**BMSAB PHYLUM CHAPTER TEMPLATE WITH INSTRUCTIONS ON FORMAT AND INFORMATION TO INCLUDE**

**Use this template as an example for the format and content of chapters on phyla that are generally understudied and comprise only a few cultured taxa. Feel free to include additional information that is available for the phylum you are covering or delete sections that are not appropriate. Your text should be entered in place of the example information provided below in black text. Continuous line numbers should be maintained throughout the manuscript including any pages containing Tables or Figures. Heading in maroon text should not be removed or edited.**

**1. MANUSCRIPT NUMBER:**

**ENTER THE MANUSCRIPT NUMBER eg.**

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**2. CHAPTER TITLE:**

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*Elusimicrobiota*

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**3. DEFINING PUBLICATION:**

**ENTER THE REFERENCE TO THE DEFINING PUBLICATION, EFFECTIVE PUBLICATION AND EMENDMENTS AS APPROPRIATE. SEE THE CONTRIBUTOR GUIDELINES FOR DETAILS ON THE NEW FORMAT. THE PAGE NUMBER IS NO LONGER REQUIRED.**

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Oren and Garrity 2021VP(synonym: ‘*Elusimicrobia*’ Geissinger et al. 2009)

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**4. AUTHORS NAMES AND INSTITUTIONS:**

**ENTER THE NAMES, INSTITUTIONS, CITY AND COUNTRY OF AUTHORS. THE ADDRESS SHOULD BE IN ITALICS eg.**

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**5. ETYMOLOGY:**

**ENTER THE ETYMOLOGY AS PRESENTED IN THE ORIGINAL TAXONOMIC DESCRIPTION OR THE LPSN WEBSITE, eg.**

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E.lu.si.mi.cro.bi.o’ta. N.L. neut. n. *Elusimicrobium*,type genus of the phylum; N.L. neut. pl. n. suff. -*ota*, ending to denote a phylum; N.L. pl. neut. n. *Elusimicrobiota*, the *Elusimicrobium* phylum.

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**7. ABSTRACT:**

**ENTER THE ABSTRACT OF THE CHAPTER. THE ABSTRACT SHOULD BE A SUMMARY OF THE INFORMATION CONTAINED IN THE MANUSCRIPT THAT GIVES THE READER AN OVERVIEW OF THE PHYLUM BEING COVERED. INFORMATION ON THE MORPHOLOGY, PHYSIOLOGY, PHYLOGENY AND ECOLOGY SHOULD BE INCLUDED eg.**

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*Elusimicrobiota* belong to the PVC superphylum and comprise at least four class-level lineages of mostly uncultured bacteria. Only the classes *Elusimicrobia* and *Endomicrobia* each have a single cultured representative. Both isolates are strictly anaerobic ultramicrobacteria with a fermentative metabolism and an unusual cell cycle. Like their uncultured relatives in the families *Elusimicrobiaceae* and *Endomicrobiaceae*, they colonize the intestinal tracts of invertebrate and vertebrate hosts and show considerable genome reduction. All other lineages seem to consist of free-living, strictly anaerobic bacteria that occur in a wide range of aquatic and terrestrial habitats. Members of several apical lineages possess the capacity for aerobic respiration.

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**7. KEYWORDS:**

**ENTER KEYWORDS THAT WILL DIRECT EXTRENAL SEARCHES TO THE CHAPTER eg.**

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PVC superphylum, animal-associated, endosymbiotic, ultramicrobacteria

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**8. DESCRIPTION:**

**ENTER THE INFORMATION THAT DESCRIBES THE PHYLUM BEING CONSIDERED. EXPAND UPON THE CHARACTERISTICS DESCRIBED IN THE ABSTRACT, INCLUDING THE MORPHOLOGY, PHYSIOLOGY, PHYLOGENY AND ECOLOGY. IF UNCULTIVATED TAXA ARE KNOWN, DISCUSS THEIR DISTRIBUTIONS AND KNOWN PROPERTIES. THE TYPE GENUS SHOULD BE INCLUDED eg.**

