

CHAPTER 7.0: REFERENCES

Aislabie, J. M., Jordan, S., & Barker, G. M. (2008). Relation between soil classification and bacterial diversity in soils of the Ross Sea region, Antarctica. *Geoderma*, *144*, 9-20.

Altschul, S. F., Gish, W., Miller, W., Myers, E. W., & Lipman, D. J. (1990). Basic local alignment search tool. *Journal of Molecular Biology*, *215*, 403-410.

Amann, R. I., Ludwig, W., & Schleifer, K. H. (1995). Phylogenetic identification and *in situ* detection of individual microbial cells without cultivation. *Microbial Review*, *59*, 143-169.

Antoon, D. L. A., Sajjad Mirza, M., Hermie, J. M. H., Herman, J. B., Paul, R. H., Angela, S., et al. (1994). Molecular ecology of microbes: A review of promises, pitfalls and true progress. *FEMS Microbiology Reviews*, *15*, 185-194.

Atlas, R. M., & Bartha, R. (1997). *Microbial Ecology: Fundamentals and Application*. (4th ed.). California: Benjamin/Cummings Science Publishing.

Audrezet, M. P., Canki Klain, N., Mercier, B., Bracar, D., Verlingue, C., Ferec, C., et al. (1994). Identification of three novel mutations (457 TAT →G, D192G, Q685X) in the Slovenian CF patients. *Human Genetics*, *93*, 659-662.

Baath, E., & Anderson, T. H. (2003). Comparison of soil fungal/bacterial ratios in a pH gradient using physiological and PLFA-based techniques. *Soil Biology & Biochemistry*, *35*, 955-963.

Bano, N., Ruyn, S., Ransom, B., & Hollibaugh, J. T. (2004) Phylogenetic composition of Arctic Ocean archaeal assemblages and comparison with Antarctic assemblages. *Applied & Environmental Microbiology*, *70*, 781-789.

Barrett, J. E., Virginia, R. A., Wall, D. H., Cary, S. C., Adams, B. J., Hacker, A. L., et al. (2006). Co-variation in soil biodiversity and biogeochemistry in northern and southern Victoria Land, Antarctica. *Antarctic Science*, *18*, 535-548.

Bauld, J. (1984). Microbial mats in marginal marine environments: Shark Bay, Western Australia and Spencer Gulf, South Australia. In Y. Cohen, R. W. Castenholz & H. O. Halvorson (Ed.), *Microbial Mats: Stromatolites* (pp.39-58). New York: Alan R. Liss.

- Belnap, J., & Lange, O. L. (2001). Structure and function of biological soil crusts: Synthesis. In J. Belnap & O. L. Lange (Ed.), *Biological Soil Crusts: Structure, Function, and Management* (pp. 471-480). Berlin: Springer.
- Bokhorst, S., Huiskes, A., Convey, P., & Aerts, R. (2007). External nutrient inputs into terrestrial ecosystems of the Falkland Islands and the Maritime Antarctic region. *Polar Biology*, *30*, 1315-1321.
- Bolter, M., Blume, H. P., Schneider, D., & Beyer, L. (1997). Soil properties and distributions of invertebrates and bacteria from King George Island (Arctowski Station), Maritime Antarctic. *Polar Biology*, *18*, 295-304.
- Boon, N., Windt, W. D., Verstraete, W., & Top, E. M. (2002). Evaluation of nested PCR-DGGE (denaturing gradient gel electrophoresis) with group-specific 16S rRNA primers for the analysis of bacterial communities from different wastewater treatment plants. *FEMS Microbiology Ecology*, *39*, 101-112.
- Borresen, A. L., Hovig, E., & Brogger, A. (1938). Detection of base mutations in genomic DNA using denaturing gradient gel electrophoresis (DGGE) followed by transfer and hybridization with gene-specific probes. *Mutation Research*, *202*, 77-83.
- Bray, J. R., & Curtis, J. T. (1957). An ordination of the upland forest communities of Southern Wisconsin. *Ecological Monographs*, *27*, 325-349.
- Brown, T. A. (2001). *Gene Cloning and DNA Analysis: An Introduction*. (4th ed.). United Kingdom: Blackwell Science.
- Canfield, D. E., Jorgensen, B. B., Fossing, H., Glud, R., Gundersen, J., Ramsing, N. B., et al. (1993). Pathways of organic carbon oxidation in three continental margin sediments. *Marine Geology*, *113*, 27-40.
- Carlsson, P., & Caron, D. A. (2001). Seasonal variation of phosphorus limitation of bacterial growth in a small lake. *Limnology & Oceanography*, *46*, 108-120.
- Casamayor, E. O., Massana, R., Benlloch, S., Ovreas, L., Diez, B., Goddard, V. J., et al. (2002). Changes in archaeal, bacterial and eukaryal assemblages along a salinity gradient by comparison of genetic fingerprinting methods in a multipond solar saltern. *Environmental Microbiology*, *4*, 338-348.

Choi, T., Chae, N., & Lee, B. (2008). Research activities of Korea Polar Research Institute: Flux observation in the Arctic and Antarctic Regions. *AsiaFlux Newsletter*, 26, 5-7.

Chong, C. W., Tan, G. Y. A., Wong, R. C. S., Martin, J. R., & Tan, I. K. P. (2009a). DGGE fingerprinting of bacteria in soils from eight ecologically different sites around Casey Station, Antarctica. *Polar Biology*, 32, 853-860.

