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Author Correction: Genome-guided isolation of the hyperthermophilic aerobe *Fervidibacter sacchari* reveals conserved polysaccharide metabolism in the Armatimonadota

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Author Correction: Genome-guided isolation of the hyperthermophilic aerobe *Fervidibacter sacchari* reveals conserved polysaccharide metabolism in the *Armatimonadota*

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In the version of this article initially published, Table 1 did not include the properties of the taxa being proposed or refer directly to another location in the main manuscript describing the properties. As such, the original manuscript did not comply with Rule 27 (2)(c) of the ICNP. Also, Table 1 listed the order *Fervidibacterales* as the nomenclatural type for the class *Fervidibacteria*, which violates latest emended version of Rule 15 stating that the nomenclatural type for a class must be a genus.

Below we provide a modification of Table 1 containing protologues with these errors corrected. We have also changed the order of the taxa in the table to meet the most common ordering.

The error has not been corrected in the PDF or HTML versions of the Article.

Corrections & amendments

Table 1 | Taxon names proposed under the ICNP

Proposed taxon	Etymology	Description
Genus <i>Fervidibacter</i>	Fer.vi.di.bac'ter. L. masc. adj. fervidus, hot, steaming; N.L. masc. n. bacter, a rod; N.L. masc. n. Fervidibacter, a hot rod	Thermophilic or hyperthermophilic inhabitants of freshwater thermal environments. All members are likely polysaccharide-degrading chemoheterotrophs with numerous carbohydrate-active enzymes encoded in their genomes. Aerobic, with high-affinity and/or low-affinity terminal oxidases present in the genomes. The oxidative pentose phosphate pathway and the tri-carboxylic acid cycle are complete in genomes belonging to the genus. Gram-stain-negative and diderm cell envelope structure. Ovoid- to rod-shaped morphology. Spores are not formed. The genus is a distinct phylogenetic lineage in the family <i>Fervidibacteraceae</i> , the order <i>Fervidibacterales</i> , and the class <i>Fervidibacteria</i> in the phylum <i>Armatimonadota</i> . The type species is <i>Fervidibacter sacchari</i> ^T .
Species <i>Fervidibacter sacchari</i>	sac'cha.ri. N.L. gen. n. sacchari, of sugar	Hyperthermophilic, microaerophilic, facultatively anaerobic, and grows chemoheterotrophically on monosaccharides and polysaccharides. Cells are ovoid- to rod-shaped, Gram-stain negative, and are 0.9–1.3 µm in width and 1.6–3.6 µm in length. Grows between 65 and 87.5 °C and an optimum temperature of 80 °C, and a pH range of 6.5–8.6 with an optimum pH of 7.5. Grows at an optimum O ₂ concentration of 5–10%. Grows on D-arabinose, D-galactose, D-glucose, D-rhamnose, D-ribose, D-xylose, chondroitin sulfate, colloidal chitin, galactan, gellan gum, guar gum, karaya gum, locust bean gum, xanthan gum, xyloglucan, β-glucan, glycogen, starch, AFEX-pretreated corn stover, miscanthus, sugarcane bagasse, acetate and casamino acids. Grows weakly on xyloglucan under fermentation conditions. The major fatty acids (>10%) are C16:0, C18:0 and/or cyclo-C17:0, and iso-C16:0. The major respiratory quinones (>10%) are MK-8 and MK-9. The isolate and genomes of the species have been recovered from geothermal springs in the Great Basin, Nevada, USA. GC content of genomes range between 51–52%. Subunits for both the high-affinity and low-affinity terminal oxidases are encoded in the genomes. Genomes also encode a Group 3d [NiFe] hydrogenase, which produces hydrogen as an electron sink for NAD ⁺ regeneration. The type strain PD1 ^T (= JCM 39283 ^T = DSM 113467 ^T) was isolated from Great Boiling Spring in Nevada, USA.
Family <i>Fervidibacteraceae</i>	Fer.vi.di.bac.te.ra'ce.ae. N.L. masc. n. Fervidibacter type genus of the family; L. suff. -aceae ending to denote a family; N.L. fem. pl. n. Fervidibacteraceae the family of the genus Fervidibacter	Thermophilic or hyperthermophilic inhabitants of freshwater thermal environments. All members are likely polysaccharide-degrading chemoheterotrophs with numerous carbohydrate-active enzymes encoded in their genomes. Aerobic, with high-affinity and/or low-affinity terminal oxidases present in the genomes. The oxidative pentose phosphate pathway and the tri-carboxylic acid cycle are complete in genomes belonging to the family. The family is a distinct phylogenetic lineage in the order <i>Fervidibacterales</i> and the class <i>Fervidibacteria</i> in the phylum <i>Armatimonadota</i> . The type genus is <i>Fervidibacter</i> .
Order <i>Fervidibacterales</i>	Fer.vi.di.bac.te.ra'les. N.L. masc. n. Fervidibacter type genus of the order; L. suff. -ales ending to denote an order; N.L. fem. pl. n. Fervidibacterales the order of the genus Fervidibacter	Thermophilic or hyperthermophilic inhabitants of freshwater thermal environments. All members are likely polysaccharide-degrading chemoheterotrophs with numerous carbohydrate-active enzymes encoded in their genomes. Aerobic or strictly anaerobic. Phylogenomic placement of this lineage within the <i>Fervidibacteria</i> and relative evolutionary divergence supports delineation of this lineage as an order within the class <i>Fervidibacteria</i> and phylum <i>Armatimonadota</i> . The type genus is <i>Fervidibacter</i> .
Class <i>Fervidibacteria</i>	Fer.vi.di.bac.te'ri.a. N.L. masc. n. Fervidibacter type genus of the type order of the class; L. suff. -ia ending to denote a class; N.L. neut. pl. n. Fervidibacteria the class of the order Fervidibacterales	Thermophilic or hyperthermophilic inhabitants of freshwater thermal environments. All members are likely polysaccharide-degrading chemoheterotrophs with numerous carbohydrate-active enzymes encoded in their genomes. Aerobic or strictly anaerobic. Phylogenomic placement of this lineage within the <i>Armatimonadota</i> and relative evolutionary divergence supports delineation of this lineage as a class within the <i>Armatimonadota</i> . The type genus is <i>Fervidibacter</i> .

Corrections & amendments

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