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.