SYSTEMATIC AND APPLIED MICROBIOLOGY
A Journal of Microbial Diversity

DESCRIPTION

*Systematic and Applied Microbiology* deals with various aspects of microbial diversity and systematics of prokaryotes. It focuses on *Bacteria* and *Archaea*; eukaryotic microorganisms will only be considered in rare cases. The journal perceives a broad understanding of microbial diversity and encourages the submission of manuscripts from the following branches of microbiology:

**Systematics**: Theoretical and practical issues dealing with classification and taxonomy, i.e. (i) new descriptions or revisions of prokaryotic taxa, including descriptions of not-yet cultured taxa in the category *Candidatus* (ii) innovative methods for the determination of taxonomical and genealogical relationships, (iii) evaluation of intra-taxon diversity through multidisciplinary approaches, (iv) identification methods.

**Applied Microbiology**: all aspects of agricultural, industrial, and food microbiology are welcome, including water and wastewater treatment.

**Comparative biochemistry and genomics**: studies concerning biochemical/metabolic and genomic diversity of cultured as well as yet-uncultured *Bacteria* and *Archaea*.

**Ecology**: polyphasic descriptions of the microbial diversity and community composition of natural and man-made ecosystems; studies quantifying the size, dynamics, and function of microbial populations; innovative research on the interaction of micro-organisms with each other and their biotic and abiotic environments. The description of candidate taxa is highly encouraged but should be based on high quality metagenomic information, as well as the in situ identification of the target bacterial or archaeal populations.

AUDIENCE

Bacteriologists, taxonomists, microbial ecologists, industrial, food and agricultural microbiologists

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Once the DP is completed, the author must submit it to the database and it can be exported subsequently either as a PDF file via the Journal Ready button or in .xls or .csv format from the main page. Alternatively, the submitter of the DP will receive the table in an email that can be formatted and then submitted to the journal as one of the manuscript submission files. However, please note that the information given for the "Date of entry", "Draft Number/Date", "Effective Publication Date", "Valid Publication Date" and "Version" should not be included in the table. The resulting table must then be sent as the Species Description Protologue. If the manuscript contains several new species or genus descriptions, a single table may be produced with as many columns as the number of taxa classified in the manuscript. Nevertheless, if the manuscript contains new genera, the genus Protologue can be given either in a unique table (preferred) or split into two tables (in the case of several genera and several species). Should the table contain citations, these must be listed in the reference section. Higher taxa Protologues must still be provided in the traditional way at the end of the manuscript.

The last sentence of the manuscript should introduce the Protologue and also specify each of the unique Taxonumbers provided in the Digital Protologue table, according to the following statement: "The formal proposal of the new genus "Genus gen. nov." and new species "Genus species sp. nov." is given in Table XX with the Taxonumbers GAXXXX and TAXXXX ".

An example of a DP table can be found here.

Submitted taxonomic manuscripts must fulfill the following standards:

(i) For any new species of a genus a type strain must be designated, this strain must be deposited in two culture collections in different countries and the accession numbers must be available on the date of the submission. This strain must be comprehensively studied by means of a polyphasic approach, including genetic and phenotypic traits.

(ii) The use of more than a single strain for descriptions of new genera and/or species is highly encouraged. It is of the utmost importance that all strains are equally studied in order to describe intraspecific diversity.

(iii) It is necessary to determine an Overall Genome Relatedness Index (OGRI; Chun and Rainey (2014) Int J Syst Evol Microbiol 64, 316 - 324), as it could be the average nucleotide identity (ANI) between genomes (either complete or in high coverage), as recommended in Richter and Rosselló- Móra (2009), PNAS, 106(45): 19126-19131. However, other widely used indexes especially devised to estimate genome relatedness are also accepted. The analyses must be carried out with the type strain of the species and the closest relatives of the putative new taxon. Also the closest relative type strain genome sequences must be used when the 16S rRNA gene sequence similarities lie above 97%. In exceptional cases, DNA-DNA hybridization analyses will be accepted, but in silico genome comparisons (ANIb, ANIm, OrthoANI, GBDP,...) are preferred.

(iv) Any taxonomic paper should be accompanied by a fingerprint of the strain/strains used to classify a new taxon by means of methods such as ERIC-, REP-, BOX-, (GTG)5- and/or RAPD-PCR, or even whole-cell protein profiles. It is obligatory to show that the different strains in use, belonging to the same taxon, are not clonal varieties. The picture of the profiles showing the differences between isolates of the same taxon should be submitted as supplementary material if they do not provide
additional information. In cases of clonality, this should be discussed in order to understand the reasons for using multiple identical clones (mainly justifiable if they have been isolated from different samples).

