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| **Lake name and location** | **Environment details** | **Techniques used** | **Organisms identified** | **Key metabolisms/ processes** | **Notes** | **Reference** | **Figure 1 map location** |
| Lakes Bonney, Hoare, Fryxell, Joyce, Miers and Vanda, McMurdo Dry Valleys | Fresh to hypersaline, permanently ice-covered | 16S and *amoA* libraries | β–proteobacteria & γ– proteobacteria | Ammonia oxidation | Nitrifying bacterial *amoA* detected in all lakes.  In meromictic lakes, the population of β– and γ– proteobacteria vertically stratified. Majority of nitrifying bacteria were β–proteobacteria. | Voytek *et al*.*,* 1999 | McMurdo Sound, Victoria Land & Transantarctic Mountains |
| Lake Bonney, McMurdo Dry Valleys | Hypersaline, meromictic, permanently ice-covered, lake separated into east and west lobes | *nifH* library of ice aggregate material and microbial mats  nitrogenase activity assays | Cyanobacteria, γ– proteobacteria. α–proteobacteria & δ–proteobacteria | Nitrogen fixation by both cyanobacteria and heterotrophic bacteria | Nitrogenase activity low compared to temperate environments.  Heterotrophs responsible for 10–30% of nitrogenase activity.  Heterotrophs likely microaerophilic. | Olson *et al*., 1998 | McMurdo Sound, Victoria Land & Transantarctic Mountains |
| Lake Bonney, McMurdo Dry Valleys&  Terrestrial cyanobacterial mats from Taylor Valley | Hypersaline, meromictic, permanently ice-covered, lake separated into east and west lobes | 16S library of sediment trapped in ice and hybridization of probes against surrounding mats | Cyanobacteria, Acidobacterium/Holophaga, Planctomycetales & Green non-sulfur Bacteria | Phototrophy and heterotrophy | Probes designed from 16S clone library of bacteria in the sediment in the ice matched that of the surrounding mats. | Gordon *et al*., 2000 | McMurdo Sound, Victoria Land & Transantarctic Mountains |
| Lake Bonney, McMurdo Dry Valleys | Hypersaline, meromictic, permanently ice-covered, lake separated into east and west lobes | 16S libraries of deep waters | γ– proteobacteria, Actinobacteria, CFB, Firmicutes, α–proteobacteria, β–proteobacteria & Planctomycetales | Heterotrophy | Population vertically stratified. East and West Lobes have overlapping but distinct communities. | Glatz *et al.*, 2006 | McMurdo Sound, Victoria Land & Transantarctic Mountains |
| Lake Bonney, McMurdo Dry Valleys | Hypersaline, meromictic, permanently ice-covered, lake separated into east and west lobes | 18S libraries of watercolumn profile | Cryptophyta, Chlorophyta, Stramenopiles, Haptophyta, Choanoflagellida, Alveolate, Fungi& Ciliates | Photosynthesis | Population vertically stratified. Crytophytes dominant in the shallow water and haptophytes in the mid-depths and chlorophtes in the deeper waters. Stramenopiles replaced haptophytes during polar night. | Bielewicz *et al.*, 2011 | McMurdo Sound, Victoria Land & Transantarctic Mountains |
| Ekho, Organic and Deep Lakes, Vestfold Hills | Hypersaline.  Ekho and Organic: meromictic and ice-covered ~9 months of the year  Deep Lake: holomictic and never freezes | 16S libraries of sediment | **Organic**: Cyanobacteria/chloroplasts, CFB, γ– proteobacteria, α–proteobacteria, Halobacteriales, Actinobacteria  **Ekho**: Firmicutes, CFB, Cyanobacteria/chloroplasts, α–proteobacteria, γ– proteobacteria, Verrucomicrobiales, Spirochaetales.  **Deep**: Halobacteriales & γ– proteobacteria | Heterotrophy | No phylotypes found in all samples. Distribution of bacterial classes similar between Ekho and Organic with *Roseovarius* common to both. *Marinobacter* and *Halomonas* common to Organic and Deep.  Coverage: 86.5%, 90.8% and 96.6% for Ekho, Organic and Deep respectively. | Bowman *et al*., 2000b | Pyrdz Bay, Vestfold & Larsemann Hills |
