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Review

Proposed nomenclature or classification changes for bacteria of medical importance: Taxonomic Update 4

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ABSTRACT

A key aspect of medical, public health, and diagnostic microbiology laboratories is the accurate identification and rapid reporting and communication to medical staff regarding patients with infectious agents of clinical importance. Microbial taxonomy continues to change at a very rapid rate in the era of molecular diagnostics including whole genome sequencing. This update focuses on taxonomic changes and proposals that may be of medical importance for years 2017 and 2018.

Contents

Over the past several years the journal of *Diagnostic Microbiology and Infectious Diseases* has published annual updates on proposed changes in bacterial taxonomy that could potentially affect the clinical and medical communities. These updates were an outgrowth of such publications previously authored by taxonomists in the 1990s that essentially ended in 2000 (Bruckner et al., 1999; Frederiksen et al., 1999). Such earlier updates attempted to include all potential taxonomic changes of medical or veterinary importance to the scientific communities.

Unfortunately, such updates are no longer feasible or manageable based upon a number of factors (Janda, 2018). These factors include the following: (1) a rapid expansion in proposed bacterial species based upon whole genome sequencing with up to one thousand newly proposed nomenspecies in a single year; (2) the limited number (<10%) of such proposed species that are recovered from clinical samples; (3) the description of >90% of these species based upon a single isolate which then becomes the type strain de facto; (4) of new species recovered from clinical specimens, the vast majority have been isolated from contaminated anatomic sites such as the gastrointestinal or urogenital tracts where their role in pathogenicity is unknown; potential pathogenic roles for some of these newly described microbes may subsequently become apparent in the future via detailed case reports or clinical series of infections; (5) many of these proposed species, identified through the Human Microbiome or Culturomics Projects (Abdullah et al., 2017), do not meet the minimum standards or requirements for validly published species under the Code (Parte, 2018; Relich et al., 2018), and finally (6) extremely limited data is presented in publications of validly published species that would help microbiologists determine whether or not these proposals could be significant to the clinical and public health sectors.

Since the format of past updates is no longer tenable yet the clinical and public health communities need to be kept aware of potential taxonomic changes of medical importance, a new approach must be sought. This update is hopefully a remedial solution to this problem. The current and subsequent updates will attempt to focus on a short narrative with limited tables on proposed nomenclature and classification changes that could impact the medical community short-term or in the foreseeable future. Such updates will occur whenever enough new taxonomic information warrants publication. Inclusion criteria for incorporation into such updates include the following: (1) a newly proposed species with a collection of at least 5 strains, the majority (typically more than half the strains described) of which have been recovered from clinical samples (see Murra et al., 2018); (2) a newly proposed species of clinical origin (<5 isolates) accompanied by enough clinical information where it is unequivocally demonstrated to be a human pathogen, or associated with an outbreak, etc. (3) proposed

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Table 1
Proposed taxonomic changes of potential clinical or public health importance

Nomenclature – New Species

Organism	Type Strain	Sources	Proposal or Comments	Ref.
Acinteobacter colistiniresistens	NIPH 2036^T (=CCM 8641^T, =CIP 110478^T, =CCUG 67966^T, =CNCTC 7573^T)	Blood, CSF, eye, pleural fluid, skin, vagina, wound	Formerly genomic species 13 and 14 (13BJ/14TU)	Nemec et al., 2017
Aggregatibacter kilianii	PN_528^T (=CCUG 70536^T, DSM 105094^T)	Blood, abdominal abscess, eye, nose, wound	Proposed species is based upon a collection of 10 strains; phenotypically most closely resembles *A. aphrophilus*	Murra et al., 2018
Elizabethkingia bruuniana	G0146^T (=DSM 2975^T, =CCUG 69503^T, =CIP 11191^T)	Blood, bronchus, urine	Formerly genomospecies 3	Nicholson et al., 2018
Klebsiella grimontii	06D021^T (=SB73^T, =CIP 111401^T, =DSM 105630^T)	AAC, blood, stool, wound	Previously listed as *K. oxytoca* phylogroups Ko2 and *K. michiganensis* Ko1. Most can be biochemically distinguished from these two species by negative melezitose reaction.	Passet and Brisse, 2018
Mycobacterium decipiens	TBL 1200985^T (=ATCC TSD-117^T; =DSM 105360^T)	Granulomatous lesion of thumb/wrist, lymph node	Closely related to the *M. tuberculosis* complex	Brown-Elliott et al., 2018
Mycobacterium grossiae	PB739^T (=DSM 104744^T, =CIP 111318^T)	Sputum, blood	Dark orange colonies	Paniz-Mondolfi et al., 2017
Rickettsia gravesii	BWI-1^T (=ATCC VR-1664^T; =CSUR R172^T)	Tick	Linked to 2004-2005 rickettsial-like illnesses on Barrow island characterized by fever, rash, and eschar	Abdad et al., 2017
Sphingobacterium cellulitidis	R-53603^T (=LMG 28764^T, =DSM 102028^T)	Pus (toe)	Case of cellulitis	Huys et al., 2017
Vibrio injenensis	M-12-1144^T (=KCTC 32233^T, =JCM 30011^T)	Blood, pus	Most closely related to *V. cincinnatiensis* and *V. metschnikovii*	Paek et al., 2017

