

Species *Allofontibacter lacus*

Etymology

[la'cus] L. gen. n. *lacus*, of a lake

Nomenclatural type

[INSDC Nucleotide: RGRP00000000.1](#)^{Ts}

Description

We propose to name PEL1, the most complete and persistent genomospecies of clade IIIb in the freshwater ecosystems sample, as *Allofontibacter lacus* sp. nov. [formerly "*Candidatus Fonsibacter lacus*"]. In addition to the previously described properties of the genus *Allonsibacter* corrig. Henson, et al (2018), the proposed species is described as follows. Small, curved rod cells of approximately 1 × 0.2 μm. Partial genome sequence WB8_6_001 with estimated completeness of 77.5% and contamination of 0.9% is 1.08 Mbp in size, with 1375 predicted genes, a coding density of 92.0%, and a G + C content of 35.9%. WB8_6_001 has an ANI of 84.9% and AAI of 87.0% with the *Allofontibacter communis* corrig. Henson et al (2018) [formerly "*Ca. Fonsibacter ubiquis*"] str. LSUCC0530T genome, the only currently described member of the *Allofontibacter* genus. The type material for this species is the genome WB8_6_001, identified in the freshwater lakes along the Chattahoochee River, Southeast USA. The representative genome is available in GenBank under accession number [SAMN10223538](#).

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Candidatus Pelagibacterales* » *Candidatus Pelagibacteraceae* » *Candidatus Allofontibacter* » "*Allofontibacter lacus*"

References

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

Corrigendum: Oren, Garrity, 2021 [2] (from "*Candidatus Fonsibacter lacus*")

Registry URL

<https://seqco.de/i:454>

References

1. Tsementzi et al. (2019). Ecogenomic characterization of widespread, closely-related SAR11 clades of the freshwater genus "*Candidatus Fonsibacter*" and proposal of *Ca. Fonsibacter lacus* sp. nov. *Systematic and Applied Microbiology*. DOI:10.1016/j.syapm.2019.03.007
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