099/00207713-52-2-493>
 52. Kook JK, Park SN, Lim YK, Choi MH, Cho E, Kong SW, et al. *Fusobacterium nucleatum* subsp. *fusiforme* Gharbia and Shah 1992 is a later synonym of *Fusobacterium nucleatum* subsp. *vincentii* Dzink et al. 1990. *Curr Microbiol.* 2013;66:414-417. <https://doi.org/10.1007/s00284-012-0289-y>
 53. Kook JK, Park SN, Lim YK, Cho E, Jo E, Roh H, et al. Genome-Based Reclassification of *Fusobacterium nucleatum* Subspecies at the Species Level. *Curr Microbiol.* 2017;74:1137-1147. <https://doi.org/10.1007/s00284-017-1296-9>
 54. Dorsch M, Lovet DN, Bailey GD. *Fusobacterium equinum* sp. nov., from the oral cavity of horses. *Int J Syst Evol Microbiol.* 2001;51:1959-1963. <https://doi.org/10.1099/00207713-51-6-1959>
 55. Jalava J, Eerola E. Phylogenetic analysis of *Fusobacterium alocis* and *Fusobacterium sulci* based on 16S rRNA gene sequences: proposal of *Filifactor alocis* (Cato, Moore and Moore) comb. nov. and *Eubacterium sulci* (Cato, Moore and Moore) comb. nov. *Int J Syst Bacteriol.* 1999;49:1375-1379. <https://doi.org/10.1099/00207713-49-4-1375>
 56. Park SN, Lim YK, Shin JH, Kim HS, Jo E, Lee WP, et al. *Fusobacterium pseudoperiodonticum* sp. nov., isolated from the Human Oral Cavity. *Curr Microbiol.* 2019;76:659-665. <https://doi.org/10.1007/s00284-019-01675-y>
 57. Downes J, Munson M, Wade WG. *Dialister invisus* sp. nov., isolated from the human oral cavity. *Int J Syst Evol Microbiol.* 2003;53:1937-1940. <https://doi.org/10.1099/ijs.0.02640-0>
 58. Rôças IN, Siqueira JF Jr, Debelian GJ. Analysis of symptomatic and asymptomatic primary root canal infections in adult Norwegian patients. *J Endod.* 2011;37:1206-1212. <https://doi.org/10.1016/j.joen.2011.05.026>
 59. Wexler HM, Reeves D, Summanen PH, Molitoris E, McTeague M, Duncan J, et al. *Sutterella wadsworthensis* gen. nov., sp. nov., bile-resistant microaerophilic *Campylobacter gracilis*-like clinical isolates. *Int J Syst Bacteriol.* 1996;46:252-258. <https://doi.org/10.1099/00207713-46-1-252>
 60. Baron EJ. *Bilophila wadsworthia*: a unique Gram-negative anaerobic rod. *Anaerobe.* 1997;3:83-86. <https://doi.org/10.1006/anae.1997.0075>