Chong, C. W., Dunn, M. J., Convey, P., Tan, G. Y. A., Wong, R. C. S., & Tan, I. K. P. (2009b). Environmental influences on bacterial diversity of soils on Signy Island, Maritime Antarctic. *Polar Biology*, 32, 1571-1582.

Clarke, K. R., & Gorley, R. N. (2006). *PRIMER v6: User Manual/Tutorial*. United Kingdom: PRIMER-E Plymouth.

Coleman, D. C., & Whitman, W. B. (2005). Linking species richness, biodiversity and ecosystem function in soil systems. *Pedobiologia*, 49, 479-497.

Cottrell, M. T., & Kirchman, D. L. (2000). Community composition of marine bacterioplankton determined by 16S rRNA gene clone libraries and fluorescence *in situ* hybridization. *Applied & Environmental Microbiology*, 66, 5116-5122.

Crump, B. C., Hopkinson, C. S., Sogin, M. L., & Hobbie, J. E. (2004). Microbial biogeography along an estuarine salinity gradient: Combined influences of bacterial growth and residence time. *Applied & Environmental Microbiology*, 70, 1494-1505.

Daniel, R. (2004). The soil metagenome: A rich resource for the discovery of novel natural products. *Current Opinion in Biotechnology*, 15, 199-204.

Davey, M. C., & Clarke, K. J. (1991). The spatial distribution of microalgae on Antarctic fellfield soils. *Antarctica Science*, 3, 257-263.

DeLong, E. F., & Karl, D. M. (2005). Genomic perspectives in microbial oceanography. *Nature*, 439, 322-325.

Dick, L. K., & Field, K. G. (2004). Rapid estimation of numbers of fecal *Bacteroidetes* by use of a quantitative PCR assay for 16S rRNA genes. *Applied & Environmental Microbiology*, 70, 5695-5697.

Dorigo, U., Volatier, L., & Humbert, J. F. (2005). Molecular approaches to the assessment of biodiversity in aquatic microbial communities. *Water Research*, *39*, 2207-2218.

Drake, H. L., & Marcus, A. H. (2007). As the worm turns: The earthworm gut as a transient habitat for soil microbial biomes. *Annual Review of Microbiology*, *61*, 169-189.

Dubey, S. K., Tripathi, A. K., & Upadhyay, S. N. (2006). Exploration of soil bacterial communities for their potential as bioresource. *Bioresource Technology*, *97*, 2217-2224.

Ferrari, V. C., & Hollibaugh, J. T. (1999). Distribution of microbial assemblages in the Central Arctic Ocean Basin studied by PCR/DGGE: Analysis of a large data set. *Hydrobiologia*, *401*, 55-68.

Ferris, M. J., & Ward, D. M. (1997). Seasonal distribution of dominant 16S rRNA-defined populations in a hot spring microbial mat examined by denaturing gradient gel electrophoresis. *Applied & Environmental Microbiology*, *63*, 1375-1381.

Fierer, N., & Jackson, R. B. (2006). The diversity and biogeography of soil bacterial communities. *Proceedings of the National Academic Sciences*, *103*, 626-631.

Friedmann, E. I. (1982). Endolithic microorganisms in the Antarctic cold desert. *Science*, *215*, 1045-1053.

Fromin, N., Hamelin, J., Tarnawski, S., Roesti, D., Jourdain Miserez, K., Forestier, N., et al. (2002). Statistical analysis of denaturing gel electrophoresis (DGE) fingerprinting patterns. *Environmental Microbiology*, *4*, 634-643.

Frostegard, A., Courtois, S., Ramišse, V., Clerc, S., Bernillon, D., LeGall, F., et al. (1999). Quantification of bias related to the extraction of DNA directly from soils. *Applied & Environmental Microbiology*, *65*, 5409-5420.

Gafan, G. P., Lucas, V. S., Roberts, G. J., Petrie, A., Wilson, M., & Spratt, D. A. (2005). Statistical analyses of complex denaturing gradient gel electrophoresis profiles. *Journal of Clinical Microbiology*, *43*, 3971-3978.

Gans, J., Wolinsky, M., & Dunbar, J. (2005). Computational improvements reveal great bacterial diversity and high metal toxicity in soil. *Science*, *309*, 1387-1390.

Giovannoni, S. J., & Rappe, M. S. (2000). Evolution, diversity, and molecular ecology of marine prokaryotes. In D.L. Kirchman (Ed.), *Microbial Ecology of the Oceans* (pp. 47-84). New York: Wiley Liss.

Graneli, W., Bertilsson, S., Philibert, A. (2004). Phosphorus limitation of bacterial growth in high Arctic lakes and ponds. *Aquatic Science*, 66, 430–439.

Hacker, J., & Carniel, E. (2001). Ecological fitness, genomic islands and bacterial pathogenicity: A Darwinian view of the evolution of microbes. *EMBO Reports*, 2, 376-381.

Hackl, E., Zechmeister Boltenstern, S., Bodrossy, L., & Sessitsch, A. (2004). Comparison of diversities and compositions of bacterial populations inhabiting natural forest soils. *Applied & Environmental Microbiology*, 70, 5057-5065.

Hammond, P. (1995). In D. Allsopp, R. R. Colwell & D. L. Hawksworth (Ed.), *Microbial Diversity and Ecosystem Function* (pp. 29-71). United Kingdom: CAB International.

Handelsman, J. (2004). Metagenomics application of genomics to uncultured microorganisms. *Microbiology & Molecular Biology Reviews*, 68, 669-685.

