**BMSAB FAMILY AND OTHER HIGHER TAXANOMIC RANK CHAPTERS TEMPLATE WITH INSTRUCTIONS ON FORMATTING AND INFORMATION TO BE INCLUDED**

**Use this template as an example for the format and content of your chapter. Feel free to include additional information that is available for the family you are covering. 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. Headings in maroon text should not be removed or edited.**

**1. PHYLUM/CLASS/ORDER:**

**ENTER THE TAXONOMIC PATH IN ITALICS eg.**

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*Actinobacteria/Actinobacteria/Frankiales*

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*Cryptosporangiaceae*

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**4. DEFINING PUBLICATION:**

**ENTER THE DEFINING PUBLICATION, EFFECTIVE PUBLICATION AND EMENDMENTS AS APPROPRIATE. THE PAGE NUMBER IS THE PAGE ON WHICH THE ACTUAL DESCRIPTION WAS PRINTED IN THE ORIGINAL PUBLICATION, NOT THE FIRST PAGE OF THAT PUBLICATION eg.**

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Zhi et al. 2009VP

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**5. AUTHORS NAMES AND INSTITUTIONS:**

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

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Peter Kämpfer, *Institut für Angewandte Mikrobiologie, Justus-Liebig Universität Giessen, Giessen, Germany*

Stefanie P. Glaeser, *Institut für Angewandte Mikrobiologie, Justus-Liebig Universität Giessen, Giessen, Germany*

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**6. ETYMOLOGY:**

**ENTER THE ETYMOLOGY AS PRESENTED IN THE ORIGINAL TAXONOMIC DESCRIPTION eg.**

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Cryp.to.spo.ran.gi.a.ce'ae. N.L. neut. n. *Cryptosporangium*, type genus of the family; suff. *‐aceae* ending to denote a family; N.L. fem. pl. n. *Cryptosporangiaceae*, the *Cryptosporangium* family.

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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 TAXON BEING COVERED. THE TYPE GENUS SHOULD BE STATED AS WELL AS THE DEFINING PUBLICATION OF THE GENUS DESCRIPTION eg.**

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Phylogenetically, a member of the order “*Frankiales*”. The family contains the genera *Cryptosporangium* and *Fodinicola*. Although most members of the order “*Frankiales*” do not form both substrate and aerial mycelia, members of this family show these structures. Sporangiospores occur occasionaly. Motile or nonmotile. Cross‐linkage of peptidoglycan is by the A type. The diagnostic diamino acids include *meso*‐diaminopimelic acid. Each peptidoglycan is directly linked without interpeptide bridges, and the muramic acid in peptidoglycan is *N*‐acetylated. Methyl 14‐methylpentadecanoate (iso‐C16:0) is the prominent fatty acid, but C17:1, 10‐methyl C17:0, and C18:1 may also be present. Menaquinones MK‐9(H6), MK‐9(H4), and MK‐9(H8) are the predominant isoprenoid quinones, and MK‐9(H2) may also be present.

DNA G+C content (mol%): 65 and 76.

*Type genus:* **Cryptosporangium** Tamura et al. 1998VP

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**8. KEYWORDS:**

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

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*Cryptosporangium*, *Fodinicola*, substrate mycelium, aerial mycelium

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**9. DESCRIPTION:**

**ENTER THE INFORMATION THAT DESCRIBES THE FAMILY BEING CONSIDERED. IMPORTANT AND DEFINING CHARACTERISTICS SHOULD BE IN BOLD FONT. THE TYPE GENUS AND DEFINING PUBLICATION, THE FAMILY CLASSIFICATION SHOULD BE INCLUDED eg.**

