

## REFERENCES

- Acinas, S.G., Anton, J., & Rodriguez-Valera, F. (1999). Diversity of free-living and attached bacteria in offshore Western Mediterranean waters as depicted by analysis of genes encoding 16S rRNA. *Applied and Environmental Microbiology*, 65: 514–522.
- 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.
- Azam, F., Smith, D.C., Steward, G.F., & Hagstrom, A. (1994). Bacteria-organic matter coupling and its significance for oceanic carbon cycling. *Microbial Ecology*, 28: 167–179.
- Bano, N., Nisa, M.-U., Khan, N., Saleem, M., Harrison, P.J., Ahmed, S.I., & Azam, F. (1997). Significance of bacteria in the flux of organic matter in the tidal creeks of the mangrove ecosystem of the Indus River delta, Pakistan. *Marine Ecology Progress Series*, 157: 1–12.
- Berney, M., Hammes, F., Bosshard, F., Weilenmann, H.-U., & Egli, T. (2007). Assessment and interpretation of bacterial viability by using the LIVE/DEAD BacLight Kit in combination with flow cytometry. *Applied and Environmental Microbiology*, 73: 3283–3290.
- Bong, C.W., & Lee, C.W. (2008). Nearshore and offshore comparison of marine water quality variables measured during SESMA 1. *Malaysian Journal of Science*, 27: 25–31.
- Bong, C.W., & Lee, C.W. (2011). The contribution of heterotrophic nanoflagellate grazing towards bacterial mortality in tropical waters: Comparing estuaries and coastal ecosystems. *Marine & Freshwater Research*, 62: 414-420.

Bostrom, K.H., Simu, K., Hagstrom, A., & Riemann, L. (2004). Optimization of DNA extraction for quantitative marine bacterioplankton community analysis. *Limnology and Oceanography: Methods*, 2: 365–373.

Bouvier, T.C., & del Giorgio, P.A. (2002). Compositional changes in free-living bacterial communities along salinity gradient in two temperate estuaries. *Limnology and Oceanography*, 47: 453–470.

Cardenas, E., & Tiedje, J.M. (2008). New tools for discovering and characterizing microbial diversity. *Current Opinion in Biotechnology*, 19(6): 544–549.

Cole, J.R., Chai, B., Farris, R.J., Wang, Q., Kulam, S.A., McGarrell, D.M., Garrity, G.M., & Tiedje, J.M. (2005). The Ribosomal Database Project (RDP-II): Sequences and tools for high-throughput rRNA analysis. *Nucleic Acids Research*, 33: D294–D296.

Crump, B.C., Armbrust, E.V., & Baross, J.A. (1999). Phylogenetic analysis of particle-attached and free-living bacterial communities in the Columbia River, its estuary, and the adjacent coastal ocean. *Applied and Environmental Microbiology*, 65: 3192–3204.

DeLong, E.F., & Karl, D.M. (2005). Genomic perspectives in microbial oceanography. *Nature*, 437: 336–342.

Díez, B., Pedrós-Alió, C., Marsh, T.L., & Massana, R. (2001). Application of denaturing gradient gel electrophoresis (DGGE) to study the diversity of marine picoeukaryotic assemblages and comparison of DGGE with other molecular techniques. *Applied and Environmental Microbiology*, 67(7): 2942–2951.

Fry, J.C. (2000). Bacterial Diversity and “unculturables”. *Microbiology Today*, 27: 186–188.

