

# **HHS Public Access**

Int J Syst Evol Microbiol. Author manuscript; available in PMC 2024 July 31.

Published in final edited form as:

Author manuscript

Int J Syst Evol Microbiol. 2023 November; 73(11): . doi:10.1099/ijsem.0.006144.

# International Committee on Systematics of Prokaryotes: Subcommittee on the taxonomy of aerobic *Bacteroidota*. Minutes of the online meeting 25 April 2023

John P. Bowman<sup>1,\*</sup>, Celia Hugo<sup>2</sup>, Ainsley Nicholson<sup>3</sup>, Richard Hahnke<sup>4</sup>, Ellen Frandsen Lau<sup>5</sup>, Barry Holmes<sup>6</sup>, Iain Sutcliffe<sup>7</sup>

<sup>1</sup>Tasmanian Institute of Agriculture, University of Tasmania, Hobart, Tasmania, Australia;

<sup>2</sup>Department of Microbial, Biochemical and Food Biotechnology, University of the Free State, Bloemfontein, South Africa;

<sup>3</sup>Special Bacteriology Reference Laboratory, Bacterial Special Pathogens Branch, Division of High-Consequence Pathogens and Pathology, Centers for Disease Control and Prevention, Atlanta, Georgia 30333, USA;

<sup>4</sup>DSMZ - German Collection of Microorganisms and Cell Cultures GmbH, Braunschweig, Germany;

<sup>5</sup>Department of Dentistry and Oral Health, Aarhus University, Aarhus, Denmark;

<sup>6</sup>National Collection of Type Cultures, Health Protection Agency, Colindale, London NW9 5EQ, UK;

<sup>7</sup>Faculty of Health & Life Sciences, Northumbria University, Newcastle Upon Tyne, Tyne & Wear, UK.

# Keywords

taxonomy; nomenclature; ICSP Subcommittee; Bacteroidota

# MINUTES OF THE MEETING

Prepared by attendees in May 2023. The original name of the Subcommittee is slightly corrected to 'Aerobic *Bacteroidota*' from 'Aerobic *Bacteroidetes*'.

Conflicts of interest

Disclaimer

<sup>\*</sup>Correspondence: John P. Bowman, john.bowman@utas.edu.au.

The authors declare that there are no conflicts of interest.

The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the Centres for Disease Control and Prevention (CDC). The mention of company names or products does not constitute endorsement by CDC.

# MINUTE 1. CALL TO ORDER

The meeting was called to order by the Chairman, J.P. Bowman, on 25 April 2023. The meeting was held as a video conference using Zoom software.

# **MINUTE 2. RECORD OF ATTENDANCE**

The members present were, J.P. Bowman (Chairman), Celia Hugo (Secretary), Ainsley Nicholson, Richard Hahnke, Ellen Frandsen Lau and Barry Holmes. Also attending was Iain Sutcliffe from the International Committee on Systematics of Prokaryotes (ICSP) Executive Board.

# MINUTE 3. APPROVAL OF AGENDA

Most of the Subcommittee have been open meetings allowing guests to attend. Separate closed meetings have not been held for a considerable period of time and thus this particular meeting was an open meeting. The proposed agenda was approved by all members. No additional points to the agenda were made. Based on the success of having an open meeting format, the online format will be utilized hereon and allow guest experts where desired.

# MINUTE 4. MINUTES OF THE PREVIOUS MEETING

The minutes of the previous meeting held 10 July 2019 were approved and have been published [1].

# **MINUTE 5. CHANGES IN MEMBERS AND OFFICERS**

J.-F. Bernardet has stepped down following his retirement. Jongsik Chun also indicated his desire to step down due to other commitments.

## MINUTE 6. CURRENT MEMBERSHIP

Taking account of minute 5, the current voting membership of the Subcommittee is as follows: J.P. Bowman (Chairman; Hobart, Tasmania, Australia); B. Holmes (Stanmore, UK), E. Frandsen Lau (Aarhus, Denmark); R. Hahnke (Braunschweig, Germany); C. Hugo (Bloemfontein, South Africa); A. Nicholson (Atlanta, GA, USA); O. Nedashkovskaya (Vladivostok, Russia). Officers are listed on the Subcommittee website (www.the-icsp.org/taxonomic-subcommittees).