(v) The nearly complete 16S rRNA gene sequence (more than 1300 nucleotides) of the type strain of the species must be studied and deposited in a public repository. The accession number must be given.

(vi) The type strains of the most closely related taxa must be simultaneously investigated. It is of the utmost importance that all reference strains are tested with the same methods as the strains of the new taxon. Submissions where the discriminative tests of the reference strains are simply taken from the literature will not be reviewed, unless they are based on results obtained with the same methods. If possible, phenotypic tests should be performed by means of standardized methods.

(vii) It is highly recommended that chemotaxonomic markers are studied, especially if these have been used as diagnostic features for the genus harboring the new taxon. It will be compulsory to show the chemical composition peculiarities for new general descriptions. Recommended markers are fatty acid profiles, polar lipid composition, quinone types, polyamine patterns, and peptidoglycan type/composition (in particular for the description of Gram-positive bacteria, but also considering that Gram-negative bacteria may differ in their diamino acid composition).

(viii) It is compulsory to give the G+C mole % values of the genome of the type strain of the type species of a new genus.

(ix) For non-ribosomal gene sequence analyses (e.g. MLSA), all accession numbers of the generated sequences must be given. In addition, it is compulsory to submit the full alignments used to generate the trees that are to be published. The alignments will be published as online supplementary material.

(x) For any new taxon, the etymology of the proposed name must be provided.

(xi) For any new taxon, a protologue indicating the discriminative traits that are characteristic of the taxon should be clearly given. One should avoid linking tables to the protologue. The text should contain all the necessary information that explains how the taxon can be identified.

(xii) The discriminative phenotype should be summarized in a diagnostic table where the most closely related taxa are also indicated.

(xiii) Each description must be accompanied at the end of the manuscript by the protologue written in accordance with the Bacteriological Code requirements.

**Single strain descriptions.** Single strain taxa descriptions (SSSD) are accepted only in exceptional cases. Exceptionalness may result from the relevance of the strain and of the work that has been done with it independently whether it has been published elsewhere. Cases such as full genome sequencing, ecological relevance in their environment, being a result of the isolation of a “candidatus” organism, or very especial metabolisms may be regarded as being of additional interest. Also, if the taxonomic work is done exhaustively and properly, adding new approaches, e.g. MLSA, ANI calculations, completing the phenotypic analyses by means of several chemotaxonomic markers and exhaustive metabolic studies, and any additional information that balances the lack of additional cultures (e.g. phage susceptibility, metabolic properties that are of biotechnological or industrial importance) would also be regarded as exceptionalness. Should this be the case, the authors must send a cover letter to the editor explaining why this new species deserves to be published in the journal, clarifying the uniqueness of the findings and the exceptionality of the new isolate. Manuscripts not fulfilling the length and the exceptionalness requirements will be directly rejected. Note, that SAM encourages compiling several SSSDs in a single manuscript when no additional strains had been isolated for each distinct species.

**Candidatus**taxa descriptions. SAM encourages the submission of new candidate taxa. The Candidatus category is be "used for describing prokaryotic entities for which more than a mere sequence is available but for which characteristics required for description according to the International Code of Nomenclature of Bacteria are lacking. In addition to genomic information, such as sequences apt to determine the phylogenetic position of the organism, all information, including structural,
metabolic, and reproductive features, should be included in the description of a provisional taxon, together with the natural environment in which the organism can be identified by in situ hybridization or other similar techniques for cell identification” (Murray and Stackebrandt (1995), Int. J. Syst. Bacteriol., 45:186-187). In general, such descriptions have been made for organisms with conspicuous characteristics related to their morphology, lifestyle or ultrastructure. However, high quality metagenome sequencing allows binning genomes of inconspicuous single prokaryotic populations whose formal description may be relevant for the scientific community.

SAM encourages the submission of proposals of candidate taxa based on high quality metagenome bins, which meet the minimal standards necessary to ensure their unequivocal identification (for recommendations see: Konstantinidis and Rosselló-Móra (2015), Syst. Appl. Microbiol., 38:223-230). All Candidatus descriptions should meet the premises established in the Bacteriological Code, and must be accompanied by the 16S rRNA gene sequence, the in situ identification of the target bacterial or archaeal populations, and the deposit of a high quality binned metagenomic sequence.

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