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Opinion

Nomenclatural Recommendations for Genera Assigned to the *Arcobacteraceae* from the Subcommittee on the Taxonomy of *Campylobacter* and Related Bacteria

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Abstract

The taxonomy of the genus *Arcobacter* has been subject to substantive turmoil in recent years following a proposal to subdivide the genus into six genera. This proposal has been challenged by a number of multidisciplinary studies employing phenotypic, genomic, and phylogenetic analyses. Following several discussions among members of the International Committee on Systematics of Prokaryotes (ICSP) subcommittee on the taxonomy of *Campylobacter* and related bacteria, this group now unanimously recommends the use of the genus term *Arcobacter* to refer to these species.

Keywords: *Arcobacter*; *Arcobacteraceae*; taxonomy; nomenclature; recommendation

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1. Introduction

The International Committee on Systematics of Prokaryotes (ICSP) is a distinct body within the International Union of Microbiological Societies (IUMS) that deals with the rules of prokaryotic nomenclature [1]. The ICSP comprises appointed representatives from—as of 20 September 2025—50 microbiology societies worldwide that subscribe to membership of the IUMS (https://www.the-icsp.org/index.php/icsp-members; accessed on 9 October 2025), as well as an Executive Board (https://www.the-icsp.org/index.php/executive-board-ics-p; accessed on 9 October 2025) that oversees ICSP activities, including coordinating the voting of members on the rules of nomenclature.

Subcommittees are specialist ICSP subgroups that have an overarching mandate that includes conducting taxonomic research on specific prokaryotic organismal groups, proposing minimal standards for describing new taxa, and making recommendations regarding the classification and nomenclature of taxa that fall under the auspices of the

subcommittee's domain of study [1]. There are currently (as of 9 October 2025) 17 such subcommittees (https://www.the-icsp.org/index.php/taxonomic-subcommittees; accessed on 9 October 2025). The subcommittee for *Campylobacter* and related organisms encompasses members that undertake research on the Campylobacterota (an elevation of the class Epsilonproteobacteria to the phylum level) [2–5], a large and taxonomically complex group that includes both host-associated and free-living species. The *Arcobacter* genus is unique among the Campylobacterota in that some species are associated with various animal species, with several implicated in diseases of humans and/or animals, and others have thus far been described only in terms of their environmental habitats [5]. Other Campylobacterota genera are, to date, either host-associated or free-living.

In recent times, the proposal [6] to subdivide members of the genus *Arcobacter* into six genera, including *Aliarcobacter*, *Halarcobacter*, *Malaciobacter*, *Poseidonibacter*, and *Pseudarcobacter*, has been challenged by a number of studies that closely examined the phenotypic, genotypic, and phylogenetic aspects of the proposal [7–9]. Members of this subcommittee have now discussed these studies in detail [10]. This paper summarises the background to these discussions and the nomenclatural recommendations following subcommittee deliberations, as has been done previously for other matters [11].

2. Background to the Recommendation

In 2018, a proposal to divide member species (27 at that time) of the genus *Arcobacter* into six additional genera (namely, *Aliarcobacter*, *Halarcobacter*, *Malaciobacter*, *Poseidonibacter*, and *Pseudarcobacter*, with '*Arcomarinus*' proposed as a candidate genus, with a formal description lacking) was put forward, leaving *Arcobacter* a monotypic genus containing *A. nitrofigilis* only [6]. The principal arguments made by these authors were as follows: (i) 16S rRNA gene sequence similarities below 95% between some taxa; (ii) phylogenomic and phylogenetic multi-locus sequence analyses, demonstrating distinct clustering, whereby these clusters were nominated as distinct genera; (iii) average nucleotide identity (ANI) and *in silico* DNA–DNA hybridization (*is*-DDH) studies that are said to support these clusters; and (iv) the correlation of phenotypic characteristics to support genus-level descriptors. These authors subsequently published two corrigenda to this study [6], predominantly to correct details including a type strain number for *A. cryaerophilus*, typographical errors in several basonym descriptors, and other nomenclatural issues that were necessary for valid publication in the *International Journal of Systematic and Evolutionary Microbiology* [12], which is the official journal of record for the description of new taxa.

