

Izemobacterium crustae sp. nov.

Submitted by Viver, Tomeu

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

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Genus <i>Izemobacterium</i>	[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	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 F ₁ F ₀ -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.	<i>Izemoplasmataceae</i>	<i>Izemobacterium crustae</i> ^{Ts}	seqco.de/i:54823
Species	[crus'tae] L. gen. n. crustae , from crust, referring to the	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 <i>Izemoplasmataceae</i> . The AAI value of the MAG and the close relative species <i>Izemoplasma acidinucleici</i> 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		NCBI Assembly:	

<i>Izemobacterium</i> <i>crustae</i> Proposed Taxon	subseafloor oceanic crust Etymology this organism was recovered	carbon fixation pathways were detected, supporting a heterotrophic mode of nutrition. Genes for β -glucosidase and pullulanase indicate Description	<i>Izemobacterium</i> Parent Taxon	GCA_052978905.1 _{Ts} Type	seqco.de/i:54822 Registry URL
		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.			