Hill, T. C. J., Walsh, K. A., Harris, J. A., & Moffett, B. F. (2003). Using ecological diversity measures with bacterial communities. *FEMS Microbiology Ecology*, 43, 1–11.

Holmes, B. (1999) The genera *Flavobacterium*, *Sphingobacterium*, and *Weeksella*. In M. Dworkin (Ed.), *The prokaryotes: An Evolving Electronic Resource for The Microbiological Community* (3rd ed.). New York: Springer.

Hovig, E., Smithsorensen, B., Brogger, A., & Borresen, A. L. (1991). Constant denaturant gel electrophoresis, a modification of denaturing gradient gel electrophoresis, in mutation detection. *Mutation Research*, 262, 63-71.

Hugenholtz, P., & Pace, N. R. (1996). Identifying microbial diversity in the natural environment: A molecular phylogenetic approach. *Trends in Biotechnology*, 14, 190-197.

Hugenholtz, P., Goebel, B. M., & Pace, N. R. (1998). Impact of culture-independent studies on the emerging phylogenetic view of bacterial diversity. *Journal of Bacteriology*, 180, 4765-4774.

Ibekwe, A. M., Papiernik, S. K., Gan, J., Yates, S. R., Yang, C. H., & Crowley, D. E. (2001). Impact of fumigants on soil microbial communities. *Applied & Environmental Microbiology*, 67, 3245–3257.

IPCC. (1996). Climate Change 1995. In *The Science of Climate Change* (pp. 572). Cambridge: Cambridge University Press.

IPCC. (2001). *Climate change 2001: Impacts, Adaptation and Vulnerability*. Cambridge: Cambridge University Press.

Iwamoto, T., Tani, K., Nakamura, K., Suzuki, Y., Kitagawa, M., Eguchi, M., et al. (2000). Monitoring impact of *in situ* biostimulation treatment on groundwater bacterial community by DGGE. *FEMS Microbiology Ecology*, 32, 129-141.

Jackson, C. R., Roden, E. E., & Churchill, P. F. (2000). Denaturing gradient gel electrophoresis can fail to separate 16S rDNA fragments with multiple base differences. *Molecular Biology Today*, 1, 49-51.

Jackson, C. R., Langner, H. W., Donahoe Christiansen, J., Inskeep, W. P., & McDermott, T. R. (2001). Molecular analysis of microbial community structure in an arsenite-oxidizing acidic thermal spring. *Environmental Microbiology*, 3, 532-542.

Janssen, P. H. (2006). Identifying the dominant soil bacterial taxa in libraries of 16S rRNA and 16S rRNA genes. *Applied & Environmental Microbiology*, 72, 1719-1728.

Jones, R. T., Robeson, M. S., Lauber, C. L., Hamady, M., Knight, R., Fierer, N. (2009). A comprehensive survey of soil acidobacterial diversity using pyrosequencing and clone library analyses. *The ISME Journal*, 3, 442– 453.

Jorgensen, B. B. (1982). Mineralization of organic matter in the sea bed: The role of sulphate reduction. *Nature*, 296, 643–645.

Junge, K., Imhoff, F., Staley, T., & Deming, W. (2002). Phylogenetic diversity of numerically important Arctic sea-ice bacteria cultured at subzero temperature. *Microbial Ecology*, 43, 315-328.

Kastovska, K., Elster, J., Stibal, M., & Santruckova, H. (2005). Microbial assemblages in soil microbial succession after glacier retreat in Svalbard (High Arctic). *Microbial Ecology*, 50, 396-407.

Kastovska, K., Stibal, M., Sabacka, M., Cerna, B., Santruckova, H., & Elster, J. (2007). Microbial community structure and ecology of subglacier sediments in two polythermal Svalbard glaciers characterized by epifluorescence microscopy and PLFA. *Polar Biology*, 30, 277-287.

Kendall, M. G. (1970). *Rank Correlation Methods*. London: Griffin.

Ki, J. S., Kang, S. H., Jung, S. W., Park, B. S., & Han, M. S. (2006). A study on a freshwater alga flora occurring in temporary ponds around the Dasan Arctic Station, Ny-Alesund (Norway), and the molecular characteristic of *Clamydomonas* 18S rDNA. *Ocean & Polar Research*, 28, 107-117.

Kim, Y. G., Choi, D. H., Hyun, S., & Cho, B. C. (2007). *Oceanobacillus profundus* sp. isolated from a deep-sea sediment core. *International Journal of Systematic & Evolution Microbiology*, 57, 409-413.

Kirk, J. L., Beaudette, L. A., Hart, M., Moutoglis, P., Klironomos, J. N., Lee, H., Trevors, J. T. (2004). Methods of studying soil microbial diversity. *Journal of Microbiological Methods*, 58, 169– 188.

Kobabe, S., Wagner, D., Pfeiffer, E. M. (2004). Characterisation of microbial community composition of a Siberian tundra soil by fluorescence *in situ* hybridization. *FEMS Microbiology Ecology*, 50, 13–23.

Korea Polar Research Institute. Accessed on May 15, 2009, from http://www.kopri.re.kr/english/eng_infra/eng_arctic/eng_arctic_intro/eng_arctic_intro.cms

Kowalchuk, G. A., Stephen, J. R., DeBoer, W., Prosser, J. I., Embley, T. M., & Woldendorp, J. W. (1997). Analysis of ammonia-oxidizing bacteria of the beta subdivision of the class *Proteobacteria* in coastal sand dunes by denaturing gradient gel electrophoresis and sequencing of PCR-amplified 16S ribosomal DNA fragments. *Applied & Environmental Microbiology*, 63, 1489-1497.

