Comments submitted February 20th

Dear colleagues,

here I am returning to my first comment, specifically to the claim that the proposed changes of the ICNP would not only cause genome sequences to be used as types of microorganisms that cannot be cultivated but also as the nomenclatural types of microorganisms that could easily be cultivated.

I had argued that even if a pure culture is already available the possibility to use a genome sequence as type instead would cause this culture to not be deposited any more in a collection, at least in the majority of the cases. Because journals like IJSEM now require a genome sequence for proposals of new taxa there is no extra effort needed to use this sequence as a nomenclatural type. The efforts to deposit a strain shall no longer be necessary. Predictably, authors will then in most cases take the line of the least resistance and not deposit strains. Journals cannot effectively control whether a culture is available and could be deposited, especially if this is not declared. Even the IJSEM has difficulties to control whether deposits are patent deposits or are subject to restrictions such as strains from Brazil or India and thus cannot serve as deposits of type strains, causing the need to deny the status of being validly published afterwards.

It has been argued by supporters of the proposal to modify the ICNP that type strains can be provided later on for a name that was validly published based on a sequence as nomenclatural type and then exchange the nomenclatural type. The proposed changes to Rule 18f are supposed to cater for that, and during the online debate it was mentioned that providing better types could easily be done within an emendation of a taxon description. However, no evidence was provided for the likelihood of such an event.

Obtaining better type material later on is indeed unlikely according to 400 mycologists (doi:10.5598/imafungus.2018.09.01.10): "An undesired side-effect that should also be considered is that, in practice, few researchers will be devoted to re- describing (or actually describing) species that have been previously named based on just a DNA sequence. This has several causes, but among them, there is an important bias in research journals disfavoring the publication of re- descriptions of already known taxa, versus the description of new taxa. Another reason is time constraints, since it is not uncommon that specialists do not have the time to properly describe all of the numerous undescribed species they are aware of. This makes them focus on those that are more likely to be published as new species and not on those that have been already described, even if previous descriptions are faulty or defective. Anyhow, having numerous names only based on DNA sequences and few descriptions of the actual organisms would create an enormous number of (validly published) names applied to taxa for which virtually no information exists."

In fact, the number of published emendations is already now much smaller than the number of names validly published under the ICNP.

Sincerely yours
Markus Göker

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Comments submitted February 20th

Dear all,

We are aware of a proposal to the ICNP to allow the use of partial or complete genome sequences as type. After much consideration, we strongly believe that genome sequence alone should not be accepted as type for the following reasons.

1. If sequence can be adopted as type, it will pose an immense risk of losing the type strain collection, as type strains are no longer needed at culture collections.

1.1. This lack of the physical presence of type strains will impair public access to this culture of type strains. This, in turn, will hinder future study and distribution of those strains for further usage and applications. It also will be difficult to obtain culture of strains for reference purposes.

1.2. Without the need to deposit type strains in culture collections, there is a higher chance that the culture of type strains will be lost or inaccessible from an individual's collection.

2. Apart from sequence data, other important information related to type strains will be lost or insufficient for further utilization. Sequence data alone most likely does not paint a complete knowledge for the genome and would be inadequate for the effective utilization of those strains.

3. The sequencing technology is not yet stable and is still evolving.

3.1. Different sequencing platforms often result in different outcomes with regards to numbers of OTUs and lengths of sequencing reads. It poses a challenge for the standardization of the quality of the sequences to be accepted as type.

3.2. As sequencing is still relatively expensive and relies on high technological expertise, it can be considered a disadvantage for many researchers. The difference in availability of the sequencing instruments and financial capability in different countries will most likely further produce a larger gap between researchers in the already developed countries and those in the developing countries. This will also discourage researchers without much instrument and financial support to discover and propose new species.

4. Acceptance of sequence as type will dissuade the culture-as-type study. This will pose a challenge in the proposal of new species. Researchers have to search and compare the culture-as-type and genome-as type information in the report of new species. In addition, there will be a complication in prioritizing the culture-as-type versus genome-as type for proposal of new species name.

5. There is not yet a proper and simple way for the public to validate or verify if the sequence data is accurately from a living organism. This is especially difficult without the strain being deposited in a reliable culture collection.

6. If the unculturable genome assembled from metagenomic study is accepted as type, there is no clear method to verify that the assembled sequence is from a single organism and there is no clear benefit from the sequence as the organisms are still unculturable.

