Register list for 7 new names including Pampinifervens gen. nov.

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Table 1: Complete list of names proposed in the current register list.

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Genus *Pampinifervens*	[Pam.pi.ni.fer'vens] **L. masc. n.** *pampinus*, tendril; **L. part. adj.** *fervens*, hot; **N.L. neut. n.** *Pampinifervens*, hot tendrils, referring to the tendrils of streamer communities growing in high-temperature geothermal springs	Cultivated members of this genus are thermophilic, microaerophilic, and autotrophic. Metagenome-assembled genomes representing members of the genus were also recovered from environmental samples consistent with these traits. Species in the genus encode genes for all five complexes of the electron transport chain, with cultivated members using oxygen as terminal electron acceptor. They are chemolithoautotrophic, with genes coding for components of the reductive tricarboxylic acid cycle conserved within the genus, likely using either hydrogen or thiosulfate as electron donors. Most members of the genus encode [NiFe] Group 1d and [NiFe] 2d uptake hydrogenases, and all species encode genes for the SOX complex for thiosulfate oxidation, and sulfide:quinone oxidoreductase (sqr) for sulfide oxidation. Cultivated members are capable of chemolithoheterotrophy using acetate. Vitamins are not required for growth. Cultivated members are negative for Gram-staining reaction, and spores are not formed. Cells are rod-shaped and motile via one or more polar flagella. Most species also encode genes required for flagellar motility. Relative evolutionary divergence places these members in a novel genus-level group and phylogenomic placement of this genus is within the *Aquificaceae*.	*Aquificaceae*	*Pampinifervens diazotrophicum*$^{\mathrm{Ts}}$	seqco.de/i:43939
	[di.a.zo.tro.phi'cum] **N.L. pref.** *diazo-*,	In addition to characteristics described for the genus, chemolithoautotrophic growth was observed using S0 as electron donor. Growth occurs in the absence of organic nitrogen sources, suggesting successful fixation of atmospheric dinitrogen. Growth occurs at 60-80 °C with an optimum at 70 °C, at pH 6.0-9.5 with an optimum at 8.5, at 0.2-10% oxygen with an optimum at 4%, and at sodium chloride concentrations ≤ 300 mM. Cells were 1.9-2.6 µm in length, and 0.3-			

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Species *Pampinifervens diazotrophicum*^{Ts}	pertaining to dinitrogen; **N.L. neut. adj.** *trophicum*, feeding from Gr. masc. adj. trophikos; **N.L. neut. adj.** *diazotrophicum*, feeding on dinitrogen	0.5 µm in width, occurring singly. Colonies that are 0.5 mm in diameter, round, and entire in shape, and cream in color form after 7 days incubation under chemoautotrophic conditions. Major fatty acids are C20:1ω9c, C20:1ω7c, C18:0 and C20:0, while minor fatty acids include C16:0, C18:1ω7c and summed feature 8. Genomic G+C content of the type strain is 43.22%. Genealogical concordance and ANI support the novelty of this species, and phylogenomics and AAI places this species in the genus *Pampinifervens* gen. nov. The nomenclatural type for the species is the genome of strain T-2 (= JCM 35475=DSM 116324) from a white streamer community in Gumingquan (Drum Beating Spring) in the Rehai Geothermal Field, Tengchong County, China. The GenBank accession number for the complete genome of strain T-2 is CP117180 (BioProject: PRJNA659730, BioSample: SAMN15924605).	*Pampinifervens*	INSDC Nucleotide: CP117180.1 ^{Ts}	seqco.de/i:43940
Species *Pampinifervens florentissimum*	[flo.ren.tis.si'mum] **L. neut. adj.** *florentissimum*, flourishing, referring to their high standing biomass in many springs in the Rehai Geothermal field	In addition to characteristics described for the genus, this species is capable of chemolithoheterotrophy using glucose, yeast extract, peptone, and casamino acids. This species can also utilize nitrate as electron acceptor during anaerobic growth, and encode all genes associated with complete denitrification of nitrate to dinitrogen, and nitrification of nitrite to nitrate. This species also encodes an arsenite transporter, arsenite oxidase, and arsenate reductase, although arsenite as an electron donor has not been tested, and arsenate was not used as electron acceptor under conditions tested before (Hedlund et al., 2015). Growth occurs at 50-80 °C with an optimum at 70 °C, at pH 5.5-10.0 with an optimum at 7.0, at 0.2-10% oxygen with an optimum of 4-6%, and at sodium chloride concentrations ≤ 200 mM. Cells are 1.9-2.2 µm in length, and 0.3-0.4 µm in width, occurring singly. Colonies are 0.5 mm in diameter, round, with entire margins, and cream in color, and form after 7 days incubation under chemoautotrophic conditions. Major cellular fatty acids are C20:1ω9c, C18:0, *cy*-21, and C16:0; minor fatty acids include C20:0, C18:1ω9c, and C19:0. Genomic G+C content range between 44.03% and 44.45%. Genealogical concordance and ANI support the novelty of this species, and phylogenomics and AAI places this species in the genus *Pampinifervens* gen. nov. The strain T-8 (= CGMC 1.5214T = JCM 33569T), was	*Pampinifervens*	INSDC Nucleotide: CP048795.1 ^{Ts}	seqco.de/i:43941

