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MINIREVIEW

What's in a Name? New Bacterial Species and Changes to Taxonomic Status from 2012 through 2015

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ABSTRACT Technological advancements in fields such as molecular genetics and the human microbiome have resulted in an unprecedented recognition of new bacterial genus/species designations by the *International Journal of Systematic and Evolutionary Microbiology*. Knowledge of designations involving clinically significant bacterial species would benefit clinical microbiologists in the context of emerging pathogens, performance of accurate organism identification, and antimicrobial susceptibility testing. In anticipation of subsequent taxonomic changes being compiled by the *Journal of Clinical Microbiology* on a biannual basis, this compendium summarizes novel species and taxonomic revisions specific to bacteria derived from human clinical specimens from the calendar years 2012 through 2015.

KEYWORDS anaerobes, bacteria, Gram-negative bacteria, Gram-positive bacteria, taxonomy

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Human microbiome studies, particularly those involving genome sequencing, have resulted in a seeming explosion of novel bacterial taxonomy. While many of these organisms appear to play a commensal role in site-specific ecology, some of the organisms may be of clinical significance in various patient populations. Moreover, enhanced studies of known bacterial genomes in a variety of applications, including those of an epidemiologic nature, have given rise to revisions and amendments to accepted bacterial taxonomy. Summaries of microbial taxonomy updates, such as those introduced in this edition of the *Journal of Clinical Microbiology*, are essential to routine practice in the clinical microbiology laboratory.

Since 2014, laboratories subscribing to the College of American Pathologists accreditation program have encountered checklist standard MIC.11375 in the context of biennial inspection exercises. The standard (1) requires laboratories to assimilate "taxonomic changes that potentially affect the choice of appropriate antimicrobials to report and/or the interpretative breakpoints to use." Cited as an example for the context of this standard is the Gram-negative bacillus with the former taxonomic designation *Actinobacillus actinomycetemcomitans*. The taxonomic revision in 1985 (2) resulting in organism classification within the genus *Haemophilus* subsequently enabled antimicrobial susceptibility testing of clinically significant isolates using standards outlined in Table 2E of CLSI supplement M100S (example provided in [3]). *Haemophilus* test medium, with a 16- to 18-hour incubation in 5% CO_2 enrichment, could be utilized for disk diffusion. *Haemophilus* test medium broth could also be inoculated for broth microdilution testing with 20- to 24-hour incubation in ambient air.

Subsequent reclassification of this organism into the genus *Aggregatibacter* (4) has resulted in the transition of susceptibility testing guidelines to those specific to (former) HACEK group organisms (*Aggregatibacter* spp., *Cardiobacterium* spp., *Eikenella corrodens*, and *Kingella* spp.) in Table 9 of the CLSI guideline M45 (5).

The shift of the former *A. actinomycetemcomitans* from Table 2E of the CLSI M100S supplement (3) to the M45 guideline (5) also impacted tested and reported antiinfective agents. While MIC interpretive criteria remained largely unchanged for trimethoprim-sulfamethoxazole, rifampin, tetracycline, ampicillin, macrolide agents, and β-lactam/β-lactamase inhibitor combinations between the two documents, the number of reportable fluoroquinolone agents via broth microdilution and disk diffusion testing in a past M100S supplement (3) was reduced from nine to two in the current M45 guideline (5). These two agents, levofloxacin and ciprofloxacin, are only assessed by broth microdilution and now possess intermediate and resistant interpretive criteria. Similarly, the number of reportable cephem agents (fifteen) in a previous M100S supplement was reduced to two for *Aggregatibacter* spp. in the context of the M45 guideline; intermediate and resistant interpretive criteria now exist. Penicillin susceptibility testing is newly available per the CLSI M45 guideline, along with *Aggregatibacter* genus-specific MIC interpretive criteria for carbapenem susceptibility testing. In an analogous fashion, clinically significant organisms in generic CLSI classifications, such as "other non-*Enterobacteriaceae*" or "*Streptococcus* spp. viridans group," could hypothetically be moved into categories that have alternative susceptibility testing guidelines or that do not allow for any testing.

The accurate identification of organisms is important for understanding the epidemiology of emerging pathogens. One contemporary example of this paradigm resides within the newly described taxon *Elizabethkingia anophelis*. This oxidase-positive Gram-negative bacillus was first isolated from the midgut of an *Anopheles gambiae* mosquito originating from McCarthy Island, The Gambia (6). Full-gene 16S rRNA sequence similarities of 98.6% and 98.2% were reported to strains *Elizabethkingia meningoseptica* ATCC 13253^T and *Elizabethkingia miricola* GTC 862^T, respectively. An initial attribution of clinical significance (7) involved a case of neonatal meningitis in Bangui, Central African Republic. Although it was identified as *E. meningoseptica* by biochemical analysis, full 16S rRNA gene sequencing of this isolate resulted in a definitive identification as *E. anophelis*. On the basis of geographic location and discovery origin, it was originally hypothesized that mosquito vectors were central to *E. anophelis* disease epidemiology.

However, Balm et al. (8) chronicled an *E. meningoseptica* outbreak in cardiothoracic and surgical intensive care units of a tertiary Singapore hospital. The organism was isolated from blood and respiratory specimens and identified by matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS). Initial epidemiologic relatedness between the clinical isolates and *E. meningoseptica* isolates derived from sampling of water taps/aerators was established by repetitive element palindromic PCR. Subsequent 16S rRNA sequencing and whole-genome alignment identified the outbreak strains as being *E. anophelis*. Additional genetic determinants were consistent with the clinical course (antimicrobial treatment failure and mortality) in a number of patients.

Moreover, Lau et al. (9) reported three cases of *E. anophelis* sepsis from one Hong Kong inpatient facility. Neonatal meningitis was additionally diagnosed in two cases, and the third involved a maternal chorioamnionitis related to one neonatal case. The isolates were originally identified as *E. meningoseptica* by both a commercial biochemical system and MALDI-TOF MS (scores $\geq$1.8). Full-gene 16S rRNA sequencing revealed 99.1% to 99.9% identity to *E. anophelis* R26^T and 97.4% to 99.9% identity to GenBank *E. meningoseptica* deposits. Draft genome sequencing not only identified the isolates as *E. anophelis*, but also implicated perinatal vertical transmission in two cases.

Lau and colleagues (10) expanded clinical and epidemiologic analyses of *Elizabethkingia* spp. bacteremia to five regional Hong Kong hospitals in the context of additional non-glucose-fermenting Gram-negative bacilli (including *Chryseobacterium* and *Flavobacterium* spp.). Bacteremia caused by *Elizabethkingia* spp. was associated with clinically significant infection ($P = 0.00009$), positive cultures from additional sources ($P = 0.005$), higher complication rates ($P = 0.01$), and increased attributable mortality rates ($P = 0.025$) compared to those of bacteremia caused by non-*Elizabethkingia* spp. Moreover,

81% of *Elizabethkingia* spp. bacteremic episodes were related to *E. anophelis*, as confirmed by full-gene 16S rRNA sequencing. The mortality rate in these patients was 23.5% (4/17), while none of the three *E. meningoseptica* bacteremia cases was fatal. Patients with *E. anophelis* bacteremia carried additional clinical diagnoses of community-acquired or nosocomial pneumonia (29.4% of cases), catheter-related bacteremia (23.5%), and neonatal meningitis (17.6%).

