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Review

Taxonomic update on proposed nomenclature and classification changes for bacteria of medical importance, 2016

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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 in the age of molecular diagnostics and phylogenetics creates changes in taxonomy at a logarithmic rate further complicating this process. This update focuses on the description of new species and classification changes proposed in 2016.

Contents

1. Introduction

In the last 2 editions of this annual update covering the years 2013–2014 (Janda, 2015) and 2015 (Janda, 2016) a total of 72 newly proposed bacterial species isolated from clinical specimens were reviewed. These newly described species did not include subspecies of clinical origin nor taxa recovered from environmental sites such as soil, marine life, plants, and other animals. In sheer numbers, this later group greatly dwarfs those reported from clinical sources.

2. Explosion in documented bacterial species

There are currently 12,391 validly published bacterial species names covered under the Rules (1 August 2013) at the time of this writing since publication of the Approved List in 1980. This makes the total number of named prokaryotic species at more than 14,300 (Hugon et al., 2015, 2017) (http://www.bacterio.net/-number.html). This number does includes homotypic and heterotypic synonyms among other nomenclature ambiguities. A recently constructed on-line database lists 2172 species that have been isolated from humans, or roughly 15.5% of the total known species to date (Hugon et al., 2015). Of these 2000 plus species more than 85% fall into the phyla belonging to the Firmicutes, Proteobacteria, and Actinobacteria, respectively.

Current estimates on the biodiversity of microbes on this planet range from 8 to 10 million (Janda, 2016) although these theoretical values are not without controversy as such numbers are calculated

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using operational taxonomic units (OTU) based upon open-reference databases of short-read 16S rRNA gene sequences (Lennon and Locey, 2016). Many of these OTUs have been rarely reported and the number of ecosystems sampled few and restricted in scope suggesting that the total number of microbial species on earth could easily exceed 11 million.

Two different resources have fueled this major expansion in the description of bacterial species associated with humans. The first involves the multi-center Human Microbiome Project (HMP) with the characterization of microbial flora associated with healthy physiologic states and indirectly disease-related conditions (Lewis et al., 2012; Lloyd-Price et al., 2016; Tuddenham and Sears, 2015). An alternative pathway involving HMP that has led to the discovery of human-associated species has been the "microbial culturnomics" studies pioneered by Didier Raoult and his colleagues (Lagier et al., 2012). Both avenues have resulted in the description of many new species associated with the human gastrointestinal tract. However non-cultivatable molecular methods, including full genome sequencing, are making significant in-roads in assessing the genetic diversity of microbes' in different ecologic environments. These facts will lead to the description of a staggering number of new species in the near future without any linkage to the human condition. As a result, the percentage of prokaryotic species associated with clinical conditions (normal flora, transient colonization, infection) will continue to decline from the current threshold approximating 15%.

3. Resources on the description of proposed new bacterial species

To add to the taxonomic and nomenclature complexity resulting from the myriad of recently named species comes the issue for clinical microbiologists of how to keep up with proposed changes and secondly are these proposals relevant to the practice of clinical microbiology and medicine. The fact that smaller and smaller percentages of newly described taxa involve species isolated from clinical sources or associated with human infections complicates this process. For instance, the website List of Prokaryotic Names with Standing in Nomenclature (LPSN) is a valuable resource for all named species based upon classification in related groups such as genera and families (see http://www.bacterio.net/index.html). However this website is not particularly useful to rapidly identify or separate clinically relevant species from environmental ones.

At the same time the landscape of scientific journals that publish articles on proposed new species continues to change. In last year's edition of this article *Antonie van Leeuwenhoek* had become the second leading journal publishing such studies after the *International Journal of Systematic and Evolutionary Microbiology* (IJSEM) (Janda, 2016). This trend has continued into 2016 with these 2 journals accounting for almost 85% of newly described species listed in Table 1. This table also shows the marked differences in the number and types (clinical associated, environmental) of species being described. Of the more than 900 proposals listed in these 7 periodicals only 94 or 9.9% have been recovered from clinical specimens obtained from healthy or ill persons. Almost 70% of these 94 publications recorded in 2016 were published in a single journal, *New Microbes and New Infections* (NMNI), whose general content is open access. Most of these species descriptions stem from the culturnomics investigations of Didier Raoult and colleagues (Lo et al., 2016a; Ndongo et al., 2016). These trends will continue in 2017.

Table 1
Publications in selected journals describing new bacterial species, 2016[a].

Journal	New Bacterial Species[b]	Associated with Clinical Sources (%)[c]
International Journal of Systematic and Evolutionary Microbiology	719	21 (2.9)
Antoine van Leeuwenhoek	80	4 (5)
New Microbes and New Infections	67	65 (97)
Archives of Microbiology	26	0
Current Microbiology	25	1 (4)
Systematic and Applied Microbiology	24	1 (4)
Anaerobe	3	2 (67)

[a] Approximate numbers.
[b] No. of publications listing one or more new bacterial species through December, 2016.
[c] Percent of articles published in selected journals describing species recovered from clinical sources.

4. Current taxonomy – issues for clinical microbiologists and related disciplines

While the present definition of a bacterial species continues to be scrutinized, analyzed, reevaluated and potentially redefined, the chasm that already exists between modern bacterial taxonomy in a post-genomic era and its relevancy to clinical and medical specialties continues to widen (Rosselló-Móra and Amann, 2015; Thompson et al., 2013, 2014; Van Regenmortel, 2010). Current bacterial taxonomy as presently defined with the description and naming of new genera and species (nomenclature, classification) has significant issues concerning its general usefulness to medical staff as it relates to the isolation, identification, diagnosis and treatment of infectious diseases. Those issues appear to be increasing in both number and scope as more and more novel taxa are described in this molecular era thereby limiting the usefulness of such data to a major user (clinical microbiology) in terms of complexity of proposed nomenclature and classification, applicability to medical diagnostics, and immediate utility.

Table 2 contrasts some of the current differences between character traits reported on proposed new species isolated from human anatomical sites [left column] to bacterial characteristics clinical microbiologists and infectious disease specialists would like to see accompany such descriptions [right column]. In addition to long-standing issues regarding the limited number of strains used to propose new bacterial species and the increasingly limited phenotypic data included in such descriptions, other trends have been observed as well. Many of the culturnomic studies published in NMNI in 2016 are incidental in nature, that is, they do not meet the minimum requirements for inclusion on a validation list in the IJSEM. These new species proposals have the scientific name published in quotation marks indicating that the name is being proposed but not for validation purposes. Two examples include "*Africanella massiliensis*" (Alou et al., 2016a) and "*Bacillus mediterraneensis*" (Alou et al., 2016b), both isolated from human gut microbiota. In addition to these new proposals each description is accompanied by only a minimal amount of microbiological information, typically including 16S rRNA sequence data and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALD-TOF MS) analysis. More than 25 such species were published in 2016 that fall into this category.

Table 2
Current taxonomic descriptions and related issues: reality vs need.

Current Taxonomy[a]	What Clinical Microbiologists Need
• Species proposals often based on a single strain [type] • Limited descriptions of some non-validly published taxa • Limited phenotypic data provided • Species often cannot be separated from nearest neighbors on a bio chemical basis • Type strain may not be "centrist" in regards to phenotypic characteristics of genus/species • Identical names or epithets often used for multiple species belonging to different genera	• Frequency and sites of isolation of new species in clinical specimens • Phenotypic data useful in identifying species with commercial-based systems • Human pathogenicity • Antimicrobial susceptibility data • Taxonomy relevant to the practice of clinical microbiology and infectious diseases

[a] For proposed species isolated from one or more clinical samples.