For these reasons, we currently oppose the proposal of the sequence as type and feel that it should be reconsidered.

Lily Eurwilaichitr
Thailand Bioresource Research Center (TBRC)
National Science and Development Agency, Thailand

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Comments submitted February 21st

7 Jan 2020

J. Dennis Pollack, Ohio State University, ret. (USA)

I don't think genome sequence is sufficient to constitute the type material of a new species.

Glenn Browning, University of Melbourne

I would accept a closed genome sequence with good depth, but not partial or draft sequences.

8 Jan

Alain Blanchard, University of Bordeaux (France)

I would accept a closed genome sequence with good depth, but not partial or draft sequences. In addition, in the pdf "It is recommended that, when possible, a sample of the DNA be deposited in at least two publically accessible service collections in different countries and the catalog numbers be indicated" is ambiguous. Indeed, the DNA of most of the uncultured bacteria is usually obtained with a high level of contamination of the DNA from the host (e.g. plant DNA for phytoplasmas). At least, the DNA sample that should be provided to the collections should be of the same quality as the one that was used to obtained the full genome sequence.

Chih-Horng Kuo, Academia Sinica (Taiwan)

I support the use of genome sequence as the type material. For more detailed considerations:

1. The complete & closed chromosome sequence should be required; plasmid(s) may be missing in the assembly but those probably are not critical for taxonomy.

2. Sometimes completing the chromosome sequence is just not practical, and draft genomes could provide some very useful information. The major concern is what would be the quantitative standards for "high quality" draft. If the community can come to a consensus, then accepting draft genomes would be fine.

3. In addition to the assembled genome, the raw sequencing data sets must be made available. In case the genomes are mis-assembled, other people can identify & verify the problem.

4. Making the DNA samples available is important but may not be always possible. Even when possible, the quantity may be quite limited. So perhaps this should be recommended and not an absolute requirement.

9 Jan

Mitchell Balish, Ohio University (USA)

A genome sequence could potentially stand as type material for a new species if at least the following criteria are met:

1) There must be evidence that the sequence is either complete (excluding episomal elements) or nearly so, accounting for difficulties in sequencing repetitive regions, etc. Evidence for completeness of a sequence that isn't closed could derive from the completeness of sets of genes encoding the proteins involved in well-established metabolic (or other) pathways, like glycolysis and protein translation (as appropriate).

2) To establish that a genome represents a new species, some stringent threshold of difference from other species – excluding elements like transposons, prophages, and pathogenicity islands – must be reached. The quantification of this difference should be established not by looking at one gene or a small number of genes; it should be derived from information integrating the entire genome (minus the aforementioned variable elements), like total percent nucleotide identity or protein similarity, or even shared gene content. Candidate criteria along these lines are proposed by the authors who are in support of the use of genome sequence as type material. It is important that the criteria are applied very strictly and regularly. I suspect many things we call different species would actually fail to meet these criteria; but I think it's better to err on the side of not calling something a new species, at least until phenotypic characterization establishes otherwise.

10 Jan

Joachim Frey, University of Bern (Switzerland)

I fully agree with the comments of Mitch.

1) The genome must be complete. Currently combining sequencing from a long read run (e.g. PacBio) with short reads run (Illumina) are standard to get a best possible full genome sequence. Both the

final full genome sequence and the short reads must be made accessible by depositing at GenBank/EMBL and SRA (short reads archive).

2) The entire genome sequence except transposons IS, CRISPR etc must be used.

3) If the type strain is deposited, (if the [organism] can be grown) the study should be reproducible. I do not know if depositing DNA will become a standard but it would certainly be useful.

13 Jan

Assunta Bertaccini, University of Bologna (Italy)

The DNA sample provided to the collections should be of the same quality as the one that was used to obtained the full genome sequence.

The complete & closed chromosome sequence should be required; making the DNA samples available may not be always possible so perhaps this should be only a recommendation but realistically based (I mean the scientific community should be sure of the existence of the strain..).

Evidence for completeness of a sequence that isn't closed could derive from the completeness of sets of genes encoding the proteins involved in well-established metabolic (or other) pathways, like glycolysis and protein translation (as appropriate).

