
Title

Taxonomic Reframe of Some Species of the Genera Haloferax and Halobellus

Abstract

Haloferax and Halobellus are the representatives of the family Haloferacaceae and they are dominant in hypersaline ecosystems. Some Haloferax and Halobellus species exhibit a close evolutionary relationship. Genomic, phylogenetic (based on 16S rRNA gene sequence), and phylogenomic analysis were performed to evaluate the taxonomic positions of the genera Haloferax and Halobellus. Based on the results we propose to reclassify Halobellus ramosii as a later heterotypic synonym of Halobellus inordinatus; Haloferax lucentense and Haloferax alexandrinum as later heterotypic synonyms of Haloferax volcanii. © The Author(s), under exclusive licence to Springer Science+Business Media, LLC, part of Springer Nature 2024.

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57194654995; 35293991900; 57194130370

Year

2024

Source title

Current Microbiology

Volume

81.0

Issue

7

Art. No.

216

DOI

10.1007/s00284-024-03695-9

Link

<https://www.scopus.com/inward/record.uri?eid=2-s2.0-85195533983&doi=10.1007%2fs00284-024-03695-9&partnerID=40&md5=40cdabb5afa2c69e475259387d46e001>

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Index Keywords

DNA, Archaeal; Haloferax; Phylogeny; RNA, Ribosomal, 16S; Sequence Analysis, DNA; archaeal DNA; RNA 16S; chemistry; classification; DNA sequencing; genetics; Haloferax; phylogeny

Chemicals/CAS

DNA, Archaeal, ; RNA, Ribosomal, 16S,

References

Castelle C.J., Banfield J.F., Major new microbial groups expand diversity and alter our understanding of the tree of life, *Cell*, 172, 6, pp. 1181-1197, (2018); Liao H., Lin X., Li Y., Qu M., Tian Y., Reclassification of the taxonomic framework of orders Cellvibrionales, Oceanospirillales, Pseudomonadales, and Alteromonadales in class Gammaproteobacteria through phylogenomic tree analysis, *mSystems*, (2020); Parte A.C., Sarda Carbasse J., Meier-Kolthoff J.P., Reimer L.C., Goker M., List of prokaryotic names with standing in nomenclature (LPSN) moves to the DSMZ, *Int J Syst Evol Microbiol*, 70, 11, pp. 5607-5612, (2020); Hwang C.Y., Cho E.S., Yoon D.J., Seo M.J., *Halobellus ruber* sp. nov., a deep red-pigmented extremely halophilic archaeon isolated from a Korean solar saltern, *Antonie Van Leeuwenhoek*, 114, 7, pp. 997-1011, (2021); Cui H.L., Yang X., Gao X., Xu X.W., *Halobellus clavatus* gen. nov., sp. nov. and *Halorientalis regularis* gen.nov,sp. nov., two new members of the family Halobacteriaceae, *Int J Syst Evol Microbiol*, 61, 11, pp. 2682-2689, (2011); Torreblanca M., Rodriguez-Valera F., Juez G., Ventosa A., Kamekura M., Kates M., Classification of non-alkaliphilic Halobacteria based on numerical taxonomy and polar lipid composition and description of *Haloarcula* gen. nov. and *Haloferax* gen. nov, *Syst Appl Microbiol*, 8, 1, pp. 89-99, (1986); Asker D., Ohta Y., *Haloferax alexandrinus* sp. nov., an extremely halophilic canthaxanthin-producing Archaeon from a solar saltern in Alexandria (Egypt), *Int J Syst Evol Microbiol*, 52, 3, pp. 729-738, (2002); Gutierrez M.C., Kamekura M., Holmes M.L., Dyall-Smith M.L., Ventosa A., Taxonomic characterization of *Haloferax* sp. (" *H. alicantei*") strain Aa 2.2: description of *Haloferax lucentensis* sp. nov, *Extremophiles*, 6, 6, pp. 479-483,