Analogous to the original Hong Kong report (9), all *E. anophelis* isolates were originally identified as *E. meningoseptica* by a commercial biochemical system; nearly 60% were identified as *E. meningoseptica* by MALDI-TOF MS. Database revision by the addition of seven *E. anophelis* spectra facilitated the identification of all *E. anophelis* isolates. An increased resistance to piperacillin and co-trimoxazole was observed within the *E. anophelis* collection compared to that of the limited subset of *E. meningoseptica* isolates (10). In summary, the recognition of current bacterial taxonomy can assist in future epidemiologic and prognostic delineations of *Elizabethkingia* spp. infections and additional emerging infectious agents.

Attempts to summarize and centralize taxonomic changes into a single resource were previously undertaken (11, 12), and there have been recent attempts to renew this practice (13, 14). The following compendium of clinically significant bacterial taxonomy changes from the calendar years 2012 to 2015 attempts to provide a comprehensive capstone for the biannual updating of bacterial taxonomy by editors of the *Journal of Clinical Microbiology*.

METHODS AND DATA

Validly published novel (Table 1) and revised (Table 2) taxa pertinent to prokaryotic species must meet one of two requirements: (i) an original investigation published in the *International Journal of Systematic and Evolutionary Microbiology* (*IJSEM*) or (ii) a study published in an alternative journal, with later inclusion on an approved list in *IJSEM*. Journals that publish studies reporting new taxa that may be relevant to the practice of clinical microbiology include *Antonie Van Leeuwenhoek*, *Current Microbiology*, *International Journal of Medical Microbiology*, *Standards in Genomic Sciences*, 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 [69]). To be considered for inclusion on this approved list, authors must submit a copy of the published manuscript to the editorial office of *IJSEM* for confirmation that all the elements necessary for valid publication have been met. In addition, type strains are to be deposited into two recognized culture collections in separate nations. Taxa on these approved lists may be subject to reclassification on the basis of a synonym designation or transfer to another genus. Accepted taxa within Tables 1 and 2 that were previously published outside *IJSEM* are represented by appropriate footnoting.

In such fashion, all issues of *IJSEM* that were published between January 2012 and December 2015 were searched for original articles describing new species taxonomy or for 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 were utilized to attempt to index subsequent case reports for further investigation; several of these case reports are referenced throughout this report. A number of *IJSEM* publications (examples provided in [35, 70–75]) 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), clinical significance of these taxa was interpreted as "not established." Future studies may be necessary to characterize the true clinical significance of novel taxa (76).

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. Two such examples of taxonomic opinion (77, 78) are presented in Table 2, with antecedent primary referenced literature (79, 80). These entries have been included with the goal of revisiting them in future *Journal of Clinical Microbiology* compendia to either ascertain true clinical significance or to determine if official taxonomic status has been granted.

RESULTS AND DISCUSSION

Table 1 lists the new taxa recovered from humans stratified by Gram reaction and morphology. Many of the new genera and species were likely discovered from studies of the human microbiome. Much of what is listed, while recovered from human clinical material, has unknown clinical significance. There are a few exceptions that warrant emphasis.

GRAM-POSITIVE COCCI

Seven new *Streptococcus* species were characterized during the study period, as highlighted in Table 1. *Streptococcus tigurinus*, a new member of the *Streptococcus mitis* group, was discovered by Zbinden et al. in 2012, when it was recovered from the blood and aortic valve of a 74-year-old Swiss patient with endocarditis (15, 16). The authors performed a retrospective review of their institution's 16S rRNA gene sequence database in the 10-year period prior to 2012, and a total of 15 patients with *S. tigurinus* infections were discovered (16). A review of the charts revealed that all of the infections were serious and invasive and included 12 cases of bacteremia, seven of which were from patients with endocarditis (16). Other invasive infections included spondylodiscitis, prosthetic joint infections, meningitis, encephalitis, and empyema (16). Others have subsequently reported similar severe infections in patients from Korea (17), Japan (18), and the United States (19). The high virulence potential of this organism has been demonstrated in a rat model of endocarditis wherein it was demonstrated that *S. tigurinus* strains have increased abilities to resist macrophage-mediated phagocytosis and to invade endothelial cells (20). The oral cavity is the presumed source of the organism. An initial study found that this organism was not prevalent in the saliva of healthy volunteers (16). However, using more sensitive molecular techniques, the same group obtained saliva and pooled plaque samples from a non-periodontitis control group and a group with periodontitis (21). The overall prevalence of *S. tigurinus* was 53% in 51 patients and there was no difference in the frequencies of detection between the two groups (21). MALDI-TOF MS misidentifies *S. tigurinus* as *Streptococcus oralis*, *Streptococcus pneumoniae*, or other member of the *mitis* group with scores $>$2.0 (16, 19, 22). Identification requires the use of 16S rRNA partial or full-gene sequencing or other molecular methods (21).

Two new subspecies of the coagulase-negative *Staphylococcus petrasii* have been characterized. Subspecies *jettensis* was recovered from wounds and implicated in bacteremia, whereas subspecies *pragensis* is believed to have caused prostatitis (23–25). One new species of coagulase-positive *Staphylococcus*, *Staphylococcus argenteus*, was isolated from the blood of a person in Australia. This organism is phenotypically very similar to *S. aureus* and has likely been misidentified as such (26). The 16S rRNA gene sequence (1,474 nucleotide [nt]) of *S. argenteus* is identical to that of *S. aureus*. However, whole-genome sequencing indicates that they are separate species. In addition, the proteomics profile of *S. argenteus* using MALDI-TOF MS is different from that of *S. aureus* (26). A study in Thailand demonstrated that 4.1% of isolates believed to be *S. aureus* were subsequently determined to be *S. argenteus* (27). This organism was associated primarily with community-acquired skin and soft tissue infections, although bacteremia and bone and joint infections were seen in three and two patients, respectively (27).