- Garneau, M.-E., Vincent, W.F., Terrado, R., & Lovejoy, C. (2009). Importance of particle associated bacterial heterotrophy in a coastal Arctic ecosystem. *Journal of Marine Systems*, 75: 185–197.
- Ghiglione, J.F., Conan, P., & Pujo-Pay, M. (2009). Diversity of total and active free-living vs. particle-attached bacteria in the euphotic zone of the NW Mediterranean Sea. *FEMS Microbiology Letters*, 299: 9–21.
- Ghiglione, J.F., Mevel, G., Pujo-Pay, M., Mousseau, L., Lebaron, P., & Goutx, M. (2007). Diel and seasonal variations in abundance, activity, and community structure of particle-attached and free-living bacteria in NW Mediterranean Sea. *Microbial Ecology*, 54: 217–231.
- Glockner, F.O., Fuchs, B.M., & Amann, R. (1999). Bacterioplankton compositions of lakes and oceans: A first comparison based on fluorescence in situ hybridization. *Applied and Environmental Microbiology*, 65: 3721–3726.
- Grasshoff, K., Kremling, K., & Ehrhardt, M. (1999). *Methods of seawater analysis* (3<sup>rd</sup> ed.). Wiley-VCH, Weinheim, Germany.
- Gregori, G., Citterio, S., Ghiani, A., Lambra, M., Sgorbati, S., Brown, S., & Denis, M. (2001). Resolution of viable and membrane-compromised bacteria in freshwater and marine waters based on analytical flow cytometry and nucleic acid double staining. *Applied and Environmental Microbiology*, 67: 4662–4670.
- Griffith, P., Shiah, F.-K., Gloersen, K., Ducklow, H.W., & Fletcher, M. (1994). Activity and distribution of attached bacteria in Chesapeake Bay. *Marine Ecology Progress Series*, 108: 1–10.

- Grossart, H.-P., Kiorboe, T., Tang, K., & Plough, H. (2003). Bacterial colonization of particles: Growth and interactions. *Applied and Environmental Microbiology*, *69*: 3500–3509.
- Gurtner, C., Heyrman, J., Piñar, Guadalupe, Lubitz, W., Swings, J., & Rölleke, S. (2000). Comparative analyses of the bacterial diversity on two different biodeteriorated wall painting by DGGE and 16S rDNA sequence analysis. *International Biodeterioration and Biodegradation*, *46*(3): 229–239.
- Hammer, O., Harper, D.A.T., & Ryan, P.D. (2001). PAST: Paleontological Statistics Software Package for Education and Data Analysis. *Palaeontologia Electronica*, *4*: 9.
- Hollibaugh, J.T., Wong, P.S., & Murrell, M.C. (2000). Similarity of particle-associated and free-living bacterial communities in northern San Francisco Bay, California. *Aquatic Microbial Ecology*, *21*: 103–114.
- Huse, S.M., Dethlefsen, L., Huber, J.A., Welch, D.M., Relman, D.A., & Sogin, H.L., (2008). Exploring microbial diversity and taxonomy using SSU rRNA hypervariable tag sequencing. *PLOS Genetics*, *4*(11): e1000255.
- Iriberry, J., Unanue, M., Barcina, I., & Egea, L. (1987). Seasonal variation in population density and heterotrophic activity of attached and free-living bacteria in coastal waters. *Applied and Environmental Microbiology*, *53*: 2308–2314.
- Jing, H., & Liu, H. (2012). Contrasting bacterial dynamics in subtropical estuarine and coastal water. *Estuaries and Coasts*, *35*: 976–990.
- Johnson, M., Zaretskaya, I., Raytselis, Y., Merezhuk, Y., McGinnis, S., & Madden, T.L. (2008). NCBI BLAST: A better web interface. *Nucleic Acid Research*, *36*: W5–W9.

- Karl, D.M. (1994). Accurate estimation of microbial loop process and rates. *Microbial Ecology*, 28: 147-150.
- Kepner, R.L., & Pratt, J.R. (1994). Use of fluorochromes for direct enumeration of total bacteria in environmental samples: Past and present. *Microbiological Reviews*, 58: 603-615.
- Kernegger, L., Zweimuller, I., & Peduzzi, P. (2009). Effects of suspended matter quality and virus abundance on microbial parameters: Experimental evidence from a large European river. *Aquatic Microbial Ecology*, 57: 161–173.
- Kunin, V., Engelbrektsen, A., Ochman, H., & Hugenholtz, P. (2010). Wrinkles in the rare biosphere: pyrosequencing errors can lead to artificial inflation of diversity estimates. *Environmental Microbiology*, 12: 118–123.
- Lalande, J., Villemur, R., & Deschenes, L. (2013). A new framework to accurately quantify soil bacterial community diversity from DGGE. *Microbial Ecology*, 66: 647–658.
- Lapoussiere, A., Michel, C., Starr, M., Gosselin, M., & Poulin, M. (2011). Role of free living and particle-attached bacteria in the recycling and export of organic material in the Hudson Bay system. *Journal of Marine Systems*, 88: 434 -445.
- Lee, C.W., & Bong, C.W. (2006). Carbon flux through bacteria in a eutrophic tropical environment: Port Klang waters. In E. Wolanski (Ed.), *The environment in Asia Pacific Harbours* (pp. 329–345). Netherlands: Springer.
- Lee, C.W., & Bong, C.W. (2008). Bacterial abundance and production, and their relation to primary production in tropical coastal waters of Peninsular Malaysia. *Marine and Freshwater Research*, 59: 10–21.