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Members of *Elusimicrobiota*, the so-called ‘Termite group I’, were first detected in 16S rRNA-based inventories of the gut microbiota of termites (Ohkuma and Kudo, 1996; Hongoh et al., 2003), where they occur in high abundance as endosymbionts of cellulolytic flagellates (Stingl et al., 2005, Ohkuma et al., 2007). *Elusimicrobium minutum* (see gbm01490) and *Endomicrobium proavitum* (see gbm01492), the only cultured representatives of the phylum, were both isolated from the intestinal tract of insects (Geissinger et al., 2009; Zheng et al., 2016). Although only distantly related, both are ultramicrobacteria that share numerous features, such as an unusual cell cycle, a strictly anaerobic, fermentative metabolism, and relatively small genomes (Hongoh et al., 2008; Herlemann et al., 2009; Zheng et al., 2017). While their uncultured relatives in the families *Elusimicrobiaceae* and *Endomicrobiaceae* are restricted to the intestinal tracts of both invertebrate and vertebrate hosts, including termites, ruminants, and humans, the majority of phylotypes appear to be free-living and were obtained from upland and wetland soils, aquifers, freshwater and marine sediments (Herlemann et al., 2007; Méheust et al., 2020; Fig. 1).

Comparative analysis of all MAGs available to date revealed that *Elusimicrobiota* lineages are quite heterogeneous (Méheust et al., 2020). While all basal lineages, including the sister groups ERL1 and ERL2, seem to consist exclusively of strictly anaerobic bacteria, several lineages in the class *Elusimicrobia* (lineages IIa, IIc, IV, V, VI) comprise MAGs that encode electron transport chains with high-affinity cytochrome oxidases, indicating the capacity for aerobic respiration (Méheust et al., 2020). Predicted genome size and G+C content vary considerably among different lineages. A substantial gene loss occurred in the host-associated lineages (*Elusimicrobiaceae* and *Endomicrobiaceae*), where genome size and G+C content are significantly lower than in their putatively free-living relatives (Fig. 2).

*Type genus: Elusimicrobium* Geissinger et al. 2009, VL132.

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**9. TAXONOMIC OUTLINE OF THE PHYLUM**

**CREATE A HIERARCHICAL TAXONOMIC OUTLINE WITH THE NAMES OF EACH CLASS, ORDER, FAMILY AND GENUS. FOR EACH TAXON, INCLUDE THE NAME, DEFINING PUBLICATION, AND ETYMOLOGY. ADD A BRIEF DESCRIPTION, WHICH COULD BE “SAME AS PHYLUM”**

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CLASS: *Elusimicrobia* Geissinger et al. 2009, VL132

E.lu’si.mi.cro’bi.a. N.L. neut. n. *Elusimicrobium*, type genus of the type order of the class; N.L. neut. pl. n. *Elusimicrobia*, class of the order *Elusimicrobiales* (nominative plural of *Elusimicrobium*)

The class *Elusimicrobia* currently contains the order *Elusimicrobiales*, which accommodates only a single species, the ultramicrobacterium *Elusimicrobium minutum*. It also comprises numerous clades of uncultured bacteria from mostly anoxic habitats (anoxic soils, aquifers, freshwater and marine sediments, and intestinal tracts), which have been detected exclusively in 16S rRNA-based surveys.

ORDER: *Elusimicrobiales* Geissinger *et al.* 2009, VL132.