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		isolated from a white streamer community in Qiao Quan (Bridge Spring) in the Rehai Geothermal Field, Tengchong County, China. The GenBank genome accession number for the complete genome sequence of strain T-8 is CP048795 (BioProject: PRJNA605417, BioSample: SAMN14057017).			
Species *Pampinifervens sericum*	[se.ri'cum] **L. neut. adj.** *sericum*, silken, referring to the silk-like appearance of the streamer communities in many of the springs in the Rehai Geothermal Field, where genomes belonging to this species were recovered from	In addition, or in contrast, to the characteristics described for the genus, the genomes of this species lack *hyaB*, required for Group 1d hydrogenases, and only encode a partial SOX complex required for thiosulfate oxidation. Additionally, structural genes for flagellar motility are absent from genomes of this species. Genomic G+C content for this species range between 42.57% and 44.77%. Genealogical concordance and ANI support the novelty of this species, and phylogenomics and AAI places this species in the genus *Pampinifervens* gen. nov. The type for this species is the genome GMQ_2011_Aq_binTs, sampled from Gumingquan (Drum Beating Spring) in the Rehai Geothermal Field, Tengchong, China, and is available under the GenBank assembly accession GCA_037722135.1. (BioProject: PRJNA1048437, BioSample: SAMN38639742).	*Pampinifervens*	INSDC Nucleotide: JBBKAW000000000$^{\mathrm{Ts}}$	seqco.de/i:43942
Species *Pampinifervens sinense*	[si.nen'se] **N.L. neut. adj.** *sinense*, of China, referring to China where genomes belonging to this species were recovered from	In addition to the genus description, this species encodes a partial denitrification pathway, with the potential to convert nitrate to nitrite, and nitrite to nitric oxide. Genomic G+C content of the species range from 44.06% to 45.27%. Genealogical concordance and ANI support the novelty of this species, and phylogenomics and AAI places this species in the genus *Pampinifervens* gen. nov. The nomenclatural type for the species is the genome ZZQ_201901_bin_7Ts, recovered from the acidic, high-temperature hot spring, Zhenzhuquan, in Tengchong County, China, and is available under the GenBank assembly accession number GCA_037927135.1. (BioProject: PRJNA1041563, BioSample: SAMN38287341).	*Pampinifervens*	NCBI Assembly: GCA_037927135.1$^{\mathrm{Ts}}$	seqco.de/i:43943
	[ten.gchon.gen'se]	In addition to traits reported for the genus, genomes of this species encode most genes for a denitrification pathway and can likely convert nitrate to dinitrogen. Genomes of this species also encode an arsenite transporter, arsenite oxidase, and arsenate reductase. The G+C content of the genomes range between			

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Species *Pampinifervens tengchongense*	**N.L. neut. adj.** *tengchongense*, referring to Tengchong	43.26% and 45.56%. Genealogical concordance and ANI support the novelty of this species, and phylogenomics and AAI places this species in the genus *Pampinifervens* gen. nov. The type for this species is the genome GXS_2011_Aq_binTs, recovered from Gongxiaoshe hot spring in Tengchong, China, and is available under the GenBank assembly accession number GCA_037722225.1. (BioProject: PRJNA1048437, BioSample: SAMN38639757).	*Pampinifervens*	INSDC Nucleotide: JBBKAY000000000 Ts	seqco.de/i:43944
Species *Pampinifervens yunnanense*	[yun.na.nen'se] **N.L. neut. adj.** *yunnanense*, referring to Yunnan, the southern Province of China	In addition, and in contrast, to the characteristics described for the genus, no hydrogenases are annotated in the genomes of this species. This would suggest that the oxidation of sulfide and thiosulfate may serve as electron donors in this species. The genomes of this species range in G+C content between 45.99% and 46.82%. Genealogical concordance and ANI support the novelty of this species, and phylogenomics and AAI places this species in the genus *Pampinifervens* gen. nov. The nomenclatural type for the species is the genome DRTY-6_201601_bin_61Ts, recovered from the hot spring Diretiyanqu-6, in Tengchong, China. The genome is available under the GenBank assembly accession GCA_037926845.1. (BioProject: PRJNA1041563, BioSample: SAMN38287353).	*Pampinifervens*	NCBI Assembly: GCA_037926845.1 Ts	seqco.de/i:43945