**Tabla 1. Clasificación taxonómica y abundancia relativa de los microorganismos encontrados secuenciando el gen 16S –** **Euryarchaeota a Actinobacteria**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  | **Género** | **Especie** | **B2** | **E1** |
| Euryarchaeota | Methanomicrobia | Methanomicrobiales | Methanoregulaceae |   | *formicica*-sp940 | 0.07% | 0.04% |
| Acidobacteria | Acidobacteria | NA | NA | *Blastocatella* | sp3023 | 0.08% | 0.13% |
|   |   |   |   | NA | sp2417; sp2420 | 0.13% | 0.08% |
| Actinobacteria | Acidimicrobiia | Acidimicrobiales | Acidimicrobiaceae | NA | sp4206-sp4230 | 1.24% | 0.94% |
|   |   |   |   | \**Microthrix* | sp4294 | 0.04% | 0.05% |
|   |   |   |   | NA | sp4624 | 0.16% | 0.15% |
|   | Actinobacteria | Corynebacteriales | Mycobacteriaceae | *Mycobacterium* | NA | 0.00% | 0.04% |
|   |   |   |   | *Mycobacterium* | *interjectum-paraense* | 0.25% | 0.30% |
|   |   |   |   | *Mycobacterium* | *moriokaense* | 0.24% | 0.27% |
|   |   |   |   | *Mycobacterium* | *mucogenicum-phocaicum* | 0.00% | 0.07% |
|   |   |   |   | *Mycobacterium* | *pallens-phocaicum* | 0.29% | 0.55% |
|   | Actinobacteria | Frankiales | Sporichthyaceae | NA | sp6155 | 0.46% | 0.58% |
|   |   |   |   | hgcI clade | sp6111 - sp6140 | 1.30% | 1.40% |
|   |   |   |   | hgcI-hgcI clade | NA | 0.32% | 0.17% |
|   |   |   |   | hgcI-hgcI clade | sp6141-sp6147 | 0.11% | 0.14% |
|   |   | Micrococcales | Microbacteriaceae | \**Aquiluna* | sp6600 | 0.10% | 0.11% |
|   |   |   |   | *\*Planktoluna* | *difficilis* | 0.00% | 0.03% |
|   |   | NA | NA | NA | sp7502-sp7508 | 0.54% | 0.53% |
|   | Thermoleophilia | Gaiellales | NA | NA | sp10836; sp10911; sp10919; sp10936 | 0.19% | 0.03% |
|   |   | Solirubrobacterales | NA | NA | sp11020; sp11037; sp11119 | 0.15% | 0.16% |
|   |   |   |   |   | **TOTAL:** | **5.67%** | **5.78%** |

**Tabla 2. Clasificación taxonómica y abundancia relativa de los microorganismos encontrados secuenciando el gen 16S –**  **Bacteroidetes**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  | **Género** | **Especie** | **B2** | **E1** |
| Bacteroidetes | Bacteroidia | Bacteroidales | Porphyromonadaceae | *Paludibacter* | sp13191 | 0.00% | 0.04% |
|   |   | NA | Draconibacteriaceae | NA | sp14889; sp14892 | 0.03% | 0.04% |
|   | Cytophagia | Cytophagales | Cytophagaceae | *Leadbetterella* | sp15250 | 0.08% | 0.10% |
|   |   |   |   | NA | sp15403; sp15445 | 0.58% | 0.59% |
|   |   |   |   | *Pseudarcicella* | sp15330 | 0.03% | 0.09% |
|   |   |   | Flammeovirgaceae | *Marinoscillum* | sp15641 | 0.03% | 0.00% |
|   |   | NA | NA | NA | sp16026-sp16029 | 0.15% | 0.11% |
|   | Flavobacteriia | Flavobacteriales | Cryomorphaceae | *Crocinitomix* | sp16191 | 0.12% | 0.11% |
|   |   |   |   | *Fluviicola* | sp16210-sp16240 | 1.13% | 1.72% |
|   |   |   | Flavobacteriaceae | *Flavobacterium* | *cheniae* | 0.24% | 0.76% |
|   |   |   |   | *Flavobacterium* | *chungnamense-koreense* | 0.00% | 0.04% |
|   |   |   |   | *Flavobacterium* | *daejeonense* | 0.00% | 0.04% |
|   |   |   |   | *Flavobacterium* | *fluvii* | 0.00% | 0.22% |
|   |   |   |   | *Flavobacterium* | *glycines-tructae* | 0.00% | 0.11% |
|   |   |   |   | *Flavobacterium* | *maotaiense* | 0.00% | 0.07% |
|   |   |   |   | *Flavobacterium* | *sasangense* | 0.18% | 0.32% |
|   |   |   |   | *Flavobacterium* | sp16957-sp17044 | 0.12% | 0.73% |
|   |   |   |   | *Flavobacterium* | *succinicans* | 0.05% | 0.04% |
|   |   |   |   | *Flavobacterium* | *terrigena* | 0.03% | 0.00% |
|   |   |   |   | *Flavobacterium*  | *tiangeerense* | 0.04% | 0.24% |
|   |   |   |   | *Flavobacterium* | *tructae* | 0.00% | 0.14% |
|   |   |   | NA | NA | sp17871 | 0.05% | 0.04% |
|   | NA | NA | NA | NA | sp11885 | 0.00% | 0.03% |