- Lee, C.W., Bong, C.W., & Hii, Y.S. (2009). Temporal variation of bacterial respiration and growth efficiency in tropical coastal waters. *Applied and Environmental Microbiology*, 75: 7594–7601.
- Lee, C.W., & Bong, C.W. (2012). The relative importance of viral lysis and grazing towards bacterial mortality in tropical coastal waters of Peninsular Malaysia. *Bulletin of Marine Science*, 88(1): 1-14.
- Lee, C.W., Kudo, I., Yanada, M., & Maita, Y. (2001). Bacterial abundance and production and heterotrophic nanoflagellate abundance in subarctic coastal waters (Western North Pacific Ocean). *Aquatic Microbial Ecology*, 23: 263–271.
- Maidak, B.L., Cole, J.R., Lilburn, T.G., Parker Jr, C.T., Saxman, P.L., Farris, R.J., Garrity, G.M., Olsen, G.J., Schmidt, T.M., & Tiedje, L.M. (2000). The RDP (Ribosomal Database Project) continues. *Nucleic Acids Research*, 28: 173–174.
- Manini, E., & Danovaro, R. (2006). Synoptic determination of living/dead and active/dormant bacterial fractions in marine sediments. *FEMS Microbiology Ecology*, 55: 416–423.
- Matcher, G.F., Dorrington, R.A., Henninger, T.O., & Froneman, P.W. (2011). Insights into the bacterial diversity in a freshwater-deprived permanently open Eastern Cape estuary, using 16S rRNA pyrosequencing analysis. *Water SA*, 37: 381–390.
- Mevel, G., Vernet, M., Goutx, M., & Ghiglione, J.F. (2008). Seasonal to hour variation scales in abundance and production of total and particle-attached bacteria in the open NW Mediterranean Sea (0–1000 m). *Biogeosciences*, 5: 1573–1586.
- Miller, D.N., Bryant, J.E., Madsen, E.L., & Ghiorse, W.C. (1999). Evaluation and optimization of DNA extraction and purification procedures for soil and sediment samples. *Applied and Environmental Microbiology*, 65: 4715–4724.

- Moller, A., Kaiser, K., & Guggenberger, G. (2005). Dissolved organic carbon and nitrogen in precipitation, throughfall, soil solution, and stream water of the tropical highlands northern Thailand. *Journal of Plant Nutrition and Soil Science*, 168: 649–659.
- Murrell, M.C., Hollibaugh, J.T., Silver, M.W., & Wong, P.S. (1999). Bacterioplankton dynamics in northern San Francisco Bay: Role of particle association and seasonal freshwater flow. *Limnology and Oceanography*, 44: 295–308.
- Muyzer, G. (1999). DGGE/TGGE a method for identifying genes from natural ecosystems. *Current Opinion in Microbiology*, 2(3): 317–322.
- Muyzer, G., & Smalla, K. (1998). Application of denaturing gradient gel electrophoresis (DGGE) and temperature gradient gel electrophoresis (TGGE) in microbial ecology. *Antonie Leeuwenhoek*, 73: 127–141.
- Muyzer, G., Brinkhoff, T., Nubel, U., Santegoeds, C., Schafer, H., & Wawer, C. (1998). Denaturing gradient gel electrophoresis (DGGE) in microbial ecology. In Akkermans, A.D.L., Van Elsas, J.D., & De Bruijin, F.J. (Eds.), *Molecular Microbial Ecology Manual* (pp. 1-27). Kluwer Academic Publishers, Dordrecht.
- Muyzer, G., Waal, E.C., & 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.
- Nocker, A., Burr, M., & Camper, A.K. (2007). Genotypic microbial community profiling: A critical technical review. *Microbial Ecology*, 54: 276–289.
- Ogino, A., Koshikawa, H., Nakahara, T., & Uchiyama, H. (2008). Succession of microbial communities during a biostimulation process as evaluated by DGGE and clone library analyses. *Journal of Applied Microbiology*, 91(4): 625–635.

