

Towards standardisation of naming novel prokaryotic taxa in the age of high-throughput microbiology

We thank Professor Oren for his interest in our work and for his constructive comments.¹ In our recent article in *Gut*, we described the discovery of a new species that rose to high abundance in the human gut after treatment with ceftriaxone.² We made the decision to propose taxonomic Latin names for this new species and for associated taxa because we wished to create a memorable, user-friendly, sustainable and transferable nomenclature that could be readily adopted by other researchers. Our proposals

included the taxonomic hierarchy: ^UComantemales ord. nov., ^UComantemaea fam. nov., ^U*Borkfalki* gen. nov., ^U*Borkfalki ceftriaxensis* sp. nov.

We adopted the superscript ‘U’ (for ‘uncultured’) prefix in line with a recent suggestion³ but accept that use of *Candidatus* has priority. However, in our defence, it is worth noting that recommendations for use of *Candidatus* cited by Professor Oren state that ‘this category should be used for describing prokaryotic entities for which more than a mere nucleic acid sequence is available’, but these recommendations remain vague on what additional information, beyond ‘mere nucleic acid sequence’ suffices.

Professor Oren criticises us for going against Recommendation 6 in the International Code of Nomenclature of Prokaryotes (ICNP) in naming a genus after ourselves. However, under General Considerations, the ICNP states that ‘Recommendations do not have the force of Rules; they are intended to be guides to desirable practice in the future. Names contrary to a Recommendation cannot be rejected for this reason’. As Oren notes, several precedents exist for scientists naming species after themselves.

We accept that we have made errors in our use of Latin. To correct these, we suggest changing the genus name to *Candidatus Borkfalkia*, and, following ICNP Rule 9 quoted by Oren,¹ the associated family name to *Candidatus Borkfalkiaceae* and the order to *Candidatus Borkfalkiales*. For a species epithet, we suggest a change to ‘ceftriaxoniphila’, from *ceftriaxonum* (N. L. neuter noun for ceftriaxone) and N.L. fem. adj. *phila*, from Gr. fem. adj. *philé*; friend, loving). Thus, the Latin binomial for our species becomes *Candidatus Borkfalkia ceftriaxoniphila*.

We proposed a novel family Erisaceae. On reviewing a recent study, we note that the newly named family Hungateiclostridiaceae appears to have priority over our proposed Erisaceae.⁴ However, in that recent study, the genus *Mageeibacillus* was included within Hungateiclostridiaceae, whereas we have shown that *Mageeibacillus* forms a distinct clade outside the Hungateiclostridiaceae, supporting the need for an additional family name, for which, in line with the ICNP Rule 9, we now propose the term Mageeibacillaceae.

A more general problem is the applicability and scalability of the ICNP’s approaches in the age of high-throughput sequencing, where the number of bacterial species discovered and described by sequencing alone vastly outweighs those that can be cultured, with individual publications now often reporting hundreds of potentially

novel species.^{5–7} Furthermore, these novel species are typically bundled into inconsistent numerical taxonomic schemes, where the same novel species will often receive multiple different numerical names. We believe that, to ensure consistency, all new species defined by sequencing deserve their own Latin binomials. We therefore welcome a recent proposal to the ICNP to accept metagenome-assembled genomes as type material for the purposes of naming new species⁸ and we encourage dialogue between taxonomists and microbial genome scientists on this pressing problem.

Falk Hildebrand ^{1,2} Mark J Pallen,^{3,4,5} Peer Bork^{6,7}

¹Gut Microbes and Health, Quadram Institute Bioscience, Norwich, Norfolk, UK

²Digital Biology, Earlham Institute, Norwich, Norfolk, UK

³Microbes in the Food Chain, Quadram Institute Bioscience, Norwich, UK

⁴School of Biological Sciences, University of East Anglia, Norwich, Norfolk, UK

⁵School of Veterinary Medicine, University of Surrey, Guildford, Surrey, UK

⁶Structural and Computational Biology, European Molecular Biology Laboratory, Heidelberg, Germany

⁷Molecular Medicine Partnership Unit, University of Heidelberg and European Molecular Biology Laboratory, Heidelberg, Germany

Correspondence to Dr Falk Hildebrand, Gut Microbes and Health, Quadram Institute Bioscience, Norwich NR4 7UQ, UK; falk.hildebrand@quadram.ac.uk

Acknowledgements We thank Mohammad Bahram and members of the Quadram Institute for helping with early versions of this manuscript.