|   | Sphingobacteriia | Sphingobacteriales | Chitinophagaceae | *Ferruginibacter* | sp18100 | 0.00% | 0.04% |
|   |   |   |   | *Ferruginibacter* | sp18126-sp18143 | 0.13% | 0.09% |
|   |   |   |   | *Lacibacter* | sp18241 | 0.08% | 0.08% |
|   |   |   |   | NA | sp18415-sp18520 | 0.19% | 0.17% |
|   |   |   |   | *Sediminibacterium* | sp18285; sp18295 | 0.05% | 0.07% |
|   |   |   | NA | NA | sp18027-sp19488 | 1.52% | 1.45% |
|   |   |   | Saprospiraceae | *\*Aquirestis* | sp18745 | 0.82% | 0.54% |
|   |   |   |   | NA | sp18870; sp18940; sp19045 | 0.22% | 0.09% |
|   |   |   | Sphingobacteriaceae | *Pedobacter* | *ruber* | 0.11% | 0.12% |
|   |   |   |   |   | **TOTAL:** | **5.98%** | **8.19%** |

**Tabla 3. Clasificación taxonómica y abundancia relativa de los microorganismos encontrados secuenciando el gen 16S –**  **Chlorobi a Planctomycetes**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  | **Género** | **Especie** | **B2** | **E1** |
| Chlorobi | Chlorobia | Chlorobiales | NA | NA | sp20026; sp20050 | 0.52% | 0.42% |
| Chloroflexi | Anaerolineae | Anaerolineales | Anaerolineaceae | *Bellilinea* | sp20241-sp20462 | 0.00% | 0.04% |
|   |   |   |   | NA | sp20453; sp20600 | 0.08% | 0.00% |
|   | Chloroflexia | Chloroflexales | Roseiflexaceae | *Roseiflexus* | sp21205 | 0.15% | 0.09% |
|   | NA | NA | NA | NA | sp21489; sp21784; sp21876; sp21965 | 0.32% | 0.25% |
|   | Thermomicrobia | NA | NA | NA | sp21846 | 0.12% | 0.06% |
| Charophyta | Conjugatophyceae | NA | NA | *Cosmarium* | *botrytis* | 0.07% | 0.04% |
|   |   | NA | NA | *Cryptomonas* | *curvata* | 0.00% | 0.08% |
|   |   | NA | NA | *Geminigera* | *cryophila* | 0.00% | 0.04% |
|   |   | NA | NA | NA | NA | 0.00% | 0.03% |
|   |   | NA | NA | *Nitzschia* | *closterium* | 0.06% | 0.07% |
|   | Cyanobacteria | NA | Microcoleaceae | *Cylindrospermosis* | sp23472-sp23474 | 0.47% | 0.46% |
|   |   | NA | Microcoleaceae | *Limnothrix* | *redekei* | 0.00% | 0.03% |
|   |   | NA | Microcoleaceae | *Planktothrix* | *agardhii* | 0.06% | 0.00% |
|   |   | NA | Microcoleaceae | *Planktothrix* | *agardhii-rubescens* | 68.34% | 66.30% |
| Firmicutes | Bacilli | Bacillales | Paenibacillaceae | *Paenibacillus* | sp27231; sp27231; sp27256 | 0.11% | 0.22% |
|   | Clostridia | Clostridiales | Clostridiaceae | *Clostridium* | *celatum* | 0.00% | 0.05% |
|   |   |   | Peptostreptococcaceae | *Intestinibacter* | sp34281 | 0.00% | 0.04% |
| Fusobacteria | Fusobacteriia | Fusobacteriales | Fusobacteriaceae | *Cetobacterium* | *somerae* | 0.00% | 0.33% |
|   |   |   |   | *Cetobacterium* | sp37384 | 0.00% | 0.05% |
|   |   |   | NA | NA | sp37488 | 0.00% | 0.09% |
| Gemmatimonadetes | Gemmatimonadetes | Gemmatimonadales | Gemmatimonadaceae | *Gemmatimonas* | sp37823; sp37864 | 0.08% | 0.05% |
|   |   |   |   | NA | sp37893-sp37988 | 0.25% | 0.25% |
| Planctomycetes | NA | NA | NA | NA | sp40445; sp40541 | 0.35% | 0.27% |
|   | Phycisphaerae | Phycisphaerales | Phycisphaeraceae | NA | sp40948; sp40951 | 0.27% | 0.19% |
|   | Planctomycetacia | Planctomycetales | Planctomycetaceae | NA | sp42137-sp42512 | 0.66% | 0.70% |
|   |   |   |   | *Pirellula* | sp41750 | 0.08% | 0.04% |
|   |   |   |   | *Rhodopirellula* | sp42027 | 0.32% | 0.31% |
|   |   |   |   |   | **TOTAL:** | **72.32%** | **70.49%** |

**Tabla 4. Clasificación taxonómica y abundancia relativa de los microorganismos encontrados secuenciando el gen 16S –**  **Proteobacteria – Clase Alphaproteobacteria**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  | **Género** | **Especie** | **B2** | **E1** |
| Proteobacteria | Alphaproteobacteria | NA | NA | NA | sp47327 | 1.23% | 1.07% |
|   |   | Rhizobiales | Methylocystaceae | *Methylocystis* | *echinoides-parvus* | 0.94% | 0.78% |
