**Supplementary Table 4 - Molecular, gene-sequence based approaches applied to the study of microbial communities associated with gypsum.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | **Site location** | **Sample description** | **Techniques used** | **Oxygenic phototrophs** | **Other microorganisms** | **References** |
| **Dry environments** |  |  |  |  |  |  |
|  | Atacama Desert, Chile | Gypsum and gypscrete rock | 16S rRNA (V3-V4 hypervariable region) gene library | *Cyanobacteriota* (*Chroococcidiopsis*) | *Pseudomonadota*, *Actinomycetota*, *Gemmatimonadota* | Casero et al., 2021 |
|  | Atacama Desert, Chile | Cyanobacterial culture isolated from gypsum rock | Almost complete 16S rRNA and 16S-23S ITS region | *Chroococcidiopsis* |  | Montero-Lobato et al., 2020 |
|  | Atacama Desert, Chile | Gypsum rock | Small subunit rRNA gene cloning, denaturing gradient gel electrophoresis, metagenomics | *Cyanobacteriota* (36–83%) and algae belonging to the *Chlorophyta* | *Actinomycetota* (10–25%), *Pseudomonadota* (13–30%). Less abundant *Chloroflexota* and *Gemmatimonadota* | Casero et al. 2020 |
|  | Atacama Desert, Chile; Mojave Desert, USA; Al-Jafr Basin, Jordan | Soil gypsum | 16S rRNA (nearly complete sequence) gene library | *Cyanobacteriota*,mainly *Chroococcidiopsis* | *Pseudomonadota*, *Verrucomicrobiota*; minor contribution of *Bacillota*, *Actinomycetota*, *Gemmatimonadota*, *Planctomycetota*, *Bacteroidota*, and a few unclassified sequences | Dong et al., 2007 |
|  | Cuatro Ciéngas Basin, Chihuahuan Desert, Mexico | Gypsum soils | 16S rRNA (nearly complete sequence) gene library; partial sequences of *nifH* | *Cyanobacteriota*; *nifH* sequences of *Cyanobacteriota* | *Pseudomonadota*, *Actinomycetota*, *Bacteroidota*, and other phyla; *nifH* sequences of *Deltaproteobacteria*, *Alphaproteobacteria* and *Gammaproteobacteria* | López-Lozano et al., 2012 |
|  | Bonneville Salt Flats, USA | Halite, gypsum | Bacterial and archaeal hypervariable region) gene libraries | *Cyanobacteriota* (*Geitlerinema*) | Archaea (*Halobacteriota*, *Thermoplasmatales*, *Hadesarchaeota*, *Nanoarchaeaeota*); Bacteria (*Acetothermia*, *Desulfovermiculus* [*Deltaproteobacteria*], *Halanaerobiales* [*Bacillota*], *Bacteroidota*); *Rhodovibrio* (anoxygenic phototroph; *Alphaproteobacteria*) were enriched in upper gypsum sediments | McGonigle et al., 2019 |
|  | Atacama Desert, Chile | Gypsum crust of an Alluvial fan | Metagenomic analysis |  | *Pseudomonadota*, *Actinomycetota*, *Bacteroidota*, *Chloroflexota*. Abundance of *Methylophilales*, *Rhizobiales*, *Caulobacterales*, and *Pseudomonadales* suggests that a methylotrophic community may have existed in the crusts | Schulze-Makuch et al., 2021 |
|  | Gallocanta and Monegros, NE Spain | Soils with different (1%-91%) gypsum content | 16S rRNA (V4 hypervariable region) gene library | *Cyanobacteriota* (~0.5% of the sequences) | *Pseudomonadota* (24-25%), *Actinomycetota* (13-18%), *Acidobacteriota* (14-17%), *Chloroflexota* (10-11%), *Bacteroidota* (7-8%), *Planctomycetota* (7-8%) | Menéndez-Serra et al., 2019 |
|  | Vena del Gesso, Apennines, Italy | Late Miocene gypsum | Partial 16S rRNA gene clone; quantitative PCR amplification using cyanobacteria-specific primers | Eleven kinds of sequence showing 94–99% identity with modern marine *Cyanobacteriota*, including *Geitlerinema*, *Chroococcidiopsis*, and *Lyngbya* |  | Panieri et al., 2010 |
|  | Sicily. Italy | Crystalline gypsum | 16S rRNA gene sequencing | *Cyanobacteriota* (Chroococcidiopsidaceae, Thermosynechococcaceae, Leptolyngbyaceae, Nostocaceae | Proteobacteria, Chloroflexota, Bacteroidota. Actinobacteriota , Acidobacteriota , Planctomycetota, and *Verrucomicrobiota* | Němečková et al., 2023 |
|  | Chott el Jerid, southern Tunisia | Gypsum crusts with endolithic communities | 16S rRNA gene libraries | Cyanobacteriota – sequences affiliated with Leptolyngbya, Nostoc, and Spirulina | *Flavobacteriota*, *Actinomycetota,* *Pseudomonadota* (*Alphaproteobacteria*, *Gammaproteobacteria*), *Deinococcales* | Stivaletta et al., 2010 |
|  | Lake St. Martin Impact Crater, Manitoba, Canada | Gypsum with cryptoendolithic communities | Partial 16S rRNA gene clones obtained with Bacteria- and Archaea-specific primers; for fungi, primers amplifying the ITS region | Cyanobacteriota (1-3% of total sequences) | Chloroflexota and Pseudomonadota dominated; also *Actinomycetota*, *Bacteroidota*, *Bacillota*, and *Synergistota*; Archaea of the phylum *Nitrososphaerota*; ITS sequences of Ascomycota and Basidiomycota. | Rhind et al., 2014 |