Kowalchuk, G. A., Drigo, B., Yergeau, E., & Van Veen, J. A. (2006). Assessing bacterial and fungal community structure in soil using ribosomal RNA and other structural gene markers. In P. Nannipieri & K. Smalla (Ed.), *Nucleic Acids and Proteins in Soil, Soil Biology* (pp. 159-188).

Kubeckova, K., Johansen, J. R., & Warren, S. D. (2002). Development of immobilized cyanobacterial amendments for reclamation of microbiotic soil crusts. *Algological Studies*, *109*, 341-362.

Lane, D. J. (1991). In E. Stackbrandt & M. Goodfellow (Ed.), *Nucleic Acid Techniques in Bacterial Systematics* (pp. 115-175). New York: Wiley.

Larose, C., Berger, S., Ferrari, C., Navarro, E., Dommergue, A., Schneider, D., Vogel, T. M. (2010). Microbial sequences retrieved from environmental samples from seasonal Arctic snow and meltwater from Svalbard, Norway. *Extremophiles*, *14*, 205-212.

Li, H. R., Yu, Y., Luo, W., Zeng, Y. X., & Chen, B. (2009). Bacterial diversity in surface sediments from the Pacific Arctic Ocean. *Extremophiles*, *13*, 233-246.

Lindstrom, E. S., Kamst Van Agterveld, M. P., & Zwart, G. (2005). Distribution of typical freshwater bacterial groups is associated with pH, temperature, and lake water retention time. *Applied & Environmental Microbiology*, *71*, 8201-8206.

Llobet Brossa, H., Rossello Mora, R., & Amann, R. I. (1998). Microbial community composition of Wadden Sea sediments as revealed by fluorescent *in situ* hybridization. *Applied & Environmental Microbiology*, *64*, 2691-2696.

Lorenz, P., & Schleper, C. (2002). Metagenome: A challenging source of enzyme discovery. *Journal of Molecular Catalysis B: Enzymatic*, *19-20*, 13-19.

Maarit Niemi, R., Heiskanen, I., Wallenius, K., & Lindstrom, K. (2001). Extraction and purification of DNA in rhizosphere soil samples for PCR-DGGE analysis of bacterial consortia. *Journal of Microbiological Methods*, *45*, 155-165.

Madigan, M. T., Martinko, J. M., & Parker, J. (1999). *Brock Biology of Microorganisms* (9th ed.). New Jersey: Prentice-Hall.

Madigan, M. T., Martinko, J. M., & Parker, J. (2000). Microbial evolution and systematics. In *Biology of Microorganisms* (pp. 423-451). New Jersey: Prentice-Hall.

Magurran, A. E. (1988). *Ecological Diversity and its Measurement*. London: Chapman and Hall.

Maidak, B. L., Olsen, G. J., Larsen, N., Overbeek, R., McCaughey, M. J., & Woese, C. R. (1996). The ribosomal database project (RDP). *Nucleic Acids Research*, 24, 82-85.

McInerney, J. O., Mullarkey, M., Wernecke, M. E., & Powell, R. (2001). Bacteria and Archaea: Molecular techniques reveal astonishing diversity. In B. S. Rushton, P. Hackney & C. R. Tyrie (Ed.), *Biological Collection and Biodiversity* (pp. 3-10). Linnean Society Occasional Publications 3.

Melillo, J. M., Kicklighter, D. W., McGuire, A. D., Peterjohn, W. T., & Newkirk, K. M. (1995). Global change and its effects on soil organic carbon stocks. In R. G. Zepp & C. H. Sontaff (Ed.), *Role of Nonliving Organic Matter in The Earth's Carbon Cycle* (pp. 175-189). New York: Wiley.

Menyailo, O. V., Hungate, B. A., & Zech, W. (2002). Tree species mediated soil chemical changes in a Siberian artificial afforestation experiment. *Plant and Soil*, 242, 171-182.

Miller, K. M., Ming, T. J., Schulze, A. D., & Withler, R. E., (1999). Denaturing gradient gel electrophoresis (DGGE): A rapid and sensitive technique to screen nucleotide sequence variation in populations. *BioTechniques*, 27, 1016-1030.

Mindl, B., Anesio, A. M., Meirer, K., Hodson, A. J., Laybourn Parry, J., Sommaruga, R., et al. (2007). Factors influencing bacterial dynamics along a transect from supraglacier runoff to proglacier lakes of a high Arctic glacier. *FEMS Microbiology Ecology*, 59, 307-317.

Molin, J., & Molin, S. (1997). CASE: Complex adaptive systems ecology. In J. G. Jones (Ed.), *Advances in Microbial Ecology* (pp. 27-79). New York: Plenum.

Moreira, D. (1998). Efficient removal of PCR inhibitors using agarose-embedded DNA preparations. *Nucleic Acids Research*, 26, 3309-3310.

Muller, A. K., Westergaard, K., Christensen, S., & Sorensen, S. J. (2001). The effect of long-term mercury pollution on the soil microbial community. *FEMS Microbiology Ecology*, 36, 11-19.

Murray, A. E., Hollibaugh, J. T., & Orrego, C. (1996). Phylogenetic compositions of bacterioplankton from two California estuaries compared by denaturing gradient gel electrophoresis of 16S rDNA fragments. *Applied & Environmental Microbiology*, 62, 2676-2680.

