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Review Article

Taxonomic update on proposed nomenclature and classification changes for bacteria of medical importance, 2015

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A B S T R A C T

A key aspect of medical, public health, and diagnostic microbiology laboratories is the accurate and rapid reporting and communication regarding infectious agents of clinical significance. Microbial taxonomy in the age of molecular diagnostics and phylogenetics creates changes in taxonomy at a rapid rate further complicating this process. This update focuses on the description of new species and classification changes proposed in 2015.

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1. Introduction

With the publication *Approved Lists of Bacterial Names* in 1980 almost 1800 bacterial species were immediately approved for retention, thus creating a starting point for bacterial nomenclature in the future (Skerman et al., 1980). The number of such approved species has escalated dramatically over the past three decades and most notably since the introduction of alternative methods to the gold standard, DNA–DNA hybridization (DDH), to define species status at the molecular or phylogenetic level. In 2002, an ad hoc committee revisited this same issue and reevaluated species definition in bacteriology. The recommendations of this committee included the addition of almost full-length 16S rRNA gene sequences in the description of new species and the use of other molecular technologies such as multilocus sequence typing (MLST) in the characterization of DNA relatedness (Stackebrandt et al., 2002). Since this publication still other innovative and robust approaches to determining species status at the molecular level have made their ways into both the research and clinical laboratories. Among these are matrix-assisted laser/desorption – time of flight mass spectrometry (MALDI-TOF MS) and average nucleotide identity (ANI). The cumulative results of these emergent technologies will undoubtedly be the redefinition of how new species are characterized and defined in the future.

From its less than auspicious start the number of validated bacterial species has risen from 1792 in 1980 to more than 10,500 by August of 2013 with a peak of 663 validly published species in 2009 (Parte, 2014). If these numbers are not staggering enough Schloss and Handelsman (2004) have estimated the minimum bacterial richness on Earth to be approximately 35,498 species. While this projected number is astounding this value is extremely low when compared to studies estimating prokaryotic diversity approximating a mind-boggling total of 8–10 million species (Curtis et al., 2002). This roughly equates to bacterial taxonomists only identifying and naming 0.1–29.5% of the estimated number of species in the world.

With the number of newly proposed species over the past decade ranging from 372 to 666 on an annual basis (Parte, 2014) it is probably an insurmountable task for most clinical microbiology laboratories to keep abreast of important changes in bacterial taxonomy including the description of new species and the reclassification of others of medical and public health importance. Two basic facts make this problem less daunting than it appears. First, >90% of the new bacterial species published in the last few years were based upon the characterization of a single (type) strain (Oren and Garrity, 2014). This is a trend that was initially noticed in the 1990s by Frederiksen in his compilation of new species of medical and veterinary importance each year. When only a single strain of a new species exist its significance to the medical community is dubious until such time as its importance can be addressed through the recovery of additional strains associated with clinical infections. Secondly, even with these newly described species consisting of a single type strain more than 90% are of environmental (ocean, sea, plants, soil) or animal origin. Finally for the few new species that are associated with clinical samples, many originate from specimens not associated with infectious processes such as feces but rather are described as part of large international research investigations such as the human microbiome project (Janda, 2015). Thus, the number

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of taxonomic issues related to the clinical diagnosis in the microbiology laboratory is reduced significantly.

2. Updates on microbial taxonomy

There are a couple of different resources for microbiologists. A number of journals actively publish peer-reviewed articles describing either the recognition of a new species or the reclassification of an older nomenspecies (e.g. *Pseudomonas maltophilia → Xanthomonas maltophilia → Stenotrophomonas maltophilia*) based upon phylogenetic data. The most important of these journals such as the *International Journal of Systematic and Evolutionary Microbiology* (IJSEM) is almost exclusively devoted to the description of new taxa or the reclassification of existing species. One surprise to readers, however, might be that *Antonie van Leuuwenhoek* is now the second leading journal handling taxonomic papers, with 13 in 2009 to 74 in 2011 and >100 thereafter (Oren and Garrity, 2014; Sutcliffe and Trujillo, 2013). In addition to these two journals *Systematic and Applied Microbiology* and *Current Microbiology* both publish on the description of many new taxa each year. Other periodicals to a lesser extent also publish papers describing new species including *Standards in Genomic Sciences, Anaerobe, Archives of Microbiology,* and *Research in Microbiology* to name several. IJSEM periodically publishes a Validation List of new names and combinations effectively but not validly published in journals other than IJSEM (Tindall, 2015; Weissfeld, 2009). These validation lists cite the source of the original publication which the reader can refer to get more detailed information. For instance, Xu et al. described a new klebsiellae recovered from heavily polluted water in 2010 they named *Klebsiella alba*. However this taxon only appeared on Validation List no. 166 in 2015 when the proposal had met the minimal standards required for description of a new species under the *Bacteriological Code* (1990 Revision) (Oren and Garrity, 2015). These minimal standards include such things as deposition of the type strain in at least two internationally recognized culture collections such as the American Type Culture Collection (ATCC) and the Collection de l'Institut Pasteur, Institut Pasteur (CIP).