Contributors FH, PB and MJP wrote the letter together.

Funding The authors gratefully acknowledge the support of the Biotechnology and Biological Sciences Research Council (BBSRC); FH’s salary is funded by the BBSRC Institute Strategic Programme Gut Microbes and Health BB/R012490/1 and its constituent project BBS/E/F/000PR10355. MJP is supported by the Quadram Institute Bioscience BBSRC-funded Strategic Program: Microbes in the Food Chain (Project No. BB/R012504/1) and its constituent project BBS/E/F/000PR10351 (Theme 3, Microbial Communities in the Food Chain) and by the Medical Research Council CLIMB grant (MR/L015080/1) PB was supported by European Union’s Horizon 2020 research and innovation Programme ec/H2020/ eS/erc-adg-669830; MicrobioS.

Competing interests None declared.

Patient consent for publication Not required.

Provenance and peer review Not commissioned; internally peer reviewed.



OPEN ACCESS

Open access This is an open access article distributed in accordance with the Creative Commons Attribution 4.0 Unported (CC BY 4.0) license, which permits others to copy, redistribute, remix, transform and build upon this work for any purpose, provided the

original work is properly cited, a link to the licence is given, and indication of whether changes were made. See: <https://creativecommons.org/licenses/by/4.0/>.

© Author(s) (or their employer(s)) 2020. Re-use permitted under CC BY. Published by BMJ.



To cite Hildebrand F, Pallen MJ, Bork P. *Gut* 2020;**69**:1358–1359.

Received 7 May 2019

Accepted 30 May 2019

Published Online First 15 June 2019

Gut 2020;**69**:1358–1359. doi:10.1136/gutjnl-2019-319045

ORCID iD

Falk Hildebrand <http://orcid.org/0000-0002-0078-8948>

REFERENCES

- Oren A. Naming novel prokaryotic taxa discovered in the human gut. *Gut* 2019;**69**:969–70.
- Hildebrand F, Moitinho-Silva L, Blasche S, et al. Antibiotics-induced monodominance of a novel gut bacterial order. *Gut* 2019;**68**:1781–90.
- Konstantinidis KT, Rosselló-Móra R, Amann R. Uncultivated microbes in need of their own taxonomy. *ISME J* 2017;**11**:2399–406.
- Zhang X, Tu B, Dai LR, et al. *Petroclostridium xylanilyticum* gen. nov., sp. nov., a xylan-degrading bacterium isolated from an oilfield, and reclassification of clostridial cluster III members into four novel genera in a new Hungateiclostridiaceae fam. nov. *Int J Syst Evol Microbiol* 2018;**68**:3197–211.
- Nielsen HB, Almeida M, Juncker AS, et al. Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. *Nat Biotechnol* 2014;**32**:822–8.
- Parks DH, Rinke C, Chuvochina M, et al. Recovery of nearly 8,000 metagenome-assembled genomes substantially expands the tree of life. *Nat Microbiol* 2017;**2**:1533–42.
- Pasolli E, Asnicar F, Manara S, et al. Extensive Unexplored Human Microbiome Diversity Revealed by Over 150,000 Genomes from Metagenomes Spanning Age, Geography, and Lifestyle. *Cell* 2019;**176**:649–62.
- Whitman WB. Modest proposals to expand the type material for naming of prokaryotes. *Int J Syst Evol Microbiol* 2016;**66**:2108–12.