Muyzer, G., Waal, E. C. D., & Uitterlinden, A. G. (1993). Profiling of complex microbial populations by denaturing gradient gel electrophoresis analysis of polymerase chain reaction-amplified genes coding for 16S rRNA. *Applied & Environmental Microbiology*, *59*, 695-700.

Muyzer, G., Teske, A., Wirsén, C. O., & Jannasch, H. W. (1995). Phylogenetic relationships of *Thiomicrospira* species and their identification in deep-sea hydrothermal vent samples by denaturing gradient gel electrophoresis of 16S rDNA fragments. *Archiv für Microbiologie*, *164*, 165-172.

Muyzer, G. (1999). DGGE/TGGE a method for identifying genes from natural ecosystems. *Current Opinion in Microbiology*, *2*, 317-322.

Nakagawa, S., Takai, K., Inagaki, F., Hirayama, H., Nunoura, T., Horikoshi, K., et al. (2005). Distribution, phylogenetic diversity and physiological characteristics of *Epsilon-proteobacteria* in a deep-sea hydrothermal field. *Environmental Microbiology*, *7*, 1619–1632.

Nakatsu, C. H. (2007). Soil microbial community analysis using denaturing gradient gel electrophoresis. *Soil Science Society of America Journal*, *71*, 562-571.

Neef, A., Amann, R., Schlesner, H., & Schleifer, K.H. (1998). Monitoring a widespread bacterial group: *In situ* detection of planctomycetes with 16S rRNA-targeted probes. *Microbiology*, *144*, 3257-3266.

Nemergut, D. R., Costello, E. K., Meyer, A. F., Pescador, M. Y., Weintraub, M. N., & Schmidt, S. K. (2005). Structure and function of alpine and arctic soil microbial communities. *Research in Microbiology*, *156*, 775–784.

Neufeld, J. D., & Mohn, W. W. (2005). Unexpectedly high bacterial diversity in Arctic tundra relative to boreal forest soils, revealed by serial analysis of ribosomal sequence tags. *Applied & Environmental Microbiology*, *71*, 5710-5718.

Newberry, C. J., Webster, G., Cragg, B. A., Parkes, R. J., Weightman, A. J., & Fry, J. C. (2004). Diversity of prokaryotes and methanogenesis in deep subsurface sediments from the Nankai Trough, Ocean Drilling Program Leg 190. *Environmental Microbiology*, *6*, 274-287.

Nubel, U., Garcia Pichel, F., Kuhl, F., & Muyzer, G. (1999). Quantifying microbial diversity: Morphotypes, 16S rRNA genes, and carotenoids of oxygenic phototrophs in microbial mats. *Applied & Environmental Microbiology*, *65*, 422-430.

O'Donnell, A. G., Seasman, M., Macrae, A., Waite, I., & Davies, J. T. (2001). Plants and fertilisers as drivers of change in microbial community structure and function in soils. *Plant Soil*, *232*, 135-145.

Oechel, W. C., & Vourlitis, G. L. (1994). The effects of climate change on land-atmosphere feedbacks in Arctic tundra regions. *TREE*, *9*, 324-329.

Ogram, A., & Feng, X. (1997). Methods of soil microbial community analysis. In J. W. Hurst, G. R. Knudsen, M. J. McInerney, L. D. Stetzenbach & M.V. Walter (Ed.), *Manual of Environment Microbiology* (pp. 422-430). Washington: ASM Press.

Ohkubo, S., Miyashita, H., Murakami, A., Takeyama, H., Tsuchiya, T., & Mimuro, M. (2006). Molecular detection of epiphytic *Acaryochloris* sp. on marine macroalgae. *Applied & Environmental Microbiology*, *72*, 7912-7915.

Olsen, G. J., Lane, D. J., Giovannoni, S. J., Pace, N. R., & Stahl, D. A. (1986). Microbial ecology and evolution: A ribosomal RNA approach. *Annual Review of Microbiology*, *40*, 337-365.

Pace, N. R. (1997). A molecular view of microbial diversity and the biosphere. *Science*, *276*, 734-740.

Parkes, R. J., Cragg, B. A., & Wellsbury, P. (2000). Recent studies on bacterial populations and processes in subsea-floor sediments: A review. *Hydrogeology Journal*, *8*, 11-28.

Paster, B. J., Boches, S. K., Galvin, J. L., Ericson, R. E., Lau, C. N., Levanos, V. A., et al. (2001). Bacterial diversity in human subgingival plaque. *Journal of Bacteriology*, *183*, 3770-3783.

Pearce, D. A. (2003). Bacterioplankton community structure in a Maritime Antarctic oligotrophic lake during period of holomixis, as determined by denaturing gradient gel electrophoresis (DGGE) and fluorescence *in situ* hybridization (FISH). *Microbial Ecology*, *46*, 92-105.

Pellegata, N. S., Losekoot, M., Fodde, R., Pugliese, V., Saccomanno, S., Renault, B., Bernini, L. F., & Ranzani, G. N. (1992). Detection of K-ras mutations by denaturing gradient gel electrophoresis (DGGE): A study on pancreatic cancer. *Anticancer Research*, *12*, 1731-1735.

Perreault, N. N., Andersen, D. T., Pollard, W. H., Greer, C. W., & Whyte, L. G. (2007). Characterization of the prokaryotic diversity in cold saline perennial springs of the Canadian High Arctic. *American Society for Microbiology*, *73*, 1532-1543.

