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MINIREVIEW

Summary of Novel Bacterial Isolates Derived from Human Clinical Specimens and Nomenclature Revisions Published in 2018 and 2019

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ABSTRACT Knowledge of novel prokaryotic taxon discovery and nomenclature revisions is of importance to clinical microbiology laboratory practice, infectious disease epidemiology, and studies of microbial pathogenesis. Relative to bacterial isolates derived from human clinical specimens, we present an in-depth summary of novel taxonomic designations and revisions to prokaryotic taxonomy that were published in 2018 and 2019. Included are several changes pertinent to former designations of or within *Propionibacterium* spp., *Corynebacterium* spp., *Clostridium* spp., *Mycoplasma* spp., *Methylobacterium* spp., and *Enterobacteriaceae*. Future efforts to ascertain clinical relevance for many of these changes may be augmented by a document development committee that has been appointed by the Clinical and Laboratory Standards Institute.

KEYWORDS nomenclature, prokaryotes, taxonomy

The *Journal of Clinical Microbiology* continues its biennial commitment to the provision of microbial nomenclature changes for its readership. Most recent endeavors from this journal have focused on the fields of parasitology (1, 2), bacteriology (3), mycology (4), human and veterinary virology (5), and mycobacteriology (6). With respect to discovery of novel taxa and revisions to prokaryotic nomenclature, these often occur as aftermaths of human microbiome studies or advancements in technologies relative to microbial genome sequencing, some of which are now commonly implemented in the routine clinical microbiology laboratory. While some have questioned the clinical relevance, and even necessity, of several taxonomic decisions that have been rendered within the past decade (7, 8), one cannot refute the importance of having access to these data in order to make informed decisions. Knowledge of current-status taxonomic nomenclature has the capability of influencing antimicrobial susceptibility testing options, performance, and reporting (9, 10); impacting daily operations of the clinical microbiology laboratory (in the context of compliance with laboratory accreditation requirements) (11); and clarifying roles of microbe pathogenicity (12) and epidemiology (13).

An increasing number of resources attempting to compile prokaryotic taxonomic changes have become available over the past 2 decades (14–21), including compendia from *Journal of Clinical Microbiology* (3, 22, 23). Approaches to performing this task have slightly diverged in recent years. Recent reports from Janda (20, 21) have restricted inclusion to novel taxa characterized by at least five strains (or taxa with substantial clinical correlation) and to taxonomic revisions having major clinical significance. Similarly, *Journal of Clinical Microbiology* compendia are based on isolates derived from human sources; however, these summaries are designed to cast a broader net with the thought that future case reports can validate the clinical significance of these taxa. We

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hereby add to these data by summarizing novel prokaryotic taxa and bacterial nomenclature revisions published in the years 2018 and 2019. Nomenclature designations of presented organisms have been accepted by the *International Journal of Systematic and Evolutionary Microbiology* (IJSEM).

METHODS

Validly published novel and revised taxa pertinent to prokaryotic species must meet one of two requirements: (i) publication of an original investigation in IJSEM or (ii) publication of a study in an alternative journal, with later inclusion on an approved list in IJSEM. Journals that have published studies providing an effective description of validly named novel taxa which may be relevant to the practice of clinical microbiology include *Antonie Van Leeuwenhoek*, *Applied and Environmental Microbiology*, *Current Microbiology*, *Frontiers in Microbiology*, *Journal of Clinical Microbiology*, *Journal of Microbiology*, *Microbiology and Immunology*, *MicrobiologyOpen*, *New Microbes and New Infections*, *Research in Microbiology*, and *Standards in Genomic Sciences*. Journals that have recently published studies reflecting revisions in prokaryotic taxonomy include *F1000Research*, *Frontiers in Microbiology*, *Genes*, and *Systematic and Applied Microbiology*. Six times per year, *IJSEM* publishes papers entitled "List of new names and new combinations previously effectively, but not validly, published" (example provided in reference 24). To be considered for inclusion on this approved list, authors must submit a copy of the published article to the editorial office of IJSEM for confirmation that all conditions for valid publication have been met. In addition, type strains are to be deposited in recognized culture collections in two separate countries. Taxa on these approved lists may be subject to reclassification on the basis of a synonym designation or transfer to another genus. In this paper, accepted taxa that were previously published outside IJSEM are noted.

All issues of IJSEM published from January 2018 through December 2019 were searched for original articles describing new species taxonomy or accepted changes in taxonomic nomenclature. This audit was further filtered by organisms recovered from human sources. When an initial organism reservoir could not be ascertained, PubMed primary literature searches (U.S. National Library of Medicine and the National Institutes of Health) of the novel or revised taxon attempted to index subsequent case reports for further investigation; several of these case reports are referenced throughout this paper. A number of IJSEM publications simply identified isolates as being derived from a specific specimen source (including sterile body sites) but did not provide contextual clinical data. Therefore, in these scenarios (including a number of novel taxa derived from blood culture), the clinical significance of these taxa was interpreted as "not established" (examples are provided in reference 25–29). (By way of PubMed primary literature searches, attempts were also made to investigate the uncertain clinical significance of previously reported novel and revised taxa [3].) Additional studies may be necessary to characterize the ultimate clinical significance of novel taxa (30).

Twice per year, IJSEM publishes papers entitled "Notification of changes in taxonomic opinion previously published outside the IJSEM." The journal publicizes these changes in taxonomic opinion simply as a service to bacteriology, rather than statements of validly published or approved taxonomy. One example of taxonomic opinion (31) will be presented later in this report, along with antecedent primary referenced literature (32). This entry is included with the goal of revisiting it in future *Journal of Clinical Microbiology* compendia either to ascertain true clinical significance or to determine if official taxonomic status has been granted.

RESULTS AND DISCUSSION

A compilation of novel taxa recovered from human sources stratified by Gram reaction, cellular morphology, and oxygen growth requirement is presented in Table 1. Correct and updated *Enterobacterales* family designations (33) for selected taxa are concomitantly provided. It should be noted that within Table 1, a subset of biochemical testing results was derived from methods that are potentially antiquated, time-

TABLE 1 New bacterial species recovered from human clinical material reported from January 2018 through December 2019[a]

Group and scientific name	Family	Source	Clinical relevance	Growth characteristics	Reference(s)
Gram-positive cocci					
Micrococcus caseolyticus subsp. *hominis* subsp. nov.	*Staphylococcaceae*	Variety of human clinical material	Acute vaginitis/cervicitis; chronic vulvitis; wound following knee surgery	Gram-positive spherical aerobic cocci occurring in pairs, clusters; nonmotile; non-spore forming; colonies on TSA are circular, flat, smooth, yellow-orange pigmented; grows in presence of 7.5% NaCl; catalase, oxidase, PYR, nitrate, VP test positive; susceptible to furazolidone (100 μg); resistant to novobiocin (5 μg) and bacitracin (10 IU)	34[b]
Micrococcus goetzii sp. nov.	*Staphylococcaceae*	Swabs, nail, mycosis	Isolated from human clinical material—swabs, nail, mycosis	Gram-positive spherical aerobic cocci occurring singly and in clusters; non-spore forming, nonmotile; colonies on TSA are circular, entire, nonpigmented; grows in presence of 7.5% NaCl; catalase, oxidase, PYR, nitrate, VP test positive; hydrolyzes gelatin; susceptibility as for above species	34[b]
Micrococcus epidermidis sp. nov.	*Staphylococcaceae*	Swab, mycosis	Isolated from human clinical material—swab, mycosis	Gram-positive, aerobic, spherical cocci occurring in pairs, tetrads; non-spore forming, nonmotile; circular, nonpigmented colonies on TSA; grows in presence of 7.5% NaCl; catalase, oxidase, PYR, nitrate, VP test positive; hydrolyzes gelatin; susceptibility as for above species	34[b]
Micrococcus bohemicus sp. nov.	*Staphylococcaceae*	Wound	Isolated from human clinical material—traumatic knee wound	Gram-positive, aerobic, spherical cocci occurring in pairs, tetrads; non-spore forming, nonmotile; circular, nonpigmented colonies on TSA; grows in presence of 7.5% NaCl; catalase, oxidase, PYR, nitrate, VP test positive; hydrolyzes gelatin; susceptibility as for above species	34[b]
Staphylococcus cornubiensis sp. nov.	*Staphylococcaceae*	Skin	Isolated from skin of a 64-yr-old man with cellulitis	Gram-positive cocci arranged in clusters; colonies on sheep blood agar are nonpigmented and surrounded by double-zone hemolysis; catalase positive; DNase producing; coagulates rabbit plasma; slide coagulase (clumping factor) negative	35
Vagococcus vulneris sp. nov.	*Enterococcaceae*	Wound	Isolated from human foot wound	Gram-positive cocci occurring in chains; colonies are gray-white, circular on 5% sheep blood agar, alpha-hemolytic after incubation at 35°C; catalase negative, nonmotile, optochin resistant, vancomycin susceptible; PYR, LAP positive; grows in presence of bile and 6.5% NaCl; esculin hydrolysis positive	36

(Continued on next page)

TABLE 1 (Continued)

Group and scientific name	Family	Source	Clinical relevance	Growth characteristics	Reference(s)
Gram-positive bacilli					
Tsukamurella ocularis sp. nov.	*Tsukamurellaceae*	Eye	Conjunctival swabs from two patients from Hong Kong with conjunctivitis	Gram-positive, nonmotile, non-spore-forming bacillus; aerobic; catalase positive; grows best at 37°C after 48 h on Columbia agar with 5% defibrinated sheep blood agar; white, yellow, or cream-colored colonies, dry, rough with irregular spreading edges; hydrolyzes tyrosine but not xanthine; assimilates many compounds	37, 108
Tsukamurella hominis sp. nov.	*Tsukamurellaceae*	Eye	Conjunctival swabs from a patient from Hong Kong with conjunctivitis	Gram-positive, nonmotile, non-spore-forming bacillus; aerobic; catalase positive; grows best at 37°C after 48 h on Columbia agar with 5% defibrinated sheep blood agar; white, yellow, or cream-colored colonies, dry, rough with irregular spreading edges; hydrolyzes tyrosine but not xanthine; assimilates many compounds	37
Corynebacterium fournieri sp. nov.	*Corynebacteriaceae*	Female genital tract	Isolated from a patient with bacterial vaginosis	Gram-positive, facultatively anaerobic rods; non-spore forming, nonmotile; catalase, urease positive; optimal growth at 37°C; grayish, circular colonies on blood agar	38[c]
Corynebacterium belfantii sp. nov.	*Corynebacteriaceae*	Throat	Previously *C. diphtheriae* biovar Belfanti; isolated from pseudomembrane in the throat of a patient in France; rhinitis, ozaena	Gram-positive pleomorphic, aerobic rods; non-spore forming; nonmotile, white or opaque colonies; maltose positive, nitrate negative; glycogen negative	39
Corynebacterium diphtheriae subsp. *diphtheriae* subsp. nov. (corresponds to lineage 1)	*Corynebacteriaceae*	Throat	Isolated from patients with diphtheria	Gram-positive pleomorphic aerobic rods; white or opaque colonies	40[d]
Corynebacterium diphtheriae subsp. *lausannense* subsp. nov. (corresponds to lineage 2)	*Corynebacteriaceae*	BAL	Isolated from a BAL specimen of a patient hospitalized in Lausanne University hospital with severe tracheobronchitis	Gram-positive aerobic rods; white or opaque colonies; nitrate reductase negative; nontoxigenic; susceptible to penicillin, amoxicillin, clindamycin, levofloxacin, ciprofloxacin, erythromycin, azithromycin	40[d]
Streptacidiphilus bronchialis sp. nov.	*Streptomycetaceae*	BAL	Not established; isolated from a BAL sample of an 80-yr-old patient from Tennessee (USA)	Gram positive, aerobic, non-acid fast, nonmotile; produces branched mycelium and aerial hyphae; forms elevated white to gray colonies on TSA supplemented with 5% sheep blood	109