E.lu.si.mi.cro.bi.al’es. N.L. neut. n. *Elusimicrobium*, type genus of the order; L. fem. pl. n. suff. *-ales*, ending to denote an order; N.L. fem. pl. n. *Elusimicrobiales*, order of the genus *Elusimicrobium*

The order *Elusimicrobiales* is identified on the basis of phylogenetic analysis of 16S rRNA gene sequences. It currently contains the family *Elusimicrobiaceae*, which accommodates a single species, the ultramicrobacterium *Elusimicrobium minutum*, and other, highly supported clades of uncultured bacteria that have been detected exclusively in 16S rRNA-based surveys (Herlemann et al., 2007; Geissinger et al., 2009). While members of the family *Elusimicrobiaceae* (cluster III) seem to occur exclusively in intestinal tracts of insects and vertebrates, other lineages (clusters IV and V) comprise uncultured bacteria from a range of other, mostly anoxic habitats (anoxic soils, aquifers, freshwater, and marine sediments).

FAMILY: *Elusimicrobiaceae* Geissinger *et al.* 2009, VL132.

E.lu.si.mi.cro.bi.a’ce.ae. neut. n. *Elusimicrobium*, type genus of the family; L. fem. pl. n. suff. *-aceae*, ending to denote a family; N.L. fem. pl. n. *Elusimicrobiaceae*, family of the genus *Elusimicrobium*

The family *Elusimicrobiaceae* currently accommodates only a single species, the ultramicrobacterium *Elusimicrobium minutum*. It also comprises numerous clades of uncultured bacteria, which have been detected in 16S rRNA-based surveys and are exclusively found in intestinal habitats, ranging from the guts of termites, cockroaches, and beetle larvae to the mammalian intestinal tract.

CLASS: *Endomicrobia* Zheng et al. 2016, VL180.

En’do.mi.cro’bi.a. N.L. neut. n. *Endomicrobium*, type genus of the type order Endomicrobiales; N.L. neut. pl. n. suff. *-ia*, ending to denote a class; N.L. neut. pl. n. *Endomicrobia*, the class of *Endomicrobium* (sic)

The class *Endomicrobia* currently contains the order *Endomicrobiales*, which accommodates only a single species, the ultramicrobacterium *Endomicrobium proavitum*. It also comprises several clades of uncultured bacteria, which have been detected exclusively in 16S rRNA-based surveys of mostly anoxic habitats (anoxic soils, aquifers, freshwater sediments, and intestinal tracts).

ORDER: *Endomicrobiales* Zheng *et al.* 2016, VL180.

En’do.mi.cro’bi.a’les. N.L. neut. n. *Endomicrobium*, type genus of the order; L. fem. pl. n. suff. *-ales*, ending to denote an order; N.L. fem. pl. n. *Endomicrobiales*, the order of *Endomicrobium*

The order *Endomicrobiales* is identified on the basis of phylogenetic analysis of 16S rRNA gene sequences. It currently contains the family *Endomicrobiaceae*, which accommodates only a single described species, the ultramicrobacterium *Endomicrobium proavitum*, and other clades of uncultured bacteria that occur almost exclusively in the intestinal tracts of insects (Ikeda-Ohtsubo et al., 2010; Mikaelyan et al., 2017). Other lineages have been detected in 16S rRNA-based surveys of mostly anoxic habitats (anoxic soils, aquifers, freshwater sediments).

FAMILY: *Endomicrobiaceae* Zheng *et al.* 2016, VL180.

En’do.mi.cro’bi.a’ce.ae. N.L. neut. n. *Endomicrobium*, type genus of the family; L. fem. pl. n. suff. *-aceae*, ending to denote a family; N.L. fem. pl. n. *Endomicrobiaceae*, the family of *Endomicrobium.*

The family *Endomicrobiaceae* currently contains the genus *Endomicrobium*, which accommodates only a single described species, the ultramicrobacterium *Endomicrobium proavitum*. All other members of the family are so far uncultured. The habitat of most lineages is the intestinal tract of insects, particularly the hindgut of termites and cockroaches. Several lineages (*Candidatus* Endomicrobium) are specific symbionts of termite gut flagellates and colonize either the cytoplasm or the external surface of their hosts. One lineage colonizes the cow rumen.