To establish that a genome represents a new species, some stringent threshold of difference from other species – excluding elements like transposons, prophages, and pathogenicity islands – must be reached. The quantification of this difference should be established not by looking at one gene or a small number of genes; it should be derived from information integrating the entire genome (minus the aforementioned variable elements), like total percent nucleotide identity or protein similarity, or even shared gene content. Candidate criteria along these lines are proposed by the authors who are in support of the use of genome sequence as type material. It is important that the criteria are applied very strictly and regularly.

The genome must be complete. Both the final full genome sequence and the short reads must be made accessible and depositing DNA would certainly be useful.

I don't agree with CH about draft genomes and raw sequencing data sets these data could/should be handled only by expert colleagues who can verify them in the most appropriate manner …

15 Jan

Ana Sofia Ramirez Corbera, Universidad de Las Palmas de Gran Canaria (Spain)

The genome sequence is sufficient to constitute the type material of a new species, but I would also add the necessity of detecting it several times (in different places or the same place at different times) as an equivalent of the need to have some isolations of the same species.

18 Jan

Christine Knox, Queensland University of Technology (Australia)

It is time to have an alternative to serotyping and DNA-DNA hybridization assays in order to define a new type species. 16S rRNA sequencing and then a closed and complete genome sequence of the strain to be designated the type strain is the way forward. It would be good to have deposits of both the culture (when possible) and the DNA.

There will be difficulties if more that one strain is described. It may not be possible to provide multiple WGSs. Sequencing and alignment of selected genes then may define phylogenetic relationships but this cannot be used to describe type strains.

30 Jan

Dmitriy V. Volokhov, US Food and Drug Administration (USA) [edited for length]

A high-quality draft (genome scaffolds) or better complete genome sequences should be provided for Candidatus species.

I disagree that ONLY complete genome sequences should be acceptable; researchers could have a lot of situations when assembly of complete genome sequences for Candidatus species may not be possible.

At least two different genome assembly algorithms should be used for Candidatus species.

The DNA sample for Candidatus species provided to the collections should be of the same quality as used to obtain the full genome sequence. But what will be acceptance criteria of this “same quality”?

I disagree that ONLY DNA and/or DNA sequence deposition for cultivable [organisms] will be sufficient instead of deposition of live culture of type strain.

A single strain per each species could be sufficient in a case when the novel species found to be genetically unique in comparison to other well-known species.

There will be difficulties if more than one strain is described for the same species if multiple WGSs are not provided, in this case MLST can be used as define phylogenetic relationships among strains. MLST should not be used to describe type strains for Candidatus species.

Comments from members of the Subcommittee on taxonomy of Mollicutes attached.

Daniel R. Brown, PhD
Chairman, UF Institutional Animal Care and Use Committee

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Comments submitted February 23rd

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"

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

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.

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 acception for microbiologists to deposit type material.

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

Fanus Venter
Professor: Department of Biochemistry, Genetics and Microbiology
Deputy Director Forestry and Agricultural Biotechnology Institute (FABI)
University of Pretoria

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Comments submitted February 23rd (interleaved with the original comments from Prof. Venter

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 acception 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

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Comments submitted February 23rd

In reply to Dr. Shivaji.

I noted the split between "chemotaxonomy" and "phenotype". There is no reason why chemical data should not be included as part of the phenotype, just as the ribosome or ATP synthase has a phenotype. While the phenotype is often referred to as "unreliable" or "uninformative" this often depends on how work is done or which parameters are studied. Genetic information can be "unreliable" if different labs submit different digital sequence information for what they claim to be the same strain or "uninformative" if it is a gene that appears to be easily lost or gained in a population.

One of the key issues is that one has forgotten is that as defined by Colwell the "polyphasic" method has moved on. Originally defined on data available at the time and clearly a phenetic approach (ie overall similarity and not limited to phenotype as often mistakenly assumed), the polyphasic method can include relevant phenotypic information as well as relevant gene based information. Co-relating the two is the next major task in the biological sciences. Annotation of genes usually requires knowledge of the phenotype. Debates with Peter Sneath missed the point that the early rRNA ctalaogue Sab values were phenetic and not (phylo)genetic = cladistic. The strength of the system that developed was that work on the lipids of what was to become the Archaea went back to 1962 and supported a completely different data set, just as early 16S rRNA catalogue and cytochrome sequences (Nature papers in the late 1970s) showed the same picture or that the respiratory lipoquinone data collected from the late 1950s onwards and published in a review by Collins and Jones quickly allowed one to make sense of re-arrangements in the genus Pseudomonas and the concept of the alpha-, beta- and gamma-subclasses. The latter being also supported by lipopolysaccharide work. Both the gene based and phenotype based systems point to an evolutionary basis for their distribution and development over geological time. A broad based “polyphasic” approach is a multi-disciplinary approach that takes us to the limits of our current methods and understanding of biology.

