



Reply to the commentary “Uncultivated microbes—in need of their own nomenclature?”

Konstantinos T Konstantinidis¹ · Ramon Rosselló-Móra² · Rudolf Amann³

Received: 25 October 2017 / Revised: 27 October 2017 / Accepted: 28 October 2017 / Published online: 15 January 2018
© International Society for Microbial Ecology 2018

In their commentary in ISME Journal [1], Oren and Garrity, two highly experienced taxonomists acting as nomenclature reviewers and senior editors for the International Journal of Systematic and Evolutionary Microbiology (IJSEM), expressed concerns on our proposal for the creation of a parallel classification for yet uncultured Bacteria and Archaea (Konstantinidis et al. 2017). We recognize that it might appear an unorthodox approach to solve the long-standing and pressing problem of a standardized and supervised taxonomy for yet uncultured Bacteria and Archaea with a parallel system. In fact, the goal of our proposal is to speed up the process of recognizing the uncultivated within the framework of the International Code of Nomenclature of Prokaryotes (ICNP) [2], which clearly represents the preferred way forward by Oren and Garrity as well as by us. However, if this cannot be realized in a timely fashion, we are convinced that the temporal generation of a parallel, yet congruent system of classification is a much better option than no action. Simultaneous to the publication of our ISME article, two of us (KTK and RRM) have been elected as new members of the 2017 class of the Judicial Commission of the International Committee on Systematics of Prokaryotes (JC-ICSP), and we will try to move forward

the proposal to use DNA sequences as type material [3] and related proposals in order to promote a harmonized classification of the cultured and the uncultured. However, based on the previous slow action of the JC-ICSP and the several pending requests (since 2007) with opinions yet to be expressed, we are not optimistic that the uncultivated majority will soon be given official standing in nomenclature. At the very least, with our perspective (Konstantinidis et al. 2017) we made microbial ecologists and taxonomists aware of the scale of the problem, which is caused by the coincidence of an unprecedented acceleration of microbial diversity research with a monolithic code of nomenclature.

Clearly, the “chaos” predicted by Oren and Garrity in their commentary is already upon us. For instance, it is not currently possible to know what has been described from the uncultivated majority since no system is in place to catalog this diversity, and the taxon names proposed are not regulated or checked for consistency, frequently resulting in unsuccessful names for describing the unique phenotype or ecology of the organisms in question. The issues with the Phylum rank to which Oren and Garrity referred is an important example of the magnitude of the problem and needs an immediate action. Although used extensively in Microbiology, Phylum is not a recognized rank of the official nomenclature, despite the fact that a proposal to recognize Phylum, made by several authors including Oren and Garrity, has been pending for two years now. Thus, the names given to candidate phyla are also not regulated. Our proposed (parallel) system would actually help greatly with this problem, not make it worse as Oren and Garrity seem to imply, since we are proposing to standardize the taxonomic ranks and use the same nomenclature rules as the official system, with the only addition of a superscript U before the name for uncultivated. This proposed naming scheme represents a rather minor difference, and thus, is easily mergeable with the official system in the future. The fact that the current practices in metagenomics and single cell genomics allow the genomic description of biological units

✉ Konstantinos T Konstantinidis
kostas@ce.gatech.edu

✉ Ramon Rosselló-Móra
rossello-mora@uib.es

✉ Rudolf Amann
ramann@mpi-bremen.de

¹ School of Civil and Environmental Engineering and School of Biological Sciences, Georgia Institute of Technology, Atlanta, GA, USA

² Marine Microbiology Group, Institut Mediterrani d'Estudis Avançats (IMEDEA; CSIC-UIB), Esporles E-07190, Spain

³ Max Planck Institute for Marine Microbiology, Bremen D-28359, Germany

with similar or even higher quality than the current taxonomic descriptions creates an urgent need to take the classification of the uncultured seriously. The single category that would permit the classification of yet uncultivated Bacteria and Archaea, *Candidatus* [4], had, from the beginning, no standing in the ICNP nor did the given names have priority (as also stated clearly by Oren and Garrity in their comment). This has effectively discouraged ecologists from making serious efforts in classification. Accordingly, nomenclatural chaos is rapidly growing for the uncultivated, and this requires immediate action, with the goal to produce harmonized classifications with homogeneous criteria for all prokaryotes. In our view, this action should start to materialize as early as next year since the genomic information available for uncultivated Bacteria and Archaea is exponentially growing. As a matter of fact, an equal, if not larger, number of sequence-discrete natural population genomes at the 95% ANI level (i.e., species-like) to the species with validly published names ($n = \sim 13,000$) have already been reported (e.g., [5]).