# **MINUTE 7. PLANS FOR FUTURE ACTIVITIES**

#### Online meetings

The meeting method was discussed including online meetings to improve their regularity. Since the coronavirus disease 2019 pandemic, video conferencing is much more popular and thus it was seen as a good option to meet. Also, given the long hiatus since the previous meeting and with the developments in the taxonomy field, the meetings will be held more frequently. The times would be determined at each meeting depending on need. The next meeting is scheduled for late 2023 with the exact day determined by member availability.

# **MINUTE 8. ACTIONS**

# 1) Expansion of the purview of the Subcommittee. From the 2019 meeting it was discussed that some members of the *Bacteroidia* should be covered by the Subcommittee since they can grow aerobically

Gram-negative anaerobes have been covered by another ICSP Subcommittee (Subcommittee for Gram-negative Anaerobes) but since the early 2000s it has been inactive. John Bowman proposed to incorporate the *Bacteroidia* in its entirety into the taxonomic coverage of the Subcommittee. Also Richard Hahnke mentioned that some prior members of the *Bacteroidota* (formerly *Bacteroidetes*) should also be included, in particular *Balneolota* Hahnke *et al.* 2021 and *Rhodothermota* Munoz *et al.* 2021. This would lead to a name change, in effect 'aerobic Bacteroidetes' to simply '*Bacteroidota* and relatives'. The exact wording will be discussed at the next Subcommittee meeting. There are no plans to incorporate other related taxa (for example *Chlorobia, Ignavabacteria, Candidatus* 'Kryptonia' and *Candidatus* 'Kappabacteria') but this requires discussion at the next meeting and requires an overview of what other ICSP Subcommittees are active or reactivating.

#### 2) Update of Minimal Standards

In the 2019 Subcommittee meeting [1] it was discussed that the Minimal Standards (published in 2002) should be updated, especially due to genome sequence usage now being prevalent in taxonomic decision making. Richard Hahnke, who has published several papers using whole genome comparisons, also mentioned that comprehensive data on gliding motility and chemotaxonomy are also needed in an updated Minimal Standards. The concept is that a paper could be coordinated within the committee and driven by a particular member. Richard Hahnke indicated he could do this. From the 2023 meeting this was reaffirmed and would be a project that would be led by Richard Hahnke with support from the other Subcommittee members. This activity will be a standing agenda item for the next Subcommittee meeting and onwards.

# 3) Alignment of List of Prokaryotes with Standing in Nomenclature (LPSN) names with names present in the Genome Taxonomy Database (GTDB)

Following discussion over the LPSN correct name policy and also encouraged by the now active SeqCode [2] (see below relevant agenda items), Ainsley Nicholson said that she would provide a comparison between LPSN and GTDB names for discussion prior to our next meeting. This will be very helpful to determine areas where the Subcommittee could provide taxonomic evaluation and also highlight knowledge gaps, i.e. non-sequenced type strains. This activity will be a standing agenda item for the next Subcommittee meeting and onwards.

#### 4) Subcommittee to provide advice on LPSN correct names

It was decided unanimously that the Subcommittee is in a good position to offer advice on the taxonomy (as opposed to the nomenclature) of *Bacteroidota* taxa that are created

through splitting of genera or changes due to amalgamation of species and genera. The stance of the LPSN is to accept these changes as opinions especially if the groups involved are monophyletic (as explained in the LPSN website FAQ section). The Subcommittee was unanimous in that doing this would help provide clarity to the scientific community especially if coupled to an updated Minimal Standards. This activity will be a permanent agenda item and key discussion point for the next Subcommittee meeting.

#### 5) New members

Ellen Frandsen suggested a new member Professor Niels Nørskov-Lauritsen (Department of Clinical Research, University of Southern Denmark, Odense) who has a keen interest in taxonomy and is involved in a Cross European project on *Capnocytophaga*. John Bowman suggested inviting one or more new members with expertize on the *Bacteroidia*. He would determine names for them to be discussed at the next Subcommittee meeting.

