Title

Reclassification of Some Exiguobacterium Species Based on Genome Analysis

Abstract

The Exiguobacterium genus comprises Gram-stain-positive and facultatively anaerobic bacteria. Some Exiguobacterium species have previously shown significant high 16S rRNA gene sequence similarities with each other. This study evaluates the taxonomic classification of those Exiguobacterium species through comprehensive genome analysis. Average nucleotide identity (ANI) and digital DNA–DNA hybridization (dDDH) values were determined for various Exiguobacterium species pairs. The ANI and dDDH values between Exiguobacterium enclense and Exiguobacterium indicum, Exiguobacterium aquaticum and Exiguobacterium mexicanum, Exiguobacterium soli and Exiguobacterium antarcticum, and Exiguobacterium sibiricum and Exiguobacterium artemiae were above the cut-off level (95–96% for ANI and 70% for dDDH) for species delineation. Based on the findings, we propose to reclassify Exiguobacterium enclense as a later heterotypic synonym of Exiguobacterium indicum, Exiguobacterium aquaticum as a later heterotypic synonym of Exiguobacterium mexicanum, Exiguobacterium soli as a later heterotypic synonym of Exiguobacterium antarcticum and Exiguobacterium sibiricum as a later heterotypic synonym of Exiguobacterium artemiae.

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Index Keywords

Bacterial Typing Techniques; DNA, Bacterial; Exiguobacterium; Genome, Bacterial; Nucleic Acid Hybridization; Phylogeny; RNA, Ribosomal, 16S; Sequence Analysis, DNA; bacterial DNA; bacterial RNA; genomic DNA; nucleotide; RNA 16S; bacterial DNA; RNA 16S; Article; DNA DNA hybridization; Exiguobacterium; Exiguobacterium antarcticum; Exiguobacterium aquaticum; Exiguobacterium artemiae; Exiguobacterium enclense; Exiguobacterium indicum; Exiguobacterium mexicanum; Exiguobacterium sibiricum; Exiguobacterium soli; gene sequence; genome; genome

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References

Collins M.D., Lund B.M., Farrow J.A.E., Schleifer K.H., Chemotaxonomic study of an alkalophilic bacterium, Exiguobacterium aurantiacum gen. nov., sp. nov, J Gen Microbiol, 129, 7, pp. 2037-2042, (1983); Chaturvedi P., Prabahar V., Manorama R., Pindi P.K., Bhadra B., Begum Z., Shivaji S., Exiguobacterium soli sp. nov., a psychrophilic bacterium from the McMurdo Dry Valleys, Antarctica, Int J Syst Evol Microbiol, 58, pp. 2447-2453, (2008); Fruhling A., Schumann P., Hippe H., Straubler B., Stackebrandt E., Exiguobacterium undae sp. nov. and Exiguobacterium antarcticum sp. nov, Int J Syst Evol Microbiol, 52, 4, pp. 1171-1176, (2002); Dastager S.G., Mawlankar R., Sonalkar V.V., Thorat M.N., Mual P., Verma A., Krishnamurthi S., Tang S.K., Li W.J., Exiguobacterium enclense sp. nov., isolated from sediment, Int J Syst Evol Microbiol, 65, pp. 1611-1616, (2015); Liu F., Li Y., He W., Wang W., Zheng J., Zhang D., Exiguobacterium algae sp. Nov. and Exiguobacterium qingdaonense sp. Nov., two novel moderately halotolerant bacteria isolated from the coastal algae, Antonie van Leeuwenhoek, 114, 9, pp. 1399-1406, (2021); Lopez-Cortes A., Schumann P., Pukall R., Stackebrandt E., Exiguobacterium mexicanum sp. nov. and Exiguobacterium artemiae sp. nov., isolated from the brine shrimp Artemia franciscana, Syst Appl Microbiol, 29, 3, pp. 183-190, (2006); Rodrigues D.F., Goris J., Vishnivetskaya T., Gilichinsky D., Thomashow M.F., Tiedje J.M., Characterization of Exiguobacterium isolates from the Siberian permafrost. Description of Exiguobacterium sibiricum sp. nov, Extremophiles, 10, 4, pp. 285-294, (2006); Yumoto I., Hishinuma-Narisawa M., Hirota K., Shingyo T., Takebe F., Nodasaka Y., Matsuyama H., Hara I., Exiguobacterium oxidotolerans sp. nov., a novel alkaliphile exhibiting high catalase activity, Int J Syst Evol Microbiol, 54, pp. 2013-2017, (2004); 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); Raichand R., Pareek S., Singh N.K., Mayilraj S., Exiguobacterium aquaticum sp. nov., a member of the genus Exiguobacterium, Int J Syst Evol Microbiol, 62, pp. 2150-2155, (2012); Zhang D., Zhu Z., Li Y., Li X., Guan Z., Zheng J., Comparative genomics of Exiguobacterium reveals what makes a cosmopolitan bacterium, mSystems, 6, 4, (2021); Richter M., Rossello-Mora R., Shifting the genomic gold standard for the prokaryotic species definition, Proc Natl Acad Sci U S A, 106, 45, pp. 19126-19131, (2009); 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); Lagesen K., Hallin P., Rodland E.A., Staerfeldt H.H., Rognes T., Ussery D.W., RNAmmer: consistent and rapid annotation of ribosomal RNA genes, Nucl Acids Res, 35, 9, pp. 3100-3108, (2007); Lowe T.M., Eddy S.R., tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence, Nucl Acids Res, 25, pp. 955-964, (1997); 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 Bioinformatics, 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, Nucl 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 Bioinformatics, 10, (2009); 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, Nucl Acids Res, 22, 22, pp. 4673-4680, (1994); Saitou N., Nei M., The neighbor-joining method: a new method for reconstructing phylogenetic trees, Mol Biol Evol, 4, 4, pp. 406-425, (1987); Felsenstein J., Evolutionary trees from DNA sequences: a maximum likelihood approach, J Mol Evol, 17, pp. 368-376, (1981); Fitch W.M., Toward defining the course of evolution: minimum change for a specific tree topology, Syst Zool, 20, pp. 406-416, (1971); 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); 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 Bioinformatics, 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, Nucl Acids Res, 32, 5, pp. 1792-1797, (2004); Buchfink B., Xie C., Huson