Similar to other *Gemella* species, the two new additions to the genus, *G. taiwanensis* and *G. parahaemolysans*, were isolated from blood cultures and are believed to be a

TABLE 1 New bacterial species recovered from human clinical material reported between January 2012 and December 2015

Scientific name	Family	Source (no. of cases)	Clinical relevance	Growth characteristics	Reference(s)
Gram-positive cocci					
Streptococcus tigurinus sp. nov.	*Streptococcaceae*	Isolated from human blood	Associated with serious clinical infections, such as endocarditis, meningitis, spondylodiscitis, and possibly also periodontitis	Gram-positive non-motile cocci arranged in chains, colonies are white to gray, alpha-hemolytic on sheep blood agar after 24 h at 37°C	15–22, 81
Streptococcus anginosus subsp. *whileyi* subsp. nov	*Streptococcaceae*	Human throat	Not established	Grow well aerobically and anaerobically, growth enhanced by CO_2, all strains are beta-hemolytic and contain Lancefield group C antigen	82
Streptococcus anginosus subsp. *anginosus* subsp. nov	*Streptococcaceae*	Human throat	Pharyngitis, pleuropulmonary, intraabdominal, and urogenital infections, bacteremia	Grow well aerobically and anaerobically, growth enhanced by CO_2, all strains are beta-hemolytic and contain Lancefield group G antigen	82
Streptococcus constellatus subsp. *viborgensis* subsp. nov.	*Streptococcaceae*	Human throat	Not established	Grow well aerobically and anaerobically, growth enhanced by CO_2, all strains are beta-hemolytic and contain Lancefield group C antigen	82
Streptococcus hongkongensis sp. nov.	*Streptococcaceae*	Infected tissue, marine fish	Wound infection	Facultatively anaerobic Gram-positive cocci, grow well on blood agar at 37°C, non-hemolytic	83
Streptococcus rubneri sp. nov.	*Streptococcaceae*	Human throat	Not established	Gram-positive ovoid cocci, grow well on CNA and 5% sheep blood agar at 37°C, 2 mm zone of beta-hemolysis	84
Streptococcus dentisani sp. nov	*Streptococcaceae*	Caries-free human tooth surfaces	Not established	Gram-positive cocci that grow in short chains, facultatively anaerobic, alpha-hemolytic on Columbia agar plates	85
Staphylococcus jettensis sp. nov. Reclassified as *S. petrassii* subsp. *jettensis* subsp. nov.	*Staphylococcaceae*	Multiple human specimen types: blood, CSF, deep wounds	Bacteremia, wounds	Facultatively anaerobic Gram-positive cocci, narrow zone of beta-hemolysis, late yellow pigment	23, 24
Staphylococcus petrasii subspecies *pragensis* subsp. nov.	*Staphylococcaceae*	Isolated from an ejaculate specimen of a man with prostatitis	Prostatitis	Spherical cocci appearing in pairs and clusters, weakly hemolytic on sheep blood agar, grow at 45°C, coagulase negative, novobiocin susceptible	25
Staphylococcus argenteus sp. nov.	*Staphylococcaceae*	Multiple specimen types, including blood	Bacteremia, skin, soft tissue, bone and joint infections	Creamy white colonies that exhibit beta-hemolysis on blood agar, coagulase positive, facultatively anaerobic	26, 27
Gemella parahemolysans sp. nov.	Not assigned Bacillales family XI incertae sedis	Isolated from blood cultures	Opportunistic infections in immunocompromised patients	Gram-positive cocci, non-hemolytic colonies on 5% SBA, grow as pinpoint colonies in 24 h at 37°C, facultatively anaerobic	28
Gemella taiwanensis sp. nov	Not assigned Bacillales family XI incertae sedis	Isolated from blood cultures	Opportunistic infections in immunocompromised patients	Gram-positive cocci, non-hemolytic colonies on 5% SBA, grow as pinpoint colonies in 24 h at 37°C, facultatively anaerobic	28
Gram-positive rods					
Dietzia aurantiaca sp. nov.	*Dietziaceae*	Isolated from human cerebrospinal fluid	Not established	Gram positive coccoid cells, oxidase and catalase positive, grow well at 10–37°C, optimal at 30°C, colonies are convex and have orange pigmentation	86
Bacillus cytotoxicus sp. nov.	*B. cereus* group *Bacillaceae*	Vegetable, potato purees, semolina	Food poisoning	Thermotolerant (grow at 20–50°C), facultative anaerobe	87
Lactobacillus saniviri sp. nov.	*Lactobacillaceae*	Isolated from feces of a healthy Japanese male	Not established	Gram-positive facultatively anaerobic rods, not spore forming, alpha hemolysis apparent after aerobic incubation for 3 d at 37°C	29
Lactobacillus senioris sp. nov.	*Lactobacillaceae*	Isolated from the feces of a 100-year-old female in Japan	Not established	Rod-shaped Gram-positive organisms that occur singly, in pairs, or in short chains, not spore forming, facultatively anaerobic, grows at 15–37°C	29
Lactobacillus hominis sp. nov.	*Lactobacillaceae*	Human intestine	Not established	Facultative anaerobe	30

(Continued on following page)

TABLE 1 (Continued)

Scientific name	Family	Source (no. of cases)	Clinical relevance	Growth characteristics	Reference(s)
Paenibacillus vulneris sp. nov	*Paenibacillaceae*	Necrotic wound	Wound infection	Aerobic spore forming	88
Nocardia amikacinitolerans	*Nocardiaceae*	Eye of a 12-year-old girl	Not established	Aerobic, orange pigmented, grows best at 25°C	89
Nocardia kroppenstedtii	*Nocardiaceae*	Isolated from a lung transplant patient with pulmonary infection	Pneumonia	Aerobic, Gram-positive partially acid fast rod forms irregular, wrinkled, matt, pale orange-yellow pigmented colonies after 5 days growth at 30°C, grows at 25–37°C, optimal at 28°C	90
Alicyclobacillus consociatus sp. nov. Reclassified as *Effusibacillus consociatus* comb. nov.	*Alicyclobacillaceae*	Blood from an adult woman	Bacteremia	Aerobic, spore-forming rods grow at 15–45°C, optimal at 30°C	91, 92
Hazenella coriacea gen. nov., sp. nov.	*Thermoactinomycetaceae*	Human blood	Bacteremia	Thin, branching Gram-positive spore-forming rods grow on sheep blood agar at 22–45°C, optimal at 42–45°C, beta-hemolysis observed at 48 h	31
Canibacter oris gen. nov., sp. nov.	*Microbacteriaceae*	Infected dog bite wound	Dog bite infections	Rod-shaped Gram-positive cells that form Y or V shapes, facultative anaerobe, non-hemolytic on sheep blood agar	32
Gordonia iterans sp. nov.	*Nocardiaceae*	Isolated from sputum of a patient with bacterial pneumonia	Pneumonia	Aerobic, Gram-positive, partially acid-fast coccobacilli, yellow-pigmented colonies, grows at 15–40°C	93
Gram-negative cocci					
Neisseria oralis sp. nov	*Neisseriaceae*	Human oral cavity and clinical samples	Bacteremia, also isolated from urine, peritoneal cavity	Gram-negative diplococci, yellow, grow best at 37°C in 5% CO_2	33
Faucicola mancuniensis gen nov. sp. nov	*Moraxellaceae*	Tonsils of a healthy adult female	Not established	Aerobic Gram-negative, non-motile coccus, growth occurs at 20–37°C on Columbia blood agar	34
Gram-negative rods					
Bartonella rochalimae sp. nov.	*Bartonellaceae*	Blood	Bacteremia in context of fever and splenomegaly	Aerobic, fastidious bacillus with unipolar flagella, growth on fresh defibrinated rabbit blood agar at 35°C with enhanced CO_2	94[a]
Haemophilus sputorum sp. nov.	*Pasteurellaceae*	Blood, throat swab (5), sputum (2), female urethra, tooth alveolitis	Occasional involvement in human infections, has been isolated from cystic fibrosis patients	Beta-hemolysis on horse blood agar and sheep blood agar, rare strains do not grow on sheep blood agar, oxidase positive, catalase variable	95[b]
Psychrobacter sanguinis sp. nov.	*Moraxellaceae*	Blood (4), cerebrospinal fluid	Not established in bacteremic patients, post-neurosurgical meningitis	Growth on blood agar, no growth on MacConkey agar, growth promoted by Tween 80, oxidase positive, non-glucose fermentative	35, 36
Legionella nagasakiensis sp. nov.	*Legionellaceae*	Bronchoalveolar lavage	Pneumonia	Growth on BCYE agar, requires L-cysteine, negative for β-galactosidase activity	96
Massilia oculi sp. nov.	*Oxalobacteraceae*	Ocular	Endophthalmitis	Beige colonies on blood agar and nutrient agar, growth on MacConkey agar, oxidase negative, assimilates D-glucose	97
Myroides phaeus sp. nov.	*Flavobacteriaceae*	Saliva	Not established	Growth of pale-yellow/brown colonies on routine laboratory medium at 6–37°C, optimal growth at 28°C, negative for β-galactosidase activity	98
Legionella steelei sp. nov.	*Legionellaceae*	Respiratory tract (2)	Not established	Growth on BCYE agar, requires L-cysteine, oxidase positive	99
Kerstersia similis sp. nov.	*Alcaligenaceae*	Leg wound (3), neck abscess	Skin and soft tissue infection	Growth on nutrient agar and blood agar, colonies are white-to-light brown and have swarming appearance, oxidase negative	100
Legionella cardiaca sp. nov.	*Legionellaceae*	Aortic valve tissue	Native valve endocarditis	Growth on BCYE agar, requires L-cysteine, non-glucose fermentative	101