(2002); Enache M., Itoh T., Kamekura M., Teodosiu G., Dumitru L., *Haloferax prahovense* sp. nov., an extremely halophilic Archaeon isolated from a Romanian salt lake, *Int J Syst Evol Microbiol*, 57, pp. 393-397, (2007); Perez-Davo A., Aguilera M., Gonzalez-Paredes A., Lujan Jimenez-Pranteda M., Monteoliva-Sanchez M., *Halobellus ramosii* sp. nov., an extremely halophilic Archaeon isolated from a saline-wetland wildfowl reserve, *Int J Syst Evol Microbiol*, 65, 11, pp. 3847-3852, (2015); Klenk H.P., Goker M., En route to a genome-based classification of Archaea and bacteria?, *Syst Appl Microbiol*, 33, 4, pp. 175-182, (2010); Liu G.H., Narsing Rao M.P., Dong Z.Y., Wang J.P., Che J.M., Chen Q.Q., Sengonca C., Liu B., Li W.J., Genome-based reclassification of *Bacillus okuhidensis* as a later heterotypic synonym of *Bacillus halodurans*, *Int J Syst Evol Microbiol*, 69, 11, pp. 3599-3602, (2019); Teng J.L., Tang Y., Huang Y., Guo F.B., Wei W., Chen J.H., Wong S.S., Lau S.K., Woo P.C., Phylogenomic analyses and reclassification of species within the genus *Tsukamurella*: insights to species definition in the post-genomic era, *Front Microbiol*, 7, (2016); Auch A.F., von Jan M., Klenk H.-P., Goker M., Digital DNA-DNA hybridization for microbial species delineation by means of genome-to-genome sequence comparison, *Stand Genomic Sci*, 2, 1, pp. 117-134, (2010); Konstantinidis K.T., Tiedje J.M., Genomic insights that advance the species definition for prokaryotes, *Proc Natl Acad Sci USA*, 102, 7, pp. 2567-2572, (2005); Parks D.H., Imelfort M., Skennerton C.T., Hugenholtz P., Tyson G.W., CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes, *Genome Res*, 25, 7, pp. 1043-1055, (2015); Felsenstein J., Evolutionary trees from DNA sequences: a maximum likelihood approach, *J Mol Evol*, 17, 6, pp. 368-376, (1981); Kumar S., Stecher G., Tamura K., MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets, *Mol Biol Evol*, 33, 7, pp. 1870-1874, (2016); Thompson J.D., Higgins D.G., Gibson T.J., CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice,

Nucleic Acids Res, 22, 22, pp. 4673-4680, (1994); Kimura M., A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences, J Mol Evol, 16, 2, pp. 111-120, (1980); Felsenstein J., Confidence limits on phylogenies: an approach using the bootstrap, Evolution, 39, 4, pp. 783-791, (1985); Eren A.M., Esen O.C., Quince C., Vineis J.H., Morrison H.G., Sogin M.L., Delmont T.O., Anvi'o: an advanced analysis and visualization platform for omics data, PeerJ, 3, (2015); Yoon S.H., Ha S.M., Kwon S., Lim J., Kim Y., Seo H., Chun J., Introducing EzBioCloud: a taxonomically united database of 16S rRNA gene sequences and whole-genome assemblies, Int J Syst Evol Microbiol, 67, 5, pp. 1613-1617, (2017); Eren A.M., Kiefl E., Shaiber A., Veseli I., Miller S.E., Schechter M.S., Fink I., Pan J.N., Yousef M., Fogarty E.C., Trigodet F., Watson A.R., Esen O.C., Moore R.M., Clayssen Q., Lee M.D., Kivenson V., Graham E.D., Merrill B.D., Karkman A., Blankenberg D., Eppley J.M., Sjodin A., Scott J.J., Vazquez-Campos X., McKay L.J., McDaniel E.A., Stevens S.L.R., Anderson R.E., Fuessel J., Fernandez-Guerra A., Maignien L., Delmont T.O., Willis A.D., Community-led, integrated, reproducible multi-omics with anvi'o, Nat Microbiol, 6, 1, pp. 3-6, (2021); Hyatt D., Chen G.L., Locascio P.F., Land M.L., Larimer F.W., Hauser L.J., Prodigal: prokaryotic gene recognition and translation initiation site identification, BMC Bioinform, 11, (2010); Eddy S.R., Accelerated profile HMM searches, PLoS Comput Biol, 7, 10, (2011); Lee M.D., GToTree: a user-friendly workflow for phylogenomics, Bioinformatics, 35, 20, pp. 4162-4164, (2019); Edgar R.C., MUSCLE: multiple sequence alignment with high accuracy and high throughput, Nucleic Acids Res, 32, 5, pp. 1792-1797, (2004); Contreras-Moreira B., Vinuesa P., Get_homologues, a versatile software package for scalable and robust microbial pangenome analysis, Appl Environ Microbiol, 79, 24, pp. 7696-7701, (2013); Li L., Stoeckert C.J., Roos D.S., OrthoMCL: identification of ortholog groups for eukaryotic genomes, Genome Res, 13, 9, pp. 2178-2189, (2003); Katoh K., Standley D.M., MAFFT multiple sequence alignment software version 7: improvements in performance and usability, Mol Biol Evol, 30, 4, pp.