|   |   |   |   | *Methylocystis* | NA | 0.53% | 0.40% |
|   |   |   | NA | *Alsobacter* | *metallidurans* | 0.05% | 0.05% |
|   |   |   | NA | NA | sp43754-sp44623 | 0.85% | 0.80% |
|   |   | Rhodobacterales | Rhodobacteraceae | *Loktanella* | *cinnabarina-hongkongensis* | 0.00% | 0.05% |
|   |   |   |   | *Rhodobacter* | sp44970-sp44985 | 0.37% | 0.39% |
|   |   |   |   | *Rubellimicrobium* | sp45100-sp45101 | 0.04% | 0.03% |
|   |   | Rhodospirillales | Acetobacteraceae | *Acidocella* | sp45542 | 0.06% | 0.04% |
|   |   |   |   | NA | sp45774 | 0.08% | 0.04% |
|   |   |   |   | *Roseomonas* | sp45724 | 0.13% | 0.09% |
|   |   |   |   | *Roseomonas*  | *stagni* | 0.06% | 0.04% |
|   |   |   | NA | NA | sp45894 | 0.12% | 0.12% |
|   |   |   | NA | *Reyranella* | *massiliensis* | 0.07% | 0.09% |
|   |   |   | Rhodospirillaceae | *Dongia* | *mobilis* | 0.04% | 0.00% |
|   |   | Rickettsiales | Holosporaceae | NA | sp46619 | 0.05% | 0.00% |
|   |   |   | Mitochondria | NA | sp46900 | 0.04% | 0.05% |
|   |   |   | NA | *\*Captivus* | sp47083 | 0.06% | 0.06% |
|   |   |   | NA | *\*Hepatincola* | sp47102 | 0.03% | 0.00% |
|   |   |   | Rickettsiaceae | NA | sp47030 | 0.04% | 0.00% |
|   |   | Sphingomonadales | Sphingomonadaceae | *Novosphingobium* | sp47641 | 0.06% | 0.05% |
|   |   |   |   | *Sphingopyxis* | *contaminans* | 0.00% | 0.05% |
|   |   |   |   | *Sphingopyxis* | *contaminans-*sp48013 | 0.07% | 0.04% |
|   |   |   |   |   | **TOTAL:** | **4.90%** | **4.24%** |

**Tabla 5. Clasificación taxonómica y abundancia relativa de los microorganismos encontrados secuenciando el gen 16S –**  **Proteobacteria – Clase Betaproteobacteria**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  | **Género** | **Especie** | **B2** | **E1** |
| Proteobacteria | Betaproteobacteria | Burkholderiales | Alcaligenaceae | NA | sp48199; sp48206; sp48312 | 0.35% | 0.41% |
|   |   |   | Burkholderiaceae | *Limnobacter* | sp48679 | 0.07% | 0.05% |
|   |   |   |   | *Polynucleobacter* | *acidiphobus* | 0.38% | 0.45% |
|   |   |   |   | *Polynucleobacter* | *cosmopolitanus* | 0.16% | 0.14% |
|   |   |   |   | *Polynucleobacter* | *difficilis* | 0.04% | 0.00% |
|   |   |   | Comamonadaceae | *Alicycliphilus* | *denitrificans* | 0.00% | 0.04% |
|   |   |   |   | *Aquincola-Zhizhongheella* | *caldifontis-tertiaricarbonis* | 0.20% | 0.22% |
|   |   |   |   | *Chlorochromatium* | sp48875 | 0.05% | 0.04% |
|   |   |   |   | *Comamonas* | sp48915 | 0.00% | 0.03% |
|   |   |   |   | *Giesbergeria* | NA | 0.04% | 0.00% |
|   |   |   |   | *Hydrogenophaga* | *bisanensis* | 0.04% | 0.00% |
|   |   |   |   | *Hydrogenophaga* | *bisanensis-pseudoflava* | 0.00% | 0.06% |
|   |   |   |   | *Hydrogenophaga* | *caeni-*sp49308 | 0.04% | 0.04% |
|   |   |   |   | *Leptothrix* | *ginsengisoli* | 0.06% | 0.11% |
|   |   |   |   | *Limnohabitans* | *curvus* | 0.90% | 1.04% |
|   |   |   |   | *Limnohabitans* | *parvus* | 0.10% | 0.17% |
|   |   |   |   | *Limnohabitans* | *planktonicus* | 0.69% | 0.73% |
|   |   |   |   | *Limnohabitans* | sp49038 | 0.08% | 0.09% |
|   |   |   |   | NA | NA | 0.13% | 0.11% |
|   |   |   |   | NA | sp49241 | 0.12% | 0.19% |
|   |   |   |   | *Pseudorhodoferax* | sp49091 | 0.03% | 0.04% |
|   |   |   |   | *Rhodoferax* | *antarcticus* | 0.00% | 0.04% |
|   |   |   |   | *Rhodoferax* | *ferrireducens* | 0.13% | 0.16% |
|   |   |   |   | *Rhodoferax* | *saidenbachensis* | 0.21% | 0.37% |
|   |   |   |   | *Sphaerotilus* | sp49144 | 0.24% | 0.19% |
|   |   |   |   | *Variovorax* | sp49185; sp49189 | 0.32% | 0.14% |
|   |   |   |   | *Zhizhongheella* | *caldifontis*-sp49244 | 0.10% | 0.09% |
|   |   |   | Oxalobacteraceae | *Paucimonas* | sp49461 | 0.12% | 0.06% |
|   |   |   |   | *Undibacterium* | *seohonense* | 0.03% | 0.17% |