| Lake Vida, McMurdo Dry Valleys | Hypersaline, meromictic, permanently ice-covered | 16S and 18S DGGE and 16S library of ice cover core | **16S**: Actinobacteria, CFB, γ– proteobacteria, Cyanobacteria. OD1, TM7 Firmicutes &Planctomycetales.  **18S**: Chlorophyta, fungi, Bacillariophyta, Apicomplexa, Cercozoa, Chrysophyceae, Chytridiomycota & Ciliophora. | Phototrophy,  heterotrophy | Cell density highest at the surface. Phylogeny shows *Marinobacter* related to Lake Bonney isolate and bacterial sequences are similar to marine and polar organisms. | Mosier *et al.*, 2007 | McMurdo Sound, Victoria Land &Transantarctic Mountains |
| Suribati Ike, Skarvsnes, Syowa Oasis | Hypersaline, meromictic sulfidic anoxic bottom waters. | 16S libraries of water at the halocline | *Marinobacter*, *Halomonas*, *Pseudomonas* &*Halocella.* | Heterotrophy | *Marinobacter* isolates capable of DMSO-respiration were relatives of those detected in the lake water.  Bacteria from the water column were unable to respire nitrate. | Matsuzaki *et al*., 2006 | Syowa Oasis |
| Clear, Pendant , Scale, Ace, Burton Lakes, Taynaya Bay, Vestfold Hills | Saline, meromictic lakes, high levels of accumulated sulphides (120 to >250mmol kg-1). | 16S libraries of anoxic sediment | **Bacteria**:Firmicutes, Cyanobacteria/chloroplasts, CFB, δ–proteobacteria, , α–proteobacteria, Planctomycetes, γ– proteobacteria, green non-sulfur bacteria, Chlamydiales, Verrucomicrobia & Actinobacteria.  **Eucarya**: (2.5% of clones)  **Archaea:***Methanosarcina barkerii* or unknown Euryarchaeota group equidistant from Thermoplasma, Methanomicrobiales and Halobacteriales. | Sulphate reduction, methanogenesis,  but also aerobic phototrophs and aerobic heterotrophy | Microbial diversity was surprisingly high. Lakes with similar physico-chemical and limnological traits had more similar microbial communities. | Bowman *et al.*, 2000a | Pyrdz Bay, Vestfold & Larsemann Hills |
| Lake Fryxell, McMurdo Dry Valleys | Brackish, meromictic permanently ice-covered. | *pufM* libraries, DGGE and RT-PCR of *pufM* transcripts in the water column. | α–proteobacteria &  β–proteobacteria related to purple non-sulfur bacteria and aerobic anoxygenic phototrophs. | Anoxygenic photosynthesis. | Vertical stratification of the community down the water column.  Purple and green sulfur bacteria not detected despite the high sulfide in the bottom waters.  *pufM*transcripts only found below 9 m even though *pufM* genes are found throughout water column. | Karr *et al.*,2003 | McMurdo Sound, Victoria Land &Transantarctic Mountains |
| Lake Fryxell, McMurdo Dry Valleys | Brackish, meromictic permanently ice-covered. | 16S and *dsrA* DGGE of water column | *Desulfovibrio*, *Desulfosarcina*, *Desulfobulbus*, and *Desulfobacter* groups. | Dissimilatory sulfate reduction | Phylogenetically diverse population of vertically stratified SRB. | Karr *et al.*,2005 | McMurdo Sound, Victoria Land & Transantarctic Mountains |
| Lake Fryxell, McMurdo Dry Valleys | Brackish, meromictic permanently ice-covered. | 16S DGGE of water column | *Methanoculleus*, *Methanosarcina,* unclassified Euryarchaea, Methanosarcinales-group euryarchaea & marine benthic group C-like Crenarchaea | Hydrogenotrophic methanogenesis, potential anoxic methanotrophy | Diverse population of methanogenic Euryarchaea, unclassified Euryarchaea and divergent Crenarchaea detected in sediments and water column. | Karr *et al.*,2006 | McMurdo Sound, Victoria Land & Transantarctic Mountains |
| Nurume-Ike, Langhovde Hills, Syowa Oasis | Saline, meromictic | 16S library of anoxic sediment | **Archaea**: Marine benthic group & unclassified Euryarchaeaota.  **Bacteria**: α–proteobacteria, δ–proteobacteria, Planctomycetes, Cyanobacteria/chloroplast, γ– proteobacteria, Actinobacteria, CFB, Verrucomicrobia & Spirochaetes. | Heterotrophy | Distribution of bacterial classes similar to lake sediment in the Vestfold Hills except α–proteobacteria relatively overrepresented and Firmicutes underrepresented. | Kurasawa *et al*., 2010 | Syowa Oasis |