# MINUTE 9. RECENT TAXONOMY DEVELOPMENTS

#### New names

John Bowman provided a list of new taxa and reclassifications covering the period of 2018–2023. The information was determined by comparing LPSN information with NCBI (National Collection of Biotechnology Information) taxonomy. Names in quotations are listed in LPSN as being effectively published outside the International Journal of Systematic and Evolutionary Microbiology (IJSEM), but still not published in a Validation list produced monthly in the IJSEM. Owing to the span of time, the taxonomic expansion is considerable and there is also a noticeable lag between description and validation for many names. Here, all classes of *Bacteroidota* are mentioned for the record. Some *Candidatus* names are also mentioned. The naming of 65000 Candidatus taxa by Pallen and colleagues in 2022 [3] is not reflected below and the list only includes names in the LPSN and does not extend to the SeqCode. This can be considered for future meetings as a discussion item and also inform a Minimal Standards document. Overall, the rate of genus- and species-level descriptions is similar to that observed for the 2015–2017 period as noted in the previous minutes. Scientists from China are making a remarkable contribution to this growth in new names. Though not detailed here, the class Bacteroidia has experienced significant taxonomic changes. Several Bacteroides and Prevotella species have been reclassified creating new genera (e.g. Hoylesella, Segatella). Owing to the popularity of gut microbiome research and interest in tackling the diversity therein, numerous Candidatus taxa have been described, including 15 genera and >120 species beyond the names already created by Pallen and colleagues. This rapid growth in *Candidatus* names now can be supported by the SeqCode. For the rest of Bacteroidota, new Candidatus taxa are so far making a much smaller impact.

**Class Flavobacteriia Bernardet 2012**—New higher rank taxa include five families (*Luteibaculaceae, Parvicellaceae, Salibacteraceae, Vicingaceae* and *Weeksellaceae*) and 43 genera ('*Paracrocinitomix*', *Putridiphycobacter,* '*Taishania*', *Abyssalbus, Aegicerativicinus, Aestuariimonas,* '*Aggregatimonas*', *Amniculibacterium, Antarcticibacterium,* '*Ascidiaceibacter*', '*Avrilella*', *Christiangramia,* '*Citreibacter*', *Cochleicola,* '*Constantimarinum*', '*Coraliitalea*', *Haloflavibacter,* '*Halomarinibacterium*',

Luteirhabdus, Mesohalobacter, Paramesonia, Pareuzebyella, Patiriisocius, Paucihalobacter, Pelagihabitans, Pontimicrobium, Poritiphilus, Pseudalgibacter, Pukyongia, 'Rasiella', Sinisalibacter, Spodiobacter, 'Spongiibacterium' (currently contains only the orphan species S. fuscum), Ulvibacterium, Urechidicola, Wocania, Parvicella, Croceimicrobium, Thermaurantimonas, Acidiluteibacter, Vicingus, Faecalibacter and Frigoriflavimonas). New species and species that were transferred to another genus number 480 (across 114 genera out of the 200 belonging to *Flavobacteriia*); 63 species names still require official validation as of the time of the meeting. Reclassification of species occurred in the genera Algibacter, Arcticiflavibacter, Arenitalea, Chryseobacterium, Epilithonimonas, Flagellimonas, Flavihalobacter, Flaviramulus, Flavobacterium, Formosa, Ichthyenterobacterium, Kaistella, Maripseudobacter, Mesoflavibacter, Muricauda, Soonwooa, Spongiibacterium, Ulvibacter and Vitellibacter. For example, the taxonomy of the genus Chryseobacterium has been redefined using genome-based taxonomy [4] and some of its species have been assigned to the genera Epilithonomonas, Kaistella, Halpernia and Soonwooa. The name Christiangramia is the replacement for the genus Gramella owing to it already being the name for fossil ostracods, described originally in 1971 [5]. The genus Flavobacterium is remarkable in that its number of species has now swelled to more than 300. Two Candidatus genera are listed in the LPSN, called Candidatus 'Prosiliicoccus' and Candidatus 'Merdimorpha'. Though not listed in the LPSN, Candidatus 'Marisimplicoccus', Candidatus 'Marivariicella', Candidatus 'Maricapacicella' and Candidatus 'Arcticimaribacter' were defined to represent genus-level groups within a major clade of uncultured marine bacteria designated the NS5 clade, located within the family *Flavobacteriaceae* [6]. Further details are mentioned in the LPSN.