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Phylogenetically, a member of the order *Frankiales*. The family contains the genera *Cryptosporangium* and *Fodinicola*. Although most members of the order *Frankiales* do not form both **substrate and aerial mycelia**, members of this family show these structures. Sporangiospores occur occasionally. Motile or nonmotile. Cross‐linkage of peptidoglycan is by the A type. The diagnostic diamino acids include ***meso*‐diaminopimelic acid**. Each peptidoglycan is directly linked without interpeptide bridges, and the muramic acid in peptidoglycan is *N*‐acetylated. Methyl 14‐methylpentadecanoate (iso‐C16:0) is the prominent fatty acid, but C17:1, 10‐methyl C17:0, and C18:1 may also be present. Menaquinones **MK‐9(H6), MK‐9(H4), and MK‐9(H8)** are the predominant isoprenoid quinones, and MK‐9(H2) may also be present. The pattern of 16S rRNA signatures consists of nucleotides at positions 66:104 (G‐C), 158:163 (G‐C), 186:191 (G‐C), 195 (U), 196 (C), 293:304 (G‐C), 600:638 (G‐C), 601:637 (A‐U), 841 (U), 952:1229 (C‐G), 986:1219 (A‐U), 1042 (U), 1251 (G), and 1003:1037 (A‐C). The polar lipid profiles include **phosphatidylethanolamine, phosphatidylglycerol, phosphatidylserine, phosphatidylinositol**, and several phospholipids and glycolipids. Mycolic acids and teichoic acids are absent. **Xylose, as a diagnostic whole‐cell sugar, is present**, and acofriose (3‐*O*‐methyl rhamnose), as a whole‐cell sugar, may also be present.

*DNA G+C content (mol%):* 65 and 76.

*Type genus:* **Cryptosporangium** Tamura 1998VP

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**10. TAXONOMIC COMMENTS:**

**ENTER INFORMATION ON THE TAXONOMIC POSITION OF THE FAMILY AND THE GENERA IT CONTAINS INCLUDING THE 16S rRNA GENE BASED PHYLOGENY, THE WHOLE GENOME BASED PHYLOGENY FROM GTDB AND ANY DIFFERENCES OBSERVED BETWEEN THESE PHYLOGENIES AND RESULTING CLASSIFICATIONS. A 16S rRNA BASED PHYLOGENETIC TREE SHOULD BE PRESENTED eg.**

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The family *Cryptosporangiaceae* currently comprises the two genera *Cryptosporangium* (Tamura et al., 1998) and *Fodinicola* (Carlsohn et al., 2008). Phylogenetic trees based on the 16S rRNA gene sequences show that members of the genus *Cryptosporangium* are grouped into a coherent clade. Already pointed out by Carlsohn et al. (2008), the genus *Fodinicola* has a phylogenetically deep branching point within the family of the order *Frankiales* (Sen et al., 2014), showing similar values in a range of 92.9–94.8% and 93.9–94.5% to type strains of both *Cryptosporangium* and *Sporichthya*, respectively, and members of the genera *Frankia* and *Acidothermus* are slightly less closely related to *Fodinicola feengrottensis* with similarity values in a range of 92.5–93.0% than to the members of the genus *Cryptosporangium*. As a consequence, Carlsohn et al. (2008) did not assign the genus *Fodinicola* to a family. Zhi et al. (2009) reevaluated and updated the 16S rRNA gene sequence‐based definition for the higher ranks of the class *Actinobacteria* and proposed the family *Cryptosporangiaceae*, and subsequently, Ludwig et al. (2012) proposed the monospecific genus *Fodinicola* (type species *Fodinicola feengrottensis*) to be tentatively classified in the family *Cryptosporangiaceae* as a genus *incertae sedis*based on the similarities in 16S rRNA gene sequence data.

On the basis of the phylogenetic analysis of the currently known taxa of *Actinobacteria*, the genera *Cryptosporangium* and *Fodinicola* formed, independent of the algorithms used for the construction of phylogenetic trees, a distinct cluster (supported by bootstrap values >70%) within the order *Frankiales* (Figure 1). Members of the genus *Cryptosporangium* formed a monophyletic clade, and the type strain of *F. feengrottensis* a separate branch next to that clade. Type strains of the genus *Cryptosporangium* shared 97.8–99.3% 16S rRNA gene sequence similarity among each other and 93.4–94.8% with the type strain of *F. feengrottensis* (pairwise sequence similarities were calculated without the use of an evolutionary model using ARB). In contrast, the stable phylogenetic relationship of the two genera, clustering to next related genera/families, varied among the phylogenetic trees constructed with different algorithms (Figure [**1**](https://onlinelibrary.wiley.com/doi/full/10.1002/9781118960608.fbm00018.pub2#fbm00018-fig-0001)) and different subsets of reference sequences (data not shown). Currently, two type strain whole‐genome sequences are available for *Cryptosporangium* species, *Cryptosporangium arvum* DSM 44712T (GCA\_000585375.1; RefSeq: NZ\_JFBT00000000.1) and *Cryptosporangium aurantiacum* DSM 46144T(GCA\_900143005.1; RefSeq: NZ\_FRCS00000000.1). Both genome sequences are draft sequences. The genomes have a size of 9,195,993 and 9,579,923 bp including 8,554 and 8,767 open reading frames (ORFs) and a mol% G + C content of 71.7 and 71.2%, respectively. The whole‐genome sequences of *Cryptosporangium japonicum* DSM 44713T (GOLD project ID Gp0220407) and *Fodinicola feengrottensis* DSM 19247T (GOLD project ID Gp0220357) are currently under construction.