Nomenclature – Other Issues

Organism	Type Strain[a]	Sources	Comments	Ref.
Acinetobacter dijkshoorniae	JVAP01^T	Blood, sputum, urine, wound	Proposed in 2016 Coisgaya et al., 2016), a later heterotypic synonym of *A. lactucae* NRRL B-41902^T. Type strains exhibit 100% homology by DDH. Rule 23 a,b and 24a,b apply	Dunlap and Rooney, 2018
Klebsiella aerogenes	NCTC 1006^T (=ATCC 13048^T, =DSM 30053^T, =JCM 1235^T)	Various sources	The epithet '*mobilis*' is illegitimate. *K. mobilis* and *Enterobacter aerogenes* are homotypic synonyms	Tindall et al., 2017
Mycobacterium africanum, M. bovis, M. caprae, M. microti, M. pinnipedii	ATCC 25420^T, ATCC 19210^T, ATCC BAA-824^T, ATCC 19422^T, ATCC BAA-688^T	Various sources	Heterotypic synonyms of *Mycobacterium tuberculosis* based upon WGS, dDDH, and ANI.	Riojas et al., 2018
Shewanella haliotis	JCM 14758^T	Blood, soft tissue	Heterotypic synonym of *S. algae* based upon WGS. *S. haliotis* has been reported to cause bacteremia and soft tissue infections.	Szeinbaum et al., 2018

Classification

Organism	Reference Strain(s)	Proposal or Comments	Ref.
Genus *Borrelia*	NA	Propose not enough evidence to subdivide the genus *Borrelia* into two distinct genera	Margos et al., 2017
Family *Enterobacteriaceae*	NA	Proposed reclassification of species into six different subfamilies based upon genome sequences, AAI, 16S, and CSIs	Alnajar and Gupta, 2017
Family *Enterobacteriaceae*	NA	Proposed division of current members of the family into 7 distinct families based upon cladistics analysis (WGS, MLSA, 16S, CSi): *Enterobacteriaceae, Erwiniaceae, Pectobacteriaceae, Yersiniaceae, Hafniaceae, Morganellaceae* and *Budviciaceae*	Adeolu et al., 2016
Escherichia hermannii	ATCC 33650^T	Proposed reclassification to a new genus, *Atlantibacter* based on MLSA	Hata et al., 2016
Escherichia vulneris	ATCC 33821^T	Proposed reclassification into a new genus *Pseudescherichia* gen. nov.	Alnajar and Gupta, 2017
Fusobacterium nucleatum subspecies	*F. animalis* (ATCC 51191^T), *F. poplymorphum* (ATCC 10953^T), *F. vincentii* (ATCC 49256^T)	Proposed reclassification and elevation of subspecies to species rank as *F. animalis, F. poplymorphum,* and *F. vincenttii,* based upon ANI and GGD	Kook et al., 2017
Haemophilus ducreyi	CIP 54.2^T (=ATCC 33940^T)	Not phylogenetically related to *H. influenzae*. Should be placed in a new genus based upon WGS and predicted protein sequences.	Christensen and Bisgaard, 2018
Mycobacterium avium complex	*M. avium* (ATCC 25921^T) *M. intracellulare* (ATCC 13950^T)	Proposed definition for inclusion as a member of the complex based upon presence of corresponding values of two of the following targets: 16S, *hsp*65, *rpoB*, WGS	van Ingen et al., 2018
Mycobacterium abscessus complex		Proposal to elevate subspecies *bolletii* and *massiliense* to species rank as *M. bolletii* and *M. massiliense*	Adekambi et al., 2017
Mycobacterium yongonense	DSM 45126^T (=KCTC 19555^T)	Proposal to transfer to *Mycobacterium intracellulare* as subsp. *yongonense* based on WGS	Castejon et al., 2018
Photorhabdus asymbiotica susp. *australis*	CIP 108025^T (ACM 5210^T)	Proposal to elevate subspecies to species status as *P. australis* based upon several techniques including WGS, MALDI-TOF, FAME, and isDDH	Machado et al., 2018

Abbreviations: 16S = 16S rRNA gene sequencing; AAC = antibiotic-associated colitis; AAI = average amino acid identity; ANI = average nucleotide identity; CSF = cerebrospinal fluid; CSI = conserved signature indels; dDDH = digital DNA-DNA hybridization; is DDH = *in silico* DNA-DNA hybridization; FAME = fatty acid methyl ester analysis; GGD = genome-to-genome distance; *hsp*65 = heat-shock protein; MLSA = multi-locus sequence analysis; NA = not applicable; *rpoB* = beta subunit of RNA polymerase; WGS = whole genome sequencing.

