

Taxonomic Note

On species descriptions based on a single strain: proposal to introduce the status *species proponenda* (sp. pr.)

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A survey of the descriptions of novel bacterial species published in the period 1996–2006 revealed that a large number of taxonomic descriptions are still based on one or a few strains. This situation determines that not only species descriptions, but also proposals to create higher ranks, are actually based on very few strains, which could produce a highly biased scenario. The encouragement to include a reasonable number of strains in species descriptions has been largely disregarded after its proposal, since acceptance of such descriptions relies mainly on editors' and reviewers' opinions. This observation and other considerations lead us to propose the creation of the status *species proponenda* (sp. pr.), as a compromise between the need for scientific description of biodiversity and exchange of data and the good taxonomic practice of including a sufficient number of strains in descriptions of species and higher taxonomic ranks.

Christensen *et al.* (2001) presented a detailed report on the trend of describing novel taxonomic units (species, genera and families) based on a very small number of isolates or even one isolate. This is not considered good taxonomic practice, since descriptions based on single isolates might not be reliable and good theoretical reasons to include many isolates in taxonomic studies have been documented (Sneath, 1976; Trüper & Schleifer, 1992).

With this premise, Christensen *et al.* (2001) suggested that Recommendation 30b of the *International Code of Nomenclature of Bacteria* (the *Bacteriological Code*; Lapage *et al.*, 1992) be modified as follows: 'Descriptions should be based on as many strains as possible (minimum five), representing different sources with respect to geography and ecology in order to be well characterized both phenotypically and genotypically, to establish the centre (from which the type strain could be chosen) and the extent of the cluster to be named. In addition, comparative studies should be performed, including reference strains that represent neighbouring species and/or genera, in order to give descriptions that are sufficiently detailed to allow differentiation from these neighbours'.

On this basis, the ad hoc committee for the re-evaluation of the species definition in bacteriology encouraged microbiologists to base a species description on more than a single strain (Stackebrandt *et al.*, 2002).

We performed a review of the descriptions of novel species and genera published between 1996 and 2006. Lists of names published each year were obtained from J. P. Euzéby's *List of Prokaryotic names with Standing in Nomenclature*, in particular from <http://www.bacterio.cict.fr/allnamesac.html>

for names validly published in 1996 and 1997 and from specific yearly lists for the years 1998–2006 (1998, <http://www.bacterio.cict.fr/twothousand/ninetyeight.html>; 1999, <http://www.bacterio.cict.fr/twothousand/ninety-nine.html>; 2000, <http://www.bacterio.cict.fr/twothousand/changestwothousand.html>; 2001, <http://www.bacterio.cict.fr/twothousand/twothousandone.html>; 2002, <http://www.bacterio.cict.fr/twothousand/twothousandtwo.html>; 2003, <http://www.bacterio.cict.fr/twothousand/twothousandthree.html>; 2004, <http://www.bacterio.cict.fr/twothousand/twothousandandfour.html>; 2005, <http://www.bacterio.cict.fr/twothousand/twothousandfive.html>; 2006, <http://www.bacterio.cict.fr/twothousand/twothousandsix.html>). Descriptions of new combinations, new subspecies and *Candidatus* were omitted, as well as descriptions of novel higher taxonomic ranks that did not contain novel species. The results of the analysis are reported in Fig. 1; species numbers are plotted for each year according to the number of strains which was included in the original description.

It is evident that, after the 'encouragement' of 2002, the trend of taxonomic descriptions has not changed, with even an increase in the incidence of proposals of novel species based on one or a few strains. It could therefore be concluded that the suggestion of the ad hoc committee (Stackebrandt *et al.*, 2002) was not properly followed by the scientific community. In the publication procedure, the encouragement becomes the responsibility of single editors and reviewers, and in practice it is extremely difficult to rule that a description based on a single strain or very few strains should be rejected simply because of the small number of strains included, if the taxonomic characterization is well

