

ecco

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To the International Committee on Systematics of Prokaryotes

Subject: proposed changes in the International Code of Nomenclature of Prokaryotes (ICNP)

Date: 27 February 2020

Dear Sir/Madam,

On behalf of the Executive Board of ECCO, I would like to transfer our position on the proposed changes in the International Code of Nomenclature of Prokaryotes (ICNP).

The decisions that is to be made shortly by the authorized international bodies in prokaryotic taxonomy with regard to the proposed changes in the ICNP could have serious consequences in the activities of our member collections and their role in biodiversity preservation and distribution for life science researchers. We therefore appreciate that we are offered the opportunity to bring forward our concerns and opinion about the proposals in front of the International Committee on Systematics of Prokaryotes (ICSP).

The ECCO Board understands and acknowledges the need for a classification system for Prokaryotes that will accommodate both culturable and not-yet-cultured organisms, and that microbiologists want to be able to place the not-yet-cultured organisms among their culturable relatives in a robust classification of the Prokaryotes, and be able to provide official taxonomic names to all these elements.

According to Rule 30 3b, the current Code requires deposit of a designated type-strain in culture collections in two different countries for valid publication of a species or sub-species. Unfortunately the proposal to allow the use of complete or partial genome sequences as type (Whitman 2016), will in our view take away the firm basis of the system. The basis are the type-strains, the biological specimens that allow for a polyphasic approach in characterizing species including DNA-based analyses as well as phenotypic traits (virulence, pathogenicity, antimicrobial resistance, metabolic catalytic activities, etc).

The specimens allow to conduct critical review of taxon names later (after valid publication) using new techniques as they develop, by which we are able to improve and adopt it when possible and needed. With the current techniques for metabolically inactive preservation available in most public culture collections, strains can be kept in their original state and this allows for future studies to successfully add new markers for improving reliable identification. By allowing DNA sequences to serve as type for valid publication of new species means that if no strains are deposited later, further research, reproducibility testing and characterization of those taxa, including re-sequencing, will not be possible, and the system will slowly but certainly be undermined.

There is no general consensus among bacterial taxonomists about whether sequence data, even high-quality whole genome sequences, can “unambiguously identify the taxonomic group” (proposed rule 18.a). It has been established that genomes of different specimens of the same taxon may comprise vastly different regions of DNA, depending on mechanisms for horizontal gene transfer or other ways of easy gain or loss of genes. Furthermore, whole genome sequencing technologies are still not fully evolved and currently available technologies do not allow for a full genome to be sequenced in one read, or fragments of genome sequences in e.g. environmental samples to be compiled reliably into single-organism genomes. Type strains allow for a polyphasic approach in characterizing species including DNA-based analyses as well as phenotypic traits, which is the optimal approach for reaching stability in classifications and a universal best practice for taxonomic research on all (microbial) life forms.

The process of isolating and sustainably preserving prokaryotes requires specific expertise and is costly. Strain deposit procedures are time-consuming, and development of new rapid technologies for biodiscovery indeed call for more efficient ways of formally describing and inventorying novel taxa. Some organisms cannot be preserved successfully and the deposit of genomic DNA extracts in a public collection can then be a good alternative that at least allows for reproducing results and verification, in contrast to sequence data.

If the proposal is accepted, it will no longer be strictly necessary to deposit any material in public collections, be it type-strains, DNA-extracts or environmental samples. This of course does not mean that we think that efforts to isolate and study new species in culture would be completely discarded nor that all scientists who have regularly been depositing strains will suddenly stop to do so, but overall the motivation to do all that is needed for depositing type-strains in a public collection will decrease. The proposal allows for later replacement of a type sequence by a type strain when the latter becomes available, but in our experience, we believe that in practice this will be forgotten or, worse, simply ignored. This should be a major concern to all stakeholders, especially in the light of climate change and the accelerated loss of biodiversity.

There are still technical and bioinformatics biases to be considered in molecular microbiology. Discrepant results can be obtained depending on the method used to extract DNA and the variety of methodologies proposed for bioinformatics analyses. Sequencing methods cannot discriminate between live bacteria and transient DNA. Furthermore, it is challenging to determine the activity and physiological state of a microorganism using DNA sequencing. Overall, recent culturomics approaches have significantly increased the number of bacterial species that have been isolated from different matrices, allowing us to investigate the phenotypes and functions of these isolates. In addition, whole genome sequencing of all these bacteria will facilitate the interpretation of future metagenomic studies. For example, culturomics has markedly increased the number of species known to be associated with humans, bringing the total to 2,671 species. Indeed, culturomics enabled ca. 23% of the current repertoire of the bacterial species to be cultured at least once from a human sample. Culturomics has led not only to an increase in the number of known human-associated bacteria but also to a change in the methods that are used to describe unknown bacteria (Lagier et al., 2018).

Regulatory pressure from the Access and benefit Sharing regimes (ABS, Nagoya protocol) and other rules and regulations such as Plant health, biosafety and biosecurity is increasing and makes it more difficult for scientists to deposit strains in public collections abroad. Collections have to follow more complex procedures causing further delay in accepting deposits. ECCO and other organisations aim to support depositors by developing tools such as best practices and model transfer agreements (MTA). The situation is already serious but could deteriorate even faster when the proposal would be accepted. The long-term sustainability of public culture collections is of great importance for all their stakeholders including the microbiology community and the health practitioners that depend on the availability of type- and other materials for diagnostics, verification, follow-up fundamental and applied research and development.

It has been suggested that the proposal could be a way to overcome the problems with regard to restricted access to biological material under the ABS regimes implemented in various countries/regions, as (at least for a long time) sequence information has been regarded to be out of scope of the Convention on Biological Diversity (CBD) and the Nagoya protocol. However, some countries that are Party to these treaties have already imposed restrictions on (genome) sequencing, and the deposit and use of sequence data (e.g. China). Moreover, international negotiations are currently taking place to bring genomic information under the Nagoya protocol framework. The ongoing discussions to include digital sequence information (DSI) under the Nagoya protocol might result in a positive decision at the 15th Conference of the Parties which planned in October this year, which could then also have major consequences for the accessibility of sequence-based types.

Finally, if accepted the proposal could open the door for short track (even automated) publication of massive numbers of new names, which some labs may consider an acceptable way or the only way of working giving limited resources. Verification, assessment and interpretation of such vast amounts of new names will pose problems to the scientific community.

On behalf of the ECCO Executive Board,



Gerard Verkley

ECCO President