|   |   |   |   | *Undibacterium* | sp49478 | 0.17% | 0.15% |
|   |   | Methylophilales | Methylophilaceae | *Methylobacillus* | *flagellatus* | 0.08% | 0.06% |
|   |   |   |   | *Methylotenera* | *mobilis* | 0.05% | 0.00% |
|   |   |   |   | *Methylotenera* | sp49684 | 0.04% | 0.00% |
|   |   | Nitrosomonadales | Nitrosomonadaceae | NA | sp50176 | 0.06% | 0.03% |
|   |   | Rhodocyclales | Rhodocyclaceae | *Dechloromonas* | denitrificans-*hortensis-*sp50348 | 0.10% | 0.11% |
|   |   |   |   | *Dechloromonas* | sp50343-sp50348-sp50527; sp50351 | 0.06% | 0.00% |
|   |   |   |   | NA | sp50512; sp50547 | 0.08% | 0.03% |
|   |   |   |   |   | **TOTAL:** | **5.26%** | **5.56%** |

**Tabla 6. Clasificación taxonómica y abundancia relativa de los microorganismos encontrados secuenciando el gen 16S –** **Proteobacteria – Deltaproteobacteria y otros grupos**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  | **Género** | **Especie** | **B2** | **E1** |
| Proteobacteria | Deltaproteobacteria | Bdellovibrionales | Bacteriovoracaceae | *Peredibacter* | sp50818 | 0.03% | 0.00% |
|   |   |   |   | *Peredibacter* | *starrii* | 0.03% | 0.07% |
|   |   | Myxococcales | NA | NA | sp53501 | 0.05% | 0.05% |
|   |   |   | Phaselicystidaceae | *Phaselicystis* | sp53959 | 0.07% | 0.06% |
|   |   |   | Sandaracinaceae | NA | sp54095 | 0.03% | 0.04% |
|   |   | Oligoflexales | NA | NA | sp54406 | 0.11% | 0.13% |
|   |   |   | Oligoflexaceae | NA | sp54323 | 0.06% | 0.05% |
|   |   | Syntrophobacterales | Syntrophaceae | *Smithella* | sp55023; sp55026; sp55045 | 0.35% | 0.37% |
|   | Gammaproteobacteria | Aeromonadales | Aeromonadaceae | *Aeromonas* | *rivuli-sobria* | 0.00% | 0.12% |
|   |   |   |   | *Aeromonas* | *sobria* | 0.35% | 0.00% |
|   |   | Cellvibrionales | Spongiibacteraceae | NA | sp57486 | 0.04% | 0.05% |
|   |   | Chromatiales | Chromatiaceae | *Rheinheimera* | *aquatica-texasensis* | 0.00% | 0.30% |
|   |   |   |   | *Rheinheimera* | *arenilitoris* | 0.00% | 0.35% |
|   |   |   |   | *Rheinheimera* | *tilapiae* | 0.04% | 0.30% |
|   |   | Methylococcales | Methylococcaceae | *Methylocaldum* | sp60855-*szegediense* | 0.50% | 0.04% |
|   |   |   |   | *Methylocaldum* | sp60866 | 0.10% | 0.05% |
|   |   |   |   | *Methylocaldum-Methyloparacoccus* | *murrellii-*sp60867 | 0.04% | 0.04% |
|   |   |   |   | *Methylomonas* | *methanica* | 0.05% | 0.00% |
|   |   | NA | NA | NA | sp60261 | 0.06% | 0.07% |
|   |   | Oceanospirillales | Oceanospirillaceae | *Pseudospirillum* | sp61724 | 0.08% | 0.00% |
|   |   | Pseudomonadales | Pseudomonadaceae | *Pseudomonas* | *anguilliseptica* | 0.47% | 0.17% |
|   |   |   |   | *Pseudomonas* | *benzenivorans-putida* | 0.07% | 0.00% |
|   |   | Xanthomonadales | NA | *Acidibacter* | sp65528; 65529 | 0.21% | 0.15% |
|   |   |   | NA | NA | sp65588 | 0.09% | 0.08% |
|   |   |   | Xanthomonadaceae | *Arenimonas* | sp64994; sp64998 | 0.00% | 0.07% |
|   | NA | NA | NA | NA | NA | 0.61% | 0.51% |
|   | NA | NA | NA | NA | sp65765; sp65842 | 0.13% | 0.16% |
| Saccharibacteria | NA | NA | NA | NA | sp66011 | 0.03% | 0.00% |
| Verrucomicrobia | NA | NA | NA | *\*Methylacidiphilum* | sp69240 | 0.06% | 0.04% |
|   | NA | NA | NA | NA | sp68500; sp68759; sp68788 | 0.12% | 0.09% |
|   | Opitutae | Opitutales | Opitutaceae | *Opitutus* | sp68908; sp68917 | 0.18% | 0.13% |
|   | Spartobacteria | Chthoniobacterales | Chthoniobacteraceae | *Chthoniobacter* | sp69045 | 0.04% | 0.03% |
|   | Spartobacteria | Chthoniobacterales | NA | NA | sp69180; sp69190; sp69211 | 0.93% | 1.26% |
|   | Verrucomicrobiae | Verrucomicrobiales | Verrucomicrobiaceae | *Brevifollis* | *gellanilyticus* | 0.04% | 0.03% |
|   |   |   |   | *Luteolibacter* | *algae* | 0.00% | 0.04% |