| Heywood Lake and Shallow Bay, Signy Island | **Heywood Lake**: ice covered for ~9 months of the year, eutrophic due to organic inputs from seals, separated into two basins by shallow inlet.  **Shallow Bay**: Coastal marine, ice-covered during winter | Archaeal 16S and universal 16S libraries of anoxic  Sediment. Northern blots probed with methanogenic archaeal probes. | **Heywood Lake blots**: *Methanomicrobiales*, *Methanogenium*,*Methanosarcinales*& *Methanosaeta*.  **Shallow Bay blots**: *Methanosarcinales*, *Methanomicrobiales*,& *Methanococcoides*.  **Heywood Lake archaea**: *Methanosaeta* &*Methanogenium*.  **Shallow Bay archaea**: *Methanogenium*, *Methanolobus* & *Methanococcoides*.  **Heywood Lake SRB**: *Desulfovibrio*, *Desulfotalea/Desulforhopalus*, *Desulfobulbus*&*Desulfobacteriaceae*.  **Shallow Bay SRB**: *Desulfotalea/Desulforhopalus*, *Desulfobacterium*, *Desulfobulbus*&*Desulfobacteriaceae*. | Acetoclastic & hydrogenotrophic methanogenesis, sulfur & metal oxidation, sulfate reduction. | Methanogeneis and sulfate reduction detected at both sites. Diversity of methanogenic archaea extremely low.  Methanogenic archaea 34% and 0.2 % of community in Heywood Lake and Shallow Bay respectively.  SRB 0.9% and 14.7% of community in Heywood Lake and Shallow Bay respectively. | Purdy *et al.*, 2003 | Antarctic Peninsula |
| Sombre Lake, Signy Island | Freshwater, ice-covered for ~9 months of the year, oligotrophic (N and P) limited. | 16S libraries, DGGE, 16S libraries and FAME analysis of isolates and FISH of water column profile | **16Sofisolates**: β–proteobacteria, Firmicutes, Actinobacteria, α–proteobacteria & γ– proteobacteria  **FAME**: Firmicutes, Actinobacteria, γ– proteobacteria, β–proteobacteria & α–proteobacteria  **Clones**: Actinobacteria, CFB, β–proteobacteria, α–proteobacteria, Spirochaetales, δ–proteobacteria, γ– proteobacteria &Verrucomicrobia  **FISH**: β–proteobacteria,CFB, α–proteobacteria & γ– proteobacteria.  **DGGE**: Actinobacteria, CFB& β–proteobacteria | Heterotrophic, mainly respiratory metabolisms | Relative abundances shown by clone libraries and FISH the same.  Few genera were found by culture-dependent and independent techniques.  16S isolate library and 16S clone library were significantly different. 16S clone library covers the largest spread of phyla but is missing Firmicutes.  Overall β–proteobacteria were dominant. | Pearce *et al*., 2003a | Antarctic Peninsula |
| Moss Lake, Signy Island | Freshwater, ice-covered for ~9 months of the year, oligotrophic (N and P) limited. | 16S DGGE and FISH of water column profile | β–proteobacteria, CFB, α–proteobacteria, γ– proteobacteria, Actinobacteria &Cyanobacteria.  < 1% of cells hybridized with Archaeal FISH probe. | Heterotrophy, mainly respiratory metabolisms, phototrophy | Very little vertical stratification of population.  16S sequences similar to temperate and cold aquatic systems. | Pearce *et al*., 2003b | Antarctic Peninsula |
| Moss, Sombre and Heywood Lakes, Signy Island | Freshwater, ice-covered for ~9 months of the year, oligotrophic to eutrophic status. | 16S DGGE of water column profile over the winter to summer transition | Not determined | Not determined | Lakes were physically and chemically stratified in winter and mixed in summer. Variation in bacterial community structure correlated with lake chemistry.  Bacterial community still unstable during holomixis. | Pearce, 2005a | Antarctic Peninsula |
| Heywood Lake, Signy Island | Freshwater, ice-covered for ~9 months of the year, eutrophic due to organic inputs from seals, separated into two basins by shallow inlet. | 16S libraries, DGGE, 16S libraries and FAME analysis of isolates and FISH of water column profile | **16Sclones**: β–proteobacteria, α–proteobacteria, & Actinobacteria.  **FAME**: Actinobacteria, Firmicutes, γ– proteobacteria & α–proteobacteria.  **FISH**: β–proteobacteria, CFB, γ– proteobacteria & α–proteobacteria.  **DGGE**: Actinobacteria, CFB, Gram-positives & β–proteobacteria. | Heterotrophy, mainly respiratory metabolisms, phototrophy | Clone library coverage 71.7%.  Similar genera to Moss and Sombre Lakes.  Actinobacteria and marine α–proteobacteria enriched compared to oligotrophic lakes while Cyanobacteria underrepresented.  Species eveness is higher than Sombre or Moss Lakes. | Pearce *et al.*, 2005b | Antarctic Peninsula |
