

Taxonomic subcommittees and minimal standards for the description of prokaryotes



Marthía E. Trujillo

Departamento de Microbiología y Genética
Edificio Departamental, Lab 205
Campus Unamuno 37007
Salamanca, Spain
Tel (34) 9232 94532
Fax (34) 9232 24876
Email met@usal.es

The preparation of minimal standards for the description of new taxa is one of the tasks of the taxonomic subcommittees working under the auspice of the International Committee on Systematics of Prokaryotes. Minimal standards are intended to provide bacteriologists involved in the taxonomy of prokaryotes a set of essential requirements for the description of new taxa.

Microbial taxonomists are constantly describing new taxa in an effort to keep an inventory of the vast microbial diversity. The number of new species described seems to advance at a rhythm that is difficult to follow and yet it appears that we are still working at the tip of the iceberg. An upmost effort will be necessary to reveal and understand microbial diversity and, in this respect, taxonomy plays a crucial role.

Formal descriptions of novel taxa remain the bedrock of taxonomy, along with the re-evaluation of established classification schemes. A novel organism should be characterised as fully as possible in order for subsequent identification systems to have a reliable basis on which to work. The more reliable the characterisation and classification, the greater chance one will have of being able to pick identification methods which are both accurate and have a long-term future¹.

But, when a researcher embarks on the task of describing a new organism, a question may form in his/her mind: which tests should be the most appropriate to perform? As Tindall *et al.*¹ point out, an orderly approach to the characterisation and identification of a strain should be adopted while a 'shotgun' strategy in which all sorts of tests are performed is not recommended. One of the main problems with the description of new species is the lack of comparison between the new taxon and existing ones because there is no uniformity in the tests performed. In many cases, the resources available or predilection for certain methods will determine which tests will be carried out by a researcher. The

failure to compare two or more organisms using a set of common tests prevents the establishment of stable identification systems. While no prescription can be given for which tests to perform because they differ among genera and species, a working framework is possible.

To ensure the optimal circumscription of novel taxa to be named, it was agreed during a meeting of the Judicial Commission of the International Committee on Nomenclature of Bacteria in Mexico City, 1970, that the *Bacteriological Code* included a recommendation to the effect that, "descriptions of new taxa contained information on certain characteristics, the list of characteristics to vary according to the taxon and to be updated as necessary"². Therefore Recommendation 30b of the *Code* states that: "Before publication of the name and description of a new species, the examination and description should conform at least to the minimal standards (if available) required for the relevant taxon of bacteria"³. The preparation of minimal standards for the description of new taxa is therefore one of the tasks of Taxonomic Subcommittees of the International Committee on Systematics of Prokaryotes (ICSP). Among others, the subcommittees are also expected to make recommendations regarding taxonomic procedures, changes in nomenclature, recognition of types of various taxa, or classification. Article 9 of the *Bacteriological Code* (1990 revision)³ refers to the organisation and functions of these taxonomic subcommittees.

Minimal standards are intended to provide bacteriologists involved in the taxonomy of prokaryotes a set of essential requirements for the description of new taxa, but in no way limiting the extent of investigation that can be performed. Instead, these recommendations are aimed at preventing the establishment of insufficiently characterised 'new' taxa, which are later difficult to handle by other microbiologists and quite often represent a source of confusion in taxonomic classification⁴. Therefore, these recommendations should not be seen as an obstacle for publishing the description of new species but rather as a working background that would benefit the taxonomic research community.

Unfortunately, minimal standards are not available for all organisms covered by the subcommittees, and even more critical, in some cases, taxonomic subcommittees for certain taxa have never been created. The ICSP web page (<http://www.the-icsp.org/>) lists 28 taxonomic subcommittees, a number that is obviously insufficient to cover the taxa currently described. Furthermore, fewer than 20 minimal standards have been published to date (a list can be found in Tindall *et al.*⁵).

Within this list, minimal standards for the description of aerobic, endospore-forming bacteria⁶; the class *Mollicutes*⁷; the family *Pasteurellaceae*⁸; the family *Halomonadaceae*⁴ or the suborder *Micrococcineae*⁹ have recently been published. In general, these guidelines have been well accepted by authors^{10–14} and in some cases adherence to the spirit of the standards has been excellent since the first publication appeared^{7,15}. This positive response should encourage the publication of additional standards and members of these subcommittees should be regarded as a group of experts offering advice to others for the description of specific taxa.

In addition, authors should expect manuscripts with the description of new taxa to be judged in part on fulfilment of minimal standards. Indeed it is highly recommended by the *International Journal of Systematic and Evolutionary Microbiology* (IJSEM) to follow standards when available for papers submitted to the journal^{16,17}. The practical application of minimal standards in the formal description of novel taxa would also facilitate the work of reviewers and editors who share responsibility in the endorsement of novel species descriptions⁷. Furthermore, if the application of these standards is also adopted by journals that support the publication of new taxa, the subsequent validation process of the new names effectively published outside the IJSEM would render less difficult. Indeed, journals such as *Antonie van Leeuwenhoek*, *Journal of Microbiology* and *Systematic and Applied Microbiology* contain specific instructions for the publication of taxonomy papers where these guidelines are recommended.