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TABLE 1 (Continued)

Group and scientific name	Family	Source	Clinical relevance	Growth characteristics	Reference(s)
Gram-negative bacilli					
Phytobacter ursingii sp. nov.	Unassigned	Sputum, perirectal tissue, intravenous fluid	Not established; archived isolates from United States (110–112) with some related to nosocomial outbreak of sepsis (113, 114)	Facultative, motile, oxidase-negative Gram-negative bacilli; 4-mm-diam nonpigmented colonies on nutrient agar; lactose-fermentative colonies on MacConkey agar; optimal growth temp, 28–37°C; VP test, citrate, esculin, indole positive; lysine decarboxylase, arginine dihydrolase, ornithine decarboxylase negative; differentiated from *Phytobacter diazotrophicus* by its ability to metabolize D-serine and L-sorbose	115
Klebsiella grimontii sp. nov.	*Enterobacteriaceae*	Blood (3 isolates), wound (2 isolates)	Clinical diagnoses of bacteremia, diabetic foot syndrome, antibiotic-associated hemorrhagic colitis provided in selected instances in Europe and South Africa (116, 117); others involved in asymptomatic fecal carriage; several isolates former members of *Klebsiella oxytoca* phylogroup Ko6	Several characteristics (nonmotile, Gram-negative bacillus; lysine decarboxylase, VP test, ONPG positive; ornithine decarboxylase negative) analogous to those of *Klebsiella* spp.; indole positive; differentiated from *K. oxytoca* and *Klebsiella michiganensis* by inability to ferment melezitose	25
Enterobacter sichuanensis sp. nov.	*Enterobacteriaceae*	Urine	Not established; isolated from patient hospitalized for chronic renal insufficiency in China	Several characteristics analogous to other *Enterobacter* spp.; differentiated from *E. cloacae* by negative motility, D-mannitol, L-rhamnose reactions, and positive inositol reaction; positive for arginine dihydrolase, ornithine decarboxylase; resistant to cefazolin, cefoxitin, ceftriaxone, imipenem, ertapenem; susceptible to cefepime, aminoglycosides, fluoroquinolones	46
Aggregatibacter kilianii sp. nov.	*Pasteurellaceae*	Eye (4 isolates), blood (2 isolates), abdomen (2 isolates), wound, sinus; isolates derived from patients in Denmark and Switzerland	Often considered commensal; clinical relevance suggested for several isolates (including dacrocystitis, abdominal abscess, and conjunctivitis)	Facultative, nonmotile, short Gram-negative bacilli, with occasional filamentous forms; 1.0- to 1.5-mm-diam convex, yellowish colonies on chocolate agar; optimal growth in air supplemented with 5–10% CO_2; neither X factor nor V factor required for growth; urease, ornithine decarboxylase, indole, catalase negative; β-galactosidase, alanine, phenylalanine-proline arylamidase, *N*-acetylglucosamine positive	26[d]
Klebsiella huaxiensis sp. nov.	*Enterobacteriaceae*	Urine	Isolated from patient with urinary tract infection in China	Classified in the *Klebsiella oxytoca* phylogroup (indole, lactose, lysine decarboxylase, mannitol, ONPG positive; urease, ornithine decarboxylase negative); differentiated from other members of the phylogroup by negative VP test result	42

(Continued on next page)

TABLE 1 (Continued)

Group and scientific name	Family	Source	Clinical relevance	Growth characteristics	Reference(s)
Gardnerella leopoldii sp. nov.	*Bifidobacteriaceae*	Vaginal swab (2 isolates)	Not established; isolated from patients in Belgium	Gram-negative to Gram-variable coccobacilli; pinpoint white to greyish colony growth on chocolate agar with 5% CO_2 enrichment; negative for sialidase and β-galactosidase activities; MALDI-TOF or avg nucleotide identity analyses necessary for unambiguous differentiation from other *Gardnerella* spp.	55
Gardnerella piotii sp. nov.	*Bifidobacteriaceae*	Vaginal swab (2 isolates)	Not established; isolated from patients in Belgium	Gram-negative to Gram-variable coccobacilli; pinpoint white to greyish colony growth on chocolate agar with 5% CO_2 enrichment; positive for sialidase and negative for β-galactosidase activities; MALDI-TOF or avg nucleotide identity analyses necessary for unambiguous differentiation from other *Gardnerella* spp.	55
Gardnerella swidsinskii sp. nov.	*Bifidobacteriaceae*	Vaginal swab (2 isolates)	Not established; isolated from patients in Belgium and Russia	Gram-negative to Gram-variable coccobacilli; pinpoint white to greyish colony growth on chocolate agar with 5% CO_2 enrichment; negative for sialidase and β-galactosidase activities; MALDI-TOF or avg nucleotide identity analyses necessary for unambiguous differentiation from other *Gardnerella* spp.	55
Pandoraea fibrosis sp. nov.	*Burkholderiaceae*	Sputum (2 isolates)	Isolated on *Burkholderia cepacia*-selective medium from cystic fibrosis patient hospitalized in Australia	Facultative, motile, oxidase-positive Gram-negative bacilli; 1- to 2-mm-diam white, convex colonies; optimal growth temp, 37°C; nitrate reduction to nitrite; inability to oxidize bromosuccinic acid and D-galacturonic acid	53
Enterobacter huaxiensis sp. nov.	*Enterobacteriaceae*	Blood	Not established; isolated from patient in China	Several characteristics analogous to other *Enterobacter* spp.; differentiated from *E. cloacae* by negative potassium gluconate, methyl-α-D-mannopyranoside reactions and positive D-arabitol reaction; positive for arginine dihydrolase, ornithine decarboxylase; resistant to ampicillin, cefazolin, cefotetan; susceptible to ceftriaxone, cefepime, carbapenems, aminoglycosides, fluoroquinolones	27
Enterobacter chuandaensis sp. nov.	*Enterobacteriaceae*	Blood	Not established; isolated from patient in China	Several characteristics analogous to other *Enterobacter* spp.; differentiated from *E. cloacae* by negative ornithine decarboxylase, D-sorbitol, melibiose, methyl-α-D-mannopyranoside reactions; positive for arginine dihydrolase; resistant to ampicillin, cefazolin, cefotetan; susceptible to ceftriaxone, cefepime, carbapenems, aminoglycosides, fluoroquinolones	27

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TABLE 1 (Continued)

Group and scientific name	Family	Source	Clinical relevance	Growth characteristics	Reference(s)
Proteus faecis sp. nov.	*Morganellaceae*	Feces (1 isolate), sputum (1 isolate)	Not established; isolated from clinic patients in China	Facultative, motile, oxidase-negative Gram-negative bacilli; swarming evident; optimal growth temp, 37°C; H_2S, sucrose, maltose positive; ornithine decarboxylase, esculin hydrolysis, salicin, L-rhamnose negative; variable indole production	48
Pseudomonas asiatica sp. nov.	*Pseudomonadaceae*	Urine (1 isolate), feces (2 isolates)	1 isolate from patient hospitalized in Myanmar with urinary tract infection; 2 isolates from patients hospitalized in Japan with diarrhea	Aerobic, motile, oxidase-positive Gram-negative bacilli; 0.5- to 2.5-mm-diam creamy, convex colonies on TSA following 2 days of incubation at 30°C; fluorescent pigment production; differentiated from closely related *Pseudomonas putida* and *Pseudomonas monteilii* by ability to utilize L-arabinose, D-mannose, L-pyroglutamic acid, D-glucuronic acid, *p*-hydroxyphenylacetic acid	51
Elizabethkingia occulta sp. nov.	*Flavobacteriaceae*	Reference collection (2 isolates)	Derived from CDC collection of 297 isolates previously designated *Elizabethkingia meningoseptica*	Non-spore-forming, nonmotile, oxidase-positive Gram-negative bacillus; growth on MacConkey agar and TSA at 28–37°C; colonies are pigmented white or yellow; nitrate reduction; urease, catalase, esculin hydrolysis, indole, β-galactosidase positive; gelatin hydrolysis, citrate, malonate negative	54[e]
Enterobacter chengduensis sp. nov.	*Enterobacteriaceae*	Blood	Not established; isolated from hospital setting in China	Several characteristics analogous to other *Enterobacter* spp.; differentiated from *E. cloacae* by negative methyl-α-D-mannopyranoside, VP reactions; positive for arginine dihydrolase, ornithine decarboxylase; resistant to cefotetan, fluoroquinolones; susceptible to ceftriaxone, cefepime, carbapenems, aminoglycosides	28[e]
Yersinia kristensenii subsp. *rochesterensis* subsp. nov.	*Yersiniaceae*	Feces	Not established; isolated from fecal specimen submitted for enteric pathogen detection in U.S.	Several characteristics analogous to other *Yersinia* spp. (motility, ornithine decarboxylase reactions more robust at 25°C than at 37°C); arabinose, ONPG reactions positive at 25°C but not 37°C; sucrose, pyrazinamidase negative; differentiated from several *Yersinia* spp. by positive lipase reaction	50

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TABLE 1 (Continued)

