

Descriptions of Novel Microbial Taxa

Key points for descriptions of novel microbial taxa

- Authors must emphasise why a proposed novel taxon is of interest (e.g. in the Abstract, Introduction and Discussion sections).
- **It is expected that descriptions of novel Archaeal and Bacterial taxa will include data from genome sequence analyses.** In addition, we expect manuscripts containing genome data to present an analysis of genomic features of interest (beyond basic metrics such as G+C content, ANI and dDDH).
- Single strain species descriptions are discouraged: manuscripts will be rejected if our Editor's analyses indicate additional strains could reasonably have been obtained
- Manuscripts in poor quality English may be rejected without review

The primary concern for Editors of *Antonie van Leeuwenhoek* handling manuscripts describing novel taxa is that the manuscript should convincingly demonstrate the novelty of the isolate(s) being described. Moreover, because *Antonie van Leeuwenhoek* is a journal of general microbiology we expect the Introduction and/or Discussion text in manuscripts to explain why the authors undertook the study being reported and also to emphasise any interesting and novel features (beyond those needed for the taxonomic argument) of the biology of the strain(s) being described, since this should increase the scientific value and raise interest in the work.

- The introduction section should avoid long lists of validly names species associated with particular genera as summary data at LPSN (<http://www.bacterio.net/index.html>) can be cited. Details of relatives of ecological or other relevance only should be cited.
- Appropriate citation of relevant literature on a particular taxon or taxa is expected (not simply the reporting of new data)
- Antibiotic susceptibility is a potentially variable characteristic as it can be greatly affected by the presence or absence of mobile genetic elements. Therefore these characteristics should not be used in a prokaryotic species description to specify the properties of a novel taxon described on the basis of a single strain. They are still relevant data and so should simply be stated in the Results section.
- Likewise, long lists of substrate utilisation and enzyme activities (e.g. API or Biolog data) should not be included in the protologues of single strain species descriptions of prokaryotes since many of these characteristics may vary within species – these characters are still relevant data and should be included in the results text (e.g. as a Table).

Descriptions of novel bacterial taxa that include analyses of whole genome sequence data are especially welcomed, as indeed are manuscripts containing other contemporary approaches to systematics (e.g. MLSA, MALDI-TOF data etc; see Sutcliffe et al. 2012 (<http://link.springer.com/article/10.1007%2Fs10482-011-9664-0>) for a commentary on contemporary approaches). Authors should emphasise in their covering letter why a proposed novel taxon is of interest, particularly

where a description is based on a single strain only (see below).

The use of bacterial names and the proposal of new taxa should follow the conventions of the International Journal of Systematic and Evolutionary Microbiology (<http://ijs.sgmjournals.org/site/misc/ifora.xhtml>).

Before submission, nomenclature may be checked by consultation with one of the following experts: Aharon Oren (aharon.oren@mail.huji.ac.il) or Bernhard Schink (bernhard.schink@uni-konstanz.de). Moreover, attention is drawn to the comments of Trüper (2005) cautioning against 'localimania' in the naming of new taxa:

International Journal of Systematic and Evolutionary Microbiology 55:1753
<http://ijs.sgmjournals.org/content/55/5/1753.full.pdf>

It is to be strongly emphasised that good practise in microbial taxonomy encourages the description of taxa based on the characterisation of several strains rather than single strains [see Felis G.E. and F. Dellaglio. 2007. On species descriptions based on a single strain: proposal to introduce the status species proponenta (sp. pr.).]

International Journal of Systematic and Evolutionary Microbiology 57:
2185-2187 <http://ijs.sgmjournals.org/content/57/9/2185.abstract>

Where minimal standards have been defined for the description of particular taxa it is important that authors give full consideration to these.

Sequence data have to be accessible for the peer reviewing process. If not yet available in an appropriate database then the sequence should be provided as supplementary material to the manuscript submission. Sequence data in final manuscript submissions must be accompanied by an Accession number for an appropriate database (e.g. EMBL or GenBank), which must be clearly stated in the text.

Our Editors reserve the option of rejecting without or after review

- descriptions of proposed novel taxa based on single strains where database searches indicate that other members of the same taxon may be available from other laboratories or culture collections.
- descriptions of proposed novel taxa (particularly those based on single strains) if the main manuscript text does not provide evidence that the proposed novel taxon is of particular interest or if it seems likely that additional strains should be readily recoverable.
- descriptions of proposed novel taxa that are considered not to meet the appropriate standards of presentation, including English Language usage. English language checking is the responsibility of the authors before submission. For authors needing assistance, the language editing service recommended by Springer can be accessed at:
<http://www.editorialmanager.com/homepage/ms/springer-msservices.html>

Authors are also advised to consult the following guidelines concerning the Valid Publication of Prokaryotic Names: Tindall, B.J. et al. (2006) Valid

publication of names of prokaryotes according to the rules of nomenclature: past history and current practice.

International Journal of Systematic and Evolutionary Microbiology 56: 2715-2720 <http://ijs.sgmjournals.org/content/56/11/2715.abstract>

Manuscripts describing new microbial taxa will only be considered acceptable if accompanied by details demonstrating that the proposed type strain(s) have been deposited in two recognised culture collections in two different countries. One of these culture collections should preferably be located in Europe and, for novel fungal species, including yeasts, one of these culture collections must be the

Centraalbureau voor Schimmelcultures, Fungal and Yeast Collection
<http://www.cbs.knaw.nl/>

The standard accepted evidence for deposition of a type strain into culture collections is copies of the certificates of deposition. Culture collection accession numbers must be provided in the manuscript text and may substitute for deposition certificates ONLY where the publically accessible culture collection catalogues already confirm that the type strain has been deposited. An extensive listing of culture collections is provided by the

World Federation of Culture Collections, <http://www.wfcc.info/>

Novel fungal taxa should also be registered in MycoBank and the MB number must be included in the manuscript.

MycoBank <http://www.mycobank.org/>

It is noted that as of January 1, 2012, it is permissible to give the description or diagnosis of novel fungi exclusively in English. A Latin diagnosis is no longer required (McNeill J. et al. 2012. International Code of Nomenclature for Algae, Fungi, and Plants (Melbourne Code). Regnum Veg, 154. Gantner Verlag, Koenigstein, Germany). In recognition of these changes, descriptions or diagnoses of novel fungi should be made in either Latin AND English or in English alone. Eventually, this journal expects to accept descriptions and diagnoses of novel fungi in English only.

International Code of Nomenclature for Algae, Fungi, and Plants (Melbourne Code) <http://www.iapt-taxon.org/nomen/main.php>

This journal strongly recommends that descriptions of new fungal taxa and new combinations of any taxonomic rank include the keywords "X new taxa". The X is to be replaced by a digit indicating the number of new taxa and combinations in the manuscript. In the case of a single taxon it should read "1 new taxon". We recommend listing the names of the new taxa either in the manuscript title, the abstract, or the keywords without exceeding the maximum number of 6 keywords in total. Where additional typifications (lectotypes, neotypes, epitypes etc.) are proposed we recommend listing those under a separate keyword, "X new typifications" under the same conditions as above. These features will help timely recording of your new taxa by the International Sequence Database Consortium (INSDC) and other relevant aggregators of taxonomic information."