**Class Sphingobacteriia Kämpfer 2012**—The sphingobacteria now include three new genera named *Albibacterium*, *Daejeonella* and *Pararcticibacter* as well as 106 new species names described across 10 genera. Most new species belong to the species rich genera, *Mucilaginibacter*, *Pedobacter* and *Sphingobacterium*. Species reclassification mainly affected genus *Pedobacter* in which eight species were reclassified as *Daejeonella* (seven species) or *Albibacterium* (one species). The type species of *Pseudosphingobacterium* (*P. domesticum*) was also transferred to the genus *Olivibacter*.

**Class Chitinophagia Munoz et al. 2017**—A total of 21 new genus names were described including *Agriterribacter*, *Aurantisolimonas*, *Deminuibacter*, *Edaphocola*, *Flavipsychrobacter*, '*Foetidibacter*', '*Ginsengibacter*', *Gynurincola*, '*Hanamia*', *Ilyomonas*, *Limnovirga*, '*Longitalea*', *Mucibacter*, *Nemorincola*, *Paracnuella*, *Paraflavisolibacter*, *Paraflavitalea*, *Parapseudoflavitalea*, *Phnomibacter*, *Pinibacter* and '*Pseudocnuella*'. Furthermore, 85 new species names (across 40 genera) were described or were created due to reclassification. Reclassification resulted in the type species of *Asinibacterium*, *Crenotalea*, *Filimonas*, *Pseudobacter* and *Vibrionimonas* being merged into other genera that had priority due to an earlier publication date. More details are provided by the LPSN.

**Class Cytophagia Nakagawa 2012**—A total of eight new family names were created between 2018–2023 mainly due to reclassification of species on the basis of genome-based taxonomy. These include *Cesiribacteraceae*, *Fulvivirgaceae*, *Mangrovivirgaceae*, *Marivirgaceae*, *Raineyaceae*, *Reichenbachiellaceae*, *Roseivirgaceae* 

Bowman et al.

and *Thermoflexibacteraceae*. In addition, 22 new genus names were described: *Arthrospiribacter, Cognataquiflexum, Pararhodonellum, Penaeicola, Pleomorphovibrio, Aquirufa, Arundinibacter, 'Chryseosolibacter', Chryseotalea, 'Dawidia', Edaphorhabdus, Sandaracinomonas, Tellurirhabdus, 'Marinigracilibium', Xanthovirga, Parachryseolinea, Pseudochryseolinea, Botryobacter, Sabulibacter, Raineya, 'Fibrivirga', Marinilongibacter* and *Rhodoflexus.* The genera *Fabibacter* and *Fabivirga* were also reclassified into the genus *Roseivirga.* Species description was highly active with more than 190 new species described across 48 genera, including major expansions of the genera *Hymenobacter* (51 new species) and *Spirosoma* (24 new species).

**Class Saprospiria Hahnke et al. 2018**—The saprospiria expanded only by four genera since 2018, including *Portibacter, Flavilitoribacter, Neolewinella* and *Membranihabitans*. The genera *Flavilitoribacter* and *Neolewinella* were created by the reclassification of most species of the genus *Lewinella*, which now includes currently only its type species *L. cohaerens*. In addition, the genus *Membranicola* was merged with *Membranihabitans*. Only two truly new saprospiria species were described from marine samples, *Flavilitoribacter nigricans* and *Membranihabitans marinus*. This lack of species descriptions suggests the saprospiria are challenging to culture. As a likely consequence several *Candidatus* 'Brachybacter', *Candidatus* 'Defluviibacterium', *Candidatus* 'Opimibacter', *Candidatus* 'Parvibacillus' and *Candidatus* 'Vicinibacter' and are in addition to what has been named by Pallen and colleagues.

