Register list for Krumholzibacterium zodletonense gen. nov. sp. nov. and their lineage

Submitted by Nguyen, Huong

Phylum *Krumholzibacteriota*

Etymology

[Krum.hol.zi.bac.te.ri.o'ta] **N.L. neut. n.** *Krumholzibacterium*, a genus name ; *-ota*, ending to denote a phylum; **N.L. neut. pl. n.** *Krumholzibacteriota*, the Krumholzibacterium phylum

Nomenclatural type

Genus *Krumholzibacterium*

Description

Youssef et al. (2019): The candidatus phylum *Krumholzibacteriota* is defined by eight genomic assemblies (Zgenome0171T, Zgenome0218, Zgenome0207_2, Zgenome0274_1, UBA2172, UBA4771, UBA4783, and ex4484_7) recovered using genome-resolved metagenomics from three distinct habitats (Zodletone spring sediment, Suncor tailing pond, and Guyamas basin), as well as 16S rRNA gene sequences from uncultured representatives in a wide range of terrestrial, marine, and aquatic habitats that are predominantly anoxic or hypoxic. The genome assembly Zgenome0171T serves as the type material and is deposited in GenBank under Biosample accession number SAMN09745294 and WGS accession number QTKG00000000. Genomic analysis predicted Gram-negative cell walls, and rod-shaped cells with heterotrophic lifestyle, and the ability to degrade glucose, mannose, alanine, aspartate, glutamate, and methionine and production of acetate and formate as fermentation end products.

Classification

Bacteria » *Krumholzibacteriota*

References

Effective publication: Youssef et al., 2019 [1]

Registry URL

https://seqco.de/i:41783

Class *Krumholzibacteriia*

Etymology
[Krum.hol.zi.bac.te.ri'i.a] **N.L. neut. n.** *Krumholzibacterium*, referring to the type genus *Krumholzibacterium*; *-ia*, ending to denote a class; **N.L. neut. pl. n.** *Krumholzibacteriia*, the *Krumholzibacterium* class

Nomenclatural type
Genus *Krumholzibacterium*

Description
Youssef et al. (2019): The description is the same as for the genus *Krumholzibacterium*. Contains the order *Krumholzibacteriales*. Genomic analysis predicts an anaerobic, Gram-negative, motile (flagellated) chemoorganoheterotrophic rod. Genomic analysis identified auxotrophies for proline, vitamin B6, lipoic acid, biotin, and vitamin B12. Substrates supporting growth based on genomic analysis include glucose, mannose, aspartate, alanine, asparagine, glutamate, glutamine, cysteine, serine, threonine, glycine, methionine, histidine, dipeptides, tripeptides, and oligpopeptides. Fermentation end products include acetate, formate, and ethanol.

Classification
Bacteria » *Krumholzibacteriota* » *Krumholzibacteriia*

References
Effective publication: Youssef et al., 2019 [1]
Corrigendum: Oren, Garrity, 2021 [2] (from “Krumholzibacteria”)

Registry URL
https://seqco.de/i:50461

Order *Krumholzibacteriales*

Etymology
[Krum.hol.zi.bac.te.ri.a'les] **N.L. neut. n.** *Krumholzibacterium*, referring to the type genus *Krumholzibacterium*; *-ales*, ending to denote an order; **N.L. fem. pl. n.** *Krumholzibacteriales*, the *Krumholzibacterium* order

Nomenclatural type
Genus *Krumholzibacterium*

Description
Youssef et al. (2019): The description is the same as for the genus Krumholzibacterium. Contains the family Krumholzibacteriaceae. Genomic analysis predicts an anaerobic, Gram-negative, motile (flagellated) chemoorganoheterotrophic rod. Genomic analysis identified auxotrophies for proline, vitamin B6, lipoic acid, biotin, and vitamin B12. Substrates supporting growth based on genomic analysis include glucose, mannose, aspartate, alanine, asparagine, glutamate, glutamine, cysteine, serine, threonine, glycine, methionine, histidine, dipeptides, tripeptides, and oligpopeptides. Fermentation end products include acetate, formate, and ethanol.