Polz, M. F., Hunt, D. E., Preheim, S. P., & Weinreich, D. M. (2006). Patterns and mechanisms of genetic and phenotype differentiation in marine microbes. *Philosophical Transactions of the Royal Society*, *361*, 2009-2021.

Post, W. M., Emanuel, W. R., Zinke, P. J., & Stangenberger, A. G. (1982). Soil carbon pools and world life zones. *Nature*, *298*, 156-159.

Powell, S. M., Bowman, J. P., Snape, I., & Stark, J. S. (2003). Microbial community in pristine and polluted nearshore Antarctic sediments. *FEMS Microbiology Ecology*, *45*, 135-145.

Powell, S. M., Bowman, J. P., Snape, I., Thompson, B. A. W., Stark, J. S., McCammon, S. A., et al. (2004). A comparison of the short term effects of diesel fuel and lubricant oils on Antarctic benthic microbial communities. *Journal of Experimental Marine Biology & Ecology*, *322*, 53-65.

Prosser, J. I. (2002). Molecular and functional diversity in soil microorganisms. *Plant Soil*, *244*, 9-17.

Rademaker, J. L. W., Louws, F. J., Rossnach, U., Vinuesa, P., & De-Bruijn, F. (1999). Computer-assisted analysis of molecular fingerprints and database construction. In A. D. L. Akkermans, J. D. Van Elsas & F. J. DeBruijn (Ed.), *Molecular Microbial Ecology Manual*. Dordrecht: Kluwer Academic Publisher.

Rappe, M. S., & Giovannoni, S. J. (2003). The uncultured microbial majority. *Annual Review of Microbiology*, *57*, 369-394.

Ravenschlag, K., Sahm, K., Pernthaler, J., & Amann, R. (1999). High bacterial diversity in permanently cold marine sediments. *Applied & Environmental Microbiology*, *65*, 3982-3989.

Ravenschlag, K., Sahm, K., & Amann, R. (2001). Quantitative molecular analysis of the microbial community in marine Arctic sediments (Svalbard). *Applied & Environmental Microbiology*, 67, 387-395.

Remenant, B., Grundmann, G. L., & Jocteur Monrozier, L. (2009). From the micro-scale to the habitat: Assessment of soil bacterial community structure as shown by soil structure directed sampling. *Soil Biology & Biochemistry*, 41, 29–36.

Rozzak, D. B., & Colwell, R. R. (1987). Survival strategies of bacteria in the natural environment. *Microbial Review*, 51, 365-379.

Sahm, K., & Berninger, U. G. (1998). Abundance, vertical distribution and community structure of benthic prokaryotes from permanently cold marine sediments (Svalbard, Arctic Ocean). *Marine Ecology Progress Series*, 165, 71-80.

Sahm, K., Knoblauch, C., & Amann, R. (1999). Phylogenetic affiliation and quantification of psychrophilic sulfate-reducing isolates in Marine Arctic sediments. *Applied & Environmental Microbiology*, 65, 3976-3981.

Saitou, N., & Nei, M. (1987). The neighbor-joining method: A new method for reconstructing phylogenetic trees. *Molecular & Biology Evolution*, 4, 406-425.

Schafer, H., & Muyzer, G. (2001). Denaturing gradient gel electrophoresis in marine microbial ecology. *Methods in Microbiology*, 30, 425-468.

Schloss, P. D., & Handelsman, J. (2005) Introducing DOTUR, a computer program for deWning operational taxonomic units and estimating species richness. *Applied & Environmental Microbiology*, 71, 1501-1506.

Sekiguchi, H., Tomioka, N., Nakahara, T., & Uchiyama, H. (2001). A single band does not always represent single bacterial strains in denaturing gradient gel electrophoresis analysis. *Biotechnology Letters*, 23, 1205-1208.

Shannon, C. E., & Weaver, W. (1971). *The Mathematical Theory of Communication*. Urbana: University of Illinois Press.

Sharp, M., Parkes, J., Cragg, B., Fairchild, I. J., Lamb, H., & Tranter, M. (1999). Widespread bacterial populations at glacier beds and their relationship to rock weathering and carbon cycling. *Geology*, 27, 107–110.

Sheffield, V. C., Cox, D. R., Lerman, L. S., & Myers, R. M. (1989). Attachment of a 40 bp G+C rich sequence (GC-clamp) to genomic DNA fragments by PCR results in improved detection of single-base changes. *Proceedings of the National Academic Sciences*, 86, 232-236.

Simas, F. N. B., Schaefer, C. E. G. R., Melo, V. F., Albuquerque Filho, M. R., Michel, F. M., Pereira, V. V., et al. (2007). Ornithogenic cryosols from Maritime Antarctica: Phosphatization as a soil forming process. *Geoderma*, 138, 191-203.

Simpson, J. M., McCracken, V. J., White, B. A., Gaskins, H. R., & Mackie, R. I. (1999). Application of denaturing gradient gel electrophoresis for the analysis of the porcine gastrointestinal microbiota. *Journal of Microbiology Methods*, 36, 167-179.

Skidmore, M. L., Foght, J. M., & Sharp, M. J. (2000). Microbial life beneath a high Arctic glacier. *Applied & Environmental Microbiology*, 66, 3214-3220.

Somerville, C. C., Knight, I. T., Straube, W. L., & Colwell, R. R. (1989). Simple, rapid method for direct isolation of nucleic acids from aquatic environments. *Applied & Environmental Microbiology*, 55, 548-554.