- Oren, A. (2004). Prokaryote diversity and taxonomy: Current status and future challenges. *Philosophical Transactions Royal Society London*, 359: 623-638.
- Ortega-Retuerta, E., Joux, F., Jeffrey, W.H., & Ghiglione, J.F. (2013). Spatial variability of particle-attached and free-living bacterial diversity in surface waters from the Mackenzie River to the Beaufort Sea (Canadian Arctic). *Biogeosciences*, 10: 2747–2759.
- Parsons, T.R., Maita, Y., & Lalli, C.M. (1984). *A manual of chemical and biological methods for seawater analysis*. Oxford: Pergamon Press.
- Pomeroy, L.R., Williams, P.J., Azam, F., & Hobbie, J.E. (2007). The microbial loop. *Oceanography*, 20(2): 28-33.
- Quince, C., Curtis, T.P., & Sloan, W.T. (2008). The rational exploration of microbial diversity. *International Society for Microbial Ecology Journal*, 2: 997–1006.
- Riemann, L., & Winding, A. (2001). Community dynamics of free-living and particle associated bacterial assemblages during a freshwater phytoplankton bloom. *Microbial Ecology*, 42: 274–285.
- Sakami, T. (2008). Seasonal and spatial variation of bacterial community structure in river mouth areas of Gokasho Bay, Japan. *Microbes and Environment*, 23: 227–284.
- Schloss, P.D., & Handelsman, J. (2005). Metagenomics for studying unculturable microorganisms: Cutting the Gordian knot. *Genome Biology*, 6(8): 229.



- Sogin, M.L., Morrison, H.G., Huber, J.A., Welch, D.M., Huse, S.M., Neal, P.R., Arrieta, J.M., & Herndl, G.J. (2006). Microbial diversity in the deep sea and the unexplored “rare biosphere”. *Proceedings of the National Academy of Sciences of the United State of America*, 103(32): 12115–12120.
- Staley, J.T., & Konopka, A. (1985). Measurements of in situ activities of nonphotosynthetic microorganisms in aquatic and terrestrial habitats. *Annual Review of Microbiology*, 39: 321–346.
- Stocker, R., Seymour, J.R., Samadani, A., Hunt, D.E., & Polz, M.F. (2008). Rapid chemotactic response enables marine bacteria to exploit ephemeral microscale nutrient patches. *Proceedings of the National Academy of Sciences USA*, 105: 4209–4214.
- Suzuki, M.T., & Giovannoni, S.J. (1996). Bias caused by template annealing in the amplification of mixtures of 16S rRNA genes by PCR. *Applied and Environmental Microbiology*, 62: 625–630.
- Winter, C., Hein, T., Kavka, G., Robert L. Mach, R.L., & Farnleitner, A.H. (2007). Longitudinal changes in the bacterial community composition of the Danube River: A whole-river approach. *Applied and Environmental Microbiology*, 73: 421–431.
- Zhang, R., Liu, B., Lau, S.C.K., Ki, J.-S., & Qian, P.-Y. (2007). Particle-attached and free living bacterial communities in a contrasting marine environment: Victoria Harbor, Hong Kong. *FEMS Microbiology Ecology*, 61: 496–508.
- Zweifel, U.L., & Hagstrom, A. (1995). Total counts of marine bacteria includes a large fraction of non-nucleoid-containing bacteria (ghost). *Applied and Environmental Microbiology*, 61: 2180–2185.