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 in particular descriptions of not-yet cultivated 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**: polyphasic studies combining multiple methods yielding in-depth data on the diversity and function of particular clades of Bacteria and Archaea in all aspects of agricultural, food, and industrial microbiology, including water and wastewater treatment. Also these studies must have a focus on prokaryotic systematics.

**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 prokaryotic populations; innovative research on the interaction of Bacteria and Archaea 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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Guidelines for taxonomic papers
In 2017 Systematic and Applied Microbiology, together with Antonie van Leeuwenhoek (Rossello-Mora et al. (2017) Syst. Appl. Microbiol. 40, 121-122) started an initiative to modernize its taxonomic papers by implementing the Digital Protologue Database (DPD) in where the protologues given in the manuscripts would be extracted from the Digital Protologue (DP) compulsorily filled by the authors. The purpose of the initiative was, for the first time, generating a public and interactive database on protologues with unique taxonumbers, and also propose the descriptions in form of a protologue table and not given at the end of the manuscript. The success of the DPD was especially dependent on the acceptance by the editorial board of the official journal of the International Committee on Systematics of Prokaryotes, who finally decided not to implement the DPs. Due to this reason, the developers of the DPD decided to streamline the information content of the DPs, and generate a database capturing all relevant metadata for strains, MAGs and SAGs that are to be published in Syst. Appl. Microbiol. and any other journal that may adhere to the initiative.

Syst. Appl. Microbiol. changes now the policy for the taxonomic papers in where all new taxa Protologues (i.e. formal descriptions) can be given in form of a table (an example of a DP table can be found here.) and or written in the text as traditionally has been done. If you go for the Protologue Table, and the manuscript contains several new species or genera, a single table may be produced with as many columns as the number of taxa classified in the manuscript. Empty fields must contain a dash (-). Should the table contain citations, these must be listed in the reference section. In this latter case, the last sentence of the manuscript should introduce the Protologue Table(s).

However, for all taxonomic papers a DP must be created for at least the type strain using the DP database (DPD) available from the http://imedea.uib-csic.es/dprotologue/ website that generates a unique Taxonumber. Authors should fill in the form with the maximum quantity of information and metadata as possible. The PDF that can be extracted from the DPD must be submitted as supplementary material. Gene and genome entries must be public at the moment of the manuscript submission, or alternatively the sequences must be submitted along with the manuscript and be available for the referees. The lack of access to these relevant data will be a reason of rejection of the manuscript.

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, as well as accompanying isolates must be comprehensively studied by means of a polyphasic approach, including genetic and phenotypic traits. The genome sequences must be generated and deposited in public repositories. At least for the type strain the DP must be generated as indicated above, but the metadata of any additional genome generated for the manuscript should also be added to the DPD and submitted as supplementary material.

(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. The almost complete sequence of the type strain of the new taxon and at least a draft genome sequence of any additional strain must be provided. The accession numbers must be given in the manuscript and the sequences must be available before submission.

(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-Mòra (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 exceptionality 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. *Syst.Appl.Microbiol.* encourages the submission of new candidate taxa. The *Candidatus* category is to 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.

*Syst. Appl. Microbiol.* encourages the submission of proposals of candidate taxa based on high quality metagenome assembled genomes (MAGs) or single amplified genomes (SAGs), 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 candidate taxa names should meet the premises established in the Bacteriological Code, but the type material. For MAGs and SAGs, *Syst. Appl. Microbiol.* will consider type material the (meta)genome sequences as recommended by Whitman (2015) *Syst. Appl. Microbiol.* 38, 217-222. High quality descriptions 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 (for standards see Konstantinidis et al. (2017) ISMEJ 11, 2399-2406). The protologues for the candidate taxa must accomplish the *Syst. Appl. Microbiol.* requirements mentioned above and must be accompanied by the DP entry as supplementary material.

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