Speksnijder, A., Kowalchuk, G. A., DeJong, S., Kline, E., Stephen, J. R., Laanbroek, H. J., et al. (2001). Microvariation artifacts introduced by PCR and cloning of closely related 16S rRNA gene sequences. *Applied & Environmental Microbiology*, 67, 469-472.

Stackebrandt, E., Brambilla, E., Cousin, S., Dirks, W., & Pukall, R. (2004). Culture-independent analysis of bacterial species from an anaerobic mat from Lake Fryxell, Antarctica: Prokaryotic diversity revisited. *Cell & Molecular Biology*, 50, 517-524.

Stahl, D. A., Lane, D. J., Olsen, G. J., & Pace, N. R. (1984). Analysis of hydrothermal vent-associated symbionts by ribosomal RNA sequences. *Science*, 224, 409-411.

Staley, J. T., & Konopka, A. (1985). Measurement of *in situ* activities of nonphotosynthetic microorganisms in aquatic and terrestrial habitats. *Annual Review of Microbiology*, 39, 321-346.

Steffan, R. J., Goksoyr, J., Bej, A. K., & Atlas, R. M. (1988). Recovery of DNA from soils and sediments. *Applied & Environmental Microbiology*, 54, 2908-2915.

Steffan, R. J., Breen, A., Atlas, R. M., & Sayler, G. S. (1989). Application of gene probe methods for monitoring specific microbial populations in freshwater ecosystems. *Canadian Journal of Microbiology*, *35*, 681-685.

Steffan, R. J., & Atlas, R. M. (1998). DNA amplification to enhance detection of genetically engineered bacteria in environmental samples. *Applied & Environmental Microbiology*, *54*, 2185-2191.

Stepanauskas, R., Moran, M. A., Bergamaschi, B. A., & Hollibaugh, J. T. (2003). Covariance of bacterioplankton composition and environmental variables in a temperate delta system. *Aquatic Microbial Ecology*, *31*, 85-98.

Tamura, K., Dudley, J., Nei, M., & Kumar, S. (2007). MEGA4: Molecular evolutionary genetics analysis (MEGA) software version 4.0. *Molecular Biology Evolution*, *24*, 1596-1599.

Tebbe, C. C., & Vahjen, W. (1993). Interference of humic acids and DNA extracted directly from soil in detection and transformation of recombinant DNA from bacteria and a yeast. *Applied & Environmental Microbiology*, *59*, 2657-2665.

Ter Braak, C. J. F., Van Tongeren, O. F. R., & Jongman, R. H. G. (1995). *Data Analysis in Community and Landscape Ecology*. United Kingdom: Cambridge University Press.

Torsvik, V., Goksoyr, J., & Daae, F. L. (1990). High diversity in DNA of soil bacteria. *Applied & Environmental Microbiology*, *56*, 782-787.

Trevors, J. T. (1998). Molecular evolution in bacteria: Cell division. *Microbiological Reviews*, *29*, 237-245.

Tsai, Y., & Olson, B. H. (1992). Rapid method for separation of bacterial DNA from humic substances in sediments for polymerase chain reaction. *Applied & Environmental Microbiology*, *58*, 2292-2295.

Van Der Gucht, K., Sabbe, K., De Meester, L., Vloemans, N., Zwart, G., Gillis, M., & Vyverman, W. (2001). Contrasting bacterioplankton community composition and seasonal dynamics in two neighbouring hypertrophic freshwater lakes. *Environmental Microbiology*, *3*, 680-690.

Van Hannen, E. J., Van Agterveld, M. P., Gons, H. J., Laanbroek, H. J. (1998). Revealing genetic diversity of eukaryotic microorganisms in aquatic environments by denaturing gradient gel electrophoresis. *Journal of Physiology*, 34, 206-213.

Vincent, W. F., Bowman, J. P., Rankin, L. M., & McMeekin, T. A. (2000). Phylogenetic diversity of *Picocyanobacteria* in Arctic and Antarctic ecosystem. In C. R. Bell, M. Brylinsky & P. Johnson-Green (Ed.), *Microbial Biosystems: New Frontiers: Proceedings of the 8th International Symposium on Microbial Ecology* (pp. 317-322). Canada: Atlantic Canada Society for Microbial Ecology.

Wadham, J. L., Bottrell, S., Tranter, M., & Raiswell, R. (2004). Stable isotope evidence for microbial sulphate reduction at the bed of a polythermal high Arctic glacier. *Earth & Planetary Science Letters*, 219, 341–355.

Waita, D. A., Aubreya, D. P., & Anderson, W. B. (2005). Seabird guano influences on desert islands: Soil chemistry and herbaceous species richness and productivity. *Journal of Arid Environments*, 60, 681-695.

Wallenstein, M. D., McMahon, S., & Schimel, J. (2007). Bacterial and fungal community structure in Arctic tundra tussock and shrub soils. *FEMS Microbiology Ecology*, 59, 428-435.

Wang, Q., Garrity, G. M., Tiedje, J. M., & Cole, J. R. (2007). Naïve Bayesian Classifier for rapid assignment of rRNA sequences into the new bacterial taxonomy. *Applied & Environmental Microbiology*, 73, 5261-5267.

Ward, D. M., Bateson, M. M., Weller, R., & Ruff Roberts, A. L. (1992). Ribosomal RNA analysis of microorganisms as they occur in nature. *Advance in Microbial Ecology*, 12, 219-286.

