

Supplementary Material



Haloglomus irregulare gen. nov., sp. nov., a New Halophilic Archaeon Isolated from a Marine Saltern

Ana Durán-Viseras, Cristina Sánchez-Porro and Antonio Ventosa*

Department of Microbiology and Parasitology, Faculty of Pharmacy, University of Sevilla, 41012 Sevilla, Spain

* Correspondence: ventosa@us.es; Tel.: +34-954556765

Accession Habitat Reference Database name Salinity number G Saline lake, Iran 5 % NaCl ERS1455389 [1] SS13 Saltern, Spain 13 % NaCl SRX328504 [2] R Saline lake, Iran 18 % NaCl ERS1455390 [1] SS19 Saltern, Spain 19 % NaCl SRX090228 [3] IC21 Saltern, Spain 21 % NaCl SRX352042 [4] [5] Tyrrell 0.1 Saline lake, Australia 29 % NaCl SRR5637210 Tyrrell 0.8 Saline lake, Australia 29 % NaCl SRR5637211 [5] 30 % NaCl S7 Saline lake, Romania Unpublished SRR8921445 W Saline lake, Iran 30 % NaCl ERS1455391 [1] 33 % NaCl SS33 Saltern, Spain SRX347883 [2] Cahuill Saltern, Chile 34 % NaCl SRX680116 [6] 37 % NaCl SS37 Saltern, Spain SRX090229 [3] [7] Gujarat Saline soil, India ND ERP005612 SMO1 Saline soil, Spain 24.0 dS/m SRR5753725 [8] SMO2 Saline soil, Spain 54.4 dS/m SRR5753724 [8]

Table S1. Features of the different metagenomic databases from hypersaline habitats used for metagenomic fragment recruitments.



Figure S1. High performance thin layer chromatography (HPTLC) of polar lipids extracted from strain F16-60^T and some other haloarchaeal species. The plate was revealed with sulfuric acid 5 % in water, and charred by heating at 160 °C. **Lanes: 1**, *Halobacterium salinarum* DSM 3754^T; **2**, *Haloglomus irregulare* gen. nov., sp. nov. (strain F16-60^T); **3**, *Natronomonas moolapensis* CECT 7526^T; **4**, *Natronomonas pharaonis* CECT 4578^T; **5**, *Halorubrum saccharovorum* DSM 1137^T.

Abbreviations: BPG, biphosphatidylglycerol; PG, phosphatidylglycerol; PGP-Me, phosphatidylglycerol phosphate methyl ester; PGS, phosphatidylglycerol sulfate; S-DGD-1, sulfated diglycosil diether; S-TGD-1-PA, sulfated triglycosyl diphytanyl archaeol ester linked to phosphatidic acid; S-TeGD, sulfated tetraglycosil diether.



Figure S2. High performance thin layer chromatography (HPTLC) of phospholipids extracted from strain F16-60^T and some other haloarchaeal species. The plate was revealed with molibden blue. **Lanes: 1**, *Halobacterium salinarum* DSM 3754^T; **2**, *Haloglomus irregulare* gen. nov., sp. nov. (strain F16-60^T); **3**, *Natronomonas moolapensis* CECT 7526^T; **4**, *Natronomonas pharaonis* CECT 4578^T; **5**, *Halorubrum saccharovorum* DSM 1137^T.

Abbreviations: BPG, biphosphatidylglycerol; PG, phosphatidylglycerol; PGP-Me, phosphatidylglycerol phosphate methyl ester; PGS, phosphatidylglycerol sulfate; S-DGD-1, sulfated diglycosil diether.



Figure S3. Photomicrograph of cells of strain F16-60^T observed under a phase-contrast microscope (1000X, immersion oil), cultured in liquid medium under optimal conditions. Scale bar, 10 μ m.



Figure S4. Venn diagram showing the number of genes shared between the genome of strain F16-60^T and closest related species *Natronomonas pharaonis* DSM 2160^T and *Natronomonas moolapensis* $8.8.11^{T}$.

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Figure S5. Metagenomic fragment recruitment plots of strain $F16-60^{T}$ against different metagenomic datasets (see Supplementary Table 1). In each panel the Y axis represents the percentage of identity and X axis represents the genome length. A restrictive cut-off 95 % of nucleotide identity in at least 30 bp of the metagenomic read was used. The black dashed line shows the threshold for the presence of the same species (95 % identity).

Abbreviations: IC21 – Metagenome from Isla Cristina solar saltern pond (Spain), 21 % salinity, Tyrrell 0.1 – Metagenome from Lake Tyrrell (Australia), 29 % salinity, Tyrrell 0.8 – Metagenome from Lake Tyrrell (Australia), 29 % salinity, S7 – Metagenome from Fara Fund hypersaline meromictic lake, 30 % salinity, SS33 – Metagenome from Santa Pola solar saltern pond (Spain), 33 % salinity, Cahuill – Metagenome from Cahuil lagoon (Chile), 34 % salinity, Gujarat – Metagenome from Little Rann of Kutch hypersaline soil (India), SMO1 – Metagenome from Marismas del Odiel Salt Marshes hypersaline soil (Spain), 24 mS/cm salinity, SMO2 – Metagenome from Marismas del Odiel Salt Marshes hypersaline soil (Spain), 54 mS/cm salinity.

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