D.H., 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, R Development Core Team, (2022); Dowle M., Srinivasan A., Data.Table: Extension of 'data.frame', R Package Version 1.14.6, (2022); Charif D., Lobry J.R., SeqinR 1.0–2: A Contributed Package to the R Project for Statistical Computing Devoted to Biological Sequences Retrieval and Analysis, Structural Approaches to Sequence Evolution Biological and Medical Physics, Biomedical Engineering, pp. 207-232, (2007); Qin Q.L., Xie B.B., Zhang X.Y., Chen X.L., Zhou B.C., Zhou J., Oren A., Zhang Y.Z., A proposed genus boundary for the prokaryotes based on genomic insights, J Bacteriol, 196, 12, pp. 2210-2215, (2014); Chun J., Oren A., Ventosa A., Christensen H., Arahal D.R., da Costa M.S., Rooney A.P., Yi H., Xu X.-W., De Meyer S., Trujillo M.E., Proposed minimal standards for the use of genome data for the taxonomy of prokaryotes, Int J Syst Evol Microbiol, 68, 1, pp. 461-466, (2018); Wayne L.G., Brenner D.J., Colwell R.R., Grimont P.A.D., Kandler O., Krichevsky M.I., Moore L.H., Moore W.E.C., Murray R.G.E., Stackebrandt E., Starr M.P., Truper H.G., Report of the Ad Hoc Committee on reconciliation of approaches to bacterial systematics, Int J Syst Evol Microbiol, 37, 4, pp. 463-464, (1987); 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); 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, 1, pp. 81-91, (2007); 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); Mukherjee S., Seshadri R., Varghese N.J., Eloe-Fadrosh E.A., Meier-Kolthoff J.P., Goker M., Coates R.C., Hadjithomas M., Pavlopoulos G.A., Paez-Espino D., Yoshikuni Y., Visel A., Whitman W.B., Garrity G.M., Eisen J.A., Hugenholtz P., Pati A., Ivanova N.N., Woyke T., Klenk H.P., Kyrpides N.C., 1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life, Nat Biotechnol, 35, pp. 676-683, (2017); Konstantinidis K.T., Rossello-Mora R., Amann R., Uncultivated microbes in need of their own taxonomy, ISME J, 11, 11, pp. 2399-2406, (2017); Chaturvedi P., Shivaji S., Exiguobacterium indicum sp. nov., a psychrophilic bacterium from the Hamta glacier of the Himalayan Mountain ranges of India, Int J Syst Evol Microbiol, 56, pp. 2765-2770, (2006)

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