

Game Changers

WHAT'S IN A NAME? DECIPHERING THE TAXONOMY OF BACTERIA, FUNGI AND PARASITES CAUSING INFECTION

JE Moore¹, BC Millar¹

¹ Laboratory for Disinfection and Pathogen Elimination Studies, NI Public Health Laboratory, Belfast City Hospital, Belfast, BT9 7AD

Microbial taxonomy, encompassing bacteria, fungi and parasites, is becoming more and more complicated, largely due to the application of newly emerging molecular methods, including whole genome sequencing. Presently, the List of Prokaryotic Names with Standing in Nomenclature lists 30,808 species from 4,954 genera.¹ In addition to this, there are a further 9,006 species from 2,196 genera, which are not validly published names.¹ Classification of these organisms has relied on phenotypic diversity, small subunit ribosomal RNA and more recently, genome-based classification.² Whilst only a small proportion of these organisms have ever caused human infection, it is daunting for the physician and surgeon to have an appreciation of (i) where these organisms are positioned taxonomically, (ii) how they are relate to each other and (iii) any recent modifications to their name. More recently, employment of improved molecular tools allows for the reclassification and splitting of established genera into new bacterial genera, with new names, which has the potential to cause confusion amongst doctors using the conventional name. An example of this is the Gram-positive anaerobe, *Clostridium difficile*, which was

reclassified and renamed as *Clostridioides difficile* in 2016.³ Other examples of recent bacterial nomenclature revisions include *Mycobacterium abscessus* to *Mycobacteroides abscessus*, *Enterobacter aerogenes* to *Klebsiella aerogenes* and *Ochrobactrum anthropi* to *Brucella anthropi*. For a full list of bacterial taxonomical revisions, please see Prinzi and Moore.⁴

A freely available online tool, LifeMap,⁵ (<https://lifemap-ncbi.univ-lyon1.fr/>) is available for interrogation, which allows the reader the opportunity to input a microbial name of interest, utilising zooming and panning tools to determine where the organism of interest is positioned taxonomically, as well as describing the most up-to-date taxonomical name (Figure 1). Employment of such a tool may aid in a better understanding of microbial taxonomy of infection-causing pathogens and an improved lexicon aiding better communication amongst physicians/surgeons and scientists.

REFERENCES:

1. Euzey JP, Parte AC. LPSN - List of Prokaryotic names with Standing in Nomenclature. [Internet]. Germany: The Leibniz Association. [cited 2024 June 5]. Available from: <https://lpsn.dsmz.de/>
2. Hugenholtz P, Chuvochina M, Oren A, Parks DH, Soo RM. Prokaryotic taxonomy and nomenclature in the age of big sequence data. *The ISME J*. 2021;**15**(7):1879-92.
3. Lawson PA, Citron DM, Tyrrell KL, Finegold SM. Reclassification of *Clostridium difficile* as *Clostridioides difficile* (Hall and O'Toole 1935) Prévot 1938. *Anaerobe*. 2016;**40**:95-9.
4. Prinzi AM, Moore NM. Change of plans: overview of bacterial taxonomy, recent changes of medical importance, and potential areas of impact. *Open Forum Infect Dis*. 2023;**10**(7):ofad269. doi.org/10.1093/ofid/ofad269
5. de Vienne DM. Lifemap: exploring the entire tree of life. *PLOS Biology*, 2016;**14**(12):e2001624. doi.org/10.1371/journal.pbio.2001624

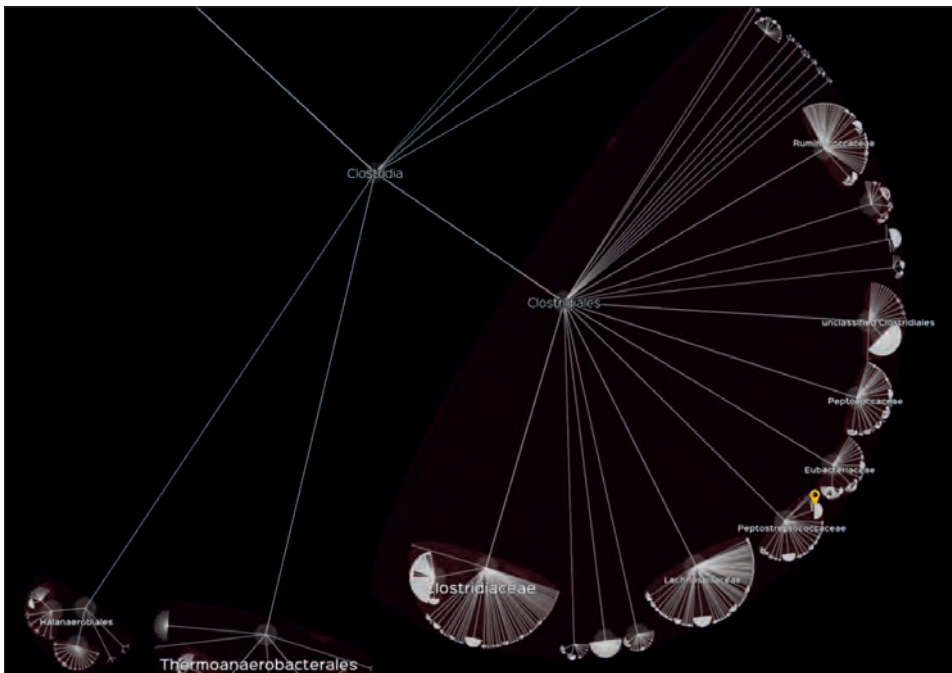


Figure 1: Description of the taxonomical lineage of *Clostridioides (Clostridium) difficile* (📍), as displayed by LifeMap (NCBI version).⁵



UMJ is an open access publication of the Ulster Medical Society (<http://www.ums.ac.uk>). The Ulster Medical Society grants to all users on the basis of a Creative Commons Attribution-NonCommercial-ShareAlike 4.0 International Licence the right to alter or build upon the work non-commercially, as long as the author is credited and the new creation is licensed under identical terms.