Group and scientific name	Family	Source	Clinical relevance	Growth characteristics	Reference(s)
Providencia huaxiensis sp. nov.	*Morganellaceae*	Rectal swab	Not established; carbapenem-resistant-*Enterobacterales* surveillance rectal swab collected from hospitalized patient in China	Facultative, nonmotile, non-spore-forming, oxidase-negative Gram-negative bacillus with growth characteristics similar to other *Enterobacterales*; citrate, urease, mannitol, indole, D-mannitol, esculin hydrolysis positive; gelatinase, sorbitol negative; resistant to several antimicrobial agents (including amikacin, ceftazidime, ciprofloxacin, colistin, imipenem, piperacillin-tazobactam)	49
Klebsiella africana sp. nov.	*Enterobacteriaceae*	Feces	Not established; isolated from asymptomatic individual in Senegal; additional report (43) characterizes human clinical isolates in Kenya	General characteristics analogous to those of *Klebsiella pneumoniae* (urease, VP test, ONPG, lysine decarboxylase positive; indole, ornithine decarboxylase negative); differentiated from other *K. pneumoniae* complex members by inability to metabolize D-arabitol	44[f]
Rickettsia monacensis sp. nov.	*Rickettsiaceae*	*Ixodes ricinus* tick collected in Germany	Recent case reports document detection in the context of acute febrile illness (57) and codetection with *Orientia tsutsugamushi* in clinically significant disease (58)	Intracellular propagation in cultures of mouse L-929, African green monkey Vero, *I. ricinus* IRE11, *Ixodes scapularis* ISE6, and *Dermacentor andersoni* DAE100 cells; organisms found free within cytoplasm of host cells (occasionally within nuclei); ultrastructure similar to other rickettsiae (size range, 1–1.5 μm by 0.3–0.4 μm)	56[f]
Kosakonia quasisacchari sp. nov.	*Enterobacteriaceae*	Wound secretion	Not established; isolated from hospital setting in China	Facultative, motile, non-spore-forming, oxidase-negative Gram-negative bacillus with growth characteristics similar to other *Kosakonia* (formerly *Enterobacter*) spp.; positive methyl-D-glucopyranoside, citrate, arginine dihydrolase, VP reactions; negative adonitol, D-arabitol, dulcitol, melibiose, ornithine decarboxylase, lysine decarboxylase reactions; resistant to cefazolin, cefoxitin; susceptible to ceftriaxone, cefepime, fluoroquinolones, carbapenems, aminoglycosides	41
Pseudomonas juntendi sp. nov.	*Pseudomonadaceae*	Sputum (1 isolate), urine (1 isolate)	Not established; isolated from patients in Japan and Myanmar	Aerobic, motile, oxidase-positive Gram-negative bacilli; 1- to 2-mm-diam creamy, convex colonies on LB agar following 2 days of incubation at 30°C; fluorescent pigment production; L-arabinose, D-mannose, D-galactose, D-fructose-6-phosphate, esterase-positive; differentiated from closely related *P. asiatica*, *P. putida* and *P. monteilii* by inability to utilize phenylmercuric acetate	118

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TABLE 1 (Continued)

Group and scientific name	Family	Source	Clinical relevance	Growth characteristics	Reference(s)
Pseudomonas nosocomialis sp. nov.	*Pseudomonadaceae*	Cerebrospinal fluid (1 isolate), BAL fluid (1 isolate), exudate (1 isolate); isolates obtained from reference collections	Clinical relevance discussed in reference 119	Aerobic, motile, oxidase-positive Gram-negative bacilli; 2- to 10-mm-diam irregular, dry, beige colonies on LB agar; freshly isolated colonies are adherent and wrinkled (similar to *Pseudomonas stutzeri*); optimal growth temp, 37°C; fluorescent pigment not produced; differentiated from closely related *Pseudomonas* spp. by ability to utilize L-fucose, acetoacetic acid, arabinose, D-arabitol; by absence of arginine dihydrolase, gelatinase; by inability to utilize phenylacetate, mannose	52
Campylobacter armoricus sp. nov.	*Campylobacteraceae*	Feces (3)	Isolated from patients with gastroenteritis in France	Non-spore-forming, motile, curved Gram-negative bacillus (0.3 μm wide and 2.5 μm long); coccoidal cells observed in older cultures; swarming observed; nonhemolytic, greyish colonies observed on blood agar at both 37°C and 42°C in microaerophilic conditions; growth at 37°C in anaerobic conditions; variable growth at 42°C in anaerobic conditions; no growth in aerobic conditions; catalase, oxidase, urease positive; hippurate hydrolysis, nitrate reduction negative	59
Gram-positive anaerobes					
Blautia hominis sp. nov.	*Lachnospiraceae*	Feces	Not established; sample from South Korean patient with diverticulitis	Nonmotile, spore forming; coccoid or oval shaped, observed in pairs; strictly anaerobic; optimal growth at 37°C; colonies are white, glistening, circular; produces acid from a variety of carbohydrates, including sucrose, lactose, maltose, and arabinose; susceptible to ampicillin, vancomycin, cefoperazone, metronidazole	120
Parolsenella catena gen. nov., sp. nov.	*Atopobiaceae*	Feces	Not established; fecal sample from healthy Japanese man in his 30s	Gram-positive coccobacillus forming chains; nonmotile, non-spore forming, nonpigmented; obligate anaerobe; optimum growth at 37°C; off-white to gray, circular, crater-like colonies; acid produced from D-glucose, maltose, D-mannose; susceptible to amoxicillin, erythromycin, gentamicin, penicillin, trimethoprim-sulfamethoxazole, vancomycin	121

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TABLE 1 (Continued)

Group and scientific name	Family	Source	Clinical relevance	Growth characteristics	Reference(s)
Ellagibacter isourolithinifaciens gen. nov., sp. nov.	*Eggerthellaceae*	Feces	Not established; isolated from feces of healthy male donor	Gram-positive, non-spore-forming short rod; nonmotile; obligate anaerobe; slow growing, requiring 5 days of incubation at 37°C; arginine, leucine arylamidase positive	122
Rubneribacter badeniensis gen nov., sp. nov.	*Eggerthellaceae*	Feces	Not established; isolated from feces of healthy 30-yr-old male donor	Gram-positive, nonmotile, rod-shaped; obligate anaerobe; pale whitish colonies after 72 h incubation at 37°C; arginine dihydrolase, proline, phenylalanine, leucine, alanine, glycine, histidine, and serine arylamidase are produced	123
Enteroscipio rubneri gen. nov., sp. nov.	*Eggerthellaceae*	Feces	Not established; isolated from feces of healthy 30-yr-old male donor	Gram-positive, nonmotile rod-shaped, obligate anaerobe; small pale-white colonies after 48–72 h incubation on BHI agar at 37°C; production of arginine dihydrolase	123
Lawsonibacter asaccharolyticus gen. nov., sp. nov.	*Ruminococcaceae*	Feces	Not established; isolated from fecal samples of a healthy 41-yr-old healthy Japanese woman	Gram-positive, obligate anaerobe; nonmotile, non-spore-forming bacillus; grows optimally at 37°C; colonies on BBA are gray to off-white, circular, smooth; susceptible to amoxicillin, bacitracin, chloramphenicol, erythromycin, oxytetracycline, penicillin, vancomycin	124
Peptoniphilus lacydonensis sp. nov.	*Peptoniphilaceae*	Sinus	Isolated from a sinus sample of an 85-yr-old man with chronic refractory sinusitis, complicating ethmoidal adenocarcinoma	Gram-positive, anaerobic and microaerophilic coccus; nonmotile, non-spore forming; optimal growth at 37°C after 48 h; translucent gray colonies; indole positive; susceptible to amoxicillin, cefepime, imipenem, gentamicin, doxycycline, tigecycline, clindamycin, fosfomycin, rifampin, ciprofloxacin, erythromycin, vancomycin	125[g]
Clostridium neonatale sp. nov.	*Clostridiaceae*	Blood, feces, spleen	Necrotizing enterocolitis in neonates	Strictly anaerobic, motile, Gram-positive bacillus; colonies are gray, with irregular-edged spreading or swarming on BHI agar; nonhemolytic on BBA; saccharolytic	61, 62
Ezakiella massiliensis sp. nov.	*Peptoniphilaceae*	Vagina	Isolated from vaginal sample of a healthy woman who had sexual relations with a woman with bacterial vaginosis	Gram-positive strictly anaerobic coccus, nonmotile, non-spore forming; clear, gray colonies after 72 h growth on blood agar; optimal growth at 37°C; catalase, oxidase positive; susceptible to amoxicillin, benzylpenicillin, ceftriaxone, imipenem, metronidazole, vancomycin	126[b]

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TABLE 1 (Continued)

Group and scientific name	Family	Source	Clinical relevance	Growth characteristics	Reference(s)
Pseudopropionibacterium rubrum sp. nov.	*Propionibacteriaceae*	Human gingival sulcus	Not established; isolated from the gingival sulci of healthy humans	Gram-positive, pleomorphic, facultative anaerobic bacillus; forms red, crinkled, nonhemolytic colonies following incubation on sheep blood agar at 37°C for 4 days; hydrolyzes esculin, arginine; indole, nitrate positive; catalase negative	63[b]
Ruminiclostridium cellobioparum gen. nov., comb. nov.	*Hungateiclostridiaceae* fam. nov	Mixture of bovine rumen and human feces	Not established; isolated from human feces, bovine rumen	Gram-positive or -negative curved obligately anaerobic bacillus; motile; oval spores swell the cells; optimum growth temp, 30–37°C; utilizes a variety of carbohydrates	127
Ruminiclostridium cellobioparum subsp. *cellobioparum* subsp. nov.	*Hungateiclostridiaceae* fam. nov.	As above	As above	As above	127
Catenibacillus scindens gen. nov., sp. nov.	*Lachnospiraceae*	feces	Not established; isolated from the feces of a healthy human in Nuthetal, Germany	Gram-positive, non-spore-forming, nonmotile short bacillus; occurs primarily in chains; colonies on sheep blood after 4 days of growth on sheep blood agar are grayish, circular, raised, nonhemolytic; main fermentation products are acetate, butyrate	128
Murdochiella vaginalis sp. nov.	*Peptoniphiliaceae*	Female genital tract	Isolated from a vaginal swab of a 33-yr-old French woman with bacterial vaginosis	Gram-positive coccus, obligate anaerobe; nonmotile, non-spore forming, occurs in pairs, short chains; after 2 days incubation on Columbia agar with 5% sheep's blood at 37°C, colonies are white, circular, opaque; acid from glucose, mannose, galactose; susceptible to oxacillin, penicillin, ceftriaxone, ciprofloxacin, clindamycin, doxycycline, erythromycin, fosfomycin, gentamicin, trimethoprim-sulfamethoxazole, vancomycin	65[c]
Romboutsia hominis sp. nov.	*Clostridiaceae*	Ileostoma effluent	Not established; isolated from the ileostoma effluent of an otherwise healthy human volunteer	Gram-positive, obligately anaerobic, motile bacillus; cells occur singly and in pairs; non-spore forming; white or light gray circular mucoid colonies after 24 h of growth; acid produced from D-fructose, D-glucose, glycerol	129
Anaerobutyricum hallii gen. nov., comb. nov.	*Lachnospiraceae*	Feces	Not established; isolated from human feces	Gram-positive, obligately anaerobic, nonmotile bacillus occurring singly, in pairs; circular colonies whitish to yellow, smooth, nonhemolytic on anaerobic blood agar; optimal growth at 37°C; acid from galactose; produces large amounts of butyric acid	130
Anaerobutyricum soehngenii sp. nov.	*Lachnospiraceae*	Feces	Not established; isolated from the stool of an infant	As above; produces acid from D-glucose, maltose, galactose, sucrose, D-mannose, D-fructose, sorbitol	130

