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Commentary

The use of genomic DNA sequences as type material for valid publication of bacterial species names will have severe implications for clinical microbiology and related disciplines

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The bacterial species is the basis for the study, identification, and diagnosis in medical and veterinary microbiology. More than 2000 species have been isolated from humans, while more than 100 are considered to be serious human pathogens (Hugon et al., 2015; Janda, 2017). The process for establishing an unequivocal nomenclature of bacteria is standardized and maintained internationally (*Prokaryotic Nomenclature Up-to-date*, n.d.; Parte, 2018). Scientific publishers are trying to comply with this nomenclature as do internal identifiers in databases, including those relevant for diagnostics. Valid publication of species names defines 1 "type" strain, e.i., as the reference standard for taxonomic investigations and standardization of diagnostics tests. The International Code of Nomenclature of Prokaryotes (the "Code") requires that "The type strain is made up of living cultures of an organism descending from a strain designated as the nomenclatural type." (Rule 18a) (Parker et al., 2019). Deposit of living cultures in "… at least two publicly accessible culture collections in different countries, from which subcultures must be available." (Rule 30) (Parker et al., 2019) is mandatory for valid publication of new species names.

Bacterial nomenclature and classification allow us to communicate effectively around the globe regarding bacterial diseases, epidemiology, and emerging genotypes/phenotypes. This transfer of knowledge could be compromised by a recent proposal arguing that genome sequences should be accepted as type material for valid publications of bacterial species names if a living culture is not available (Whitman, 2015; Whitman, 2016). One argument for this proposal has been that a large proportion of bacteria cannot yet be cultured and are recognized only at the DNA level. For such species, the *Candidatus* category was established (Murray and Stackebrandt, 1995), although a species name with *Candidatus* status does not have nomenclatural priority.

We do not argue that closed or draft genomic DNA cannot be used as a decisive criterion for delineating novel species, but the implications for the microbiology scientific community, if the proposal of Whitman (Whitman, 2015; Whitman, 2016) is to be implemented in the Code, are far reaching and several problems can be predicted:

1. The scientific data supporting the description of a species may not be reproducible, particularly if the original material (DNA) is damaged or lost or if no scientific distribution of nonproliferating material is anticipated.
2. The changing standards for genomic DNA sequence quality present potential complications when DNA sequence type material is replaced by new versions and the species descriptions have to be consequently revised (Chun et al., 2018).
3. To date, functional assessments for genomes are limited and do not necessarily allow recognition or prediction of distinguishing phenotypic traits that may define the taxa.
4. Genomic data do not always correlate with gene expression such that apparent features at the genome level may infer misleading phylogenomic or taxonomic relationships.
5. The problems of defining what is required to present new taxa will increase. It is already current practice to describe novel species on the basis of single strains (Christensen et al., 2001), while their intraspecies diversity at the genotypic and phenotypic level is *a priori* unknown. The proposal of Whitman (Whitman, 2015; Whitman, 2016) is likely to lead to the proposal of unknown numbers of novel species based on the description of single DNA sequences only and will lead to taxonomic and nomenclatural chaos.

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6. The motivation for researchers to cultivate and preserve strains and to attempt to investigate phenotypes will decrease, resulting in unknown intra- and interspecies diversity, at the phenotypic levels.

Another proposal has suggested establishing an independent nomenclature for not-yet-cultivated taxa (Konstantinidis et al., 2017). Although this proposal is not directly including changes to the Code, several problems have been predicted (Overmann et al., 2019). A comprehensive critical treatment of both proposals for naming uncultured prokaryotes has recently been published with overlaps to the points mentioned above and considering, as well, genomic assemblies derived from metagenomic data (microbiome DNA shotgun sequences) (Overmann et al., 2019).

Although the Code offers the possibility to reject names that may compromise clinical diagnostics (*nomina rejicienda*) and represent a risk to the diagnostics of bacterial diseases, the procedure might take years. If the proposal of Whitman (Whitman, 2015; Whitman, 2016) and Konstantinidis et al. (Konstantinidis et al., 2017) is implemented, we doubt that new species named only on the basis of genome sequences as type material will be used by the whole scientific community. Without experimental conformation of functional activities, e.g., virulence, pathogenicity, antimicrobial resistance, metabolic catalytic activities, etc., microbiologists involved in clinical human and veterinary microbiology and perhaps other fields of applied microbiology will either retain the established names or invent another system that preserves the quality of these disciplines.

What is to be done? We recommend that this far-reaching proposal be discussed throughout the wider microbiological scientific community. Decisions about changes in the Prokaryotic Code, including proposals to allow genome sequences to be accepted as the type material for new species, are to be considered by the International Committee on Systematics of Prokaryotes (ICSP) (http://www.the-icsp.org/, n.d.). The members of ICSP are delegates from their respective national microbiological societies. In-depth discussions of delegates and their societies are recommended for supporting decisions by ICSP on this topic.

Authors' contributions

HC presented the original idea and wrote first draft of the manuscript. MB, DC, LD, JMJ, AN, NN-L, ERBM, JO, and FAGR all contributed to the writing of the manuscript.

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