Unfortunately, the "phylogenetic" system (priority being given to sequence based interpretation) has also had its down side. Work by Imhoff in the 1990s on the chemical composition of the genus Rhodobacter has only recently resulted in a realisation that the "phylogenetic interpretation" can be

refined by relevant phenotypic (chemical) data. Major theories on the nature of "genera" in the planctomycetes, or Methanognium were quietly silenced with the help of the chemical data. The genus Peptoclostridium Yutin and Galperin 2013 was put into perspective by Gerritsen et al. 2014. Placing Deinobacter in the genus Deinococcus was also a major dis-service to the existing chemical data on this "genus" and we continue to founder on a clear definition of the genus Clostridium, where chemical data (with its underlying genetic information) points to a radical split.

Dr. Brian J. Tindall

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Comments submitted February 23rd

Dear Colleagues,

Given the fact that these discussions involve the International Committee on Systematics or Prokaryotes and the International Journal of Systematics and Evolutionary Microbiology it would be appropriate to highlight the science of systematics. Systematics is a fundamental part of the biological sciences and can be succinctly described as the cradle of comparative biology. Sadly one often sees this science reduced to the naming of biological entities. The latter element is nomenclature and is part of the elements nomenclature (the naming of classified biological entities), classification (the science of grouping biological entities based on their properties and theoretical and philosophical considerations), characterisation (the collecting of data on the biological entities that is potentially limited only by the methods available to us). Together these are regarded as comprising taxonomy, where a taxonomic system is a pre-requisite for the identification of a biological entity either as a member of an existing taxon (irrespective of rank) or novel at one or more ranks. Identifications typically rely on a limited data set that may none-the-less allow predictions to be made about features not included in the identification system, but included as part of the original taxonomy. As such taxonomies are open ended and nomenclatures serve as pointers to the classification and properties of the biological entity in question. Limiting those properties to only digital sequence information or reducing the classification to ANI, AAI or POCP values could be considered to be a reductionist, minimalistic approach that also precludes alternative methods or interpretation, as well as excluding relevant biological information.

Systematics certainly uses the underlying taxonomic system, but it should neither be reduced to taxonomy nor nomenclature. It is a fallacy to assume that either systematics (in the wider sense) or taxonomy has either a limited goal or inherently limits the data sets I consider myself to be a systematist with some 44 years of standing and reading relevant papers in Journal of Biological Chemistry, Molecular Microbiology, PNAS, Journal of Molecular Evolution. Journal of Lipid Research, Genome Biology or Systematic Biology contributes to the scope of systematics and the need to appreciate the current limitations that seem to have been self-imposed that many seem to have identified as the root cause of problems, but where the alternatives do not address the needs of systematics, nor does it break with what could be considered to be a limited view of the purpose of either taxonomy or its component parts (nomenclature, classification, characterisation).

Systematics is indeed a multi-disciplinary science and genomics is also one element in appreciating biological diversity. Given the magnitude of the task it would be far more beneficial to get the diverse range of experts together and to illuminate biology from its very different angles that would enrich both systematics and the appreciation of taxonomy with its underlying infrastructure. I recall a paper I wrote 27 years ago where I cited Dobzhansky and the fragmentation of the biological sciences. Little has changed in the intervening years.

Dr. Brian J. Tindall

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Comments submitted February 24th (interleaved with the original proposals to change the Code.

Dear Colleagues,
My specific comments (in red) on the wording of the proposed changes that for clarity has been inserted into the original text.

Proposal 1 (Whitman 2016). Extend the nature of the type acceptable for valid publication of a species or subspecies name to allow the use of complete or partial genome sequences as type (Whitman 2016). The new rules would be worded [new text is underlined]:
Rule 18a. The type of a species or subspecies must unambiguously identify the taxonomic group and is a designated strain or other material. Whenever possible, the type of a species or subspecies is a designated strain.