(Continued on next page)

TABLE 1 (Continued)

Group and scientific name	Family	Source	Clinical relevance	Growth characteristics	Reference(s)
Mediterraneibacter massiliensis gen. nov., sp. nov.	*Ruminococcaceae*	Feces	Not established; isolated from the stool of a morbidly obese French woman	Gram-positive, nonmotile, asporogenous, coccobacillary anaerobe; optimum growth at 37°C; translucent colonies; catalase positive	94[d]
Citroniella saccharovorans gen. nov., sp. nov.	*Peptoniphilaceae*	Feces	Not established; isolated from a fecal sample from a member of a traditional coastal Peruvian community	Gram-positive, nonmotile, strictly anaerobic coccus; colonies are small, white, smooth, circular after 6 days of growth at 37°C on BBA; ferments glucose and maltose	131
Collinsella vaginalis sp. nov.	*Coriobacteriaceae*	Vaginal sample	Isolated from a vaginal sample of a French patient with bacterial vaginosis	Gram-positive, strictly anaerobic, nonmotile, non-spore-forming bacillus; saccharolytic; gray, opaque, circular colonies on 5% sheep blood-enriched Columbia agar after 2 days at 37°C	66
Faecalibacillus intestinalis gen nov., sp. nov.	*Erysipelotrichaceae*	Feces	Not established; isolated from fecal samples of healthy Korean subjects	Gram-positive, obligately anaerobic, non-spore-forming, nonmotile long bacillus; optimal growth at 37°C; acid production from glucose, maltose, cellobiose, lactose, sucrose, salicin	132
Faecalibacillus faecis sp. nov.	*Erysipelotrichaceae*	Feces	Not established; isolated from fecal samples of healthy Korean subjects	As above; also esculin hydrolysis positive	132
Olsenella faecalis sp. nov.	*Atopobiaceae*	Feces	Not established; isolated from the feces of a healthy Korean	Gram-positive, nonmotile, strictly anaerobic bacillus; optimum growth at 37°C; creamy, white, irregular colonies; hydrolyzes esculin; produces acid from a variety of carbohydrates	133
Massiliimalia massiliensis gen nov., sp. nov.	*Ruminococcaceae*	Feces	Not established; isolated from the stool of a healthy 19-yr-old Saudi Arabian Bedouin man	Differs from the majority of species within this family by staining Gram negative; organisms are nonmotile and non-spore forming; optimal growth temp, 37°C; colonies are beige and nonhemolytic	134[f]
Massiliimalia timonensis gen. nov., sp. nov.	*Ruminococcaceae*	Feces	Not established; isolated from a stool sample of a healthy 32-yr-old Senegalese male	Gram-positive, non-spore-forming anaerobic and microaerophilic bacillus; optimal growth temp, 37°C; colonies are transparent and nonhemolytic	134[f]

(Continued on next page)

TABLE 1 (Continued)

Group and scientific name	Family	Source	Clinical relevance	Growth characteristics	Reference(s)
Gram-negative anaerobes					
Fenollaria massiliensis gen. nov., sp. nov.	Unassigned	Osteoarticular sample	Not established; isolated from a patient in France	Obligately anaerobic, non-spore-forming, nonmotile Gram-negative bacillus; very small, punctiform, grey colonies on blood-enriched Columbia agar; optimal growth temp, 37°C; leucine arylamidase, valine arylamidase, arginine arylamidase positive; susceptible to penicillin G, cefotetan, imipenem, vancomycin, metronidazole	135[h]
Veillonella infantium sp. nov.	*Veillonellaceae*	Biofilm	Not established; tongue biofilm from healthy 10-yr-old in Thailand demonstrating good oral hygiene	Obligately anaerobic, non-spore-forming, nonmotile Gram-negative coccus occurring singly or in pairs; 0.5- to 2-mm-diam opaque, greyish-white, nonhemolytic colonies on BHI blood agar after 5 days incubation; optimal growth temp, 37°C; esterase, esterase lipase, acid phosphatase positive; major end products are acetic acid and propionic acid; susceptible to colistin, kanamycin, metronidazole; resistant to vancomycin	71
Libanicoccus massiliensis gen. nov., sp. nov.	*Atopobiaceae*	Feces	Not established; isolated from healthy 35-yr-old female in Congo	Obligately anaerobic, non-spore-forming, nonmotile Gram-negative coccus; 0.8- to 1.2-mm-diam rough, dark-white colonies on blood-enriched Columbia agar; optimal growth temp, 37°C; esterase lipase, esculin hydrolysis, acid phosphatase, valine arylamidase positive; catalase, C_4 esterase, C_{14} lipase negative; major fatty acids are 9-octadecanoic and hexadecenoic acid	67, 68[i]
Prevotella rara sp. nov.	*Prevotellaceae*	Feces	Not established; isolated from healthy 43-yr-old female in Russia	Obligately anaerobic, non-spore-forming, nonmotile, short Gram-negative bacillus; 0.5-mm-diam colorless colonies on anaerobe basal agar; colonies turned light brown after 1 wk; optimal growth temp, 37°C; susceptible to bile; major metabolic end products are succinic acid and acetic acid; unable to ferment lactose	136
Mesosutterella multiformis gen. nov., sp. nov.	*Sutterellaceae*	Feces	Not established; isolated from healthy 38-yr-old female in Japan	Obligately anaerobic, non-spore-forming, nonmotile Gram-negative bacillus or coccobacillus; 0.5- to 1.0-mm convex and translucent colonies on BBA; weak growth in 20% bile; optimal growth temp, 37°C; positive for nitrate reduction and acid phosphatase; susceptible to penicillin, kanamycin; resistant to vancomycin, bacitracin, colistin	70

(Continued on next page)

TABLE 1 (Continued)

Group and scientific name	Family	Source	Clinical relevance	Growth characteristics	Reference(s)
Sutterella megalosphaeroides sp. nov.	*Sutterellaceae*	Feces	Not established; isolated from healthy 37-yr-old male in Japan	Obligately anaerobic non-spore-forming, nonmotile Gram-negative coccus; 0.5- to 1.0-mm-diam flat and translucent colonies on BBA; weak growth in 20% bile; optimal growth temp, 37°C; negative for nitrate reduction, acid phosphatase; susceptible to bacitracin, colistin, kanamycin; resistant to penicillin, vancomycin	70
Prevotella phocaeensis sp. nov.	*Prevotellaceae*	Feces	Not established; isolated from 81-yr-old female in France with *Clostridioides difficile* infection	Obligately anaerobic, non-spore-forming, nonmotile Gram-negative bacillus; 1.0- to 1.5-mm-diam white, hemolytic colonies on Columbia agar with 5% sheep blood; optimal growth temp, 37°C; predominant fatty acid is hexadecanoic acid; unable to ferment lactose, glucose, maltose, mannose, mannitol	137[d]
Parabacteroides acidifaciens sp. nov.	*Porphyromonadaceae*	Feces	Not established	Obligately anaerobic, non-spore-forming, nonmotile Gram-negative bacillus; grey to off-white colonies on YCFA medium; optimal growth temp 37–40°C; resistant to 20% bile; catalase, trehalose, β-glucosidase, melezitose negative; serine arylamidase, β-glucuronidase positive; susceptible to penicillin, vancomycin; resistant to clindamycin, kanamycin	138
Butyricimonas faecalis sp. nov.	*Odoribacteraceae*	Feces	Not established; isolate derived from healthy 31-yr-old female	Obligately anaerobic, non-spore-forming, nonmotile, short Gram-negative bacillus; 1- to 2-mm-diam nonpigmented colonies on YCFA agar; optimal growth temp 37°C; susceptible to bile; unable to produce acid from glycerol; α-galactosidase, gelatinase, esculin hydrolysis negative; catalase, arginine dihydrolase, pyroglutamic acid arylamidase positive; major end product is propionic acid	139
Parabacteroides chongii sp. nov.	*Porphyromonadaceae*	Blood	Not established; isolate derived from 63-yr-old male in South Korea with peritonitis secondary to resection of rectosigmoid junction	Obligately anaerobic, non-spore-forming, nonmotile Gram-negative bacillus; 1- to 2-mm-diam grey, circular colonies on BBA; optimal growth temp, 37°C; resistant to 20% bile; esculin hydrolysis, trehalose, raffinose, melezitose negative; catalase, α-fucosidase, β-glucosidase, β-glucuronidase positive	29[i]

(Continued on next page)

TABLE 1 (Continued)

Group and scientific name	Family	Source	Clinical relevance	Growth characteristics	Reference(s)
Bacteroides faecalis sp. nov.	*Bacteroidaceae*	Feces	Not established; isolate derived from healthy individual in South Korea	Obligately anaerobic, non-spore-forming, nonmotile Gram-negative bacillus; 0.5- to 2-mm diam greyish colonies on blood agar; optimal growth temp 37°C; catalase, leucine arylamidase, α-arabinosidase, α-fucosidase negative; acid production from glycerol and D-rhamnose	140
Prevotella brunnea sp. nov.	*Prevotellaceae*	Foot wound	Isolate derived from 67-yr-old male with diabetic foot syndrome and malodorous wound populated with mixture of Gram-positive and Gram-negative bacteria	Obligately anaerobic, non-spore-forming, nonmotile, pleomorphic, short Gram-negative bacillus; 1-mm-diam brown-pigmented colonies on BHI agar supplemented with sheep blood; optimal growth temp, 35–40°C; susceptible to bile; weak production of acid from glucose; variable production of acid from mannose, raffinose; α-fucosidase, *N*-acetyl-β-glucosaminidase activity absent	72
Spirochetes					
Leptospira venezuelensis sp. nov.	*Leptospiraceae*	Urine	Patient in Venezuela with moderately severe leptospirosis characterized by fever, myalgia, arthralgia, and elevated liver enzymes	Motile, helical bacterium, 6–20 μm by 0.1 μm; curved at each end, forming a semicircular hook; optimal growth in typical *Leptospira*-specific semisolid medium at 30°C	60