We also see the description of the uncultivated as an opportunity to provide a new standardized classification system that will be predictive of the genetic and phenotypic relatedness of the organisms grouped under the same taxonomic ranks because it will be based on generally approved standards. No “official classification” exists for the cultivated as we already stated in the very first paragraph of our ISME article. Oren and Garrity highlighted the unrestricted degree of freedom for taxonomists to describe their taxa as the main justification for the lack of official classification rules. This is, however, only partially true as reviewers and editors of journals publishing taxonomic papers are already restricting the actions of taxonomists by requesting specific “recommended” parameters and standards (beyond the naming rules) for taxa descriptions. These recommended parameters are not universally accepted, and different reviewers employ varied standards, which has resulted in non-standardized classifications. We do not see a problem in having “official” standards, which could be relaxed for cases in which strong justification can be provided, as also discussed in our perspective article (e.g., a highly important phenotype for human or ecosystem health that differentiates two otherwise homogenous sets of genomes). Notably, Oren and Garrity apparently did not find any issues with the standards we proposed based on current best practices, and we believe that these standards could serve as a starting point for discussions towards establishing official standards. Furthermore, in our era of database and internet dominance in science, where a single supervised website could harbor lists, digitalized protologues, type material (e.g., DNA sequences), and even phenotype annotations, along with additional metadata not given in the

protologues, all supervised by an official committee and supported by a worldwide recognized society such as IUMS, BISMIS or ISME, an “official” classification of cultivated and uncultivated prokaryotes appears to be a doable and highly needed endeavor.

Finally, Oren and Garrity complained that we did not cite Whitman [3] in his “Modest proposals to expand the type material for naming of prokaryotes” addressed to the ICSP in our article, but they neglected to mention that we cited the source of the proposal, the very first manuscript on this topic [6]. In the latter article, Whitman explains the benefits of making the abovementioned changes in ICNP, addressing to larger community than (just) the Judicial Commission of the ICSP. Similarly, they seem to argue that we did not cite one of their authored papers dealing with the pluralism in the *Cyanobacteria*, and the fact that one of the two systems is used more often than the other, but this does not change our main conclusion that parallel systems do exist and serve their own purposes like in the case of *Cyanobacteria*. The constraints in the number of citations allowed for perspective articles, and the fact that the nomenclature was only one of several topics covered by our article did not permit us to cite all pertinent literature.

In our view, the time to standardize and accelerate the classification of the uncultivated majority has arrived. With a serious collective effort by ecologists and taxonomists, we could lay solid foundations, which will facilitate future research and communication among scientists. We thank Oren and Garrity for their commentary which started a debate that we hope will soon result in action.

Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

References

- Oren A, Garrity G. Uncultivated microbes—in need of their own nomenclature? ISME J. 2017; in press.
- Parker CT, Tindall BJ, Garrity GM. International code of nomenclature of prokaryotes. Int J Syst Evol Microbiol. 2015.
- Whitman WB. Modest proposals to expand the type material for naming of prokaryotes. Int J Syst Evol Microbiol 2016;66:2108–12.
- Murray RG, Stackebrandt E. Taxonomic note: implementation of the provisional status *Candidatus* for incompletely described prokaryotes. Int J Syst Bacteriol 1995;45:186–7.
- Parks DH, Rinke C, Chuvochina M, Chaumeil PA, Woodcroft BJ, Evans PN, et al. Recovery of nearly 8,000 metagenome-assembled genomes substantially expands the tree of life. Nat Microbiol 2017;2:1533–42.
- Whitman WB. Genome sequences as the type material for taxonomic descriptions of prokaryotes. Syst Appl Microbiol 2015;38:217–22.