

Izemobacterium crustae sp. nov.

Submitted by Viver, Tomeu

Abstract

Description of *Izemobacterium crustae* sp. nov. recovered from oceanic crust.

Genus *Izemobacterium*

Etymology

[I.ze.mo.bac.te'ri.um] **Gr. neut. n.** *izema*, a settling down, sediment; **N.L. neut. n.** *bacterium*, rod; **N.L. neut. n.** *Izemobacterium*, a bacterium from settling or subsurface environments

Nomenclatural type

Species *Izemobacterium crustae*^{Ts}

Description

The description of the genus is identical to that given for the type species.

The MAG encodes a nearly complete glycolytic pathway and a complete lactate fermentation pathway, while gluconeogenesis and the tricarboxylic acid cycle are absent, consistent with a fermentative lifestyle and partial oxidative metabolism typical of anaerobic or microaerophilic organisms. An F₁F_o-type ATP synthase is present, suggesting energy generation linked to proton or sodium motive force. No carbon fixation pathways were detected, supporting a heterotrophic mode of nutrition. Genes for β-glucosidase and pullulanase indicate conserved oligosaccharide degradation, and biosynthetic pathways for several amino acids (serine, threonine, glutamine, cysteine, and glycine) are present. The MAG also encodes ferrous iron uptake systems, a complete DNA degradation locus (including extracellular nucleases, ABC transporters, and salvage enzymes), and a conserved sporulation gene set (*spoIIIE*, *spoVG*, *kapD*, *spsF*), consistent with endospore formation.

Classification

Bacteria » *Bacillota* » *Bacilli* » *Izemoplasmatales* » *Izemoplasmataceae* » *Izemobacterium*

References

Effective publication: Viver, Robador, 2026 [1]

Registry URL

<https://seqco.de/i:54823>

Species *Izemobacterium crustae*^{Ts}

Etymology

[crus'tae] **L. gen. n.** *crustae*, from crust, referring to the seafloor oceanic crust from which this organism was recovered

Nomenclatural type

[NCBI Assembly: GCA_052978905.1](#)^{Ts}

Description

The MAG is 2.2 Mb with a GC content of 33.6%, completeness 97.78%, contamination 5.58%. Phylogenomic analysis places it within the family *Izemoplasmataceae*. The AAI value of the MAG and the close relative species *Izemoplasma acidinucleici* was 57.18%. The MAG encodes a nearly complete glycolytic pathway and a complete lactate fermentation pathway, while gluconeogenesis and the tricarboxylic acid cycle are absent, consistent with a fermentative lifestyle and partial oxidative metabolism typical of anaerobic or microaerophilic organisms. No carbon fixation pathways were detected, supporting a heterotrophic mode of nutrition. Genes for β -glucosidase and pullulanase indicate conserved oligosaccharide degradation, and biosynthetic pathways for several amino acids (serine, threonine, glutamine, cysteine, and glycine) are present. The MAG also encodes ferrous iron uptake systems, a complete DNA degradation locus (including extracellular nucleases, ABC transporters, and salvage enzymes), and a conserved sporulation gene set (*spolIIE*, *spoVG*, *kapD*, *spsF*), consistent with endospore formation.

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Bacteria » *Bacillota* » *Bacilli* » *Izemoplasmatales* » *Izemoplasmataceae* » *Izemobacterium* » *Izemobacterium crustae*^{Ts}

References

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References

1. Viver, Robador (2026). Genomic insights into *Izemobacterium crustae* gen. nov., sp. nov., reveal metabolic adaptations for persistence in the oceanic crust. *Systematic and Applied Microbiology*. DOI:10.1016/j.syapm.2025.126679

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:bdqeb1q2** submitted by **Viver, Tomeu** and including 2 new names has been successfully validated.

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