[a]Abbreviations: BAL, bronchoalveolar lavage; BBA, brucella blood agar; BHI, brain heart infusion; CDC, U.S. Centers for Disease Control and Prevention; i.v., intravenous; LAP, leucine aminopeptidase; ONPG, *o*-nitrophenyl-β-D-galactopyranoside; PYR, pyrrolidonyl arylamidase; TSA, tryptic soy agar; VP, Voges-Proskauer; YCFA, yeast extract Casitone fatty acid.
[b]Taxonomic designation subsequently added in Validation List no. 183 (141).
[c]Taxonomic designation subsequently added in Validation List no. 184 (82).
[d]Taxonomic designation subsequently added in Validation List no. 185 (24).
[e]Taxonomic designation subsequently added in Validation List no. 188 (47).
[f]Taxonomic designation subsequently added in Validation List no. 189 (45).
[g]Taxonomic designation subsequently added in Validation List no. 182 (77).
[h]Taxonomic designation subsequently added in Validation List no. 180 (142).
[i]Taxonomic designation subsequently added in Validation List no. 181 (69).
[j]Taxonomic designation subsequently added in Validation List no. 187 (73).

consuming, and/or not routinely available in clinical microbiology laboratories; furthermore, definitive identification of other novel taxa may necessitate matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS), molecular, or sequencing modalities. Table 2 provides taxonomic revisions for organisms originally recovered from human sources. On the basis of recent peer-reviewed publications from the past 2 years, Table 3 attempts to retrospectively ascribe clinical and additional significance to a number of organisms whose clinical significance was "not established" in the previous taxonomy compendium (3). Findings that warrant emphasis are discussed below.

Novel taxa. Among the newly described Gram-positive cocci (Table 1) are several species and one novel subspecies in the genus *Macrococcus*. While macrococci are known to cause infections in animals, they have not been thought to cause human disease. Mašlaňová et al. (34) performed extensive comparative genomics of several new strains recovered from human sources. *Macrococcus caseolyticus* subsp. *hominis* subsp. nov. was recovered from several different individuals with a variety of infections, including vaginitis, cervicitis, and vulvitis, and in one individual with a postsurgical wound infection. *Macrococcus goetzii* sp. nov. and *Macrococcus epidermidis* sp. nov. seemed to be associated with nail and skin mycoses, respectively. *Macrococcus bohemicus* sp. nov. was recovered from an infected traumatic wound of the knee. In addition to describing these new taxa, the authors characterized resistance and virulence factors among the members of this genus, including a novel staphylococcal chromosomal cassette *mec* (SCC*mec*) element that the authors describe as a putative "missing link" between the class E *mec* complex in other macrococci and the class A *mec* complex among staphylococci (34).

The *Staphylococcus intermedius* group (SIG), which until recently consisted of three species, *Staphylococcus intermedius*, *Staphylococcus pseudintermedius*, and *Staphylococcus delphini*, consists of opportunistic pathogens primarily associated with infections in animals and is responsible for a variety of infections in humans who have contact with them. Murray et al. (35), in a study to improve identification of members of the SIG among isolates recovered from humans, discovered a unique strain based upon sequencing the *hsp*60 and *sodA* genes. The isolate was recovered from the skin of a 64-year-old man with cellulitis who attended a primary care clinic in Cornwall, United Kingdom. Unfortunately, there were no details provided regarding dog ownership or contact. Whole-genome sequencing confirmed that this was a unique species which the authors named *Staphylococcus cornubiensis* sp. nov. (pertaining to Cornwall). Phenotypically this organism is indistinguishable from some of the other species in the SIG.

Another novel species (*Vagococcus vulneris* sp. nov.) associated with human infections was described by Shewmaker et al. (36). The patient from whom it was recovered had a foot wound. Phenotypically, this isolate was unique compared to other *Vagococcus* type strains, except for *Vagococcus penaei*, by testing negative for hippurate hydrolysis and pyruvate (36). *V. vulneris* can be differentiated from *V. penaei*, as it does not ferment lactose but does produce acid from α-D-glucopyranoside (36).

Members of the genus *Tsukamurella* are typically associated with infections related to indwelling devices in patients who are immunocompromised. Teng et al. (37) described three new isolates that were recovered from patients in Hong Kong with conjunctivitis. Two of the three isolates were genetically similar and were given the novel species designation of *Tsukamurella ocularis* sp. nov. The third isolate has been designated *Tsukamurella hominis* sp. nov. (37). Its phenotypic characteristics are similar to those of other members of the genus (Table 1).

A novel species, *Corynebacterium fournieri* sp. nov., joins the list of coryneforms associated with genitourinary disease (38), as it was isolated from a woman with bacterial vaginosis (Table 1). Significant taxonomic reclassifications have impacted other members of the genus *Corynebacterium*, leading to new species and subspecies. The most important human pathogen in this genus is *Corynebacterium diphtheriae*, which causes the severe and once-prevalent disease diphtheria. This heterogeneous

TABLE 2 Revised bacterial taxa from January 2018 through December 2019

Organism type and former name	Revised name	Other information	Reference(s)
Gram-positive bacilli			
Turicella otitidis	*Corynebacterium otitidis* comb. nov.	Initial description of *T. otitidis* isolated from the ear of a patient with otitis media in reference 74; based on phylogenomic and comparative genomic analyses, *Turicella* is reclassified in the genus *Corynebacterium*	75
Streptomyces griseoplanus	*Streptacidiphilus griseoplanus* comb. nov.	Initial description provided in reference 143; in addition, optimal growth is at 28°C	109
Gram-negative bacilli			
Acinetobacter dijkshoorniae	*Acinetobacter lactucae*	Initial description of *A. dijkshoorniae* taxonomic status in reference 144; clinical significance and features summarized in reference 3	145
Bisgaard taxon 5	*Caviibacterium pharyngocola* gen. nov., sp. nov.	Initial description of Bisgaard taxon 5 in reference 146; new taxonomy accommodates all isolates in taxon 5; reference 147 describes clinical human infection derived from a guinea pig bite wound	147
Shewanella haliotis	*Shewanella algae*	Initial description of *S. haliotis* in reference 148; clinical significance in hepatobiliary disease and soft tissue infection summarized in references 149–151	152
Pantoea calida	*Mixta calida* comb. nov.	Initial description of *P. calida* in reference 153; organism often associated with infant formula production; clinical significance in postsurgical meningitis, bacteremia, and antimicrobial resistance reservoirs summarized in references 154–156	80
Pantoea intestinalis	*Mixta intestinalis* comb. nov.	Initial description of *P. intestinalis* in reference 157; originally isolated from feces of healthy human subject	80
Borrelia afzelii	*Borreliella afzelii* comb. nov.	Initial description of *B. afzelii* in reference 158	76[a]
Borrelia americana	*Borreliella americana* comb. nov.	Initial description of *B. americana* in reference 159	76[a]
Borrelia valaisiana	*Borreliella valaisiana* comb. nov.	Initial description of *B. valaisiana* in reference 160; recovery from human clinical specimen documented in reference 161	76[a]
Photorhabdus asymbiotica subsp. *australis*	*Photorhabdus australis* sp. nov.	Initial description of *P. asymbiotica* subsp. *australis* in reference 162; description of clinical isolates in references 162 and 163	81
Photorhabdus asymbiotica subsp. *asymbiotica*	*Photorhabdus asymbiotica*	Initial description of *P. asymbiotica* subsp. *asymbiotica* in reference 163; description of clinical significance in references 164 and 165	81
Photorhabdus luminescens subsp. *luminescens*	*Photorhabdus luminescens*	*P. luminescens* subsp. *luminescens* initially classified as *Xenorhabdus* spp. (166); clinically significant human infections, often found in Australia and United States, have been reviewed (167–170)	81
Methylobacterium extorquens	*Methylorubrum extorquens* comb. nov.	*M. extorquens* initially classified as *Protomonas extorquens* (171) and known by a number of synonyms (172); report of catheter-related infection in reference 173	84
Methylobacterium aminovorans	*Methylorubrum aminovorans* comb. nov.	Initial description of *M. aminovorans* in reference 174; case report of hospital-acquired bacteremia (catheter related) in reference 175	84
Methylobacterium podarium	*Methylorubrum podarium* comb. nov.	Initial description of *M. podarium* in reference 176; clinical relevance discussed in references 176 and 177	84

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TABLE 2 (Continued)