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**11. FURTHER COMMENTS**

**ENTER INFORMATION ON OTHER PROPOERTIES OF TEH GENERA OF THE FAMILY. THIS COULD INCLUDE DIFFERENTIATING MORPHOLOGICAL AND CHEMOTAXONOMIC PROPERTIES. A TABLE SHOWING THE CHARARCTERS THAT DIFFERENTIATE TEH GENERA OF THE FAMILY COULD BE INCLUDED INFORMATION ON THE ECOLOGY AND DIVERSITY OF THE MEMBERS OF THE FAMILY COULD BE INCLUDED eg.**

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Chemotaxonomic markers have significantly contributed to the differentiation of the genera *Cryptosporangium* and *Fodinicola* as shown in Table 1. *Cryptosporangium* species show cell walls containing glutamic acid, glycine, alanine, and *meso*‐diaminopimelic acid. This corresponds to the wall chemotype II according to Lechevalier and Lechevalier (1970), and peptidoglycan type A1γ according to Schleifer and Kandler (1972). Glucose and acofriose are detected as whole‐cell sugars. The major fatty acids comprise C17:1, C18:1, and iso‐C16:0. The major menaquinones include MK‐9(H6), MK‐9(H4), and MK‐9(H8). Phosphatidylethanolamine is present as the diagnostic phospholipid (phospholipid pattern type PII).

In *Fodinicola* species, the cell‐wall sugars contain xylose and minor amounts of an unidentified compound. The predominant menaquinones include MK‐9(H4), MK‐9(H6), and MK‐9(H8). Polar lipids comprise diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylserine, phosphatidylinositol, and several unidentified phospholipids and glycolipids, together with unidentified ninhydrin‐positive compounds. The cellular fatty acid profile is characterized by the predominance of iso‐C16:0, 10‐methyl C17:0, C17:1 cis9, 10‐methyl iso‐C18:0, and C17:0. Members of the genus *Cryptosporangium* form branching hyphae. Nonfragmentary substrate and aerial mycelia are present. These organisms develop round or irregularly shaped sporangia that are 3–10 µm in diameter.

*Cryptosporangium aurantiacum* and *Cryptosporangium minutisporangium* were originally reported as “*Actinoplanes aurantiacus*” (Ruan et al., 1976) and *Actinoplanes minutisporangius* (Ruan et al., 1986), respectively. However, the muramic acid in peptidoglycan allows differentiation between the genera *Cryptosporangium* (acetyl) and *Actinoplanes* (glycolyl).

Some sporangia, particularly on the central region of the colony, are submerged under thick mycelia. Sporangiospores are motile when they are suspended in water.

*Fodinicola* strains form branched substrate mycelium and have sparse to abundant white aerial mycelium. Aerial hyphae break up into irregular rod‐like elements.

Members of the genus *Cryptosporangium* were isolated from various sources, such as soils of vegetable fields, lake muds, acidic and heavy metal‐containing rocks, leaf litter, and from *Eucalyptus camaldulensis* roots (Ruan et al., 1976, 1986; Tamura et al., 1998; Tamura and Hatano, 2001; Ara et al., 2012; Himaman et al., 2017). *F. feengrottensis*, the only species of the genus, was isolated from a medieval mine (Carlsohn et al., 2008).