| Lakes Boeckella, Esperanza, Flora, Encantado, Chico and Pingüi, Hope Bay, Antarctic Peninsula and Lakes L, M, W and Z, King George Island | Freshwater, oligotrophic except Pingüi and Boeckella which were eutrophic and mesotrophic respectively. | 18S DGGE of surface water (20—3 μm) | Chrysophyta, Chlorophyta, Dictyochophyceae, Bacillariophyceae & Cerozoa. | photosynthesis | Molecular surveys showed greater level of diversity exists than can be determined by light microscopy.  Lake communities varied depending on trophic status.  Lakes in both regions shared bands belonging to Chrysophyta although they were 220 km apart.  Dictyochophyceae and Cercozoa restricted to oligotrophic lakes. | Unrein *et al*.,2005 | Antarctic Peninsula |
| Lakes Boeckella, Esperanza, Flora, Encantado, Chico and Pingüi, Hope Bay, Antarctic Peninsula and Lakes W and Z, King George Island | Freshwater, oligotrophic except Pingüi and Boeckella which were eutrophic and mesotrophic respectively. | 16S DGGE of surface water (3—0.2 μm) | CFB, Actinobacteria, β–proteobacteria & Cyanobacteria. | Heterotrophy, photosynthesis | Cluster analysis showed Lake communities from the Hope Bay formed one group while Lakes Chico, Pingüi and Boeckella formed another subgroup with King George Island lakes.  63.7% of variance is explained by axis 1 and 2 of Canonical Correspondence Analysis (40.4% phosphate, dissolved inorganic nitrogen and pH; 23.3% dissolved inorganic nitrogen).  Temporal variation is not as pronounced as differences due to trophic status. | Schiaffino *et al*., 2009 | Antarctic Peninsula |
| Lakes Limnopolar, Midge, Chester, Chica, Turbio, Somero & Refugio, Livingston Island. | Fresh to saline, all oligotrophic except for Refugio which was eutrophic. | 16S DGGE of from surface water | CFB & α–proteobacteria | Heterotrophy, phototrophy | Cluster analysis showed deep lakes of the plateau grouped together while Somero and Refugio were separate groups.  Over 90% of variance was explained by chemical parameters related to trophic status and salinity. | Villaescusa *et al*., 2010 | Antarctic Peninsula |
| Lake Vostok | Largest subglacial lake, isolated from surface 420, 000 years | 16S library of accretion ice core from 3590 m | α–proteobacteria, β–proteobacteria, & Actinomycetes | Potential heterotrophy | No Archaea were amplified using Archaeal primers.  No biological incorporation of selected substrates. | Priscu *et al*., 1999 | Lake Vostok |
| Lake Vostok | Largest subglacial lake, isolated from surface 420, 000 years | 16S library of accretion ice core from 3590 and 3603 m and isolation of bacteria | α–proteobacteria, β–proteobacteria, Firmicutes, Actinobacteria & CFB | Potential heterotrophy | Bacteria appear related to isolates from similarly cold environments.  No archaea were amplified using archaeal primers. | Christner *et al.*, 2001 | Lake Vostok |
| Lake Vostok | Largest subglacial lake, isolated from surface 420, 000 years | 16S, *cbbL*/*rbcL* and *hoxV-hupL* library of accretion ice core from 3561 m | *Hydrogenophilus themoluteolus* | Potential hydrogenotrophy | Thermophilic chemolithoautotrohpic *Hydrogenophilus thermoluteolus* 16S rRNA, RubisCO and NiFe-Hydrogenase genes detected. | Lavir *et al*., 2006 | Lake Vostok |
| Lake Vostok | Largest subglacial lake, isolated from surface 420, 000 | 16S library of Vostok drilling fluid recovered from 4 depths of the bore hole. | *Sphingomonas*, potential contaminants related to human/animal pathogens or saprophytes and environmental contaminants. | Hydrocarbon degrading heterotrophs | New contaminant bacteria identified that were associated with hydrocarbon-based drilling fluid. | Alekhina *et al*., 2007 | Lake Vostok |

16S, 16S rRNA gene sequencing; 18S, 18S rRNA gene sequencing, DGGE, Denaturing gradient gel electrophoresis; CFB-group, Cytophaga/Flavobacteria/Bacteroidetes, SRB, sulfate-reducing bacteria.