Organism type and former name	Revised name	Other information	Reference(s)
Methylobacterium rhodesianum	*Methylorubrum rhodesianum* comb. nov.	Initial description of *M. rhodesianum* in reference 178; *Methylobacterium lusitanum* is synonym designation (179); case report of hospital-acquired bacteremia (catheter related) in reference 175	84
Methylobacterium thiocyanatum	*Methylorubrum thiocyanatum* comb. nov.	Initial description of *M. thiocyanatum* in reference 180; cases of bacteremia discussed in references 175 and 181	84
Methylobacterium zatmanii	*Methylorubrum zatmanii* comb. nov.	Initial description of *M. zatmanii* in reference 178; case report of septicemia in reference 182	84
Enterobacter cloacae complex Hoffmann cluster III	*Enterobacter hormaechei* subsp. *hoffmannii* subsp. nov.	Initial description of isolate in reference 183; taxonomic designation made on basis of genome computational analysis	32[b]
Enterobacter cloacae complex Hoffmann cluster IV	*Enterobacter roggenkampii* sp. nov.	Initial description of isolate in reference 183; taxonomic designation made on basis of genome computational analysis	32[b]
Mycoplasma arginini	*Mycoplasmopsis arginini* comb. nov.	Initial description of *M. arginini* in reference 184; report of detection from human specimens in reference 185	85[b]
Mycoplasma arthritidis	*Metamycoplasma arthritidis* comb. nov.	Initial description of *M. arthritidis* in reference 186; reports of detection from human specimens in references 187 and 188	85[b]
Mycoplasma buccale	*Metamycoplasma buccale* comb. nov.	Initial description of *M. buccale* in reference 189	85[b]
Mycoplasma canis	*Mycoplasmopsis canis* comb. nov.	Initial description of *M. canis* in reference 190; report of isolation from human specimens in reference 191	85[b]
Mycoplasma caviae	*Mycoplasmopsis caviae* comb. nov.	Initial description of *M. caviae* in reference 192; report of detection from human specimen in reference 193	85[b]
Mycoplasma edwardii	*Mycoplasmopsis edwardii* comb. nov.	Initial description of *M. edwardii* in reference 194; case report of canine bite-induced puncture of peritoneal dialysis tubing in reference 195	85[b]
Mycoplasma faucium	*Metamycoplasma faucium* comb. nov.	Initial description of *M. faucium* in reference 189	85[b]
Mycoplasma fermentans	*Mycoplasmopsis fermentans* comb. nov.	Initial description of *M. fermentans* in reference 190	85[b]
Mycoplasma genitalium	*Mycoplasmoides genitalium* comb. nov.	Initial description of *M. genitalium* in reference 196	85[b]
Mycoplasma hominis	*Metamycoplasma hominis* comb. nov.	Initial description of *M. hominis* in reference 197	85[b]
Mycoplasma lipophilum	*Mycoplasmopsis lipophila* comb. nov.	Initial description of *M. lipophilum* in reference 198	85[b]
Mycoplasma maculosum	*Mycoplasmopsis maculosa* comb. nov.	Initial description of *M. maculosum* in reference 190; case report of meningitis in reference 199	85[b]
Mycoplasma orale	*Metamycoplasma orale* comb. nov.	Initial description of *M. orale* in reference 200	85[b]
Mycoplasma penetrans	*Malacoplasma penetrans* comb. nov.	Initial description of *M. penetrans* in reference 201	85[b]
Mycoplasma pirum	*Mycoplasmoides pirum* comb. nov.	Initial description of *M. pirum* in reference 202	85[b]
Mycoplasma pneumoniae	*Mycoplasmoides pneumoniae* comb. nov.	Initial description of *M. pneumoniae* in reference 203	85[b]
Mycoplasma primatum	*Mycoplasmopsis primatum* comb. nov.	Initial description of *M. primatum* in reference 204	85[b]
Mycoplasma pulmonis	*Mycoplasmopsis pulmonis* comb. nov.	Initial description of *M. pulmonis* in reference 186; report of detection in humans in reference 205	85[b]
Mycoplasma salivarium	*Metamycoplasma salivarium* comb. nov.	Initial description of *M. salivarium* in reference 190	85[b]

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TABLE 2 (Continued)

Organism type and former name	Revised name	Other information	Reference(s)
Burkholderia endofungorum	*Mycetohabitans endofungorum* comb. nov.	Initial description of *B. endofungorum* in reference 206; characterization of blood isolate forwarded to the CDC in reference 207	208[b]
Burkholderia rhizoxinica	*Mycetohabitans rhizoxinica* comb. nov.	Initial description of *B. rhizoxinica* in reference 206; characterization of blood and wound isolates forwarded to the CDC in reference 207	208[b]
Enterobacter muelleri	*Enterobacter asburiae*	*E. muelleri*, originally described in reference 209, is a later heterotypic synonym of *E. asburiae*	32[c]
Mycoplasma felis	*Mycoplasmopsis felis* comb. nov.	Initial description of *M. felis* in reference 210; reports of detection in humans in references 211, 212	85[d]
Acinetobacter genospecies 8	*Acinetobacter pseudolwoffii* sp. nov.	Initial description of 12 *Acinetobacter* genospecies in reference 213; characterization of outpatient conjunctival and inpatient vaginal isolates in reference 214	215[e]
Elizabethkingia genomospecies 3	*Elizabethkingia bruuniana* sp. nov.	Five distinct groups of *Elizabethkingia* strains were initially characterized by DNA-DNA hybridization (216); clinical significance reviewed in reference 78	54[e]
Elizabethkingia genomospecies 4	*Elizabethkingia ursingii* sp. nov.	Five distinct groups of *Elizabethkingia* strains were initially characterized by DNA-DNA hybridization (216); clinical significance reviewed in reference 79	54[e]
Klebsiella pneumoniae phylogenetic group 5	*Klebsiella variicola* subsp. *tropica* subsp. nov.	*K. pneumoniae* phylogenetic group 5 initially described in reference 83; isolates described in reference 44 were derived from human feces (Madagascar)	44[f]
	Klebsiella variicola subsp. *variicola* subsp. nov.	By code, second subspecies automatically created as a result of novel *Klebsiella variicola* subsp. *tropica* subsp. nov. designation	44[f]
Gram-positive anaerobes			
Eubacterium budayi	*Clostridium budayi* comb. nov.	Isolated from a cadaver by Buday and later from nonhuman sources by Prevot (217); description identical to that proposed by Prevot	61
Eubacterium nitritogenes	*Clostridium nitritogenes* comb. nov.	Description identical to that of Prevot (217) with review by Wade (218); isolated from human infections and soil	61
Eubacterium combesii	*Clostridium combesii* comb. nov.	Description reviewed by Wade (218); isolated from human infections and African soil. Dobritsa et al. (219) proposed to reclassify *E. combesii* as a later synonym of *Clostridium botulinum*. *E. combesii* does not produce botulinum toxin.	61
Propionibacterium acnes subsp. *elongatum*	*Cutibacterium acnes* subsp. *elongatum*	Description is as reported by Dekio et al. (91); strains can be found on the human skin of the lower back (associated not with acne but with progressive macular hypomelanosis)	92
Propionibacterium acnes subsp. *acnes*	*Cutibacterium acnes* subsp. *acnes*	Description is the same as given for *P. acnes* by McDowell et al. (220) along with list of mass ions by MALDI-TOF MS (92) and G+C content of the type strain genome of 60.0 mol%	92

(Continued on following page)

TABLE 2 (Continued)

Organism type and former name	Revised name	Other information	Reference(s)
Propionibacterium acnes subsp. *defendens*	*Cutibacterium acnes* subsp. *defendens*	Description is the same as previously provided by Nouioui et al. (93); prominent mass ions obtained by MALDI-TOF MS are provided in reference 92	92
Gordonibacter faecihominis	*Gordonibacter urolithinfaciens*	*G. faecihominis* is now considered a later heterotypic synonym of *Gordonibacter urolithinfaciens*, a Gram-positive anaerobic bacillus isolated from the feces of a healthy male (221)	222
Pseudopropionibacterium propionicum	*Arachnia propionica* emend.	Properties of the emended species are as reported in reference 90	64, 90
Pseudopropionibacterium rubrum	*Arachnia rubra* comb. nov.	Properties provided in a novel taxon report (63) and IJSEM addition (141) (Table 1)	64
Ruminococcus faecis	*Mediterraneibacter faecis* comb. nov.	Properties are as reported for *Ruminococcus faecis* in reference 223	94
Ruminococcus lactaris	*Mediterraneibacter lactaris* comb. nov.	Description is the same as that given for *Ruminococcus lactaris* in reference 224	94
Ruminococcus torques	*Mediterraneibacter torques* comb. nov.	Description is the same as that given in reference 225	94
Ruminococcus gnavus	*Mediterraneibacter gnavus* comb. nov.	Description is the same as that for *Ruminococcus gnavus* in reference 224	94
Clostridium glycyrrhizinilyticum	*Mediterraneibacter glycyrrhizinilyticum* comb. nov.	Description is the same as that in reference 226	94
Propionibacterium namnetense	*Cutibacterium namnetense*	Description is the same as that in reference 3	93[b]

[a]Taxonomic designation subsequently added in Validation List no. 182 (77).
[b]Taxonomic designation subsequently added in Validation List no. 184 (82).
[c]Taxonomic designation not recognized on Validation List in *International Journal of Systematic and Evolutionary Microbiology*; offered as a component of List of Changes in Taxonomic Opinion no. 29 (31).
[d]Taxonomic designation subsequently added in Validation List no. 186 (87).
[e]Taxonomic designation subsequently added in Validation List no. 188 (47).
[f]Taxonomic designation subsequently added in Validation List no. 189 (45).

species has been categorized into four biovars based on a variety of phenotypic characteristics (Gravis, Mitis, Intermedius, and Belfanti). While the first three possess the *tox* gene and are named after the severity of disease they cause, this is not true of biovar Belfanti. It lacks the *tox* gene, causes ozaena, a chronic nonspecific rhinitis, and is nitrate negative (39). Based on multilocus sequence typing (MLST) and DNA-DNA hybridization studies, it has been given a novel species designation, *Corynebacterium belfantii* sp. nov. (39). Nontoxigenic infections, such as endocarditis, osteomyelitis, cutaneous infections, and even respiratory infections associated with *C. diphtheriae* are not uncommon (40). In addition to lacking the *tox* gene, some of these strains may also be deficient in other virulence factors, such as genes related to iron uptake and the three operons that encode pili.

As mentioned above, *C. diphtheriae* has been traditionally divided into four biovars. Subsequent genomic studies do not support this phenotypic biovar classification (40). Studies using MLST identified two distinct lineages, lineage 1 (containing most strains of *C. diphtheriae*) and lineage 2, which includes the biovar Belfanti, subsequently assigned its own species designation as mentioned above (39). Tagini et al. (40) characterized a *C. diphtheriae* strain recovered from a patient with a history of bronchiectasis who developed multiple whitish lesions on the distal trachea and mainstem bronchi associated with severe tracheobronchitis. Whole-genome sequencing and subsequent comparative genomics of this isolate with 56 other *C. diphtheriae* isolates found that this strain and two others shared a lower average nucleotide identity with the type strain of *C. diphtheriae*. The isolate recovered from this patient was assigned to a novel subspecies, *Corynebacterium diphtheriae* subsp. *lausannense* subsp. nov., to replace the lineage 2 designation along with two other strains recovered from nasal swabs in the United Kingdom and India (40) (Table 1). This subspecies lacks the pilus-associated operons and nitrate reductase-encoding genes but does possess genes involved in iron uptake, an important virulence factor (40). The other novel subspecies,

TABLE 3 Update on clinical relevance for selected novel taxonomic designations described in *Journal of Clinical Microbiology* in 2019 (3)