A detailed description of the requirements for valid publication of names of prokaryotes is offered by Tindall *et al.*¹⁷. Briefly, the first requirement towards complying with valid publication of a new name is that it must be effectively published (rule 25 of the *Bacteriological Code*), which usually means in the form of a peer-reviewed article. Publication of a name in the IJSEM constitutes effective publication, but only if it conforms to the requirements laid down in the *Bacteriological Code*. However, publication of an original article in the IJSEM does not automatically constitute valid publication¹⁷. When a name is effectively published in another journal or in a book and it meets the requirements for valid publication, authors may request that the proposed name be included on a Validation List (authors must provide three hard copies or an electronic copy of the published paper to the editorial office of the IJSEM).

It is essential to involve as many scientists (both young and experienced) as possible in the preparation of minimal standards to ensure a consensus document. It is also important that taxonomists directly working with the specific taxon for which the minimal standards are invited to participate. Despite many efforts, participation and activity in some of the current taxonomic subcommittees is lower than desired. Concern for this apparent inactivity has already been discussed by members of some of these working groups¹⁸. One reason may be the lack of scientists

willing to participate (retired, no longer interested, unaware of these subcommittees, and so on) or even just a lack of time for those interested in joining these subcommittees; therefore, a clear drawback in the preparation of these documents appears to be the number of taxonomists involved, willing or with sufficient time to contribute their knowledge and experience in the field.

While some may argue that insufficient information is available to propose a set of characterisation methods for certain taxa, it is still possible to propose a common framework which can be updated as additional information is gathered. Even if the 'complete list' of procedures is not (and cannot be) presented in a single document, an initial list of guidelines (or tests) that will be common to all species descriptions for a specific group would be very useful. We should not forget that the description of minimal standards is a dynamic process and periodic revision of these documents is necessary to include new information.

In summary, there is an urgent need for experienced and new taxonomists to join efforts in the preparation of minimal standards, which will be of great value to newcomers in the area of taxonomy. The future of this discipline and our ability to attract young scientists into the field will be in part in our ability to offer new taxonomists a consensus working procedure which will facilitate their work and hopefully will contribute to a better characterisation of established and new taxa, which after all, is a key element in prokaryote systematics, regardless of the methodology used and consequently an advancement in our understanding of microbial diversity.

Acknowledgements

The author acknowledges D Labeda and L Wayne for fruitful discussions in the preparation of this manuscript.

References

1. Tindall, B.J. *et al.* (2007) Phenotypic characterisation and the principles of comparative systematics. In *Methods for General and Molecular Microbiology* (Reddy, C.A. ed), pp. 330–393, ASM Press.
2. Lessel, E.F. (1971) Judicial Commission of the International Committee on Nomenclature of Bacteria. Minutes of meeting, 5 August 1970. *Int. J. Syst. Bacteriol.* 21, 100–103.
3. Lapage, S.P. *et al.* (1992) *International Code of Nomenclature of Bacteria* (1990 Revision). Bacteriological Code. American Society for Microbiology.
4. Arahal, D.R. *et al.* (2007) Recommended minimal standards for describing new taxa of the family *Halomonadaceae*. *Int. J. Syst. Evol. Microbiol.* 57, 2436–2446.
5. Tindall, B.J. *et al.* (2010) Notes on the characterization of prokaryote strains for taxonomic purposes. *Int. J. Syst. Evol. Microbiol.* 60, 249–266.
6. Logan, N.A. *et al.* (2009) Proposed minimal standards for describing new taxa of aerobic, endospore-forming bacteria. *Int. J. Syst. Evol. Microbiol.* 59, 2114–2121.
7. Brown, D.R. *et al.* (2007) Revised minimal standards for description of new species of the class Mollicutes (division Tenericutes). *Int. J. Syst. Evol. Microbiol.* 57, 2703–2719.
8. Christensen, H. *et al.* (2007) Proposed minimal standards for the description of genera, species and subspecies of the *Pasteurellaceae*. *Int. J. Syst. Evol. Microbiol.* 57, 166–178.
9. Schumann, P. *et al.* (2009) Proposed minimal standards for describing new genera and species of the suborder *Micrococcineae*. *Int. J. Syst. Evol. Microbiol.* 59, 1823–1849.