While these resources are extremely useful for microbiologists they are time-consuming to review, analyze, and extract whatever information is needed. To many or most clinical microbiologists or laboratory directors they need a more efficient and easy method to digest summaries of taxonomic changes that can be important to the diagnostic laboratory in the future. A recent effort to revive Dr. Frederiksen's wonderful updates was recently made for calendar years 2013–2014 and published in *Diagnostic Microbiology and Infectious Diseases* (Janda, 2015). This report is a continuation of this update process with a review of proposed taxonomic changes of clinical and public health importance for calendar year 2015. Not all of the new genera and species listed in the tables below were validated at the time of submission of this update.

3. 2015 update

3.1. Proposed new taxa

Recently proposed gram-negative and gram-positive bacterial species associated with human samples are listed in Tables 1 and 2 respectively. These 2015 proposals include three novel genera namely *Faucicola, Ezakiella,* and *Mageebacillus* (Austin et al., 2015; Humphreys et al., 2015; Patel et al., 2015). Of the 28 proposed species and/or new genera and species listed in these two tables exactly half are based upon the description and characterization of a single strain which de facto becomes the type strain. Rules governing the proposal of new bacterial taxa are listed in the 1990 *Bacteriological Code* with sporadic updates or changes in the code published in the IJSEM. For those taxa not originally published in the IJSEM, validation awaits meeting the minimal criteria for description of a new species plus publication on a validation list in IJSEM (Oren and Garrity, 2015; Tindall et al., 2006). Additional proposed standards for the description of new species and

genera in specific families or suborders are posted periodically in IJSEM (Schumann et al., 2009). Updates on species without standing in nomenclature can be found at http://www.bacterio.net/-nonvalid.html.

3.2. Classification issues and nomenclature issues

Several published studies in 2015 may have potential impact among the medical and scientific communities (Table 3). One phylogenetic investigation proposes separating all *Burkholderia* species into two groups with the species pathogenic for humans retained within the genus *Burkholderia* while the remaining non-pathogenic taxa reclassified into a new genus *Paraburkholderia* (Sawana et al., 2014). A second proposal that is almost the reverse of this involves the unification of all current species under the genus *Chlamydia* which would result in the elimination of *Chlamydophila* which currently includes such species as *C. pneumoniae* and *C. psittaci* (Sachse et al., 2015). Still another proposed classification change is to remove both *Actinobaculum schaalii* and *A. urinale*, both of which are human pathogens, from the genus and transfer them to a new genus, *Actinotignum* (Fendukly and Osterman, 2005; Yassin et al., 2015a). Finally, the legitimacy of two other species (*Actinobaculum massilense, Serratia glossinae*) has been questioned which has some, albeit minor, potential ramifications for clinical microbiologists (Yassin et al., 2015a, 2015b).

4. Discussion

The current update lists most of the proposed new species or classification changes associated with bacteria of potential clinical and public health importance for the year 2015 and reaffirms and extends existing and emerging trends in bacterial nomenclature and taxonomy. Although a proposal to amend Recommendation 30b of Rule 30 of the *Bacteriological Code* to require a minimum of 5 strains to base the description of a new species upon (Christensen et al., 2001), this request has never been officially accepted, and in fact, it appears fewer and fewer strains are now being used in the characterization and description of new taxa. Of the 28 proposed species listed in Tables 1 and 2, only 5 studies (17.8%) met the standard of 5 strains with only 3 of these (10.7%) analyzing 10 or more isolates. For clinical microbiologists this is problematic in that the reader of such articles has no idea concerning the clinical relevance of such species based upon frequency, environmental and global distribution, and pathogenicity. A second trend previously noted (Janda, 2015) involves the clinical sources from which these bacterial species originate. Overall, 10 species (35.7%) were either solely recovered from human feces or were listed as from a clinical source of unknown origin. These two trends together are a reflection of basic developments among taxonomists spurred by the analysis of the human microbiome through traditional methods, culturnomics, and taxonomogenomics (Fournier et al., 2015).

Of primary importance to laboratorians is the clinical relevance of these proposed nomenclature changes. Among the taxa listed in Tables 1 and 2 their individual clinical importance is presently unknown. The description of two patients with infective endocarditis by Sohn et al. (2015) in this journal clearly documents the pathogenicity of *B. cardium* but leaves unanswered questions regarding prevalence and geographic distribution. Previously this species was mis-identified as *Brevundimonas* using Vitek 2 (Table 1). Similarly, the description of 16 strains each of *A. seifertii* and *A. variabilis*, particularly from non-intestinal sites such as blood, wounds, and urine suggest a likely but unproven causal relationship with human disease (Krizova et al., 2015; Nemec et al., 2015). Other taxa that appear to be potential human pathogens include *Mycobacterium saopaulense* (cornea, cervical abscess) and *Paracoccus sanguinis* (multiple blood isolates) (McGinnis et al., 2015; Nogueira et al., 2015). Further confirmation of these facts by independent investigators or other case report descriptions is needed.

In addition, 2 newer trends in this year's update are apparent. First, the traditional gold standard of defining a new species by DDH is quickly