

- Nomenclature

New Microbial isolates

For any attempt to affiliate an isolate to a validly described prokaryotic species the stretch of the 16S rRNA gene sequence should be at least 1000 nt long. Shorter sequences result in an uncertain affiliation.

The 16S rRNA gene sequence must be compared to those of type strains when assigning a name to an isolate, e.g. when using BLAST-NCBI tick the option 'Limit to sequences from type material' or, in the case of EzBioCloud restrict the search only to type strains and denote the type strain with a superscript ^T after the strain number.

In those cases in which the 16S rRNA gene sequence similarity is higher than 98.7% to a group of highly related species, additional evidence must be provided before a name is given to an isolate, such as generated by wet-lab DNA hybridization or genome based dDDH, or ANI analysis between an isolate and type strains of the most highly related species, to test the genomic uniqueness of a novel isolate. Also, MALDI-TOF or the phylogenetic assessment by one or more housekeeping gene sequences are helpful to confirm the membership of an isolate to a validly named species. In the absence of any of these data authors should be prudent to actually name an isolate but either use the name of a species group or the Genus spp category.

As ITS regions alone are insufficient to unambiguously name a new fungal isolate in a given genus or genus complex the literature must be searched for more discrimination barcoding regions to support the naming. In the absence of such data the authors must refrain of applying an explicit species name to an isolate.

Names given for OTU- defined 'species' at a 97% cut-off value of short 16S rRNA gene sequence stretches (e.g. V3, V3/V4 regions) are highly speculative, not re-assessed by different approaches but once published, taken for granted. As species name-attached sequences enter databases the likelihood for a future even higher erroneous identification is predictable and author should be refrain from naming species on the basis of such shaky scientific grounds.

Please, see: This [Editorial paper](#) for further information about affiliations of new isolates.

The genus, species, and variety name (in italics), strain number, and culture collection number and source of all strains under investigation should be given in the Materials and Methods section. The scientific names should be given in full (e.g., *Escherichia coli*) in the title, in the abstract, and the first time referred to in the text. When a new bacterial name is proposed (see [this document](#) for details), an international authority on nomenclature should be contacted, and the name should be approved by sending a letter to the editor-in-chief of International Journal of Systematic and Evolutionary Microbiology. Newly isolated microorganisms must be deposited in an internationally recognized culture collection if the scientific content of the manuscript is essentially dependent on the strain. Publication of an article in Archives of Microbiology is subject to the understanding that authors will distribute freely any strains, clones, or antibodies described therein for use in academic research. Nucleotide sequences are not published; citation of the database accession number in the text suffices. However, the sequence data, separate from the manuscript, must be provided for reviewing if a functional EMBL/GenBank/DBJ database accession number is not yet given in the manuscript; the accession number must be provided before acceptance.

Standard nomenclature should be used according to the following sources:

Bacterial names: DSMZ Bacterial Nomenclature up-to-date (<http://www.dsmz.de/bactnom/bactname.htm>); validation lists of the International Journal of Systematic and Evolutionary Microbiology.

Genetics: J Bacteriol (first issue of each year); Microbiol Mol Biol Rev (1998) 62:814-984 (*Escherichia coli* K-12); Genetics (1966) 54:61-76; Microbiol Rev (1988) 52:485-532 (*Salmonella typhimurium*); Microbiol Rev (1985) 49:158-179 (*Bacillus subtilis*); Annu Rev Microbiol (1986) 40:79-105 (*Pseudomonas*); Microbiol Rev (1982) 46:426-570 (*Neurospora crassa*); Nature (1997) 387 (6632 Suppl):67-73 (*Saccharomyces cerevisiae*).

Chemistry/Biochemistry: International Union of Biochemistry and Molecular Biology (IUBMB; <http://www.chem.qmw.ac.uk/iubmb/>); International Union of Pure and Applied Chemistry (IUPAC; <http://www.chem.qmw.ac.uk/iupac/index.html>); Enzyme Handbook (1990) Springer, Berlin Heidelberg New York; Enzyme Nomenclature (1992) Academic Press, London New York.