Organism	Source (3)	Updated clinical relevance	Reference
Neisseria dumasiana	Clinical sputum isolates submitted to a U.S. reference laboratory in 2009 and 2012	Deep bite wound dermatitis in a dog	95
Enterobacter bugandensis	Neonatal septicemia outbreak in Tanzania	Isolates from International Space Station; high frequency of decreased susceptibility to tobramycin, gentamicin, ciprofloxacin	105
		In vitro studies demonstrating highest virulence potential among *Enterobacter* spp.	107
		Recovered from clinical specimens (blood, throat swab) in Germany	106
Acinetobacter dijkshoorniae[a]	Clinical strains, including those from wound, sputum, blood, urine, catheter, and nephrology drain specimens	Demonstrated greater *in vitro* and *in vivo* pathogenicity potential than other *Acinetobacter* spp. (including *Acinetobacter baumannii*)	227
		Clinically significant and antimicrobial-managed agent of urinary tract infection	228
Citrobacter europaeus	Fecal isolate from a U.S. patient with diarrhea	Colistin resistance determinant *mcr-1* detected in pediatric fecal isolate from Bolivia	96
Kingella negevensis	Oropharyngeal isolates from healthy Israeli and Swiss children	Review of the laboratory diagnosis and differentiation of *Kingella negevensis* from *Kingella kingae*	100
		Organism detected from corneal scrapings from a United States patient diagnosed with microbial keratitis	101
Propionibacterium namnetense[b]	Infected tibial fracture	Rifampin-resistant isolate derived from pyogenic granuloma secondary to *Staphylococcus aureus* osteomyelitis (originally treated with rifampin and levofloxacin)	97
		1% prevalence of *C. namnetense* among osteoarticular infections; potential to be misidentified as *Cutibacterium acnes* via MALDI-TOF	98
Megasphaera massiliensis	Fecal isolate from HIV-positive patient	*In vitro* model revealed protective effect of this organism vs. neuron cytotoxicity	102
Ruthenibacterium lactatiformans	Fecal isolate from healthy Russian male	A small study suggested that reduced abundance of *R. lactatiformans* and other gut organisms can characterize gut dysbiosis in rheumatoid arthritis	103

[a]Taxonomic revision to *Acinetobacter lactucae* summarized in Table 2.
[b]Taxonomic revision to *Cutibacterium namnetense* summarized in Table 2.

proposed to replace the lineage 1 designation, is *Corynebacterium diphtheriae* subsp. *diphtheriae* subsp. nov. (40). Clinical laboratories traditionally have not assigned *C. diphtheriae* isolates to the biovar level and will likely not be able to identify isolates to the subspecies level under the new classification system. These organisms will likely continue to be identified by rapid kits and MALDI-TOF MS as *C. diphtheriae*, and they should be referred to public health laboratories for toxin testing.

Several novel Gram-negative bacillus taxa in Table 1 are members of order *Enterobacterales*. Representatives of the recently revised family *Enterobacteriaceae* include three *Klebsiella* spp., four *Enterobacter* spp., and *Kosakonia quasisacchari* sp. nov. (41). Several isolates within *Klebsiella grimontii* sp. nov. (25) were previously classified as *Klebsiella oxytoca* phylogroup Ko6. This novel taxon is believed to have clinical significance in the context of diabetic foot syndrome and antibiotic-associated colitis. The Voges-Proskauer (VP)-negative *Klebsiella huaxiensis* sp. nov. isolate described by Hu et al. (42) was isolated from a Chinese patient diagnosed with a urinary tract infection. *Klebsiella africana* sp. nov. (43–45) shares several biochemical traits with *Klebsiella pneumoniae*, but its clinical significance has not been fully established. Despite being isolated from blood culture in a number of instances, the clinical significance of the nonmotile *Enterobacter sichuanensis* sp. nov. (46), the ornithine decarboxylase-negative *Enterobacter chuandaensis* sp. nov. (27), the VP-negative *Enterobacter chengduensis* sp. nov. (28, 47), and *Enterobacter huaxiensis* sp. nov. (27) has not been clearly established. Two taxa have been added to the family *Morganellaceae*. Hydrogen sulfide-negative *Proteus faecis* sp. nov. (48) was recovered from sputum and fecal specimens derived

from Chinese patients, while *Providencia huaxiensis* sp. nov. (49) was recovered during routine carbapenem-resistant *Enterobacterales* surveillance efforts at an inpatient facility in China. The latter demonstrated resistance to a number of antimicrobial agents, including colistin, imipenem, ciprofloxacin, and piperacillin-tazobactam. Finally, lipase-positive *Yersinia kristensenii* subsp. *rochesterensis* subsp. nov. (50) was identified following an initial requisition for molecular microbiology diagnosis of gastrointestinal disease. The subsequent isolate produced motility, ornithine decarboxylase, and *o*-nitrophenyl-β-D-galactopyranoside (ONPG) reactions that were more distinctive upon incubation at 25°C than 37°C.

Several non-glucose-fermentative Gram-negative bacilli have been discovered. *Pseudomonas asiatica* sp. nov. (51) was cultivated from patients in Japan and Myanmar, one of whom was diagnosed with a urinary tract infection. Selected isolates from reference collections (including those derived from cerebrospinal fluid and bronchoalveolar lavage) have been designated *Pseudomonas nosocomialis* sp. nov. (52). A new member of the family *Burkholderiaceae*, *Pandoraea fibrosis* sp. nov. (53), was isolated on *Burkholderia cepacia*-specific medium on two occasions (with an 11-month interval) from respiratory secretions of a cystic fibrosis patient. A subset of urease- and indole-positive isolates from a CDC reference collection of *Elizabethkingia meningoseptica* isolates was given the taxonomic designation *Elizabethkingia occulta* sp. nov. in 2018 (54) and was added by IJSEM in 2019 (47).

Three novel *Gardnerella* spp. (namely, *Gardnerella leopoldii* sp. nov., *Gardnerella piotii* sp. nov., and *Gardnerella swidsinskii* sp. nov.) that were isolated from vaginal swabs of residents of Belgium and Russia required MALDI-TOF MS or average nucleotide identity analyses to be distinguished from other *Gardnerella* spp. (55). The often commensal *Aggregatibacter kilianii* sp. nov. (24, 26) has been recovered from clinical specimens collected in Switzerland and Denmark; clinical significance has been suggested for a subset of isolates derived from ocular and abdominal abscess specimens. The initial 2002 report of *Rickettsia monacensis* sp. nov. was based on its recovery from an arthropod vector in Germany (56); this organism was added by IJSEM in 2019 (45). Data published within the past 2 years have documented identification of this rickettsial agent in the context of acute febrile illness (57) and codetection with *Orientia tsutsugamushi*, both in South Korea (58).

The novel taxon *Campylobacter armoricus* sp. nov. (59) had previously been isolated from three patients with gastroenteritis in France from 2014 to 2016. This bacterium, previously identified by MALDI-TOF MS as *Campylobacter lari*, was capable of growth on blood agar at both 37°C and 42°C in a microaerophilic environment. While additional epidemiologic data from the patients were not available, researchers also recovered the organism from river water samples in a region of France known for shellfish harvesting. The novel spirochete *Leptospira venezuelensis* sp. nov. (60) was recovered from urine of a South American patient whose clinical presentation was characterized as moderately severe leptospirosis (fever and elevated liver enzymes but no renal or pulmonary involvement). The same isolate was additionally recovered from a local cow and rat.

A large number of novel Gram-positive anaerobes were identified during this 2-year period as a consequence of research on gut, vaginal, and oral microbiomes (Table 1). For most of these, the pathogenicity has not been established, and they are not discussed in detail. However, *Clostridium neonatale* sp. nov. does not fall into this category. In 2002, an outbreak of neonatal necrotizing enterocolitis (NEC) in a neonatal intensive care unit in a hospital in Winnipeg, Manitoba (Canada), was observed. Six neonates within a 2-month period developed NEC, and blood cultures and stool cultures from some of the affected infants grew a *Clostridium* species that was identified by conventional methods as *Clostridium clostridioforme*. However, historically the hospital had never recovered this organism from patients in their unit, and *C. clostridioforme* is not a common cause of NEC (61). A reference laboratory concluded that this was a novel species, *Clostridium neonatale* sp. nov., which is described in detail in reference 62. This novel species is saccharolytic but not proteolytic (62). Lactose fermentation and the production of butyric acid and gas during fermentation are

believed to contribute to the intestinal wall gas (pneumatosis intestinalis) observed in patients with NEC when these organisms translocate from the gut.

The name *Pseudopropionibacterium rubrum* sp. nov. was initially published in 2018 (63); however, the name is illegitimate, and this species appears both in Table 1, as a novel organism isolated from human gingival sulci, and in Table 2, because the name has been changed to *Arachnia rubra* comb. nov. (64). This is one example illustrating how taxonomic changes may occur frequently and why it may be prudent for laboratories to wait a few years to implement these changes.

Although the contributions of these new species to the pathophysiology of bacterial vaginosis are not clear, two novel Gram-positive anaerobes, *Murdochiella vaginalis* sp. nov. and *Collinsella vaginalis* sp. nov., were both recovered from women with this syndrome. *M. vaginalis* is an anaerobic coccus in the family *Peptoniphilaceae*, and *C. vaginalis* is a Gram-positive bacillus in the family *Coriobacteriaceae*. Both are strict anaerobes (65, 66).

Table 1 also highlights additional changes that have been made to the family *Clostridiaceae* with the expansion of novel genera and species in this family as listed and the creation of a new family, *Hungateiclostridiaceae*. Additional changes to these groups are noted in Table 2.

The majority of the dozen novel anaerobic Gram-negative bacteria listed in Table 1 were recovered from stool specimens collected from healthy individuals. These include the anaerobic Gram-negative cocci *Libanicoccus massiliensis* sp. nov. (67–69) and *Sutterella megalosphaeroides* sp. nov. (70). A third anaerobic Gram-negative coccus, *Veillonella infantium* sp. nov., was recovered from tongue biofilm (71). Three new *Prevotella* spp. were published or added by IJSEM; *Prevotella brunnea* sp. nov. (72) was isolated from a patient with diabetic foot syndrome. Its clinical significance remains uncertain, because the organism was one of several Gram-positive and Gram-negative organisms derived from the primary clinical specimen. Of the two *Parabacteroides* spp. published or added by IJSEM, *Parabacteroides chongii* sp. nov. (29, 73) may warrant additional study relative to clinical significance. This organism was isolated upon blood culture of a patient that was diagnosed with peritonitis secondary to gastrointestinal surgery.

Taxonomic revisions. As for the novel taxa listed in Table 1, most of the revisions to taxonomy of Gram-positive organisms have occurred among the anaerobes. It is worth mentioning, before the anaerobes are discussed, that *Turicella otitidis*, originally described by Funke et al. in 1994 (74), has been reclassified in the genus *Corynebacterium* based upon phylogenetic and comparative genomics analyses (75).

