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: [U]Comantemales ord. nov., [U]Comantemaea fam. nov., [U]*Borkfalki* gen. nov, [U]*Borkfalki ceftriaxensis* sp. nov.

We adopted the superscript 'U' (for 'uncultured') prefix in line with a recent suggestion[3] 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 species[8] and we encourage dialogue between taxonomists and microbial genome scientists on this pressing problem.

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