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TABLE 1 (Continued)

Scientific name	Family	Source (no. of cases)	Clinical relevance	Growth characteristics	Reference(s)
Cruoricaptor ignavus gen. nov. sp. nov.	*Flavobacteriaceae*	Blood	Septicemia	Yellowish-orange, non-hemolytic colonies on Columbia agar with 5% sheep blood, chocolate agar, no growth on MacConkey agar, optimal growth in microaerobic or capnophilic environments, cells are non-motile, oxidase positive, acid not generated from D-glucose	102[c]
Herbaspirillum massiliense sp. nov.	*Oxalobacteraceae*	Feces	Not established	2-mm diam convex, cream-colored, opaque colonies on BHI agar, optimal growth at 30–37°C in aerobic conditions, oxidase negative	103[d]
Enterobacter massiliensis sp. nov.	*Enterobacteriaceae*	Feces	Not established	0.5-mm diam light-brown, opaque colonies on blood agar, optimal growth at 37°C in aerobic conditions, oxidase-positive, curved Gram-negative bacillus	104[d]
Acidovorax wautersii sp. nov.	*Comamonadaceae*	Blood (1), non-specified human isolate (1)	Not established	Growth on routine media in 37°C aerobic environment but not at 42°C, oxidase positive, urease positive, indole negative	70
Achromobacter animicus sp. nov.	*Alcaligenaceae*	Sputum (3)	Not established, has been isolated from cystic fibrosis patients	Growth of some strains at 42°C, tolerates 3% NaCl, no acid generated from D-glucose, no glucose assimilation	105[e]
Achromobacter mucicolens sp. nov.	*Alcaligenaceae*	Sputum (4), epiglottis swab (1)	Not established, has been isolated from cystic fibrosis patients	Growth of most strains at 42°C, tolerates 3% NaCl, no acid generated from D-glucose, no glucose assimilation	105[e]
Achromobacter pulmonis sp. nov.	*Alcaligenaceae*	Sputum (3)	Not established, has been isolated from cystic fibrosis patients	Growth of most strains at 42°C, tolerates 3% NaCl, no acid generated from D-glucose, glucose assimilation is strain-dependent	105[e]
Achromobacter spiritinus sp. nov.	*Alcaligenaceae*	Sputum (3)	Not established	Growth of some strains at 42°C, tolerates 3% NaCl, no acid generated from D-glucose, no glucose assimilation	105[e]
Burkholderia pseudomultivorans sp. nov.	*Burkholderiaceae*	Sputum (10)	Not established, has been isolated from cystic fibrosis patients	Growth capable at 42°C, growth on blood agar and MacConkey agar, oxidase positive, lysine decarboxylase positive, ornithine decarboxylase negative	106[d]
Frederiksenia canicola gen. nov., sp. nov.	*Pasteurellaceae*	Skin and soft tissue (3)	Canine bite wound	Non-hemolytic colonies on blood agar, oxidase positive, indole positive, glucose fermentation without gas production, CAMP test positive	107[f]
Yersinia wautersii sp. nov.	*Enterobacteriaceae*	Feces, one other human isolate not well defined	Putative pathogenicity elucidated only by characterization of genetic determinants, taxonomic status questioned by reference 108	Overnight growth on routine media at 28°C and 37°C, urease positive, indole negative	108, 109[f]
Pelistega indica sp. nov.	*Alcaligenaceae*	Feces	Not established	Growth on TSA and MacConkey agars at 20–40°C, optimal growth at 30–35°C, motile organisms that are catalase negative and oxidase positive	110
Campylobacter fetus subsp. *testudinum* subsp. nov.	*Campylobacteraceae*	Feces, blood, pleural fluid, hematoma, bile	Diarrhea, pulmonary edema, cellulitis documented in references 38, 40	Growth on blood agar in microaerobic conditions at 25–42°C, majority of strains grow microaerobically on MacConkey agar, oxidase positive, catalase positive, urease negative, non-hydrolysis of hippurate and indoxyl acetate	37–40
Streptobacillus hongkongensis sp. nov.	*Bacteroidaceae*	Aspirate, olecranon fluid	Peritonsillar abscess, septic arthritis	Optimal growth after 48 h on Columbia agar with 5% sheep blood either incubated in 37°C anaerobic environment or in 37°C aerobic environment supplemented with 5% CO_2, no growth on MacConkey agar, oxidase negative	111
Klebsiella quasipneumoniae subsp. *quasipneumoniae* subsp. nov.	*Enterobacteriaceae*	Human infection (9), type strain derived from blood	Not established	Growth characteristics similar to other *Klebsiella* spp., utilizes tricarballylic acid, lysine decarboxylase positive, ornithine decarboxylase negative, indole negative, urease positive	71