|   |   |   |   | NA | sp69418; sp69448; sp69458 | 0.54% | 0.59% |
| Otros |   |   |   |   |   | 0.38% | 0.33% |
|   |   |   |   |   | **TOTAL:** | **5.88%** | **5.75%** |

**Tabla 7. Abundancia relativa y clasificación taxonómica de los microorganismos encontrados secuenciando el gen 16S que solamente se encontraron a cero metros de profundidad (en la superficie)**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  | **Género** | **Especie** | **E1** |
| Actinobacteria | Actinobacteria | Corynebacteriales | Mycobacteriaceae | *Mycobacterium* | NA | 0.044% |
|   |   |   |   | *Mycobacterium* | *mucogenicum-phocaicum* | 0.066% |
|   |   | Micrococcales | Microbacteriaceae | *\*Planktoluna* | *difficilis* | 0.030% |
| Bacteroidetes | Bacteroidia | Bacteroidales | Porphyromonadaceae | *Paludibacter* | sp13191 | 0.039% |
|   | Flavobacteriia | Flavobacteriales | Flavobacteriaceae | *Flavobacterium* | *chungnamense-koreense* | 0.039% |
|   |   |   |   | *Flavobacterium* | *daejeonense* | 0.039% |
|   |   |   |   | *Flavobacterium* | *fluvii* | 0.215% |
|   |   |   |   | *Flavobacterium* | *glycines-tructae* | 0.105% |
|   |   |   |   | *Flavobacterium* | *maotaiense* | 0.072% |
|   |   |   |   | *Flavobacterium* | *tructae* | 0.135% |
|   | NA | NA | NA | NA | sp11885 | 0.030% |
|   | Sphingobacteriia | Sphingobacteriales | Chitinophagaceae | *Ferruginibacter* | sp18100 | 0.041% |
| Chloroflexi | Anaerolineae | Anaerolineales | Anaerolineaceae | *Bellilinea* | sp20241-sp20462 | 0.041% |
| Cyanobacteria | Chloroplast | NA | NA | *Cryptomonas* | *curvata* | 0.083% |
|   |   | NA | NA | *Geminigera* | *cryophila* | 0.036% |
|   |   | NA | NA | NA | NA | 0.030% |
|   | Cyanobacteria | NA | Microcoleaceae | *Limnothrix* | *redekei* | 0.033% |
| Firmicutes | Clostridia | Clostridiales | Clostridiaceae | *Clostridium* | *celatum* | 0.047% |
|   |   |   | Peptostreptococcaceae | *Intestinibacter* | sp34281 | 0.044% |
| Fusobacteria | Fusobacteriia | Fusobacteriales | Fusobacteriaceae | *Cetobacterium* | *somerae* | 0.331% |
|   |   |   | Fusobacteriaceae | *Cetobacterium* | sp37384 | 0.047% |
|   |   |   | NA | NA | sp37488 | 0.094% |
| Proteobacteria | Alphaproteobacteria | Rhodobacterales | Rhodobacteraceae | *Loktanella* | *cinnabarina-hongkongensis* | 0.052% |
|   |   | Sphingomonadales | Sphingomonadaceae | *Sphingopyxis* | *contaminans* | 0.047% |
|   | Betaproteobacteria | Burkholderiales | Comamonadaceae | *Alicycliphilus* | *denitrificans* | 0.039% |
|   |   |   |   | *Comamonas* | sp48915 | 0.030% |
|   |   |   |   | *Hydrogenophaga* | *bisanensis-pseudoflava* | 0.061% |
|   | Gammaproteobacteria | Aeromonadales | Aeromonadaceae | *Aeromonas* | *rivuli-sobria* | 0.124% |
|   |   | Chromatiales | Chromatiaceae | *Rheinheimera* | *aquatica-texasensis* | 0.295% |
|   |   |   |   | *Rheinheimera* | *arenilitoris* | 0.345% |
|   |   | Xanthomonadales | Xanthomonadaceae | *Arenimonas* | sp64994; sp64998 | 0.074% |
| Verrucomicrobia | Verrucomicrobiae | Verrucomicrobiales | Verrucomicrobiaceae | *Luteolibacter* | *algae* | 0.039% |
|  |  |  |  | **ABUNDANCIA TOTAL:** | **2.747%** |

**Tabla 8. Abundancia relativa y clasificación taxonómica de los microorganismos encontrados secuenciando el gen 16S que solamente se encontraron a dos metros de profundidad**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  | **Género** | **Especie** | **B2** |
| Bacteroidetes | Cytophagia | Cytophagales | Flammeovirgaceae | *Marinoscillum* | sp15641 | 0.031% |
|   | Flavobacteriia | Flavobacteriales | Flavobacteriaceae | *Flavobacterium* | *terrigena* | 0.029% |
| Chloroflexi | Anaerolineae | Anaerolineales | Anaerolineaceae | NA | sp20453; sp20600 | 0.081% |