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**12. REFERENCES**

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

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Carlsohn, MR,  Groth, I, Saluz, HP,  Schumann, P, &  Stackebrandt, E (2008) *Fodinicola feengrottensis* gen. nov., sp. nov., an actinomycete isolated from a medieval mine. *Int J Syst Evol Microbiol*  **58**:  1529– 1536.

Felsenstein, J ( 2005) PHYLIP (Phylogeny Inference Package) version 3.6. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

Ludwig, W,  Euzéby, J, &  Whitman, WB ( 2012)  Phylogenetic trees of the phylum *Actinobacteria*. In  *Bergey's Manual of Systematic Bacteriology, vol 5, The Actinobacteria*,  2nd ed.,  W Whitman,  M Goodfellow,  P Kämpfer,  H‐J Busse,  M Trujillo,  W Ludwig et al. (eds). Springer,  New York.

Tamura, T ( 2014)  The family *Cryptosporangiaceae*. In  *The Prokaryotes – Actinobacteria*,  E Rosenberg,  EF DeLong,  S Lory,  E Stackebrandt, &  F Thompson (eds), doi: [10.1007/978-3-642-30138-4\_181](https://doi.org/10.1007/978-3-642-30138-4_181)

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**13. TABLES AND FIGURES**

**PROVIDE TABLES AND FIGURES IN THE FORMAT PROVIDED BELOW**

Table 1. Diagnostic properties of the genera *Cryptosporangium* and *Fodinicola* belonging in the family *Cryptosporangiaceae* (Tamura, 2014)

| **Taxon** | ***Cryptosporangium*** | ***Fodinicola*** |
| --- | --- | --- |
| Cellular morphology | Substrate and aerial hyphae; sporangia | Substrate and aerial hyphae |
| Spore/bud formation | Sporangiospores | − (Fragmentation of aerial hyphae) |
| Motility | + | − |
| Cell‐wall diamino acid(s) | *meso*‐A2pm | *meso*‐A2pm |
| Polar lipid(s)[a](https://onlinelibrary.wiley.com/doi/full/10.1002/9781118960608.fbm00018.pub2#fbm00018-note-0004_19) | PE | DPG, PE, PS, PI, PL, and GL |
| Major menaquinone(s) | MK‐9(H6), MK‐9(H4), and MK‐9(H8) | MK‐9(H4), MK‐9(H6), and MK‐9(H8) |
| Predominant fatty acid(s) | Iso‐C16:0, C17:1; C18:1 | Iso‐C16:0, 10‐methyl C17:0, and C17:1cis9 |
| DNA G + C content (mol%) | 70–76 | 65 |

* +, present; −, absent.
* *a* DPG, diphosphatidylglycerol; GL, unknown glycolipid(s); PE, phosphatidylethanolamine; PI, phosphatidylinositol; PS, phosphatidylserine; PL, unidentified phospholipid(s).

**14. FIGURE CAPTIONS**

**Figure 1.** Maximum‐likelihood tree based on nearly full‐length 16S rRNA gene sequences showing the monophyletic cluster formed by species of the genera *Cryptosporangium* and *Fodinicola,* the current members of the family *Cryptosporangiaceae,* among the closest related families within the order *Frankiales*. The phylogenetic tree was constructed with ARB (Ludwig et al., 2004) and the “All species living tree project” (LTPs) database LTPs123 (September 2015) using RAxML version 7.04 (Stamatakis, 2006) with GTR‐GAMMA and rapid bootstrap analysis (100 replications). The tree is based on nucleotide sequences between gene termini 81 and 1424 (*Escherichia coli* numbering, Brosius et al., 1978). The tree is entirely composed of type strain sequences. GenBank/EMBL/DDBJ Accession numbers are given in brackets. Type species are given in bold. Numbers at nodes represent bootstrap values ≥70%. Nodes marked with circles were also present in a maximum‐parsimony tree calculated with DNAPARS v 3.6 (Felsenstein, 2005); large circles thereby represent nodes with bootstrap values ≥70%. Numbers in sequence clusters represent the number of sequences included in a cluster. Bar = 0.10 nucleotide substitutions per nucleotide position.

[](https://wol-prod-cdn.literatumonline.com/cms/attachment/f167c7eb-0ce9-4cd6-9d5b-3e446feaca3b/nfg001.gif)

**Figure 1**