This proposal was challenged in 2020 [7] in a study that involved the comparison of the whole-genome sequences of 26 *Arcobacter* species (representing members of the proposed newly described taxa) and 58 other representatives of the Campylobacterales (including *Campylobacter*, *Helicobacter*, *Hydrogenimonas*, *Nitratifractor*, *Sulfuricurvum*, *Sulfurimonas*, *Sulfurispirillum*, and *Wolinella* species) for wider phylogenetic context. The wider availability and accessibility of whole-genome sequencing has assisted the development of a wide range of overall genome relatedness indices (OGRI) for evaluating the taxonomic relatedness between strains, including calculating the percentage of conserved proteins (POCP), the average amino acid identity (AAI), BLAST-based and genome-wide ANI, *is*-DDH, alignment fractions, and G + C percentages. Comparative analyses using established single-gene phylogenetic markers (16S rRNA, *atp*A, and *gro*EL) and a SplitsTree analysis employing 342 concatenated gene sequences were also performed in the study in question [7]. The phylogenetic analyses showed that *Arcobacter* formed a distinct, monophyletic clade among the other Campylobacterales species studied [7]. Moreover, disparities were identified [7] among the relationships between certain species considered by Pérez-Cataluña

et al. (2018) to represent distinct genera [6]. The other genomic metrics applied by On et al. (2020) [7] also demonstrated a clear genus-level separation between *Arcobacter sensu strictu* and the other genera in the Campylobacterales but not among the novel genera proposed by Pérez-Cataluña et al. (2018) [6]. It was noted [7] that some of the data for POCP, AAI, BLAST-based ANI, and *is*-DDH indicated taxonomic clustering, not separation, in both studies [6,7]. Phenotypically, all *Arcobacter* species examined to date are unified by their ability to grow aerobically and at temperatures ranging from 18 to 30 °C [7,9], whereas the clear phenotypic criteria for novel genera are lacking [6,7]. The phylogenomic and phenotypic results described support the description of the family *Arcobacteraceae* [3,13], a proposal previously ratified by the relevant ICSP subcommittee [14].

A subsequent study (published in 2021 [8]) examined the taxonomic position of several newly proposed species that had been assigned to some of the proposed novel genera, namely, *P. parvus* [15], *P. antarcticus* [16], *Ali. vitoriensis* [17], *A. caeni* [18], *A. lacus* [18], and *H. arenosus* [19]. The same phylogenomic and OGRI methods were used for this purpose. The results, again, assigned the novel taxa to a single phylogenetic group and indicated that these species exhibit the core phenotypes of aerotolerance and the ability to grow at lower temperatures, as were previously described as genus-level characteristics. This study was used to formally transfer several of these species to *Arcobacter* (namely, *A. parvus*, *A. antarcticus*, *A. vitoriensis*, and *A. arenosus*) and to define each of the proposed genera—i.e., *Aliarcobacter*, *Halarcobacter*, *Malaciobacter*, *Poseidonibacter*, and *Pseudarcobacter*—as later synonyms of *Arcobacter* [8].

3. Recommendations from the Subcommittee

The results of these studies were robustly presented and discussed during meetings of this subcommittee in 2024 [10]. Most of the members present concurred that the evidence presented supported the taxonomic status of *Arcobacter* as a single genus. It should be noted that M. J. Figueras (corresponding author for the 2018 proposal [6]) reiterated her belief that *further* scientific studies will corroborate her scientific position that the genus *Arcobacter* embraces several other genera. However, she also stated that she did not want to be the only member of the subcommittee who hampers the possibility of making a formal nomenclatural recommendation.

Given these discussions, and considering that two of the core principles in bacterial nomenclature [1] are to aim for the stability of names and to avoid names that may cause error or confusion, the subcommittee have now reached a unanimous consensus to *recommend* to the wider scientific community that species assigned to this phylogenetic group be referred to as *Arcobacter* species. The use of the names *Aliarcobacter*, *Halarcobacter*, *Malaciobacter*, *Poseidonibacter*, and *Pseudarcobacter* are therefore to be discouraged, subject to further studies (e.g., alternative OGRI metrics, comparative whole-cell phenotyping) that may more clearly distinguish them from each other at the genus level. We trust that this announcement will provide stability and certainty to the wider scientific community on this complex nomenclatural issue.

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