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TABLE 1 (Continued)

Scientific name	Family	Source (no. of cases)	Clinical relevance	Growth characteristics	Reference(s)
Klebsiella quasipneumoniae subsp. *similipneumoniae* subsp. nov.	*Enterobacteriaceae*	Human infection (3), type strain derived from blood	Not established	Growth characteristics similar to other *Klebsiella* spp., utilizes tricarballylic acid, lysine decarboxylase positive, ornithine decarboxylase negative, indole negative, urease-positive	71
Vibrio metoecus sp. nov.	*Vibrionaceae*	Blood, stool	Hypothesized to be an opportunistic pathogen	Typical *Vibrio cholerae*-like appearance after 30°C incubation on thiosulfate citrate bile salts medium, negative Voges-Proskauer reaction, utilizes D-glucuronic acid	72
Pseudocitrobacter faecalis sp. nov.	*Enterobacteriaceae*	Feces	Clinical significance not established, isolate possessed NDM-1 carbapenemase and CTX-M-15 extended spectrum β-lactamase	Non-hemolytic, oxidase-negative, facultative anaerobe, lysine decarboxylase negative, ornithine decarboxylase negative	112[g]
Pseudocitrobacter anthropi sp. nov.	*Enterobacteriaceae*	Feces	Clinical significance not established, isolate possessed NDM-1 carbapenemase and CTX-M-15 extended spectrum β-lactamase	Non-hemolytic, oxidase-negative, facultative anaerobe, weakly positive for lysine and ornithine decarboxylases	112[g]
Myroides injenensis sp. nov.	*Flavobacteriaceae*	Urine	Febrile illness	Pale-yellow or ivory colonies on TSA, strictly aerobic, cells are non-motile, grow at 10–45°C (optimal at 37°C), oxidase positive, urease positive	113[h]
Acinetobacter variabilis sp. nov.	*Moraxellaceae*	Urine (2), feces (1), ocular (2), blood (2), leg (2), peritoneal dialysis fluid (1), toe (1)	Not established	Strictly aerobic, oxidase-negative Gram-negative cocci, non-hemolytic colonies generated following overnight incubation at 25–41°C	73
Acinetobacter seifertii sp. nov.	*Moraxellaceae*	Blood (9), ulcer (1), respiratory (3)	Not established	Growth similar to other *Acinetobacter* spp.	74
Citrobacter pasteurii sp. nov.	*Enterobacteriaceae*	Feces	Diarrhea outbreak	Growth similar to other *Citrobacter* spp., catalase negative, indole negative	114
Rouxiella chamberiensis sp. nov.	*Enterobacteriaceae*	Parenteral nutrition bag (6)	Nutrition intended for premature newborns (NICU)	Growth on routine media (lemon yellow colonies) at 4–30°C, optimal growth at 30°C, non-hemolytic on blood agar, non-lactose fermenter on MacConkey agar, cells are non-motile, positive Voges-Proskauer reaction	115
Paracoccus sanguinis sp. nov.	*Rhodobacteraceae*	Blood (4)	Not established	Grow at 22–37°C, optimal at 28°C, pale-yellow, non-hemolytic colonies on blood agar, oxidase positive, urease negative, no decarboxylation of ornithine, lysine, or arginine	75
Tatumella saanichensis sp. nov.	*Enterobacteriaceae*	Sputum	Not established, has been isolated from cystic fibrosis patients	Growth on blood agar, incubation at 25–35°C, cells are non-motile, oxidase negative, lactose fermentative, negative Voges-Proskauer reaction	116
Burkholderia stagnalis sp. nov.	*Burkholderiaceae*	Tracheal aspirate, sputum	Not established, has been isolated from cystic fibrosis patients	Growth on blood, *Burkholderia cepacia*-selective, and MacConkey agar, rare beta-hemolysis, majority can be cultivated at 42°C, cells are motile, delayed oxidase-positive reaction	117
Bartonella ancashensis sp. nov.	*Bartonellaceae*	Blood (2)	Verruga peruana	Growth on TSA and Columbia agars with 5% sheep blood, growth on BHI with 10% sheep blood, no growth on chocolate agar, optimal growth after 10 d in 30°C 5% CO_2, oxidase negative, catalase negative, urea negative, cells are non-motile	118
Pantoea intestinalis sp. nov.	*Enterobacteriaceae*	Feces	Not established	Growth on routine laboratory medium at 15–45°C, optimal growth at 35°C, urease negative, oxidase negative	119
Bordetella bronchialis sp. nov.	*Alcaligenaceae*	Respiratory (2)	Not established, has been isolated from cystic fibrosis patients	Non-hemolytic on blood agar, no growth on centrimide agar, growth in 3% NaCl, no growth in 4.5% NaCl	120
Bordetella flabilis sp. nov.	*Alcaligenaceae*	Sputum	Not established, has been isolated from cystic fibrosis patient	Non-hemolytic on blood agar, no growth on centrimide agar, no growth in 3% NaCl, no growth in 4.5% NaCl	120

(Continued on following page)

TABLE 1 (Continued)