772-780, (2013); Minh B.Q., Schmidt H.A., Chernomor O., Schrempf D., Woodhams M.D., von Haeseler A., Lanfear R., IQ-TREE 2: new models and efficient methods for phylogenetic inference in the genomic era, *Mol Biol Evol*, 37, 5, pp. 1530-1534, (2020); Pritchard L., Glover R.H., Humphris S., Elphinstone J.G., Toth I.K., Genomics and taxonomy in diagnostics for food security: soft-rotting enterobacterial plant pathogens, *Anal Methods*, 8, 1, pp. 12-24, (2016); Kurtz S., Phillippy A., Delcher A.L., Smoot M., Shumway M., Antonescu C., Salzberg S.L., Versatile and open software for comparing large genomes, *Genome Biol*, 5, 2, (2004); Meier-Kolthoff J.P., Auch A.F., Klenk H.P., Goker M., Genome sequence-based species delimitation with confidence intervals and improved distance functions, *BMC Bioinform*, 14, (2013); Meier-Kolthoff J.P., Carbasse J.S., Peinado-Olarte R.L., Goker M., TYGS and LPSN: a database tandem for fast and reliable genome-based classification and nomenclature of prokaryotes, *Nucleic Acids Res*, 50, D1, pp. D801-d807, (2022); Camacho C., Coulouris G., Avagyan V., Ma N., Papadopoulos J., Bealer K., Madden T.L., BLAST+: architecture and applications, *BMC Bioinform*, 10, (2009); Buchfink B., Xie C., Huson D., Fast and sensitive protein alignment using diamond, *Nat Methods*, 12, 1, pp. 59-60, (2015); R: A language and environment for statistical computing; r foundation for statistical computing, (2022); Kolde R., Pheatmap: Pretty Heatmaps, (2012); Page A.J., Cummins C.A., Hunt M., Wong V.K., Reuter S., Holden M.T., Fookes M., Falush D., Keane J.A., Parkhill J., Roary: rapid large-scale prokaryote pan genome analysis, *Bioinformatics*, 31, 22, pp. 3691-3693, (2015); Seemann T., Prokka: rapid prokaryotic genome annotation, *Bioinformatics*, 30, pp. 2068-2069, (2014); Fu L., Niu B., Zhu Z., Wu S., Li W., CD-HIT: accelerated for clustering the next-generation sequencing data, *Bioinformatics*, 28, pp. 3150-3152, (2012); Kim M., Oh H.S., Park S.C., Chun J., Towards a taxonomic coherence between average nucleotide identity and 16S rRNA gene sequence similarity for species demarcation of prokaryotes, *Int J Syst Evol Microbiol*, 64, pp. 346-351, (2014); Qiu X.X., Mou Y.Z., Zhao M.L., Zhang W.J., Han D., Ren M., Cui H.L., *Halobellus inordinatus* sp nov., from a marine solar

saltern and an inland salt lake of China, *Int J Syst Evol Microbiol*, 63, 11, pp. 3975-3980, (2013); Richter M., Rossello-Mora R., Shifting the genomic gold standard for the prokaryotic species definition, *Proc Natl Acad Sci USA*, 106, 45, pp. 19126-19131, (2009); Goris J., Konstantinidis K.T., Klappenbach J.A., Coenye T., Vandamme P., Tiedje J.M., DNA-DNA hybridization values and their relationship to whole-genome sequence similarities, *Int J Syst Evol Microbiol*, 57, pp. 81-91, (2007); Konstantinidis K., Rossello-Mora R., Amann R., Uncultivated microbes in need of their own taxonomy, *ISME J*, 11, pp. 2399-2406, (2017); Oren A., Arahal D.R., Goker M., Moore E.R.B., Rossello-Mora R., Sutcliffe I.C., International code of nomenclature of Prokaryotes. Prokaryotic code revision (2022 revision), *Int J Syst Evol Microbiol*, (2023); Oren A., Taxonomy of the family Halobacteriaceae: a paradigm for changing concepts in prokaryote systematics, *Int J Syst Evol Microbiol*, 62, 2, pp. 263-271, (2012); Euzéby J.P., Validation of publication of new names and new combinations previously effectively published outside the IJSEM, *Int J Syst Evol Microbiol*, 54, 1, pp. 1-2, (2004)

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Publisher

Springer

ISSN

03438651

CODEN

CUMID

PubMed ID

38850425.0

Language of Original Document

English

Abbreviated Source Title

Curr. Microbiol.

Document Type

Article

Publication Stage

Final

Source

Scopus

EID

2-s2.0-85195533983