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**10. PHYLOGENY**

**INCLUDE A PHYLOGENETIC TREE OF THE MAJOR TAXA IN THE PHYLUM. IF THE GENOMES ARE SEQUENCED FROM ALL THE MAJOR GROUPS, USE A PHYLOGENOMIC TREE. IF THE GENOME SEQUENCES ARE NOT KNOWN FOR MANY OF THE GROUPS, USE A RRNA TREE. FOR EACH ‘LEAF’ OF THE TREE, INCLUDE THE NAME AND ACCESSION NUMBER. DO NOT INCLUDE THE OUTGROUP(S) IN THE TREE, BUT IDENTIFY THEM IN THE FIGURE LEGEND. IF THERE A MULTIPLE TAXA AT EACH RANK, LABEL THE RANKS WITH BRACKETS.**

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The genome-based phylogeny is presented in Figure 1.

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**11. TAXONOMIC COMMENTS**

**DISCUSS ANY POINTS OF INTEREST OR DIFFERING OPINIONS REGARDING THE TAXONOMIC OUTLINE AND PHYLOGENY. eg.**

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The scope of the phylum *‘Elusimicrobia’* was originally defined exclusively on the basis of phylogenetic analyses of 16S rRNA gene sequences (Herlemann et al., 2007; Geissinger et al., 2009; Yarza et al., 2014). Meanwhile, large-scale sequencing efforts yielded a substantial number of MAGs representing the mostly uncultured members of the phylum, which allowed a more precise definition of the individual lineages using concatenated gene trees. A comprehensive phylogenomic analysis of the more than 240 genomes available to date placed *Elusimicrobiota* in the PVC superphylum, with the Elusimicrobia-related lineages ERL1 (phylum UBA6262) and ERL2 (phylum CG03), ‘*Candidatus* Desantisbacteria’, and ‘*Candidatus* Omnitrophota’ as closest relatives (Méheust et al., 2020; Fig. 1).

The current Genome Taxonomy Database (GTDB) taxonomy (release 07-RS207; Parks et al., 2022) recognizes four class-level lineages, *Elusimicrobia* and *Endomicrobia*, which harbor the only cultured representatives of the phylum, and two lineages without any cultured representatives (GTDB names class UBA5214 and class UBA8919). Together with additional metagenome-assembled genomes (MAGs) not yet included in GTDB, the most recent genome tree (Fig. 1) comprises candidate taxa from all major lineages that are represented in the more comprehensive 16S rRNA-based dataset (lineages I – IX; Méheust et al., 2020, and references therein). Only lineages IIb and IId, whose members have been detected in soils and other so far under sampled habitats, are not yet represented by any MAGs.

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**12. OTHER POINTS OF INTEREST**

**USE THIS SECTION TO DISCUSS OTHER AREAS OF INTEREST, SUCH AS UNUSUAL PROPERTIES OF MEMBERS OF THE PHYLUM, BIOTECHNOLOGICAL APPLICATIONS, ETC. eg.**

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**19. REFERENCES**

**ENTER FULL REFERENCE FOR EACH CITATION IN THE CHAPTER INCLUDING THOSE CITED IN THE DEFINING PUBLICATIONS, TABLES AND FIGURE LEGENDS. REFERENCES SHOULD BE LISTED IN ALPHABETICAL ORDER BASED ON THE NAME OF THE FIRST AUTHORS. THE FORMAT PROVIDED BELOW SHOULD BE FOLLOWED EXACTLY. DOIs SHOULD BE INCLUDED WHEN AVAILABLE eg.**

