Prosiliicoccus vernus gen. nov. sp. nov.

Submitted by Nguyen, Huong

Genus *Prosiliicoccus*

Etymology

[Pro.si.li.i.coc'cus] **L. v.** *prosilio*, to leap, jump, rush, spring forth; **Gr. masc. n.** *kokkus*, a grain; **N.L. masc. n.** *Prosiliicoccus*, a coccus that springs forth

Nomenclatural type

Species *Prosiliicoccus vernus*[Ts]

Description

Francis et al. (2019): Members of the genus *Ca.* Prosiliicoccus are predicted to be obligate aerobes, with currently no indication of fermentation or anaerobic respiration. They are heterotrophic, marine surface water dwelling bacteria, capable of using glycans and proteins as primary sources of organic matter. The three species have been detected in seawater sampled in the North Sea during spring phytoplankton blooms via metagenomic assembly and fluorescence in situ hybridisation. Cells are coccoid, and may be detected using FISH probe ULV995 [49]. High quality 16S rRNA gene sequences share approximately 94% identity with closely related genera *Ulvibacter* and *Gilvibacter*. G + C content for all three species is between 36% and 37%. The genus *Ca.* Prosiliicoccus belongs to the family *Flavobacteriaceae*, order *Flavobacteriales*, class *Flavobacteriia*, and phylum *Bacteroidetes*. Type species is *Candidatus* Prosiliicoccus vernus.

Classification

Bacteria » *Bacteroidota* » *Flavobacteriia* » *Flavobacteriales* » *Flavobacteriaceae* » *Prosiliicoccus*

References

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

Registry URL

https://seqco.de/i:39015

Species *Prosiliicoccus vernus*[Ts]

Etymology
[ver'nus] **L. masc. adj.** *vernus*, pertaining to spring

Nomenclatural type
Genome sc|0006303 [Ts]

Description
Francis et al. (2019): Genome annotation allows prediction of consumption of protein, peptides, and amino acids, as well as putatively the polysaccharide laminarin. The spectrum of glycans putatively available to *Candidatus* Prosiliicoccus vernus is restricted, with laminarin appearing to be the most significant polysaccharide, while it may also consume chitin. Genome size is small relative to described *Flavobacteriia*, at an estimated 1.9 Mbp. Fluorescence microscopy reveals the cells to be coccoid, with diameter ranging between 0.5 and 1 µm. Bloom-forming behaviour is observed in *Candidatus* Prosiliicoccus vernus during and immediately after phytoplankton blooms in the North Sea.

Type material is the metagenome assembled genome 'Prosiliicoccus_vernus_reassembled_20100413' submitted to ENA in project PRJEB28156, and also to the Digital Protologue database under TaxoNumber CA00022.

Classification
Bacteria » *Bacteroidota* » *Flavobacteriia* » *Flavobacteriales* » *Flavobacteriaceae* » *Prosiliicoccus* » *Prosiliicoccus vernus*[Ts]

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

Registry URL
https://seqco.de/i:318

References

1. Francis et al. (2019). Candidatus Prosiliicoccus vernus, a spring phytoplankton bloom associated member of the Flavobacteriaceae. *Systematic and Applied Microbiology*. DOI: 10.1016/j.syapm.2018.08.007

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:3uw2rga6** submitted by **Nguyen, Huong** and including 2 new names has been successfully validated.

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