Register list for 5 new names including Chordibacter gen. nov.

Submitted by Wilkie, Isabella Maria

Family *Seribacteraceae*

Etymology

[Se.ri.bac.te.ra'ce.ae] **N.L. masc. n.** *Seribacter*, referring to the type genus Seribacter; *-aceae*, ending to denote a family; **N.L. fem. pl. n.** *Seribacteraceae*, the Seribacter family

Nomenclatural type

Genus *Seribacter*

Description

Members of the family *Seribacteraceae* are predicted to be aerobic and heterotrophic marine bacteria dwelling in surface waters. A total of 71 MAGs belonging to this family were recovered in the 2010, 2011, 2012, 2016, 2018 and 2020 Helgoland spring blooms which fell into 6 clusters. *Seribacteraceae* belongs to the order *Opitutales*, class *Verrucomicrobiae*, and phylum *Verrucomicrobiota* (based on GTDB taxonomy). Formerly identified as family MB11C04. Two FISH probes for members of this family have been developed (probe c17-1166 and c21-472 from Orellana *et al.*, 2022) and previously used to describe that members of this genus are short rods (Orellana *et al.*, 2022). The type genus is *Seribacter* and the corresponding type material is the metagenome-assembled genome r4, which shows 99.5% ANI to a previously described representative of the MB11C04 family (MB5 from Orellana *et al.*, 2022).

Classification

Bacteria » *Verrucomicrobiota* » *Opitutia* » *Opitutales* » *Seribacteraceae*

References

Effective publication: Wilkie, Orellana, 2025 [1]

Registry URL

https://seqco.de/i:44057

Genus *Chordibacter*

Etymology

[Chor.di.bac'ter] **L. masc. adj.** *chordus*, late-born; **N.L. masc. n.** *bacter*, rod; **N.L. masc. n.** *Chordibacter*, late blooming rod-shaped bacteria

Nomenclatural type

Species *Chordibacter forsetii*^{Ts}

Description

Members of the *Chordibacter* genus are predicted to be aerobic and heterotrophic marine bacteria dwelling in surface waters. A total of 17 MAGs belonging to this genus were recovered in the 2011, 2012, 2016, and 2018 Helgoland spring blooms. *Chordibacter* belongs to the family *Seribacteraceae*, formerly known as MB11C04, order *Opitutales*, class *Verrucomicrobiae*, and phylum *Verrucomicrobiota*. Formerly identified as genus MB11C04. A FISH probe for this family has been developed (probe c17-1166 from Orellana *et al.*, 2022) and previously used to describe that members of this genus are short rods of length and width 0.9 and 0.8 µm respectively (Orellana *et al.*, 2022).

Classification

Bacteria » *Verrucomicrobiota* » *Opitutia* » *Opitutales* » *Seribacteraceae* » *Chordibacter*

References

Effective publication: Wilkie, Orellana, 2025 [1]

Registry URL

https://seqco.de/i:44038

Genus *Seribacter*

Etymology

[Se.ri.bac'ter] **L. masc. adj.** *serus*, late; **N.L. masc. n.** *bacter*, rod; **N.L. masc. n.** *Seribacter*, late blooming rod-shaped bacteria

Nomenclatural type

Species *Seribacter sulfatis*$^{\mathrm{Ts}}$

Description

Members of the *Seribacter* genus are predicted to be aerobic and heterotrophic marine bacteria dwelling in surface waters. A total of 45 MAGs belonging to this genus were recovered in the 2010, 2011, 2012, 2016, 2018 and 2020 Helgoland spring blooms. *Seribacter* belongs to the family *Seribacteraceae* fam. nov., order *Opitutales*, class *Verrucomicrobiae*, and phylum *Verrucomicrobiota*. Formerly identified as genus MB11C04 in family MB11C04. A FISH probe for this family has been developed (probe c21-472 from Orellana *et al.* 2022) and previously used to describe that members of the this genus are short rods of length and width 1.2 and 1.0 µm respectively (Orellana *et al.* 2022).

Orellana, L.H., Francis, T.B., Ferraro, M., Hehemann, J.-H., Fuchs, B.M., Amann, R.I. (2022) *Verrucomicrobiota* are specialist consumers of sulfated methyl pentoses during diatom blooms. ISME J, 630–41, Doi: 10.1038/s41396-021-01105-7.