A) The Code is neutral on a number of points, including whether a nomenclatural type "must unambiguously identify the taxonomic group". The "nomenclatural type if that element of a taxon with which a name is permanently attached", but at the same time does not preclude that it may be considered later on that a name is a heterotypic synonym of another name. This wording should be deleted. It would be appropriate to substitute "nomenclatural type" in all instances in the Code where the term "type" is used alone.

B) The use of the term "material" implies a physical object. In the case of genome sequences there is a difference between the sequence chemically encoded on a piece of DNA and the digital sequence information that is obtained by experimental procedures and deposited in an electronic database as an electromagnetic signal in binary code.

(3) [first section] As from 1 April 2020*, sequences of genomic DNA may also serve as the type when it unambiguously identifies the species. When possible, it should be a high quality draft or better genome sequence.

C) For "sequences of genomic DNA" read "digital sequence information that is obtained by experimental procedures and deposited in an electronic database". Remove "unambiguously identifies the species" since this is outside of the remit of the Code. In essence "digital sequence information" is the same as a description.

Rule 30.3.c. [new rule] When a sequence is the type, the accession number in a publically available database or the sequence must be given. It is recommended that, when possible, a sample of the DNA be deposited in at least two publically accessible service collections in different countries and the catalog numbers be indicated.

D) We are not talking about a physical sequence, but digital sequence information obtained by experimental procedures and deposited in an electronic database as an electromagnetic signal in binary code. This is essentially a description at the level of the genome.

E) The term “catalog” is incorrect and should be replaced by “accession”. DNA deposited in at least two publically accessible service collections constitutes as preserved specimen. It is also questionable what purpose this would serve, since, In contrast to a written description, illustration or preserved specimen on a microscope slide of the organism the only way of examining the preserved DNA with regards its physical nature (i.e. by determining the nucleotide sequence by current methods) would be to destroy it. See also Sneath and Neimark:
https://doi.org/10.1099/00207713-45-1-188
https://doi.org/10.1099/ijs.0.63718-0

Proposal 2 (Whitman 2016). Articulates a general concept for what can serve as type for a species.
Rule 18a (3). [*second section*] As new methods are developed, they may serve as the type material so long as they unambiguously identify the species or subspecies and can be readily archived and compared.

F) This is already covered by Principle 1 (4), but also makes the mistake that a method cannot serve as a nomenclatural type. This can be deleted.
Proposal 3 (Whitman 2016). Allows valid publication of the name of a genus in the absence of a type species if the type is too ambiguous to circumscribe a species.

The rule would be:
"Rule 20a. The nomenclatural type (see Rule 15) of a genus or subgenus is the type species or the sequence of one or more genes that unambiguously identifies the genus or subgenus. The type species is the single species or one of the species included when the name was originally validly published. Only species whose names are legitimate may serve as types."
G) This links back to the issue of “unambiguously identifying” a taxon, which is not part of the remit of the Code. It also makes a claim that one or more genes may unambiguously identify the genus or subgenus. Since different authors may evaluate the same information differently this would not preclude the establishment of heterotypic synonyms, ie the two taxa were not unambiguously identified. “Or the sequence of one or more genes that unambiguously identifies the genus or subgenus” should be deleted.

Proposal 4 (Whitman et al. 2019). Upon acceptance of Proposal 1, the priority of the names of *Candidatus* taxa published before 1 April 2020* which are otherwise in accordance with the rules of the Code will have priority based upon their date of publication in the IJSEM unless a synonymous name already exists based upon deposition of type cultures.
Whitman et al. (2019) also provides a simple nomenclature for identifying the nature of the type material:

‘When the type is a culture, the superscript “T” will be used immediately following the name or strain identifier. If the type is a sequence, the superscript “Ts” will be used. If the type is a description, preserved specimen or illustration, the superscript “Td” will be used. If a representative of a taxon is brought into culture, the type strain is then designated as described in Rule 18f. The name may be emended by the new authors, and the superscript “Ts” or “Td” is replaced by the superscript “T”.’

H) As indicated previously, at the rank of species and subspecies this would apply to the nomenclatural type and not to the corresponding name.

*The original date of 1 January 2020 is changed to reflect the time necessary to bring this matter to a vote.
I) In the past all changes to the Code were documented in articles in the IJSEM, in the minutes of the appropriate committees/commissions and applied from their date of publication of the version of record.

Dr. Brian J. Tindall

PS I note with some concern that this is not happening
"As comments accumulate, the Editorial Board will transfer them to the ICSP website, and the edited comments will serve as the minutes of the meeting.