**Class Bacteroidia Krieg 2012**—Amongst members of class *Bacteroidia* able to utilize oxygen (*Marinifilaceae, Marinilabiliaceae, Prolixabacteraceae*) a number of new genera were described since 2018 including *Aquipluma, Maribellus, Labilibaculum* and *Puteibacter*. The genus *Breznakibacter* was also created to accommodate the long misclassified species [*Cytophaga*] *xylanolyticus* while the genus *Labilibacter* was merged into the genus *Saccharicrinis*. This still leaves the species *Labilibacter sediminis* as an orphan species. Ignoring new combinations collectively 25 species were created across the facultatively anaerobic members of *Bacteroidia*.

**Phylum Balneolota Hahnke et al. 2021**—A proposal was made to combine the genera *Fodinibius* and *Aliifodinibius*; however, as indicated on the LPSN at the time of the Subcommittee meeting, the resulting nomenclature remains to be validated. A new family called '*Cyclonatronaceae*' was defined containing the genera '*Cyclonatronum*' and '*Natronogracilivirga*', isolated from hypersaline soda lakes. Another soil-derived genus called *Halalkalibaculum* which possesses a single species was also described separately. A further six species have been proposed for the genera *Fodinibius*, *Aliifodinibius*, *Gracilimonas* and *Rhodohalobacter*.

**Phylum Rhodothermota Munoz et al. 2021**—This former clade of *Bacteroidota* shows continual slow expansion. The genus *Rhodocaloribacter* was added to the family *Rhodothermaceae*. The genus *Rhodothermus* acquired one additional species while in the case of *Salinibacter* five species were described since 2018. The genus *Salinivenus* 

(belonging to family *Salinibacteraceae*) and its two species was validly described in 2018. A new genus called *Roseithermus* was described within the family *Salisaetaceae* while another member of this family, the genus *Natronotalea*, acquired an additional species.

# MINUTE 10. TAXONOMIC/NOMENCLATURAL DISCUSSION – LPSN CORRECT NAMES

A discussion occurred on the LPSN policy to make notes for some taxa in which taxonomic opinions are defined, mostly related to splitting or lumping of monophyletic groups. Iain Sutcliffe reminded the Subcommittee members, the ICSP focuses only on nomenclature while the International Code of Nomenclature of Prokaryotes (ICNP) is not independent of zoological and botanical nomenclature. Since the LPSN is being more widely used by microbiologists and other scientists, there is the possibility of confusion on which name to use. As noted above under action items 2, 3 and 4, a series of tasks may help with this situation by creating Minimal Standards incorporating genome based taxonomic methods, aligning the taxonomy against the GTDB, seen as a 'gold standard' for higher rank taxonomy (genus and above) and finally enabling the Subcommittee to also voice informed opinions that may help provide some greater clarity to the taxonomy of names under its purview. The latter ideal may take some socialisation since it would be a precedent and may need to be contextualized due to different interests. Some minor controversy that has arisen due to application of genome taxonomy were discussed, including the genus Arcobacter (split into six genera in 2019) while Ainsley Nicholson, Barry Holmes and Iain Sutcliffe mentioned Brucella, Yersinia and Frankia, respectively, as well as other examples.

# MINUTE 11. CANDIDATUS NAMES

Due to the large amount of discussion in relation to correct names, there was not enough time to discuss *Candidatus* names in any depth, in particular those of Pallen *et al.* [3] that may be relevant to *Bacteroidota* and other closely related phyla. Iain Sutcliffe informed the Subcommittee that the SeqCode was operational and was designed to work in parallel with the ICNP. The discussion on *Candidatus* taxa will be moved to the next or future Subcommittee meetings. Action 3 will aid in defining the location of *Candidatus* names in the current taxonomy of *Bacteroidota*. As noted above, the class *Bacteroidia* is clearly the most affected groups as compared to more environmental taxa that predominate across the other classes in terms of numbers of described *Candidatus* taxa.

# MINUTE 12. GTDB AND POSSIBLE 'HETEROGENOUS' GENERA

A brief discussion occurred on the application of GTDB to the taxonomy of the *Bacteroidota*. This led to action item 3 as detailed above. Ainsley Nicholson mentioned her team was developing software that can rapidly analyse genomes and associate them accurately within the existing taxonomic (e.g. GTDB) framework. This is analogous to the GTDB with their rank normalization tool kit. This approach is useful to back up more evolved appraisals of taxonomy especially concerning genera and associated species.

