



Editorial

Moving the cataloguing of the “uncultivated majority” forward



There is little doubt that we are approaching an era where changes will occur in the traditional way we taxonomically classify microbes; the accumulating genomic, and multi-omic data in general, are simply calling for it! More specifically, an exponentially increasing number of metagenome-assembled genomes (MAGs) and single-cell amplified genomes (SAGs) are becoming available these days, most of which are representatives of yet uncultured species that are important for ecosystem functions, and sometimes disease. Last year alone, more than 3000 MAGs were reported, each of which would represent a new species by genomic standards, vastly outnumbering the ~1000 newly classified species based on classic taxonomic approaches and isolates. Thus, there is an urgent need to start naming (nomenclature component of taxonomy) and devising standards to classifying (classification component of taxonomy) the important uncultivated *Bacteria* and *Archaea* in order to facilitate communication among scientists and the public. For instance, it is not uncommon nowadays that different scientists are working on the same uncultured microorganism(s), but they do not know it in the absence of a supervised and stable taxonomic framework for the uncultured. Furthermore, the alphanumeric names (e.g., SUP05, SAR11) tentatively given to uncultivated taxa are not informative of the phenotype or ecology of the corresponding organisms; neither are these names regulated, creating a chaotic situation that is already difficult to manage. Unfortunately, the existing approach for cataloguing uncultivated taxa, the *Candidatus* concept, in its current form, is unable to deal with the type and volume of accumulating omic data without substantial changes. The changes would likely include – but not be limited to – the adoption of new, genome-based techniques and standards for classification to complement the traditional techniques that are not well applicable to uncultivated organisms, as well as the acceptance of the DNA sequence as the type material in the Bacteriological Code and the prioritization of taxonomic names for nomenclature in order to further promote the description of uncultivated taxa.

While these changes are the topic of ongoing intense discussions, the present special issue (SI) of *Systematic and Applied Microbiology* includes a collection of eleven manuscripts that attempt to break new ground in the topic of cataloguing the “uncultivated majority” and defining the standards to use. The articles of the SI include both theoretical discussions of the challenges associated with the nomenclature and the classification of uncultivated taxa, as well as specific examples of robust taxonomic descriptions of such taxa and the best practice(s) and standards to follow.

More specifically, Rossello-Mora and Sutcliffe argue for the need to digitize metadata information about the MAGs and SAGs using a digital prologue or a similar format in order to make metadata easily searchable by computers [11]. Rossello-Mora and Whitman [8] provided a dialogue on the history of naming uncultivated taxa and their views on how to proceed in the “big data” era, which should be highly educational to any student or scientist who wishes to perform taxonomic studies or get introduced to prokaryotic taxonomy. Chuvochina et al. [2] discuss the need to designate type material for uncultured taxa and name higher ranks starting from the species and genus, while Overmann et al. [6] call for more stringent and phenotype-based information for naming MAGs and SAGs than those that have been recently put forward. The SI also includes several examples of the description of important (uncultivated) taxa across a range of habitats such as soils, coastal ocean, deep subsurface, wastewater treatment plants and symbionts of archaeal hosts. These taxa include a clade of *Flavobacteriia* that follows algal blooms in the North Sea and is likely responsible for the mineralization of algal biomass in coastal oceans [3], abundant and deep-branching (phylum level) soil bacteria that respond to the climate change in northern latitudes [5], deep-branching bacterial populations in deep-subsurface Siberia [4] and sulfur-rich sediments of a freshwater spring in Midwest USA [10], bulking-causing filamentous chloroflexi in wastewater treatment plants [1], and nanoarchaeal symbionts of crenarchaeal hosts [9]. To further highlight the challenges (and solutions) associated with obtaining high-quality MAGs from metagenomes, and the need for standardization of this process, the SI also includes a manuscript describing the process of population genome binning and its limitations based on real metagenomic data [7].

While it will become obvious to the reader that these taxonomic studies of yet uncultured *Bacteria* and *Archaea* differ substantially in the data used for describing the (potential) phenotype, it is important to point out that they follow standards that are not inferior to taxonomic descriptions based on cultivated strains. Therefore, cataloguing the uncultivated majority is a doable and highly needed goal, and the articles mentioned above represent good reference examples. We sincerely hope that this special issue will motivate microbiologists to define and follow standards for the classification of the yet uncultured majority. The taxonomy section of *Systematic and Applied Microbiology* will strongly welcome such taxonomic contributions in the future.

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