

Comments posted 23rd February 2020 in response to Dr. Fanus Venter

All comments added are in red

Dear colleagues

After spending some time to have a relook at all the comments raised so far I would like to make a few comments. It is clear from the discussion that people feel strongly about the issues and that their viewpoints are clearly shaped by their current field of research or work environment.

I think the concerns towards these proposals have been well articulated. For me the main issues are quality of the sequences (completeness and contamination), incorrect assignment of taxa and the accompanying instability of the system, the ability to replicate findings, descriptions with limited phenotypes as well as concerns that cultures will no longer be shared (only for organisms that have been cultured). Various participants have responded to these concerns and I don't want to address these again. I would rather focus on the implications if we do not accept these proposals and continue with "business as usual"

There is a general issue of the quality of data associated with publications proposing names of new taxa or new combinations for existing taxa.

For me these proposals are primarily to create a reliable phylogenetically based taxonomy/classification system for all Bacteria and Archaea.

The use of the term "phylogenetic" is often misleading because it is now taken to include only gene or protein sequences and effectively tries to exclude the "phenotype". Unless I have misunderstood something genes primarily encode for RNA, that in turn (with the exception of tRNA and rRNA) may be translated into protein sequences that themselves are either structural entities or enzymes. Enzymes may be single entities (i.e. an amylase) or part of a biochemical pathway (TCA cycle). As such most of the genome encodes for phenotypic features, providing one gets away from the definition "phenotype" = biochemical/physiological tests". I noted some years ago the work on the ribosome that culminated the Nobel Prize work (two publications in Science) highlighted the importance of the structural aspects i.e. the phenotype of the expressed genes. The Hennigian definition of "phylogenetic systematics" is about character analysis and became known as cladistics. This is in contrast to phenetics that is based on overall similarity and may include phenotypic and genetic data (see Cain and Harrison's original definition. The third alternative is to combine the two.

If one substitutes "evolutionary framework" for "phylogenetic" this might be more realistic. Evidence is that different genes have different "phylogenies" as a result of their different structural and functional roles (that is also reflected in codon usage and amino acid usage). Whole organism "phylogenies" in the prokaryotes have a network like structure (ie vertical and horizontal inheritance (gene loss and gain, gene duplication with change of function) that we are trying to press into a tree like structure.

The desire to be able to place the uncultured bacteria within our existing classification and the ability to refer to them by a binomial name will remain. I foresee that if these proposals are not accepted, we will see the establishment of a parallel nomenclature code to deal with the uncultivated prokaryotes. This

idea has support especially among the researchers working in the field of environmental microbiology and ecology. As this "Code" will potentially deal with the majority of bacteria, it will have a major impact on all fields of microbiology including traditional bacterial taxonomy.

We already have parallel systems - see my earlier e-mail. Given the fact that it can now take up to 4 months to get a name published on the Validation Lists there is also a two tier system, with names published in original articles in the IJSEM being given favour to those names being published in other journals.

The second benefit that accepting these proposals would have, is that it will allow taxonomists in many of the developing countries to continue to catalogue their unique prokaryotic diversity.

The resolve of many of the developing countries to exercise their sovereign rights over their biological resources to ensure benefit sharing when used for commercial gain, will remain. To ensure that benefit sharing is done these countries will still enforce measures to keep track of who outside their country has access to these resources. If genome sequences will not be accepted as alternative type material, the ICSP will have to address this issue by re-evaluating their requirement for deposits of cultures with no restrictions on access. I am of the opinion that the need to keep track of access to cultures differ from "safe deposits" and should be allowed. I have been in discussions with our national government for a number of years now and can assure everybody that changing the Code will be far easier than addressing national regulations that deal with all biodiversity to make acceptance for microbiologists to deposit type material.

There is nothing in the text that I sent around that was written 12 years ago that infringes the rights of the sovereign states to determine what happens to the biological diversity over which they exercise sovereign rights. However, by restricting access to the biological entities themselves (including of course parts of it such as DNA specimens) or the digital sequence information already creates a two tier system whereby one set of nomenclatural types are readily available for verification/further work and the others not. Spain makes exceptions to comply with the Code.

Imagine a national football committee that has different rules:

- 1) 15 players (two goal keepers) and a goal that is half the size
- 2) only the "home team" is allowed to have the ball

When applying to play by their rules in the World Cup by their rules they are turned down.

As in the case of one former member of the EU there are now consequences for future funding (perhaps even for the EBI-EMBL in Hinxton) and decisions have been made to withdraw from a common science forum perhaps to the detriment of scientists involved. One has to accept that.

The issue of changes to the Code that affect Rule 30 have not been submitted and are not part of the

current debate.

Dr. Brian J. Tindall

No affiliation with an employer or organisation is intended or to be inferred

I would therefore urge the members of the ICSP to carefully consider the concerns and consequences of accepting / rejecting the proposals when casting their votes.

Regards

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