Scientific name	Family	Source (no. of cases)	Clinical relevance	Growth characteristics	Reference(s)
Bordetella sputigena sp. nov.	*Alcaligenaceae*	Sputum	Not established, has been isolated from cystic fibrosis patient	Weakly-hemolytic on blood agar, weak growth on centrimide agar, growth in 3% NaCl, no growth in 4.5% NaCl	120
Gram-positive anaerobes					
Methanomassiliicoccus luminyensis gen. nov, sp. nov.	Not assigned	Isolated from human feces from a person in Marseille France	Not established	Regular, non-motile Gram-positive cocci, obligate anaerobe, produces methane	121
Ruminococcus champanellensis sp. nov.	Ruminococcaceae	Human feces	Not established	Non-motile Gram-positive cocci, strictly anaerobic-grow at 33–39°C	122
Blautia stercoris sp. nov.	*Lachnospiraceae*	Isolated from human feces	Not established	Strictly anaerobic Gram-positive cocci, non-motile, non-spore-forming, grow well at 37°C	123
Blautia faecis sp. nov.	*Lachnospiraceae*	Human intestine	Not established	Strict anaerobe Gram-positive cocci	124
Peptoniphilus duerdenii sp. nov.	*Peptoniphilaceae*	Isolated from human vaginal abscess	Wound infections	Anaerobic Gram-positive cocci, cells are gray, convex, circular on Brucella blood agar at 37°C after 5 d, indole-positive assacharolytic	41
Peptoniphilus koenoeneniae sp. nov.	*Peptoniphilaceae*	Isolated from a human buttock abscess	Wound infections	Obligately anaerobic Gram-positive cocci, cells are gray, convex, circular on Brucella blood agar at 37°C after 5 d, indole-positive assacharolytic	41
Lachnoanaerobaculum umeaense gen. nov. sp. nov.	*Lachnospiraceae*	Isolated from the small intestine of a child with celiac disease	Not established	Obligately anaerobic, saccharolytic spore-forming Gram-positive rod, easily decolorized, colonies are spreading and flat on blood agar 72 h at 37°C	125
Lachnoanaerobaculum orale gen. nov. sp. nov	*Lachnospiraceae*	Isolated from saliva of a healthy man	Not established	Obligately anaerobic, saccharolytic spore-forming Gram-positive rod, easily decolorized, colonies are spreading and circular with rhizoid edges on blood agar 72 h at 37°C	125
Stomatobaculum longum gen. nov., sp. nov	*Lachnospiraceae*	Human oral cavity	Human periodontal infection	Strict anaerobic rods that stain Gram variable	126
Fusicatenbacter saccharivorans gen nov., sp. nov.	*Lachnospiraceae*	Human feces	Not established	Gram-positive non-spore-forming rods, spindle shaped in pairs and chains, grow well on Brucella agar at 37°C, non-hemolytic	127
Anaerostipes rhamnosivorans	*Lachnospiraceae*	Human feces	Not established	Spore-forming rods that form curly cells in old cultures, stain Gram variable, optimal growth at 37°C	128
Gordonibacter urolithinfaciens sp. nov.	*Coriobacteriaceae*	Human feces	Not established	Obligately anaerobic, non-spore-forming Gram-positive coccobacilli	129
Oribacterium parvum sp. nov.	*Lachnospiraceae*	Human subgingival dental plaque	Periodontal disease?	Gram-positive short ovoid rods that stain Gram variable, yeast extract required for growth, grow at 30–42°C, strict anaerobe	130
Oribacterium asaccharolyticum sp. nov.	*Lachnospiraceae*	Human subgingival dental plaque	Periodontal disease	Gram-positive short ovoid rods that stain Gram variable, yeast extract required for growth, grow at 30–42°C, strict anaerobe	130
Bifidobacterium faecale sp. nov.	*Bifidobacteriaceae*	Human feces	Unknown	Gram-positive Y-shaped short rods, obligately anaerobic, grow at 30–42°C (optimal at 37°C)	131
Atopobium deltae sp. nov.	*Coriobacteriaceae*	Blood of a patient with Fournier's gangrene	Bacteremia	Gram-positive obligately anaerobic short rod, non-hemolytic	43
Actinotignum schaalii comb. nov[a]	*Actinomycetaceae*	Urine of humans	Urinary tract infections	Gram-positive, non-motile, non-spore-forming slightly curved rods, facultatively anaerobic, do not branch	42, 132, 133
Actinotignum sanguinis sp. nov.	*Actinomycetaceae*	Blood cultures of a human with sepsis	Bacteremia/sepsis	Gram-positive, non-motile, non-spore-forming slightly curved rods, facultatively anaerobic, do not branch	132

(Continued on following page)

TABLE 1 (Continued)

Scientific name	Family	Source (no. of cases)	Clinical relevance	Growth characteristics	Reference(s)
Gram-negative anaerobes					
Christensenella minuta gen nov., sp. nov.	*Christensenellaceae* fam. nov.	Isolated from human feces	Not established	Non-spore-forming, short, anaerobic, Gram-negative rods, grow at 25–43°C, optimal growth at 37–40°C	134
Fretibacterium fastidiosum sp. nov.	*Synergistaceae*	Human oral cavity	Human periodontal infection	Strict anaerobe, require co-cultivation with other oral bacteria	135
Veillonella tobetsuensis sp. nov.	*Veillonellaceae*	Human tongue biofilm	Not established	Anaerobic cocci	136
Veillonella seminalis sp. nov.	*Veillonellaceae*	Human semen	Not established	Gram-negative anaerobic cocci arranged in pairs or short chains, grow well anaerobically on Columbia blood agar at 37°C	137
Alloprevotella rava gen. nov. sp. nov.	*Prevotellaceae*	Human oral cavity	Not established	Strict anaerobe grows best at 35°C, range 30–42°C	138
Coprobacter fastidiosus gen nov., sp. nov.	*Porphyromonadaceae*	Infant feces	Not established	Strict anaerobic, Gram-negative rod grows on enriched media at 30–37°C	139
Prevotella jejuni sp. nov.	*Prevotellaceae*	Small intestine of a child with celiac disease	Not established	Strict anaerobe, Gram negative, grow slowly on blood agar plates at 37°C, beta-hemolytic	140
Eisenbergiella tayi gen nov., sp. nov.	*Lachnospiraceae*	Isolated from the blood of an elderly man	Bacteremia	Strict anaerobe	44
Megasphaera indica sp. nov.	*Veillonellaceae*	Isolated from stool of healthy humans	Not established	Strict anaerobic cocci, grow at 15–37°C (optimal at 37°C)	141
Butyricimonas faecihominis sp. nov.	*Porphyromonadaceae*	Human feces	Not established	Obligately anaerobic, non-pigmented, rods, grow optimally at 37°C	142
Butyricimonas paravirosa sp. nov.	*Porphyromonadaceae*	Human feces	Not established	Obligately anaerobic, non-pigmented rods, grow optimally at 37°C	142
Parabacteroides faecis sp. nov.	*Porphyromonadaceae*	Human feces	Not established	Obligately anaerobic, non-pigmented, non-spore forming rods, grow optimally at 37°C	143
Porphyromonas pasteri sp. nov.	*Porphyromonadaceae*	Human saliva	Not established	Obligately anaerobic, non-pigmented, non-spore-forming rods, grow slowly at 37°C	144
Spirochetes					
Borrelia kurtenbachii sp. nov.	Member of the *Borrelia burgdorferi sensu lato* species complex in North America	*Ixodes scapularis*	Not established	BSK and BSK-K5 medium[i]	145
Leptospira mayottensis sp. nov.	*Leptospiraceae*	Isolated from blood of patients with leptospirosis in Mayotte	Leptospirosis	Strains grow well in EMJH medium at 30°C and 37°C	45

[a]Taxonomic designation subsequently accepted in validation list no. 144 (146).
[b]Taxonomic designation subsequently accepted in validation list no. 146 (147).
[c]Taxonomic designation subsequently accepted in validation list no. 149 (148).
[d]Taxonomic designation subsequently accepted in validation list no. 155 (149).
[e]Taxonomic designation subsequently accepted in validation list no. 152 (150).
[f]Taxonomic designation subsequently accepted in validation list no. 158 (151).
[g]Taxonomic designation subsequently accepted in validation list no. 157 (60).
[h]Taxonomic designation subsequently accepted in validation list no. 163 (152).
[i]BSK medium is the name applied to a selective medium used to grow the Lyme disease spirochete. BSK-K5 has kanamycin and 5 fluorouracil.

cause of opportunistic infections in immunocompromised patients (28). All of the patients from whom these isolates were recovered had significant comorbidities, including various types of solid tumors (28). These organisms grow slowly on 5% sheep blood agar and are nonhemolytic. They are easily decolorized during Gram staining (28). Biochemical tests can be used to differentiate them from other species of *Gemella* (28).

