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The proposed changes to the International Code of Nomenclature of Prokaryotes (ICNP) currently under consideration by the International Committee on Systematics of Prokaryotes (ICSP) would greatly harm the culture collections, their end users, and the scientific community at large. There are numerous flaws in the proposed changes, and their incorporation into the ICNP will have many unintended consequences that reverberate throughout the scientific, medical, agricultural, and regulatory communities.

Proposal 1: Allow sequences of genomic DNA serve as the nomenclatural type of a species or subspecies

As the primary scientific argument, allowing the nomenclatural type for species and subspecies to be DNA sequences minimizes the critical importance of viable biological specimens and reduces biology to mere sets of very limited data. An organism's biology may derive from its genome, but the full scope of its complex and sometimes unpredictable biology cannot be extrapolated from its genome. Post-translational modifications, epigenetics, metabolome, and the phenotypic and functional consequences of the interaction between complex biochemical pathways (to name only a few) are characteristics that cannot necessarily be predicted from the genome. All of these characteristics would be lost under the current proposals. Allowing type sequences will limit the definition of an organism to specific nucleotides and nothing more.

In terms of logistical implementation, DNA sequences in GenBank and other databases are frequently updated or deaccessioned entirely. The assignment of a specific genetic accession or set of accessions would inevitably result in frequent conflicts where a type sequence was no longer available, leading to both taxonomic and nomenclatural chaos. The nomenclatural system specified by the ICNP and the taxonomy that derives from its governance of validly published taxa require stability far greater than any current DNA databases can provide.

Acceptance of the proposed changes and their incorporation into the ICNP would do irreparable harm to the entire scheme of prokaryotic systematics. The nomenclatural type of species and subspecies must remain the type strain.

Proposal 2: Further extends acceptable nomenclatural types to new methods

The scientific arguments against Proposal 2 mirror those against Proposal 1. The full breadth and depth of an organism's biology is a function of a viable organism and cannot be captured by any specific methodology.

However, Proposal 2 also suffers from an additional mistake that makes it unworkable and unimplementable. The construction of the proposed text states that new *methods* may serve as types. A method is a procedure that is performed, the performance of which may result in the collection of scientific data. Microscopy and whole-genome sequencing are methods; microscopic

observations and genomic sequence are the respective data collected through these methods. While the presumed intention of this specific proposal is that such *data* may serve as a nomenclatural type in the future, the specific text that has been submitted to the ICSP for a vote is logically flawed and cannot be implemented into the ICNP. At a minimum, this proposal should be rejected in the current vote, and properly constructed text should be submitted as a future proposed change.

Proposal 3: Allows valid publication of a novel genus without a type species

This proposed change directly contradicts the taxonomic system universally used today. An order is composed of a family or a group of defined and related families. A family is composed of a genus or a group of defined and related genera. A genus is composed of a species or a group of defined and related species. To allow creation of genera without species is illogical and serves no practical purpose. This proposal would result in more confusion among scientists, as the definition of a genus is already at best loosely defined. Acceptance of the proposed changes will make the classification of related organisms more difficult in the future.

Proposal 4: Combines the official nomenclatural system of validly published taxa with the list of unofficial *Candidatus* taxa

The current system of nomenclature already allows the description of publication of organisms that are not culturable or cannot be fully characterized as *Candidatus* taxa. The only element that is missing from the *Candidatus* system is the recognition of nomenclatural priority. However, granting *Candidatus* organisms such priority would inevitably degrade the quality of science performed around these taxa. Rather than requiring that these organisms be properly isolated and cultured, this proposal would encourage researchers to shortcut the full and proper characterization of these taxa.

The value of genomics and advancing technology cannot be overstated. The latest technologies can and should be used to delineate, characterize, and authenticate prokaryotic organisms throughout the microbiological community. However, this is not the issue currently under consideration. These methods and the data derived from them should not be conflated with the necessity or appropriateness for them to serve as nomenclatural types. Adoption of the proposed changes would harm the field of microbiology as a whole and cause a cascade of confusion throughout the scientific, medical, agricultural, and regulatory communities.

In summary, the proposed changes to the ICNP are both scientifically misguided and logistically unworkable. The current proposals should be rejected by the members of the ICSP.