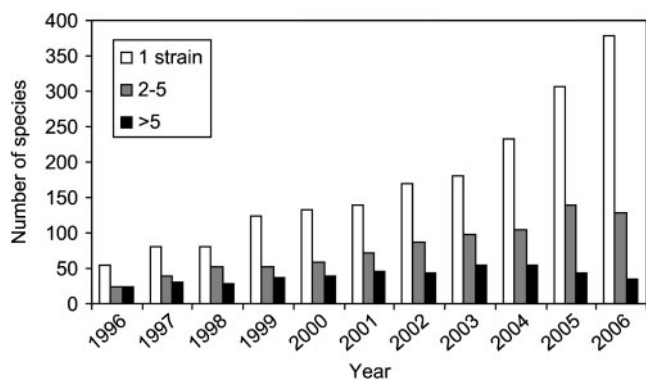


Fig. 1. Numbers of new names of prokaryote species (domains *Archaea* and *Bacteria*) based upon new isolates and published in the literature between 1996 and 2006, plotted according to the number of isolates used for the species descriptions. Data for some species (55 in 1996, 31 in 1997, 16 in 1998, 3 in 1999, 6 in 2000, 20 in 2001, 5 in 2002, 2 in 2003, 3 in 2005 and 4 in 2006) were not included as the relevant literature was not available.

documented. This non-rejection is, in our opinion, also sometimes desirable, since, for instance, some bacterial species could be highly niche-adapted and therefore isolation from different sources and/or different geographical locations could be impossible.

Furthermore, cataloguing biodiversity even if *initially* constituted by few strains could allow other scientists to identify and compare different strains of the same taxon isolated from different sources and locations, which could become impossible if the initial description is denied as based on a single strain or few strains. As a paradox, many scientists could have independently isolated and characterized small numbers of strains potentially belonging to novel species; such strains, together, could constitute novel taxa, but, if the single scientists are prevented from describing novel species separately, such strains will be confined to their laboratories and do not become the heritage of the scientific community.

In this light, we propose to introduce formally the concept of a transitory position for putative novel species. We suggest to indicate this novel category as *species proponenda* (abbreviation sp. pr.), i.e. species to be proposed, awaiting formal validity.

The procedure would be conceptually similar to that concerning the category *Candidatus*, which has to be used for well-characterized but as-yet uncultured organisms (Murray & Schleifer, 1994; Murray & Stackebrandt, 1995; Stackebrandt *et al.*, 2002) until a complete taxonomic study can be performed. The intermediate status of *species proponenda* should be applied to single strains or very small numbers of strains, e.g. up to five, presenting unique characteristics, which could become the basis for a species description.

It is proposed that the description of *species proponenda* should follow the same rules of the full species description, with particular reference to diagnostic properties and deposit of the strain/strains in at least two culture collections, but without formal indication of the type strain. It is an idea of a provisional status for the strains, which could be included in a *species novum* when a sufficient number of other similar strains are available and a type strain could be chosen, more representative of the species.

We believe that this new concept, introduced at the taxonomic level of species, and grouped in apposite lists, separate from the lists of validly published bacterial names published in IJSEM and online, is an acceptable compromise to accommodate:

- (i) the need of 'good taxonomic practice' to include several strains in species descriptions,
- (ii) the practical problem of isolating different strains from different sources,
- (iii) the requirement of availability of data on existing biodiversity to the scientific community, since *single* strains, which could sometimes be dominant in some niches, do exist.

The main advantages of the proposed status are that:

- (i) atypical strains could be described and made available to the scientific community, so that existing biodiversity is preliminarily characterized and scientists all over the world could be helped in the diagnosis of their own single strains;
- (ii) novel species, for their names to be validly published, would be based on a reasonable number of strains, and this would guarantee the choice of a type strain representative of its species or, at least, less biased by initial knowledge on the taxon;
- (iii) the creation of novel taxonomic ranks above species level (genera, families etc.) would be based on a significant number of strains.

Moreover, journal editors and reviewers would be given formal rules to decide on the description of taxa based on few strains, and the publication procedure could become more objective.

As a result, we would also expect an increase in the deposit of newly isolated strains in Biological Resource Centres by scientists not primarily involved in taxonomy and in facilitated communication among different scientists interested in the definition of the species that could putatively include the strains they are working on.

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