| Cyanobacteria | Cyanobacteria | NA | Microcoleaceae | *Planktothrix* | *agardhii* | 0.064% |
| Proteobacteria | Alphaproteobacteria | Rhodospirillales | Rhodospirillaceae | *Dongia* | *mobilis* | 0.036% |
|   |   | Rickettsiales | Holosporaceae | NA | sp46619 | 0.050% |
|   |   |   | NA | *\*Hepatincola* | sp47102 | 0.026% |
|   |   |   | Rickettsiaceae | NA | sp47030 | 0.036% |
|   | Betaproteobacteria | Burkholderiales | Burkholderiaceae | *Polynucleobacter* | *difficilis* | 0.040% |
|   |   |   | Comamonadaceae | *Giesbergeria* | NA | 0.043% |
|   |   |   |   | *Hydrogenophaga* | *bisanensis* | 0.040% |
|   |   | Methylophilales | Methylophilaceae | *Methylotenera* | *mobilis* | 0.050% |
|   |   |   |   | *Methylotenera* | sp49684 | 0.040% |
|   |   | Rhodocyclales | Rhodocyclaceae | *Dechloromonas* | sp50343-sp50348-sp50527; sp50351 | 0.059% |
|   | Deltaproteobacteria | Bdellovibrionales | Bacteriovoracaceae | *Peredibacter* | sp50818 | 0.031% |
|   | Gammaproteobacteria | Aeromonadales | Aeromonadaceae | *Aeromonas* | *sobria* | 0.345% |
|   |   | Methylococcales | Methylococcaceae | *Methylomonas* | *methanica* | 0.048% |
|   |   | Oceanospirillales | Oceanospirillaceae | *Pseudospirillum* | sp61724 | 0.078% |
|   |   | Pseudomonadales | Pseudomonadaceae | *Pseudomonas* | *benzenivorans-putida* | 0.067% |
| Saccharibacteria | NA | NA | NA | NA | sp66011 | 0.031% |
|   |   |   |   |  **ABUNDANCIA TOTAL:** | **1.225%** |

**Tabla 9. Clasificación taxonómica y abundancia relativa de los microorganismos encontrados secuenciando el gen 18S –Archaeplastida a Opisthokonta**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  | **Género** | **Especie** | **B2** | **E1** |
| Archaeplastida | Chloroplastida | Chlorophyta | Chlorophyceae | Other | Other | 0.00% | 0.10% |
|   |   |   | Chlamydomonadales | Other | Other | 4.64% | 3.29% |
|   |   |   | Chlorodendrales | *Tetraselmis* | Other | 0.00% | 0.05% |
| Archaeplastida | Chloroplastida | Chlorophyta | Sphaeropleales | Other | Other | 0.11% | 0.18% |
| Cryptophyceae | Cryptomonadales | Cryptomonas | Other | Other | Other | 0.18% | 1.75% |
|   |   | Teleaulax | Other | Other | uncultured marine eukaryote | 0.00% | 0.14% |
|   |   |   |   |   | Other | 0.00% | 0.09% |
|   |   | Other | Other | Other | Other | 0.00% | 0.21% |
|   | Goniomonas | uncultured Cryptomonadaceae | Other | Other | uncultured  | 0.14% | 0.08% |
|   | Kathablepharidae | uncultured | Other | Other | uncultured *katablepharidophyte* | 0.78% | 0.52% |
|   | Other | Other | Other | Other | Other | 2.32% | 3.54% |
| Excavata | Discoba | Discicristata | Eubodonida | *Bodo* | *Bodo saltans* | 0.07% | 0.00% |
|   |   |   | Euglenaceae | *Trachelomonas*  | *Trachelomonas sp.* T201 | 0.12% | 0.33% |
|   |   |   |   |   | Other | 0.04% | 0.11% |
| Opisthokonta | Holozoa | Ichthyosporea | Ichthyophonidae | Freshwater *Ichthyosporeans* | 1 uncultured *Ichthyosporea* | 0.00% | 0.05% |
|   |   | Metazoa (Animalia) | Bilateria | Uncultured | uncultured *Glenodinium* | 1.23% | 1.57% |
|   |   |   | Monogononta | Other | Other | 0.28% | 0.19% |
|   |   |   | Rhabdocoela | *Neodalyellida* | Other | 0.00% | 0.05% |
|   |   |   | Copepoda  | *Calanoida* | Other | 0.07% | 3.81% |
|   |   |   |   | *Cyclopoida* | Other | 13.53% | 13.02% |
|   |   |   | Phyllopoda  | *Diplostraca* | *Bosmina longirostris* | 6.78% | 6.18% |
|   |   |   |   | *Diplostraca* | Other | 7.87% | 0.00% |
|   | Nucletmycea | Discicristoidea | Incertae | Sedis | uncultured eukaryote | 0.15% | 0.06% |
|   |   | Fungi | Cryptomycota | LKM11 | uncultured eukaryote | 0.08% | 0.15% |
|   |   |   |   | LKM11 | uncultured fungus | 0.16% | 0.19% |
|   |   |   |   | LKM11 | Other | 0.10% | 0.16% |
|   |   |   | Chytridiomycetes | Chytridiales | *Rhizoclosmatium sp.* JEL347-h | 0.00% | 0.05% |