Culture Collections: ACM = Australian Collection of Microorganisms; ATCC = American Type Culture Collection; CCUG = Culture Collection University of Göteborg, Department of Clinical Bacteriology, Institute of Clinical Bacteriology, Immunology, and Virology, Göteborg, Sweden; CIP = Collection de l'Institut Pasteur, Institut Pasteur, Paris Cedex 15, France; CNCTC = Czech National Collection of Type Cultures, National Institute of Public Health, Praha, Czech Republic; CSUR = Collection de Souches de l'Unité des Rickettsies; DSM = DSMZ-Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, Germany; JCM = Japan Collection of Microorganisms, RIKEN BioResource Center, Japan; KCTC = Korean Collection for Type Cultures, Korea Research Institute of Bioscience & Biotechnology, Republic of Korea; LMG = Collection of the Laboratorium voor Microbiologie en Microbiele Genetica, Belgium; NIPH = Collection A. Nemec, National Institute of Public Health, Prague, Czech Republic.

[a] The type strains listed for Roijas et al. (2018) are in chronological order of the species listed under "Organism" (e.g., *M. microtii* = ATCC 19422^T).

classification changes involving genera or species of major clinical or public health significance; (4) taxonomic issues of clinical importance related to nomenclature such as illegitimate names, heterotypic synonyms, etc.

Proposed taxonomic changes listed below are an update from the last edition in *Diagnostic Microbiology and Infectious Diseases* (Janda, 2017) through the end of November of 2018. The basic information was derived from the following sources: (1) a monthly review of the leading 20 or 30 peer-reviewed publications dealing with bacterial taxonomy and nomenclature some of which are listed in Table 1 of the previous update (Janda, 2017); (2) literature searches using key words related to bacterial nomenclature, classification, and taxonomy at such sites as PubMed (https://www.ncbi.nlm.nih.gov/pubmed); (3) several web links with inclusive journal databases on microbiology and infectious diseases such as Free Medical Journals (http://freemedicaljournals.com/). Some other sites not listed here but used in this update no longer exist; (4) ongoing communications with various taxonomists in the field. At the time of writing, most but not all of these newly proposed species were validated (exception see: *Elizabethkingia bruuniana*). The reader is referred to the List of Procaryotic Names with Standing in Nomenclature (LPSN) for up-to-date information (http://www.bacterio.net/elizabethkingia.html).

The table lists a compilation of such proposed changes covering 2017 and 2018. The table is subdivided into three areas, (i) the description of potentially new species, (ii) nomenclature issues involving species already with taxonomic standing in the literature that need to be resolved, and (iii) proposals to reclassify existing groups into new species, genera, or families. Among notable new species proposals were the description of 10 isolates of *Aggregatibacter kilianii* by Murra et al. (2018) from various clinical specimens and five strains of *Klebsiella grimontii* isolated from human blood ($n=3$) and two wounds or soft tissue ($n=2$) (Passet and Brisse, 2018). Nemec et al. (2017) also described a new species of *Acinetobacter, A. colistiniresistens* (genomic species 13BJ/14TU), based upon a characterization of 24 human isolates recovered from a catheter, conjunctiva/conjunctivitis, and skin in addition to those listed in the table. Both the numbers and sources of strains reported in these publications suggest that these may potentially be important new pathogens of clinical or public health importance in the future. Among other important nomenclature issues is the proposal that several species of the *M. tuberculosis* complex be reclassified as heterotypic synonyms of M. *tuberculosis sensu stricto* (Riojas et al., 2018) and that the species name *Klebsiella aerogenes* replace the epithet "*mobilis*" for *K. mobilis* because of illegitimacy issues (Tindall et al., 2017). These later formal proposals require an opinion to be rendered by the Judicial Commission of the International Committee on Systematics of Prokaryotes (Tindall, 2014). Major classification changes proposed include division of current genera in the family *Enterobacteriaceae* into multiple families (Adeolu et al., 2016; Alnajar and Gupta, 2017) and transfer of some *Escherichia* species into newly proposed genera (Alnajar and Gupta, 2017; Hata et al., 2016).

In summary then, this update should be viewed as an aid to clinical microbiologists in need for keeping up with accrediting agency requirements regarding bacterial taxonomy. It is in no way meant to be exhaustive or comprehensive. This is simply one of several methods at the disposal of clinical laboratories to remain current in regards to bacterial systematics (see table 3, Janda, 2018).

Conflict of interest

There are no conflicts of interest.

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