Classification

Bacteria » *Verrucomicrobiota* » *Opitutia* » *Opitutales* » *Seribacteraceae* » *Seribacter*

References

Effective publication: Wilkie, Orellana, 2025 [1]

Registry URL

https://seqco.de/i:44039

Species *Chordibacter forsetii*$^{\mathrm{Ts}}$

Etymology

[for.se.ti'i] **N.L. gen. masc. n.** *forsetii*, of Forseti, the Scandinavian god of justice and reconciliation resident on Helgoland

Nomenclatural type

NCBI Assembly: GCA_964187505.1 $^{\mathrm{Ts}}$

Description

Members of the *Chordibacter* genus are predicted to be aerobic and heterotrophic marine bacteria dwelling in surface waters. A total of 17 MAGs belonging to this genus were recovered in the 2011, 2012, 2016, and 2018 Helgoland spring blooms. This genome is estimated to be 92.7% complete with 2.2% redundancy. It has a GC content of 44.3% and a genome size of 2.12 Mbp. The 5S, 16S, and 23S rRNA genes were identified in the genome. *Chordibacter forsetii* belongs to the family MB11C04, order *Opitutales*, class *Verrucomicrobiae*, and phylum *Verrucomicrobiota*. Formerly identified as genus MB11C04 and species MB11C04. A FISH probe for this family has been developed (probe c17-1166 from Orellana et al., 2022) and previously used to describe that members of this genus are short rods of length and width 0.9 and 0.8 µm respectively (Orellana et al., 2022). The type species is *Chordibacter forsetii* and the corresponding type material is the metagenome-assembled genome ERZ814923, which shows 99.3% ANI to a previously described representative of the MB11C04 family (MB1 from Orellana et al., 2022).

Classification

Bacteria » *Verrucomicrobiota* » *Opitutia* » *Opitutales* » *Seribacteraceae* » *Chordibacter* » *Chordibacter forsetii*$^{\mathrm{Ts}}$

References

Effective publication: Wilkie, Orellana, 2025 [1]

Registry URL

https://seqco.de/i:44036

Species *Seribacter sulfatis*^{Ts}

Etymology

[sul.fa'tis] **N.L. gen. n.** *sulfatis*, of sulfate, referring to the Marine Verrucomicrobiota encoding many sulfatases

Nomenclatural type

NCBI Assembly: GCA_964187635.1 ^{Ts}

Description

Members of the *Seribacter* genus are predicted to be aerobic and heterotrophic marine bacteria dwelling in surface waters. A total of 45 MAGs belonging to this genus were recovered in the 2010, 2011, 2012, 2016, 2018 and 2020 Helgoland spring blooms. This genome is estimated to be 94.2% complete with 0% redundancy. It has a GC content of 42.6% and a genome size of 2.53 Mbp. The 5S, 16S, and 23S rRNA genes were identified in the genome (Table S8). *Seribacter sulfatis* belongs to the family *Seribacteraceae* fam. nov., order *Opitutales*, class *Verrucomicrobiae*, and phylum *Verrucomicrobiota*. Formerly identified as genus MB11C04 and species MB11C04, in the family MB11C04. A FISH probe for this family has been developed (probe c21-472 from Orellana *et al.*, 2022) and previously used to describe that members of this genus are short rods of length and width 1.2 and 1.0 µm respectively (Orellana *et al.*, 2022). The type species is *Seribacter sulfatis* and the corresponding type material is the metagenome-assembled genome ERZ816379, which shows 99.5% ANI to a previously described representative of the MB11C04 family (MB5 from Orellana *et al.*, 2022).

Classification

Bacteria » *Verrucomicrobiota* » *Opitutia* » *Opitutales* » *Seribacteraceae* » *Seribacter* » *Seribacter sulfatis*^{Ts}

References

Effective publication: Wilkie, Orellana, 2025 [1]

Registry URL

https://seqco.de/i:44037

References

1. Wilkie, Orellana (2025). Elusive marine Verrucomicrobiota: Seasonally abundant members of the novel genera Seribacter and Chordibacter specialize in degrading sulfated glycans. *Systematic and Applied Microbiology*. DOI:10.1016/j.syapm.2024.126562

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:vjimgryf** submitted by **Wilkie, Isabella Maria** and including 5 new names has been successfully validated.

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