Warren, S. D. (2001). Biological soil crusts and hydrology in North American deserts. In J. Belnap & O. L. Lange (Ed.), *Biological Soil Crusts: Structure, Function, and Management* (pp. 327–338). Berlin: Springer Verlag.

Wartiainen, I., Hestnes, A. G., & Svenning, M. M. (2003). Methanotrophic diversity in high arctic wetlands on the islands of Svalbard (Norway) - denaturing gradient gel electrophoresis analysis of soil DNA and enrichment cultures. *Canadian Journal of Microbiology*, 49, 602–612.

Weber, S., Stubner, S., & Conrad, R. (2001). Bacterial populations colonizing and degrading rice straw in anoxic paddy soil. *Applied & Environmental Microbiology*, *67*, 1318-1327.

Webster, G., Newberry, G. J., Fry, J. C., & Weightman, A. J. (2003). Assessment of bacterial community structure in the deep sub-seafloor biosphere by 16S rDNA-based techniques: A cautionary tale. *Journal of Microbiological Methods*, *55*, 155-164.

Weintraub, N. M., & Schimel, J. P. (2003). Interactions between carbon and nitrogen mineralization and soil organic matter chemistry in arctic tundra soils. *Ecosystems*, *6*, 129-143.

Whitman, W. B., Coleman, D. C., & Weibe, W. J. (1998). Prokaryotes: The unseen majority. *Proceedings of the National Academic Sciences*, *95*, 6578-6589.

Widmer, F., Fliessbach, A., Laczko, E., Schulze Aurich, J., & Zeyer, J. (2001). Assessing soil biological characteristics: A comparison of bulk soil community DNA-PLFA, and BiologyTM analysis. *Soil Biology & Biochemistry*, *33*, 1029-1036.

Wintzingerode, F. V., Gobel, U. B., & Stackebrandt, E. (1997). Determination of microbial diversity in environmental samples: Pitfalls of PCR-based rRNA analysis. *FEMS Microbiology Reviews*, *21*, 213-229.

Wise, M. G., McAurthur, J. V., & Shimkets, L. J. (1999). Methanotroph diversity in landfill soil: Isolation of novel type I and type II methanotrophs whose presence was suggested by culture-independent 16S ribosomal DNA analysis. *Applied & Environmental Microbiology*, *65*, 4887-4897.

Woese, C. R., Weisburg, W. G., Paster, B. J., Hahn, C. M., Tanner, R. S., Krieg, N. R., et al. (1984). The phylogeny of purple bacteria: The beta subdivision. *Systematic & Applied Microbiology*, *5*, 327-336.

Wollast, R. (1991). The coastal organic carbon cycle: fluxes, sources, and sinks. In R. F. C. Mantoura, J. M. Martin & R. Wollast (Ed.), *Ocean margin processes in global change* (pp. 365-381). New York: John Wiley & Sons.

Wu, Y., Berends, M. J. W., Mensink, R. G. J., Kempinga, C., Sijmons, R. H., Van Der Zee, A. G. J., et al. (1999). Association of hereditary nonpolyposis colorectal cancer-related tumors displaying low microsatellite instability with MSH6 germline mutations. *The American Journal of Human Genetics*, *65*, 657-824.

Wynn Williams, D. D. (1993). Microbial processes and initial stabilisation of fellfield soil. In J. Miles & D. W. H. Walton (Ed.), *Primary Succession on Land* (pp. 17-32). Oxford: Blackwell.

Yang, C. H., Crowley, D. E., & Menge, J. A. (2001). 16S rDNA fingerprinting of rhizosphere bacterial communities associated with healthy and phytophthora infected avocado roots. *FEMS Microbiology Ecology*, *35*, 129–136.

Yannarell, A. C., & Triplett, E. W. (2005). Geographic and environmental sources of variation in lake bacterial community composition. *Applied & Environmental Microbiology*, *71*, 227-239.

Yao, H., He, Z., Wilson, M. J., & Campbell, C. D. (2000). Microbial biomass and community structure in a sequence of soils with increasing fertility and changing land use. *Microbial Ecology*, *40*, 223–237.

Yeates, C., Gillings, M. R., & Davison, A. D. (1998). Methods for microbial DNA extraction from soil for PCR amplification. *Biological Procedure Online*, *1*, 40-47.

Yergeau, E., Bokhorst, S., Huiskes, A. H. L., Boschker, H. T. S., Aerts, R., & Kowalchuk, G. A. (2007). Size and structure of bacterial, fungal and nematode communities along an Antarctic environmental gradient. *FEMS Microbiology Ecology*, *59*, 436-451.

Zhang, Z. (2004). *The report of 2003 Chinese Arctic Research Expedition (in Chinese)*. Beijing: Ocean Press.

Zhou, J. Z., Bruns, M. A., & Tiedje, J. M. (1996). DNA recovery from soils of diverse composition. *Applied & Environmental Microbiology*, *62*, 316-322.

Zhou, J. Z., Davey, M. E., Figueras, J. B., Rivkina, R., Gilichinsky, D., & Tiedje, J. M. (1997). Phylogenetic diversity of a bacterial community determined from Siberian tundra soil DNA. *Microbiology*, *143*, 3913-3919.

Zhou, J. Z., Beicheng, X., Huanf, H., Treves, D. S., Hauser, L. J., Mural, R. J., et al. (2003). Bacterial phylogenetic diversity and a novel candidate division of two humid region, sandy surface soils. *Soil Biology & Biochemistry*, *35*, 915-624.