|   |   |   | Rhizophydiales | uncultured | uncultured Chytridiomycota | 0.05% | 0.00% |
|   |   |   | Rhizophydiales | uncultured | Other | 0.37% | 0.38% |
|   |   |   | Didymellaceae  | *Boeremia* | Other | 0.00% | 0.06% |
|   |   | LKM15 | uncultured | Eimeriidae | uncultured Eimeriidae | 0.00% | 0.07% |
|   |   |   |   |   | **Abundancia Total:** | **39.07%** | **36.36%** |

**Tabla 10. Clasificación taxonómica y abundancia relativa de los microorganismos encontrados secuenciando el gen 18S –SAR y otros**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  | **Género** | **Especie** | **B2** | **E1** |
| SAR | Alveolata | Ciliophora | Choreotrichia | *Metacylis* | uncultured tintinnid ciliate | 1.26% | 0.39% |
|   |   |   |   | *Pelagostrobilidium* | Other | 1.21% | 7.48% |
|   |   |   |   | *Tintinnidium* | Other | 0.32% | 0.63% |
|   |   |   | Haptoria | Other | Other | 0.13% | 0.00% |
|   |   |   | Hypotrichia | Other | Other | 0.00% | 0.10% |
|   |   |   | Oligotrichia | *Pseudotontonia* | Other | 0.00% | 0.27% |
|   |   |   |   | *Strombidium* | Other | 0.00% | 0.05% |
|   |   |   | Prostomatea | *Cryptocaryon* | uncultured alveolate | 0.93% | 0.50% |
|   |   |   |   | *Cryptocaryon* | Other | 0.33% | 0.50% |
|   |   |   | Peritrichia | *Epicarchesium* | Other | 0.00% | 0.10% |
|   |   |   | Peritrichia | *Telotrochidium* | Other | 0.16% | 0.13% |
|   |   |   |   | *Zoothamnium* | Other | 0.18% | 0.06% |
|   |   |   |   | Other | Other | 0.24% | 0.26% |
|   |   |   | Scuticociliatia | uncultured | uncultured ciliate | 0.00% | 0.06% |
|   |   |   |   | Other | Other | 0.28% | 0.12% |
|   |   |   | Other | Other | Other | 0.37% | 0.32% |
|   |   | Dinoflagellata | Incertae | Sedis | Azadinium | 0.12% | 0.07% |
|   |   |   | Thoracosphaeraceae | Other | Other | 0.00% | 0.12% |
|   |   |   | Other | Other | Other | 5.08% | 0.81% |
|   |   | Protalveolata | Colpodellida | *Colpodella* | uncultured eukaryote | 0.60% | 0.19% |
|   |   |   | Perkinsidae  | A31 | uncultured alveolate | 0.05% | 0.00% |
|   |   |   | Perkinsidae | A31 | uncultured eukaryote | 0.32% | 0.32% |
|   |   |   | Syndiniales | Other | Other | 0.00% | 0.11% |
|   |   | Other | Other | Other | Other | 0.13% | 0.50% |
|   | Rhizaria | Cercozoa | Cercozoa sp. ATCC 50530 | *Cercozoa sp.* ATCC 50530 | *Cercozoa sp.* ATCC 50530 | 0.13% | 0.10% |
|   |   |   | Glissomonadida | *Heteromita* | *Cercozoa sp.* ATCC PRA130 | 0.00% | 0.05% |
|   |   |   | Thecofilosea | NW617 | uncultured eukaryote | 0.22% | 0.00% |
|   |   |   | Other | Other | Other | 2.61% | 0.41% |
|   | Stramenopiles | Bicosoecida | Bicosoeca | uncultured stramenopile | uncultured stramenopile | 0.31% | 0.32% |
|   |   |   | Bicosoeca | Other | Other | 1.59% | 1.52% |
|   |   |   | uncultured eukaryote | uncultured eukaryote | uncultured eukaryote | 0.28% | 0.18% |
|   |   | Incertae | Sedis | *Pirsonia* | *formosa* | 0.09% | 0.00% |
|   |   | MAST-12 | MAST-12C | uncultured Eimeriidae | uncultured Eimeriidae | 1.08% | 1.15% |
|   |   | MAST-6 | Other | Other | Other | 0.06% | 0.00% |
|   |   | Ochrophyta | Chrysophyceae | Ochromonadales | Spumella-like flagellate JBC27 | 0.26% | 0.45% |
|   |   |   | Bacillariophytina | Other | Other | 0.19% | 0.00% |
|   |   |   | Ochromonadales | *Paraphysomonas* | Chrysophyceae sp. I8 | 0.05% | 0.10% |
|   |   |   |   | *Paraphysomonas* | uncultured *chrysophyte* | 0.13% | 0.16% |
|   |   |   |   | *Paraphysomonas* | uncultured *marine* eukaryote | 0.08% | 0.07% |
|   |   |   |   | *Paraphysomonas* | Other | 1.15% | 2.81% |
|   |   |   | Bacillariophyceae | *Navicula* | Other | 0.00% | 0.10% |
|   |   |   |   | *Sellaphora* | *pupula* | 0.04% | 0.22% |
|   |   |   |   | *Sellaphora* | Other | 0.17% | 0.22% |