GRAM-POSITIVE RODS

Many aerobic or facultatively anaerobic Gram-positive rods were discovered during the 4-year period of this review. The new species of lactobacilli were recovered from the feces of patients who were otherwise healthy and likely represent a component of the normal intestinal microbiota (29, 30). Several new aerobic actinomycetes in the *Nocardia* and *Gordonia* genera were recovered from patients with pneumonia, thereby contributing to the growing list of opportunistic pathogens in immunocompromised patients. Two new genera were also described. *Hazenella coriacea* grows optimally between 42 and 45°C and was recovered from the blood of three separate patients, although the details of their illnesses were not provided (31). *Canibacter oris* was recovered from both a swab and purulent material from an infected dog-bite wound on the finger of a 58-year-old patient in Australia (32).

GRAM-NEGATIVE COCCI

Two new Gram-negative cocci have been characterized. *Neisseria oralis* (33) is a new species that is found in the human oral cavity and is associated with a variety of infections. The clinical significance of the new genus and species *Faucicola mancuniensis*, recovered from the tonsils of an otherwise healthy woman, has not been established (34).

FACULTATIVE GRAM-NEGATIVE RODS

With respect to novel Gram-negative bacillus taxa, the oxidase-positive *Psychrobacter sanguinis* sp. nov. was first identified from four archival blood culture isolates originating from New York (35). Clinical significance was uncertain among any of these cases, as pertinent clinical data were not provided. Full-gene 16S rRNA sequencing reported 99.7% genetic similarity to *Psychrobacter* sp. PRwf-1, a strain originating from a fish species caught in Puerto Rico. The aquatic strain was subsequently reclassified as *P. sanguinis*. A French group recently reported a case of post-neurosurgical meningitis with *P. sanguinis* etiology (36). An external ventricular drain was instilled into a 64-year-old female to relieve elevated intracranial pressure. Approximately 1 week after the procedure, the organism was cultivated following a lumbar puncture. It was hypothesized that the patient repeatedly touched the drain with her bare hands, facilitating the introduction of organisms from an environmental (nosocomial) source.

In 1985, Harvey and Greenwood (37) reported the isolation of *Campylobacter fetus* from a pet turtle in the context of three clinically ill household members and concomitant isolation of *Salmonella enterica* serovar Agona. Molecular analysis of a *C. fetus* subsp. *fetus* blood culture isolate derived from a precursor T lymphocyte acute lymphoblastic leukemia patient indicated a reptilian origin (38). This isolate and other archival human strains were paired with five *C. fetus*-like organisms from reptiles, subjected to a number of characterizations (including MALDI-TOF MS and whole-genome sequencing), and granted the novel taxon *Campylobacter fetus* subsp. *testudinum* subsp. nov. (39). Epidemiologic investigation indicated that afflicted individuals were largely Asian men who reported consumption of Asian foods or had previous exposure to reptiles (40).

ANAEROBES

Many new anaerobes have been discovered. Some have been recovered from the stool of healthy children and adults and likely represent components of the normal microbiota. Others have been isolated from dental plaque, but whether they cause periodontal disease is unclear at present. A few organisms are worth highlighting.

Among the Gram-positive anaerobes, two new *Peptoniphilus* species, namely, *duerdenii* and *koenoeneniae* were recovered from abscesses of the vagina and buttocks, respectively (41). *Actinobaculum schaalii* has been moved into the genus *Actinotignum*. The three species in this genus, *schaalii*, *urinale*, and *sanguinis*, are part of the urinary microbiota, but they are also associated with urinary tract infections in men and young children (42). MALDI-TOF MS can identify these species, and the correct identification is important, as *A. schaalii*, the most common pathogen in the genus, is resistant to trimethoprim-sulfamethoxazole and ciprofloxacin, which are the agents commonly used for the treatment of urinary tract infections (42). *Atopobium deltae*, another novel Gram-positive anaerobe, was recovered from the blood of a patient with Fournier's gangrene (43). Most of the newly discovered Gram-negative anaerobes have not been clearly associated with clinical infections, except for the new genus and species *Eisenbergiella tayi* (44), which was associated with bacteremia in an elderly patient. Of the spirochetes recently characterized, *Leptospira mayottensis* has been associated with clinical disease in patients from Mayotte in the Indian Ocean (45).

TAXONOMIC REVISIONS

Table 2 lists the taxonomic revisions for organisms recovered from humans, stratified by Gram reaction and morphology. A recent report describing the successful culture propagation of what was formerly classified as "*Candidatus Helicobacter heilmannii*" from feline gastric mucosa resulted in its assignment to the taxon *Helicobacter heilmannii* sp. nov. (46). While most descriptions of this organism are associated with veterinary bacteriology, evidence does exist for the presence of this organism in human tissue (reviewed in reference 47).

Aeromonas hydrophila subsp. *dhakensis* and *Aeromonas aquariorum* were reclassified in 2013 under the singular taxon *Aeromonas dhakensis* sp. nov. comb. nov. (48). Formal acceptance by the *IJSEM* was granted in 2015 (49). The initial characterization of *A. hydrophila* subsp. *dhakensis* occurred in the context of diarrheal illness in Bangladesh (50). In addition to gastroenteritis, reports have suggested a significant distribution of (the former) *A. aquariorum* extraintestinal infections in a variety of geographic locations (51, 52). Chen et al. (53) reviewed 80 cases of *Aeromonas* spp. wound infections in Taiwan. It was found that 46.3% of these infections were caused by *A. dhakensis*, while 16.3% were of *A. hydrophila* etiology. Compared to other *Aeromonas* spp., *A. dhakensis* was also associated with antecedent environmental water exposure, biofilm formation, and increased *in vitro* cytotoxicity. Furthermore, the organism generated increased MIC values for ceftriaxone, gentamicin, and imipenem.

Wautersiella falsenii was reclassified in 2014 as *Empedobacter falsenii* comb. nov. (54). Twenty-six human isolates from Belgium (including blood, ear discharge, oral cavity, pleural fluid, pus, respiratory tract, wound, and vaginal swab) contributed to the initial *W. falsenii* designation (55). Again, clinical manifestations of illness were not described in this report. van der Velden et al. (56) presented the case of a febrile 1-year-old girl with pyelonephritis caused by *W. falsenii*. The identification of the organism was facilitated by MALDI-TOF MS and confirmed by partial-gene 16S rRNA sequencing. An intravenous 2-week ciprofloxacin regimen brought about clinical and microbiologic improvement. Traglia et al. (57) described the isolation of *E. falsenii* from a cervical neck abscess specimen obtained from an 18-year-old female with acute otitis media. Similar to the previous clinical report (56), the *E. falsenii* isolate exhibited decreased susceptibilities to colistin, ceftazidime, piperacillin-tazobactam, representative carbapenems, and additional β-lactam/β-lactamase inhibitor combinations.

