Title

Assessing the metabolism, phylogenomic, and taxonomic classification of the halophilic genus Halarchaeum

Abstract

In this study, a genomic approach was employed to evaluate the metabolic potentials and taxonomic classification of the halophilic genus Halarchaeum. Genomic analysis revealed that Halarchaeum members exhibit a predilection for amino acids as their primary energy source in high-salinity environments over carbohydrates. Genome analysis unveiled the presence of crucial genes associated with metabolic pathways, including the Embden–Meyerhof pathway, semi-phosphorylative Entner–Doudoroff pathway, and the urea cycle. Furthermore, the genomic analysis indicated that Halarchaeum members employ diverse mechanisms for osmotic regulation (encompassing both salt-in and salt-out strategies). Halarchaeum members also encode genes to alleviate acid and heat stress. The average nucleotide identity value between Halarchaeum solikamskense and Halarchaeum nitratireducens exceeded the established threshold (95%–96%) for defining distinct species. This high similarity suggests a close relationship between these two species, prompting the proposal to reclassify Halarchaeum solikamskense as a heterotypic synonym of Halarchaeum nitratireducens. The results of this study contribute to our knowledge of taxonomic classification and shed light on the adaptive strategies employed by Halarchaeum species in their specific ecological niches. © The Author(s) 2024. Published by Oxford University Press on behalf of FEMS. All rights reserved.

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Index Keywords

DNA, Bacterial; Glycolysis; Halarchaeum; Halobacteriaceae; Metabolic Networks and Pathways; Phylogeny; RNA, Ribosomal, 16S; Sequence Analysis, DNA; betaine; glycerol; glycine; RNA 16S; sucrose; trehalose; bacterial DNA; Article; energy resource; Halarchaeum; Halarchaeum nitratireducens; Halarchaeum solikamskense; Halobacteriaceae; Halobacterium salinarum; halophile; osmoregulation; DNA sequencing; genetics; glycolysis; metabolism; phylogeny

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betaine, 107-43-7, 590-46-5; glycerol, 56-81-5; glycine, 56-40-6, 6000-43-7, 6000-44-8; sucrose, 122880-25-5, 57-50-1; trehalose, 99-20-7, 6138-23-4; DNA, Bacterial, ; RNA, Ribosomal, 16S,

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