



Same meat, different gravy: ignore the new names of mycobacteria

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A new name for most *Mycobacterium* species has been recently proposed. According to taxonomic rules novel and previous nomenclature coexist and are synonyms. The use of the latter has the advantage of avoiding confusion for healthcare and harm for patients. <http://bit.ly/2XhTACc>

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In a recent article, GUPTA *et al*. [1] have proposed a revision of the taxonomy of mycobacteria with the redistribution of 150 species of the genus *Mycobacterium* into five different genera; the four newly proposed genera hosting the nontuberculous mycobacteria (NTM) are called *Mycobacteroides*, *Mycolicibacter*, *Mycolicibacterium* and *Mycolicibacillus*. The proposed taxonomy is based on the theory of synapomorphies, molecular markers that most likely appeared early in an ancestor and then were vertically

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transmitted to descendants [2]. The detection of a number of such molecular markers, represented either by specific amino acid insertions/deletions or by whole proteins, selectively present in evolutionary-related groups of species, clearly depicts five major clades within the conventional genus *Mycobacterium*. The work is mostly sound and the emerging phylogeny impressively overlaps the ones originated by other phylogenomic approaches [3, 4]. The novelty is that GUPTA *et al.* [1] have suggested to assign to each of these clades the status of independent genera.

What has caused most confusion among mycobacteriologists was not the study by GUPTA *et al.* [1], but the validation of the novel nomenclature [5] published by the *International Journal of Systematic and Evolutionary Microbiology (IJSEM)*, the official publication of the International Committee on Systematics of Prokaryotes. We believe the new nomenclature has the potential to cause confusion and provides no benefits to the field of clinical mycobacteriology. Investigating the rules regulating the nomenclature of prokaryotes, unknown to the majority of microbiologists and clinicians, produced surprising results. Accordingly, in this editorial, we aim to provide clinicians involved in the management of patients with NTM disease state of the art information about rules regulating the nomenclature of prokaryotes and that, in spite of this recent publication [1], the currently used nomenclature of NTM can remain unchanged.

The bacterial taxonomy is ruled by the Code of nomenclature of prokaryotes [6] (previously Bacteriological code) that, differently from common assumptions, does not provide instructions on description of novel species nor in making decisions in case of divergent opinions among taxonomists. We were indeed surprised to read that, as stated by Tindall [7], “an ‘official’ taxonomy has not been introduced” in accordance with the principle of “freedom of taxonomic thought and action”.

Actually the Code only provides valid names of bacteria, given that two major conditions are fulfilled: the valid publication and the priority [8]. To be valid, a publication describing a new taxon needs to contain a protologue. The protologue is a short paragraph including the name of the taxon followed by the specification *nov.* (in case of a new species, *sp. nov.*; in case of a new genus *gen. nov.* etc.), the etymology with its syllabication and accentuation, and by a description of the salient features of the new taxon, the designation of the type strain, and the accession numbers certifying its deposition in at least two international culture collections located in different countries. Priority means that in cases where the proposed new name has been previously assigned to another validly published taxon, the latter has the priority and a novel name must be proposed prior to validation.

The publication in *IJSEM* automatically grants validity to a new name; in contrast, in order for an organism name to be recognised as valid if published in other journals, the authors must request the new name to be included in a Validation list published, upon check of conformity, by *IJSEM*.

When a change of a validly published species or genus name is proposed, the new name, once validly published becomes a heterotypic synonym of the previous ones. Thus, both are correct (valid) and can be used without restriction. The common thought that the most recent name replaces the previous one is groundless. A validly published name is not ever withdrawn.

The article by GUPTA *et al.* [1] is indeed validly published (it contains the protologue for all the species taken into account, where the respective type strains are confirmed) and the new names have been included in a validation list by *IJSEM* [5]. As a consequence, the species allocated in genera other than *Mycobacterium* (*Mycobacteroides*, *Mycolicibacter*, *Mycolicibacterium* and *Mycolicibacillus*) have synonyms, both of which can correctly be used. The authors of this editorial, and probably the majority of microbiologists and clinicians, were not acquainted with this possibility.

The nomenclature based on five genera also has two major pitfalls; first, it applies and is validly published with limit to the 150 species investigated by GUPTA *et al.* [1]; however, at least 40 others continue to have *Mycobacterium* as the only valid name. Second, four of the genomes investigated in the study of GUPTA *et al.* [1]: *M. rhodesiae*, *M. szulgai*, *M. tusciae* and *M. vulneris* were mislabelled [4]. *M. rhodesiae* and *M. tusciae* proved to be unidentified rapidly growing mycobacteria; *M. szulgai* proved to be *M. kubicae* and *M. vulneris* proved to be *M. porcinum*. This means that the transfer of *M. vulneris* (a slow grower) to the genus *Mycolicibacter* is incorrect [9].

Overall, the updated nomenclature and its adoption in *IJSEM* and in databases used for sequence-based strain identification (*e.g.* GenBank) or MALDI-TOF mass spectra databases does a disservice to microbiologists, clinicians and patients. Nontuberculous mycobacteria may be diverse in their genetics and biology, but they produce remarkably similar disease manifestations in distinct populations at risk. This uniformity and the lessons to be learned from it are important for both clinicians as well as the affected patients. Hence, to repeat the words of Amalio Telenti, now 20 years ago: “clinical meaningfulness should be the key to taxonomic precision” [10]. The pragmatic solution is to choose the nomenclature less prone to errors and, in this view, the one based on the single genus, *Mycobacterium*, has important advantages.

Significant progress has been gained in recent years by promoting evidence-based clinical care, treatment outcomes and clinical trials in nontuberculous mycobacterial infections as a group, sharing a simple term familiar to clinicians and patients (mycobacteria) and an appropriate acronym (NTM) [11–14]. The proposed new nomenclature does not help this cause.

As it seems, GUPTA *et al.* [1] did rather not solve a burning taxonomic problem within the genus *Mycobacterium*; their findings, while being mostly correct and scientifically sound, do however not justify the disruption caused by the splitting and renaming of this medically important genus. Substantial cost and effort will be needed to update procedures and laboratory information management systems in hospitals and laboratories which support physicians and care-givers in their daily work, to enable them to deal with the new names and their synonyms without confusion. All this is in fact without a perceivable advantage for the patients nor healthcare in general.

We are confident that microbiologists and clinicians will clearly support the possibility, offered by the Code, to wilfully ignore renaming of clinically important organisms such as nontuberculous mycobacteria.

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