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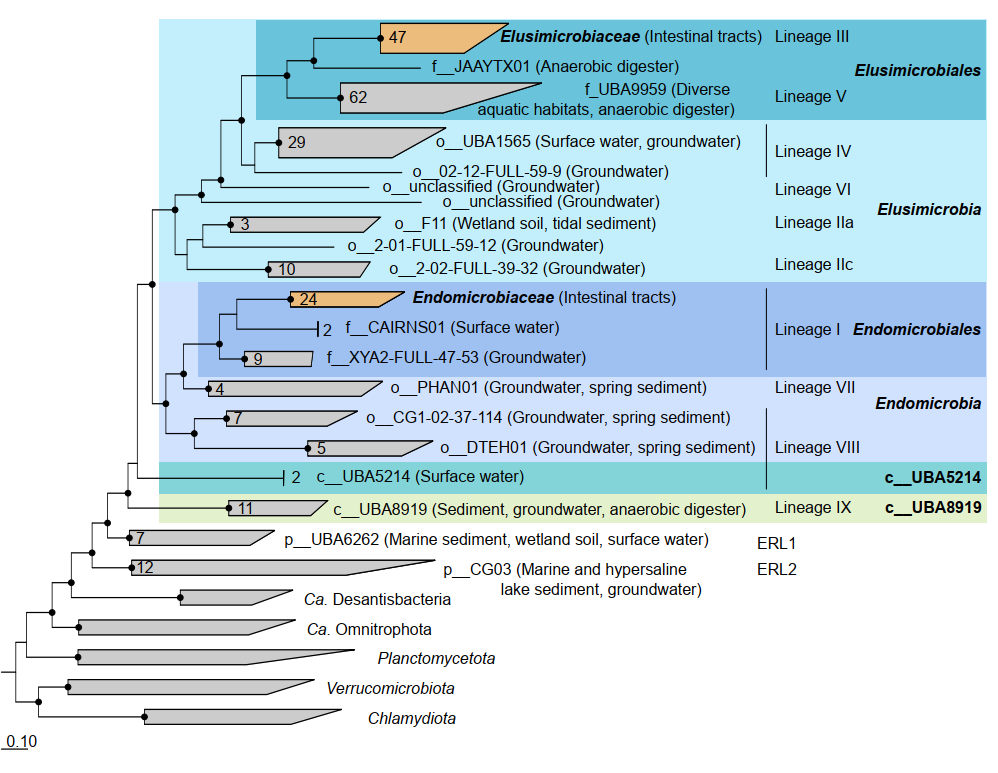
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**20. TABLES AND FIGURES**

**PROVIDE TABLES AS WORD OR EXCEL DOCUMENTS. NONE ARE USED IN THIS MANUSCRIPT.**

**21. FIGURE CAPTIONS**



**Fig. 1. Genome-based phylogeny of the phylum *Elusimicrobiota*.** The taxonomic ranks follow the Genome Taxonomy DataBase (GTDB r06-RS202; Parks et al., 2022). Clades are labelled with the number of genomes included and their general habitats; the families represented by isolates are marked in orange. Lineage numbering introduced in previous publications is indicated (Herlemann et al., 2007; Geissinger et al., 2009; Méheust et al., 2020). The maximum-likelihood tree was constructed from an alignment of 120 bacterial single-copy marker genes (4,847 amino acid positions; Parks et al. 2017), which was filtered using trimAL v1.3 with the gappyout method (Capella-Gutiérrez et al., 2009). Tree topology was inferred with IQ-TREE (multicore version 1.6.1, Nguyen et al., 2015) using a LG+F+R9 model of evolution, as suggested by ModelFinder under the Bayesian Information Criterion (Kalyaanamoorthy et al., 2017), and with 1,000 ultrafast bootstrap iterations (Minh et al., 2013); only highly supported nodes are indicated. The tree was rooted with selected members of the PVC superphylum. The scale bar indicates 0.10 amino acid substitutions per site. Figure 3.

Timeline

Description automatically generated with medium confidence

**Fig. 2. Genome size and G+C content in the phylum *Elusimicrobiota*.**  Average genome sizes (± standard deviation) for major lineages were calculated from assembly size and completeness of the respective MAGs upon analysis with CheckM (Parks et al., 2015). Lineages and color codes are as defined in Fig. 2.