POTENTIAL EMERGING PATHOGENS

While not included within the formal tables of this review, the following encompass examples of new taxa that could conceivably transcend into the realm of human clinical disease. *Rickettsia buchneri* sp. nov. (58) is a Gram-negative bacillus isolated from ovaries of the *Ixodes scapularis* vector already known to deliver a number of bacterial and parasitic species to accidental human hosts. Mediannikov

TABLE 2 Revised bacterial taxa between January 2012 and December 2015

Old name	Revised name	Other information	References
Aerobic Gram-positive rod			
Bacillus massiliensis	*Lysinibacillus massiliensis* comb. nov.	Isolated from human cerebrospinal fluid	153, 154
Anaerobic Gram-positive cocci			
Ruminococcus obeum	*Blautium obeum* comb. nov.	Isolated from human feces	155
Anaerobic Gram-negative rods			
Prevotella tannerae	*Alloprevotella tannerae* gen. nov.	Endodontic infections	138
Bifidobacterium stercoris	*Bifidobacterium adolescentis*	Isolated from human feces	156
Anaerobic Gram-positive rods			
Eubacterium saburreum	*Lachnoanaerobaculum saburreum* comb. nov.	Isolated from dental plaque	125
Clostridium hathewayi	*Hungatella hathewayi* gen. nov., comb. nov.	Isolated from human feces	157
Actinobaculum urinale	*Actinotignum urinale* comb. nov.	Urinary tract infections	132
Actinobactulum schaalii	*Actinotignum schaalii* gen. nov., comb. nov.	Urinary tract infections	132
Gram-negative cocci			
Neisseria mucosa var. *heidelbergensis*	*Neisseria oralis*	*Neisseria oralis* sp. nov. referenced in Table 1 of this minireview	33, 158
Aerobic and facultative Gram-negative rods			
"*Candidatus Helicobacter heilmannii*"	*Helicobacter heilmannii* sp. nov.	Newly recognized due to *in vitro* cultivation of the organism, significance in humans described in reference 47	46, 47
Cronobacter genomospecies 1	*Cronobacter universalis* sp. nov.	Pathogenicity of strain 731 previously demonstrated in leg infection	159
Pasteurella species B	*Pasteurella oralis* sp. nov.	Type strain isolated in 1981 from cat bite wound of human	160
Selected CDC group II-i isolates	*Sphingobacterium mizutaii*	Two isolates recovered from blood culture (one from patient with septicemia)	161
Yersinia frederiksenii genospecies 2	*Yersinia massiliensis*	Phylogenetic analysis grouped 15 strains of *Y. frederiksenii* genospecies 2/*Y. massiliensis* apart from *Y. frederiksenii* genospecies 1 and 3	162
142 group	*Chryseobacterium bernardetii* sp. nov.	Isolated from tongue swab, sputum, blood, finger abscess	163
78 group	*Chryseobacterium nakagawai* sp. nov.	Isolated from kidney abscess, urine	163
212 group (contribution of CDC groups IIc and IIe)	*Chryseobacterium taklimakanense* comb. nov.	Isolated from blood, wound, cerebrospinal fluid	163
Aeromonas hydrophila subsp. *dhakensis*	*Aeromonas dhakensis* sp. nov. comb nov.	Pathogenicity in humans described in references 50, 53	48[a], 50, 53
Aeromonas aquariorum	*Aeromonas dhakensis* sp. nov. comb nov.	Pathogenicity in humans described in references 51, 52	48[a], 51, 52
Aeromonas hydrophila subsp. *anaerogenes*	*Aeromonas caviae*	Original taxonomy discussed in reference 164	79[b], 164
Enterobacter gergoviae	*Pluralibacter gergoviae* comb. nov.	*E. gergoviae* sp. nov. pathogenicity first characterized in reference 165	63[c], 165
Enterobacter amnigenus	*Lelliottia amnigena* comb. nov.	One recent example of *E. amnigenus* pathogenicity was bloodstream isolate harboring both bla_{KPC} and *rmtB* on single plasmid, as published in reference 166	63[c], 166
Achromobacter genogroup 2	*Achromobacter insuavis*	Isolated from cystic fibrosis, non-cystic fibrosis patient sputum	167[d]
Achromobacter genogroup 5	*Achromobacter aegrifaciens*	Isolated from cystic fibrosis, non-cystic fibrosis patient sputum	167[d]
Achromobacter genogroup 7	*Achromobacter anxifer*	Isolated from cystic fibrosis patient sputum	167[d]
Achromobacter genogroup 14	*Achromobacter dolens*	Isolated from cystic fibrosis, non-cystic fibrosis patient sputum	167[d]
Wautersiella falsenii	*Empedobacter falsenii* comb. nov.	Pathogenicity in humans described in references 56, 57	54–57
Rahnella genomospecies 2	*Rahnella variigena* sp. nov.	Type strain isolated from human burn specimen	80[e]

[a]Taxonomic designation subsequently accepted in validation list no. 161 (49).
[b]Taxonomic designation not recognized on validation list in *International Journal of Systematic and Evolutionary Microbiology*; offered as component of changes in taxonomic opinion no. 19 (77).
[c]Taxonomic designation subsequently accepted in validation list no. 154 (64).
[d]Taxonomic designation subsequently accepted in validation list no. 155 (149).
[e]Taxonomic designation not recognized on validation list in *International Journal of Systematic and Evolutionary Microbiology*; offered as component of changes in taxonomic opinion no. 22 (78).

et al. (59) isolated and characterized the Gram-negative bacillus *Bartonella senegalensis* sp. nov. from the soft tick *Ornithodoros sonrai*, a vector of relapsing fever. This novel taxon was subsequently approved by *IJSEM* (60). *Klebsiella michiganensis* sp. nov. (61) is a newly characterized Gram-negative bacillus isolated from a toothbrush holder, with taxonomy subsequently accepted by *IJSEM* (62). Brady et al. (63) described taxonomic reclassification of *Enterobacter oryzae* and *Enterobacter turicensis* as *Kosakonia oryzae* comb. nov. and *Cronobacter zurichensis* nom. nov., respectively, with subsequent acceptance by *IJSEM* (64). In antecedent publications, the former *E. oryzae* and *E. turicensis* were recovered from wild rice (65) and fruit

powder (66), respectively. Stephan et al. (67) published the taxonomic reclassification of *Enterobacter pulveris* as *Franconibacter pulveris* comb. nov. Isolation of this organism from infant formula was previously described (68). These organisms with inferred pathogenic potential provide the basis for follow-up database searches in future *Journal of Clinical Microbiology* taxonomy compendia.

In summary, over the 4-year period of this review, both the expansion of new technologies and the characterization of the human microbiome have led to the discovery of a broad range of bacterial organisms that are part of the normal human microbiota. In addition, the new tools have enabled a more comprehensive assessment of closely related pathogens and the discovery of novel clinically significant organisms. We attempted to highlight those pathogens and, where possible, to describe their epidemiologic and clinical niches.

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