# MINUTE 13. MEMBER-FOCUSED ACTIVITIES AND OTHER BUSINESS

General discussions completed the meeting. Richard Hahnke mentioned he is analysing the Reichenbach collection which contains about 8000 strains. Though focused mainly on myxobacteria, Richard Hahnke indicated some *Bacteroidota* genera have been described (e.g. '*Chryseosolibacter*', '*Dawidia*') [7] and further new discoveries could be possible. Ellen Frandsen heralded her retirement in October 2023 and also suggested a new member for the Subcommittee (action item 5). Richard Hahnke mentioned that the LPSN has a newsletter which will be ideal for the Subcommittee to subscribe to in order to be informed of new taxonomic updates. Furthermore Iain Sutcliffe mentioned that Bergey's International Society for Microbial Systematics also has a semi-regular newsletter (BISMIS Bulletin) and a regular seminar series (www.bismis.net/bismislive.html). The main contact for BISMIS is Kamlesh Jangrid.

# **Funding Information**

The authors received no specific grant from any funding agency.

# Abbreviations:

GTDB	genome taxonomy database
ICNP	International Code of Nomenclature of Prokaryotes
ICSP	International Committee on Systematics of Prokaryotes
IJSEM	International Journal of Systematic and Evolutionary Microbiology
LPSN	list of prokaryotes with standing in nomenclature
NCBI	National Collection of Biotechnology Information

### References

- Bowman JP. International Committee on Systematics of Prokaryotes: Subcommittee on the taxonomy of Aerobic Bacteroidetes (formerly *Flavobacterium* and *Cytophaga*-like bacteria). Minutes of the open meeting, 10th July 2019, Glasgow, UK. Int J Syst Evol Microbiol 2023;73:005966.
- Hedlund BP, Chuvochina M, Hugenholtz P, Konstantinidis KT, Murray AE, et al. SeqCode: a nomenclatural code for prokaryotes described from sequence data. Nat Microbiol 2022;7:1702– 1708. [PubMed: 36123442]
- 3. Pallen MJ, Rodriguez-R LM, Alikhan NF. Naming the unnamed: over 65,000 Candidatus names for unnamed Archaea and Bacteria in the Genome Taxonomy Database. Int J Syst Evol Microbiol 2022;72:005482.
- 4. Nicholson AC, Gulvik CA, Whitney AM, Humrighouse BW, Bell ME, et al. Division of the genus *Chryseobacterium*: Observation of discontinuities in amino acid identity values, a possible consequence of major extinction events, guides transfer of nine species to the genus *Epilithonimonas*, eleven species to the genus *Kaistella*, and three species to the genus *Halpernia* gen. nov., with description of *Kaistella daneshvariae* sp. nov. and *Epilithonimonas vandammei* sp. nov. derived from clinical specimens. Int J Syst Evol Microbiol 2020;70:4432–4450. [PubMed: 32735208]

Bowman et al.

- 5. Deshmukh UB, Oren A. Proposal of *Christiangramia* gen. nov., *Neomelitea* gen. nov. and *Nicoliella* gen. nov. as replacement names for the illegitimate prokaryotic generic names *Gramella* Nedashkovskaya *et al.* 2005, *Melitea* Urios *et al.* 2008 and *Nicolia* Oliphant *et al.* 2022, respectively. Int J Syst Evol Microbiol 2023;73:5806.
- 6. Priest T, Heins A, Harder J, Amann R, Fuchs BM. Niche partitioning of the ubiquitous and ecologically relevant NS5 marine group. ISME J 2022;16:1570–1582. [PubMed: 35169264]
- Octaviana S, Lorenczyk S, Ackert F, Fenske L, Wink J. Four new members of the family *Cytophagaceae: Chryseosolibacter histidini* gen. nov., sp. nov., *Chryseosolibacter indicus* gen. nov., sp. nov., *Dawidia cretensis*, gen. nov., sp. nov., and *Dawidia soli*, gen. nov., sp. nov. isolated from diverse habitat. Antonie van Leeuwenhoek 2022;115:1059–1072. [PubMed: 35732971]