10. Li, H.B. *et al.* (2008) *Halomonas korlensis* sp. nov., a moderately halophilic, denitrifying bacterium isolated from saline and alkaline soil. *Int. J. Syst. Evol. Microbiol.* 58, 2582–2588.
11. Sánchez-Porro, C. *et al.* (2009) Description of *Kushneria aurantia* gen. nov., sp. nov., a novel member of the family *Halomonadaceae*, and a proposal for reclassification of *Halomonas marisflavi* as *Kushneria marisflavi* comb. nov., of *Halomonas indalini* as *Kushneria indalini* comb. nov. and of *Halomonas avicenniae* as *Kushneria avicenniae* comb. nov. *Int. J. Syst. Evol. Microbiol.* 59, 397–405.
12. Kuhnert, P. *et al.* (2010) *Basfia succiniciproducens* gen. nov., sp. nov., a new member of the family *Pasteurellaceae* isolated from bovine rumen. *Int. J. Syst. Evol. Microbiol.* 60, 44–50.
13. Gregersen, R.H. *et al.* (2009) Comparative studies on [*Pasteurella*] *testudinis* and [*P.*] *testudinis*-like bacteria and proposal of *Chelonobacter oris* gen. nov., sp. nov. as a new member of the family *Pasteurellaceae*. *Int. J. Syst. Evol. Microbiol.* 59, 1583–1588.
14. Spengler, J. *et al.* (2010) *Mycoplasma mucosicanis* sp. nov., isolated from the mucosa of dogs. *Int. J. Syst. Evol. Microbiol.* (in press) DOI:10.1099/ijss.0.015750-0.
15. ICSB Subcommittee on the Taxonomy of Mycoplasmatales (1972) Proposal for minimal standards for descriptions of new species of the order Mycoplasmatales. *Int. J. Syst. Bacteriol.* 22, 184–188.
16. Logan, N.A. (2005) International Committee on Systematics of Prokaryotes; Subcommittee on the taxonomy of the genus *Bacillus* and related organisms: Minutes of the meeting, 30 July 2002, Paris, France. *Int. J. Syst. Evol. Microbiol.* 55, 977–979.
17. Tindall, B.J. *et al.* (2006) Valid publication of names of prokaryotes according to the rules of nomenclature: past history and current practice. *Int. J. Syst. Evol. Microbiol.* 56, 2715–2720.
18. Holmes, B. and Farmer III, J.J. (2009) International Committee on Systematics of Prokaryotes Subcommittee on the taxonomy of *Aeromonadaceae*, *Vibrionaceae* and related organisms. *Int. J. Syst. Evol. Microbiol.* 59, 2638–2640.

Biography

Martha E Trujillo is a senior lecturer in the Department of Microbiology and Genetics at the University of Salamanca (Spain) and Vice-Dean of the Faculty of Agricultural and Environmental Sciences. Martha undertook a PhD in Bacterial Systematics at the University of Newcastle upon Tyne, UK, followed by a postdoctoral position in the Department of Microbiology at Novartis AG in Switzerland. She joined the University of Salamanca in 2002, where she currently carries out her research on plant–bacteria interactions with special emphasis on the relationship between *Micromonospora* and nitrogen-fixing nodules of legumes. In addition, she is interested in bacterial communities that thrive in deteriorated rock monuments.

Under the Microscope

Prokaryotic taxonomy in the sequencing era and the role of MLSA in classification



Peter Kämpfer

Institut für Angewandte
Mikrobiologie
Justus-Liebig-Universität Giessen
Heinrich-Buff-Ring 26, D-35392
Giessen, Germany
Email peter.kaempfer@umwelt.
uni-giessen.de



Stefanie P Glaeser

Institut für Mikro- und
Molekularbiologie
Justus-Liebig-Universität Giessen
Heinrich-Buff-Ring 26, D-35392
Giessen, Germany
Email peter.kaempfer@umwelt.
uni-giessen.de

The initial step in prokaryote species and genera descriptions is now largely based on the 16S rRNA gene sequencing approach followed often by a very restricted additional phenotypic characterisation of the representatives of the potential novel taxa. Despite the advantages of the sequence-based approaches, there appears to be a tendency to classify new species on the basis of comparative sequence analyses of 16S rRNA gene sequences and other gene sequence data (multilocus sequence analyses, MLSA), contrary to the indications of other data. However, the biological meaning behind these sequence data is not always clear, and one should be careful with comprehensive taxonomic rearrangements until there is better insight of these data.

Organisms can be classified in different ways, but the resulting classification systems remain abstract ideas (mental representations). In biology, the ultimate goal of taxonomy is to establish a system that mirrors the “order in nature”. The term “natural” is now most often associated with evolution. In prokaryote microbiology, the taxonomic concepts try to mirror the origin of life, hence the cell as the basic unit of life remains the level of consideration.

The analysis of the small subunit ribosomal RNA (16S rRNA) gene has clearly revolutionised prokaryotic taxonomic studies. For the first time, a hierarchical taxonomy on the basis of a practical molecular marker was possible.

The advantages and the pitfalls of 16S rRNA sequence-based