|  | Axel Heiberg Island, Canadian high Arctic | Polar desert with an evaporitic gypsum diapir | Clone libraries of partial sequences of bacterial 16S rRNA genes, archaeal 16S rRNA genes, eukaryal/fungal 18S rRNA genes and chloroplast 23S rRNA genes | *Cyanobacteriota* (21% of the bacterial reads, related to *Nostoc*, *Loriellopsis*, *Chroococcidiopsis* and *Cyanothece.* Algal sequences affiliated with lichenizing symbionts *Trebouxia* and *Trichosarcina* | *Pseudomonadota*: *Alphaproteobacteria* (35% of total reads) related to *Rhizobiales*, *Rubellimicrobium*, *Caulobacter*, *Sphingomonas*) and *Betaproteobacteria* (21% of total reads), related to *Delftia* and *Rubrivivax*; *Actinomycetota* (16% of total reads; related to *Rubrobacter* and *Patulibacter*. Archaeal sequences of *Nitrososphaerota*. Fungal sequences related to *Verrucaria*, *Thalidium*, and *Bagliettoa* | Ziolkowski et al., 2013a |
| **Aquatic environments** |  |  |  |  |  |  |
|  | LagunaTebenquiche, Salar de Atacama, Chile | Gypsum evaporite dome (salinity 116 g l-1) | 16S rRNA (V4 hypervariable region) gene library |  | *Bacteroidota* (*Rhodothermaceae*), *Pseudomonadota* (*Alphaproteobacteria* and *Deltaproteobacteria*) | Fernandez et al., 2016, Fernández et al., 2020 |
|  | Salar de Llamara, Atacama Desert. Chile | Evaporitic gypsum domes | 16S rRNA (V4 hypervariable region) gene library | *Cyanobacteriota* (few) | *Pseudomonadota* (mainly *Alphaproteobacteria* and *Gammaproteobacteria*, *Planctomycetota*, *Bacteroidetes* (*Sphingobacteriales*), *Bacillota*; a few sequences of Archaea and Eukarya | Rasuk et al., 2014, Rasuk et al., 2020 |
|  | Guerrero Negro, Mexico | Endoevaporitic gypsarenite microbial mat | Small subunit rRNA gene cloning, denaturing gradient gel electrophoresis | *Cyanobacteriota*, mainly *Euhalothece* (Chroococcales); one Oscillatoriales sequence | *Pseudomonadota* (*Gammaproteobacteria -* 20% including phototrophic *Ectothiorhodospiraceae*, *Alphaproteobacteria* - 13%, *Deltaproteobacteria* - 13%); *Bacteriodota* 30%); also anoxygenic phototrophs of the *Chloroflexota* and *Chlorobiota* | Jahnke et al., 2014 |
|  | Guerrero Negro, Mexico | Salterns and sabkha | 16S rRNA gene libraries using Bacteria- and Cyanobacteria-specific primers | *Cyanobacteriota*: *Euhalothece*, *Arthrospira*, *Halospirulina* | *Pseudomonadota*, *Bacteroidota* | Vogel et al., 2009 |
|  | Lake Lucero Playa, White Sands National Monument, New Mexico, USA | Gypsum-rich hypersaline ephemeral playa | 16S rRNA (V4 hypervariable region) gene library for Bacteria and Archaea; 18S rRNA (V1-V3 region) gene library for eukaryotic microorganisms | *Cyanobacteriota* (at the surface and in low abundance): *Euhalothece*, *Chroococcidiopsis*, *Calothrix*, *Halospirulina*, *Leptolyngbya*, *Phormidium* | *Pseudomonadota* (predominant genera: *Delftia*, *Pseudomonas*), *Actinomycetota*, *Bacteroidota*, *Bacillota*, *Gemmatimonadota*; *Truepera* (*Deinococcota*); Archaea: *Candidatus* Halobonum, *Nitrososphaera*; Eukaryotes including diatoms and fungi | Sirisena et al., 2018 |
|  | Eilat, Israel | Saltern evaporation pond | 16S rRNA (nearly complete sequence) gene library for Bacteria and Archaea; denaturing gradient gel electrophoresis | *Cyanobacteriota*: two sequences affiliated with the *Halothece* cluster, one remotely affiliated with *Coleofasciculus* and *Lyngbya* | Bacteria: *Bacteroidota*, phototrophic and chemotrophic groups of *Alphaproteobacteria* (*Pseudomonadota*); *Chloroflexota*, *Planctomycetota*, *Bacillota*, *Spirochaetota*. Archaeal sequences affiliated with *Methanosarcinales* and *Halobacteria* | Sørensen et al., 2005, Oren et al., 2009 |
|  | Eilat, Israel | Saltern evaporation pond | Real-time PCR of 16S rRNA (nearly complete sequence) genes of Bacteria and Archaea, dissimilatory sulfite reductase (*dsrAB*), and methyl coenzyme M reductase (*mcr*) genes; denaturing gradient gel electrophoresis |  | Sulfate reducers were affiliated with the *Desulfovibrionales*, *Desulfotomaculum*, and two deeply branching groups with no close cultured relatives; the DSR gene copy number was ~1.5% that of the 16S rRNA gene copy number. Methanogens affiliated with the genera *Methanohalophilus* and *Methanohalobium*. Methanogens were little abundant; the number of MCR gene copies never exceeded 0.1% of the number of 16S rRNA gene copies | Sørensen et al., 2009 |

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