A number of Gram-negative organisms have been subject to taxonomic revision in the past 2 years. On the heels of the major taxonomic revision of Lyme disease spirochetes to the genus *Borreliella* (76), the taxonomic revision of *Borrelia afzelii*, *Borrelia americana*, and *Borrelia valaisiana* to *Borreliella afzelii*, *Borreliella americana*, and *Borreliella valaisiana* was added by IJSEM in 2018 (77). *Elizabethkingia* genomospecies 3 and 4 received novel genus/species designations in 2018 that were added by IJSEM in 2019 (47). *Elizabethkingia bruuniana* sp. nov. and *Elizabethkingia ursingii* sp. nov., described by Nicholson et al. (54) and cited in Validation List no. 188 (47), have recently become problematic in Asian nations (78, 79).

Additional revisions apply to members of the order *Enterobacterales* (33). Isolates of *Pantoea calida* and *Pantoea intestinalis*, typically associated with infant formula production and normal fecal flora, respectively, are now members of the novel genus *Mixta* gen. nov. (80). *Photorhabdus asymbiotica* subsp. *australis*, *Photorhabdus asymbiotica* subsp. *asymbiotica*, and *Photorhabdus luminescens* subsp. *luminescens* have each had their former subspecies designation converted to genus/species nomenclature (81). Two Hoffmann cluster designations of *Enterobacter cloacae* have been granted genus/species designations (*Enterobacter hormaechei* subsp. *hoffmannii* subsp. nov. and *Enterobacter roggenkampii* sp. nov.) (32), with this revision added by IJSEM (82). It has been opined that the former *Enterobacter muelleri* is a synonym of *Enterobacter asburiae*

(31, 32). Two novel subspecies of *Klebsiella variicola* (44, 45) have emerged from *Klebsiella pneumoniae* phylogenetic group 5, which was reported in 2017 (83).

Perhaps the most noteworthy nomenclature changes to Gram-negative prokaryotes involve genus-level revisions. Green and Ardley (84) reclassified 11 species within the *Methylobacterium* genus into novel designations within the new genus *Methylorubrum*. Included are six species that have been isolated from human clinical material: *Methylorubrum extorquens* comb. nov. (type species), *Methylorubrum aminovorans* comb. nov., *Methylorubrum podarium* comb. nov., *Methylorubrum rhodesianum* comb. nov., *Methylorubrum thiocyanatum* comb. nov., and *Methylorubrum zatmanii* comb. nov. Approximately three dozen species retained the genus designation *Methylobacterium*, including the type species *Methylobacterium organophilum*.

A second significant genus-level reclassification involves *Mycoplasma* spp. Gupta et al. (85) proposed the removal of several former members of the genus *Mycoplasma* and placement into *Mycoplasmopsis* gen. nov., *Metamycoplasma* gen. nov., *Mycoplasmoides* gen. nov., *Malacoplasma* gen. nov., and *Mesomycoplasma* gen. nov. A summary of the 105 total nomenclature revisions, relative to both human and nonhuman isolates, can be found elsewhere (86). Novel genera containing species of human origin include *Mycoplasmopsis* gen. nov., *Metamycoplasma* gen. nov., *Mycoplasmoides* gen. nov., and *Malacoplasma* gen. nov. (Table 2). These designations have been added by IJSEM (82, 87). Specific reclassifications include *Metamycoplasma hominis* comb. nov., *Mycoplasmoides pneumoniae* comb. nov., and *Mycoplasmoides genitalium* comb. nov. The new genera are encompassed by the families *Metamycoplasmataceae* fam. nov. and *Mycoplasmoidaceae* fam. nov.

A cohort of 20 researchers recommended rejection of these findings (88). *The International Code of Nomenclature of Prokaryotes* (89) allows for a process called *nomina rejicienda*, by which a taxonomic designation can be formally challenged and rejected upon adjudication. Several arguments were presented for this recommendation; one of the more interesting ones was tied to a rule within that Code that states, "A name may be placed on [the list of rejected names] for various reasons, including. . .a perilous name, i.e., a name whose application is likely to lead to accidents endangering health or life or both or of serious economic consequences." Balish et al. (88) attempted to invoke this rule in the context of both human (*M. genitalium*, *M. pneumoniae*, and *M. hominis*) and veterinary (*Mycoplasmopsis agalactiae*, *Mycoplasmopsis bovis*, and *Mesomycoplasma hyopneumoniae*) pathogens, some of which are reportable agents to selected world and U.S. health agencies and may have downstream treatment, import/export, and quarantine consequences. Moreover, an additional Code recommendation states, "Avoid names of epithets that are very long or difficult to pronounce."

With respect to anaerobic bacteria, three species of *Eubacterium* have been reclassified as members of the emended genus *Clostridium*, as they are more closely related to species in this genus (>98% sequence similarity by 16S rRNA gene sequence analysis) than to the type strain in the genus *Eubacterium* (82 to 85% sequence similarity) (61). In 2016, the genus *Propionibacterium* was divided into four genera based on whole-genome sequencing, namely, *Cutibacterium*, *Acidipropionibacterium*, *Pseudopropionibacterium*, and the original *Propionibacterium* (90). At the same time, three distinct groups of *Propionibacterium acnes* designated types I, II, and III were described and subsequently were given subspecies names (91). With the subsequent changes in genus nomenclature, these types have been assigned subspecies status in the genus *Cutibacterium* as *Cutibacterium acnes* subsp. *elongatum*, *Cutibacterium acnes* subsp. *acnes*, and *Cutibacterium acnes* subsp. *defendens* (92). Likewise, *Propionibacterium namnetense* has been renamed *Cutibacterium namnetense* (93). Two of the previously designated *Pseudopropionibacterium* species, *Pseudopropionibacterium propionicum* and *Pseudopropionibacterium rubrum*, have been reassigned to the genus *Arachnia* (Table 2) because the name *Pseudopropionibacterium* is considered illegitimate when applied to these species (64).

Finally, in keeping with the dramatic taxonomic changes occurring among the clostridia, *Clostridium glycyrrhizinilyticum* has been reassigned to a new genus, *Medi-*

terraneibacter, along with four species in the genus *Ruminococcus* (Table 2). All of these species have been recovered from the gut of otherwise healthy humans (94).

Recently ascribed and additional clinical significance. Several novel taxa were described in a previous *Journal of Clinical Microbiology* compendium (3), only to have their clinical relevance reported as "not established." While clinical infection by *Neisseria dumasiana* has yet to be documented in humans, a veterinary dermatitis case report has been published (95). Reports of important antimicrobial-resistant phenotypes have subsequently been described for *Citrobacter europaeus* (colistin) (96) and the former *Propionibacterium namnetense* (rifampin) (97). The latter anaerobic Gram-positive bacillus, whose taxonomy revision to *Cutibacterium namnetense* is listed in Table 2, was documented as the etiologic agent in 1% of osteoarticular infections caused by *Cutibacterium* spp. and can be misidentified as *Cutibacterium acnes* even by advanced diagnostic modalities such as MALDI-TOF MS (98). Ruffier d'Epenoux et al. used a *gyrB* sequencing method, a tool that is likely available only in reference laboratories, to differentiate *C. namnetense* from *C. acnes* (98). The latter scenario brings to light a recent change in requirements for defining novel taxa in IJSEM. As of 2018, scientists describing novel taxa must additionally provide whole-genome sequencing data for isolates designated type strains (99). While providing an increased level of complexity and specificity to these novel designations, this mandate may also preclude the ability of routine clinical microbiology laboratories to readily recognize a novel prokaryotic species.

A recent review by Yagupsky (100) speaks to the importance of differentiating the newer taxon *Kingella negevensis* from the well-established pediatric pathogen *Kingella kingae*. Pendela et al. (101) recently described the recovery and identification of *K. negevensis* (among multiple organisms) from an ocular infection. Two feces-derived anaerobic Gram-negative bacilli were recently demonstrated to potentially have effects on host function in noninfectious models. Using an *in vitro* model, Ahmed et al. (102) showed that *Megasphaera massiliensis* potentially has protective capacity versus neuronal cell cytotoxicity. A report by Lee et al. (103) revealed that increased abundance of *Ruthenibacterium lactatiformans* was found in patients with rheumatoid arthritis. Limitations of these findings included the increased abundance of additional gut microbiota beyond *Ruthenibacterium* spp.

Perhaps the most relevant example of an organism for which additional clinical and epidemiologic relevance has been elucidated is *Enterobacter bugandensis*. The bacterium was initially characterized from an outbreak of sepsis among 17 neonates in Tanzania. Isolates were also significant from an antimicrobial resistance perspective, as they demonstrated resistance to aminoglycoside agents, fluoroquinolone agents, and tetracycline; isolates furthermore harbored the CTX-M-15 resistance determinant (104). Since this report, isolates of *E. bugandensis*, with similar antibiograms, have been recovered from the International Space Station (105). The organism has also been isolated from pediatric blood and adult upper respiratory tract specimens derived from patients in Germany (106). As researchers further investigate these isolates, increased virulence potential for this organism has been ascertained. Falgenhauer et al. (106) identified *E. bugandensis* as the most pathogenic species of the genus *Enterobacter*. Pati et al. (107) characterized the type strain of *E. bugandensis* (derived from a Tanzanian pediatric patient) and described its pathogenicity in a mouse model as being as efficient as that of *Salmonella enterica* serotype Typhimurium in terms of elicitation of proinflammatory cytokines. The isolate was additionally capable of growth in high concentrations of human serum. Finally, genetic determinants for pathogenicity were associated with the chromosome, while those potentiating antimicrobial resistance were found on organism plasmids.

CONCLUSION

In summary, communication of prokaryotic taxonomic changes (in clinically relevant fashion) to our clinical colleagues may tremendously impact the care of patients. While published resources, such as *Journal of Clinical Microbiology* and other compendia (3,

16–23), have sought to provide such updates, additional on-line resources can be of assistance. One such service, LPSN (List of Prokaryotic Names with Standing in Nomenclature) (bacterio.net), does provide notations of whether a given taxonomic designation has been "validly" or "nonvalidly" named. With this stated, readers should be cognizant of both the scope of organisms selected for discussion and criteria used for inclusion within these publications.

Because the field of prokaryotic taxonomy is one that will not likely experience a slow-down any time soon, Clinical and Laboratory Standards Institute (CLSI) has appointed a document development committee to prepare a report entitled "Guideline for Implementation of Taxonomy Nomenclature Changes" as an effort to assist clinical and veterinary microbiology laboratories in managing taxonomic revisions in a relevant fashion. The document will be revised every 2 years incorporating new scientific publications and feedback from users through the CLSI process. Document publication is slated for 2022.

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