Classification
Bacteria » *Krumholzibacteriota* » *Krumholzibacteriia* » *Krumholzibacteriales*

References
Effective publication: Youssef et al., 2019 [1]

Registry URL
https://seqco.de/i:42781

Family *Krumholzibacteriaceae*

Etymology
[Krum.hol.zi.bac.te.ri.a'ce.ae] **N.L. neut. n.** *Krumholzibacterium*, referring to the type genus *Krumholzibacterium*; *-aceae*, ending to denote a family; **N.L. fem. pl. n.** *Krumholzibacteriaceae*, the *Krumholzibacterium* family

Nomenclatural type
Genus *Krumholzibacterium*

Description
Youssef et al. (2019): The description is the same as for the genus *Krumholzibacterium*. Genomic analysis predicts an anaerobic, Gram-negative, motile (flagellated) chemoorganoheterotrophic rod. Genomic analysis identified auxotrophies for proline, vitamin B6, lipoic acid, biotin, and vitamin B12. Substrates supporting growth based on genomic analysis include glucose, mannose, aspartate, alanine, asparagine, glutamate, glutamine, cysteine, serine, threonine, glycine, methionine, histidine, dipeptides, tripeptides, and oligpopeptides. Fermentation end products include acetate, formate, and ethanol.

Classification
Bacteria » *Krumholzibacteriota* » *Krumholzibacteriia* » *Krumholzibacteriales* » *Krumholzibacteriaceae*

References
Effective publication: Youssef et al., 2019 [1]

Registry URL
https://seqco.de/i:42782

Genus *Krumholzibacterium*

Etymology
[Krum.hol.zi.bac.te'ri.um] **N.L. neut. n.** *bacterium*, a bacterium; **N.L. neut. n.** *Krumholzibacterium*, A bacterium named after Professor Lee Krumholz for his contributions to the fields of diversity, genetics, and physiology of micro-organisms in anaerobic habitats

Nomenclatural type
Species *Krumholzibacterium zodletonense*^{Ts}

Description
Youssef et al. (2019): Genomic analysis predicts an anaerobic, Gram-negative, motile (flagellated) chemoorganoheterotrophic rod. Genomic analysis identified auxotrophies for proline, vitamin B6, lipoic acid, biotin, and vitamin B12. Substrates supporting growth based on genomic analysis include glucose, mannose, aspartate, alanine, asparagine, glutamate, glutamine, cysteine, serine, threonine, glycine, methionine, histidine, dipeptides, tripeptides, and oligpopeptides. Fermentation end products include acetate, formate, and ethanol.

Classification
Bacteria » *Krumholzibacteriota* » *Krumholzibacteriia* » *Krumholzibacteriales* » *Krumholzibacteriaceae* » *Krumholzibacterium*

References
Effective publication: Youssef et al., 2019 [1]

Registry URL
https://seqco.de/i:23550

Species *Krumholzibacterium zodletonense*[Ts]

Etymology
[zo.dle.to.nen'se] **N.L. neut. adj.** *zodletonense*, referring to Zodletone Spring, Oklahoma

Nomenclatural type
Genome sc|0006276 [Ts]

Description
Youssef et al. (2019):
Genomic analysis predicts an anaerobic, Gram-negative, motile (flagellated) chemoorganoheterotrophic rod. Genomic analysis identified auxotrophies for proline, vitamin B6, lipoic acid, biotin, and vitamin B12. Substrates supporting growth based on genomic analysis include glucose, mannose, aspartate, alanine, asparagine, glutamate, glutamine, cysteine, serine, threonine, glycine, methionine, histidine, dipeptides, tripeptides, and oligpopeptides. Fermentation end products include acetate, formate, and ethanol.

Appears to be a slow-growing member of the rare biosphere. Possesses catalase and peroxidase-encoding genes. Lacks CRISPR-Cas system. The genome assembly Zgenome0171T serves as the type material and is deposited in GenBank under Biosample accession number SAMN09745294 and WGS accession number QTKG00000000.

Classification
Bacteria » *Krumholzibacteriota* » *Krumholzibacteriia* » *Krumholzibacteriales* » *Krumholzibacteriaceae* » *Krumholzibacterium* » *Krumholzibacterium zodletonense*[Ts]

References
Effective publication: Youssef et al., 2019 [1]

Registry URL
https://seqco.de/i:307

References

1. Youssef et al. (2019). Candidatus Krumholzibacterium zodletonense gen. nov., sp nov, the first representative of the candidate phylum Krumholzibacteriota phyl. nov. recovered from an anoxic sulfidic spring using genome resolved metagenomics. *Systematic and Applied Microbiology*. DOI: 10.1016/j.syapm.2018.11.002
2. Oren, Garrity (2021). Candidatus List No. 2. Lists of names of prokaryotic Candidatus taxa. *International Journal of Systematic and Evolutionary Microbiology*. DOI: 10.1099/ijsem.0.004671

Register List Certificate of Validation

On behalf of the *Committee on the Systematics of Prokaryotes Described from Sequence Data* (SeqCode Committee), we hereby certify that the Register List **seqco.de/r:tv5uw9c7** submitted by **Nguyen, Huong** and including 6 new names has been successfully validated.

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