|   |   |   |   | Other | Other | 0.13% | 0.12% |
|   |   |   | Fragilariales | *Licmophora* | Other | 0.00% | 0.08% |
|   |   |   | Other | Other | Other | 0.57% | 1.70% |
|   |   | Peronosporomycetes | Aphanomyces | Other | Other | 0.07% | 0.20% |
|   |   |   | Pythium | *Pythium* | *insidiosum* | 0.07% | 0.08% |
|   |   |   |   | Other | Other | 0.05% | 0.00% |
|   |   |   | Saprolegnia | *Saprolegnia* | *Saprolegnia* sp. SAP1 | 0.71% | 0.43% |
|   |   | Peronosporomycetes  | Other | Other | Other | 1.44% | 0.47% |
|   |   | Other | Other | Other | Other | 0.39% | 0.29% |
|   | Other | Other | Other | Other | Other | 0.09% | 0.00% |
| Other |   | Other | Other | Other | Other | 11.86% | 12.87% |
| Other | Other | Other | Other | Other | Other | 25.37% | 26.45% |
|   |   |   |   |   | **Abundancia Total:** | **60.93%** | **63.64%** |

**Tabla 11. Abundancia relativa y clasificación taxonómica de los microorganismos encontrados secuenciando el gen 18S que solamente se encontraron a dos metros de profundidad o en la superficie (cero metros de profundidad).**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  | **Género** | **Especie** | **B2** | **E1** |
| Archaeplastida | Chloroplastida | Chlorophyta | Chlorophyceae | Other | Other | 0.00% | **0.10%** |
|   |   |   | Chlorodendrales | *Tetraselmis* | Other | 0.00% | **0.05%** |
| Cryptophyceae | Cryptomonadales | Teleaulax |   |   | uncultured marine eukaryote | 0.00% | **0.14%** |
|   |   |   | Other | Other | Other | 0.00% | **0.09%** |
|   |   | Other | Other | Other | Other | 0.00% | **0.21%** |
| Opisthokonta | Holozoa | Ichthyosporea | Ichthyophonidae | Freshwater *Ichthyosporeans* | 1 uncultured *Ichthyosporea* | 0.00% | **0.05%** |
|   |   | Metazoa (Animalia) | Rhabdocoela | *Neodalyellida* | Other | 0.00% | **0.05%** |
| Opisthokonta | Nucletmycea | Fungi | Chytridiomycetes | Chytridiales | *Rhizoclosmatium* sp. JEL347-h | 0.00% | **0.05%** |
|   |   | Fungi | Didymellaceae  | *Boeremia* | Other | 0.00% | **0.06%** |
|   |   | LKM15 | uncultured | Eimeriidae | uncultured Eimeriidae | 0.00% | **0.07%** |
| SAR | Alveolata | Ciliophora | Hypotrichia | Other | Other | 0.00% | **0.10%** |
|   |   |   | Oligotrichia | *Pseudotontonia* | Other | 0.00% | **0.27%** |
|   |   |   |   | *Strombidium* | Other | 0.00% | **0.05%** |
|   |   |   | Peritrichia | *Epicarchesium* | Other | 0.00% | **0.10%** |
|   |   |   | Scuticociliatia | uncultured | uncultured ciliate | 0.00% | **0.06%** |
|   |   | Dinoflagellata | Thoracosphaeraceae | Other | Other | 0.00% | **0.12%** |
|   |   | Protalveolata | Syndiniales | Other | Other | 0.00% | **0.11%** |
|   | Rhizaria | Cercozoa | Glissomonadida | *Heteromita* | Cercozoa sp. ATCC PRA130 | 0.00% | **0.05%** |
|   | Stramenopiles | Ochrophyta | Bacillariophyceae | *Navicula* | Other | 0.00% | **0.10%** |
|   |   |   | Fragilariales | *Licmophora* | Other | 0.00% | **0.08%** |
| Opisthokonta | Nucletmycea | Fungi | Rhizophydiales | uncultured | uncultured Chytridiomycota | **0.05%** | 0.00% |
| SAR | Alveolata | Ciliophora | Haptoria | Other | Other | **0.13%** | 0.00% |
|   |   | Protalveolata | Perkinsidae  | A31 | uncultured alveolate | **0.05%** | 0.00% |
|   | Rhizaria | Cercozoa | Thecofilosea | NW617 | uncultured eukaryote | **0.22%** | 0.00% |
|   | Stramenopiles | Incertae | Sedis | *Pirsonia* | *formosa* | **0.09%** | 0.00% |
|   |   | MAST-6 | Other | Other | Other | **0.06%** | 0.00% |
|   |   | Ochrophyta | Bacillariophytina | Other | Other | **0.19%** | 0.00% |
|   |   | Peronosporomycetes | Pythium | Other | Other | **0.05%** | 0.00% |
|   | Other | Other | Other | Other | Other | **0.09%** | 0.00% |
|   |   |   |   |   | **Abundancia Total:** | **0.94%** | **1.89%** |