

- bacteria: a challenging task for molecular taxonomists. *ASM News* **60**, 360-365.
2. Aminin, A.L.N., Madayanti F., Aditiawati P., Akhmaloka (2008a) Simple Enrichment and Independent Cultures to Expand Bacterial Community Analysis from Gedongsongo Hot Spring. *Journal of Bioscience and Bioengineering*, Vol. 106, No. 2, (August issue, 2008)
 3. Aminin, A.L.N., Madayanti F., Aditiawati P., Akhmaloka (2008b) Culture-Independent and Culture-Dependent Approaches on Microbial Community Analysis at Gedongsongo (GS-2) Hot Spring. *International Journal of Integrative Biology*, **2**, 145-152
 4. Bøkken, L.R. (1995) Separation and purification of bacteria from soil. *Appl. Environ. Microbiol.* **49**, 143-169.
 5. Bassam, B. J., G. Caetano-Anolles, and P. M. Greshoff. 1991. Fast and sensitive staining of DNA in polyacrylamide gels. *Anal. Biochem.* **196**:80-83.
 6. Nakatsu, C.H., Vigdis Torsvik, and Lise Øvrea's, 2000, Soil Community Analysis Using DGGE of 16S rDNA Polymerase Chain Reaction Products, *Soil Sci. Soc. Am. J.* **64**:1382-1388.
 7. Fuhrman, J. A., McCallum, K., and Davis, A.A., 1993. Phylogenetic diversity of subsurface marine microbial communities from the Atlantic and Pacific Oceans. *Applied & Environmental Microbiology*, **59**:1294-1302.
 8. Klijn, N., Weerkamp, A. H., and de Vos, W. M., 1991, Identification of Mesophilic Lactic Acid Bacteria by Using Polymerase Chain Reaction-Amplified Variable Regions of 16S rRNA and Specific DNA Probes, *Applied & Environmental Microbiology*, Vol. **57**, No. 11, p. 3390-3393
 9. Moyer, C.L., Dobbs, F.C., and Karl, D.M., 1995, Phylogenetic Diversity of the Bacterial Community from a Microbial Mat at an Active, Hydrothermal Vent System, Loihi Seamount, Hawaii, *Applied & Environmental Microbiology*, Vol. **61**, No. 4, p. 1555-1562.
 10. Rondon, M., August, P.R., Bettermann, A.D., Brady, S.F., Grossman, T.H. and Liles, M.R. et al. (2000) Cloning the soil metagenome: a strategy for accessing the genetic and functional diversity of uncultured microorganisms. *Appl. Environ. Microbiol.* **66**, 2541-2547.
 11. Orita, M., Iwahana, H., Kanazawa, H., Hayashi, K. and Sekiya, T. (1989) Detection of polymorphisms of human DNA by gel electrophoresis as single strand conformation polymorphisms. *Proc. Natl. Acad. Sci. USA* **86**, 2766-2770.
 12. Lee, D., Zo, Y. and Kim, S. (1996) Nonradioactive method to study genetic profiles of natural bacterial communities by PCR-single-strand-conformation polymorphism. *Appl. Environ. Microbiol.* **62**, 3112-3120.
 13. Hayashi, K. (1991) PCR-SSCP: a simple and sensitive method for the detection of mutations in genomic DNA. *PCR Methods Applic.* **1**, 34-38.
 14. Schwieger, F. and Tebbe, C. (1998) A new approach to utilize PCR-single-strand-conformation polymorphism for 16S rRNA gene-based microbial community analysis. *Appl. Environ. Microbiol.* **64**, 4870-4876.
 15. Ueda, K., Ohno, M., Yamamoto, K., Nara, H., Mori, Y., Shimada, M., Hayashi, M., Oida, H., Terashima, Y., Nagata, M., and Beppu, T., 2001, Distribution and Diversity of Symbiotic Thermophiles, *Symbiobacterium thermophilum* and Related Bacteria, in Natural Environments, *Applied & Environmental Microbiology*, Vol. **67**, No. 9, p. 3779-3784
 16. Woese, C.R., 1987, The Universal Ancestor, *Proc. Natl. Acad. Sci. USA*, Vol. **95**, pp. 6854-6859.
 17. Peters, S., Koschinsky, S., Schwieger, F. and Tebbe, C. (2000) Succession of microbial communities during hot composting as detected by PCR-single-strand-conformation polymorphism-based genetic profiles of small-subunit rRNA genes. *Appl. Environ. Microbiol.* **66**, 930-936.
 18. Zumstein, E., Moletta, R. and Godon, J.-J. (2000) Examination of two years of community dynamics in an anaerobic bioreactor using fluorescence polymerase chain reaction (PCR) single-strand conformation polymorphism analysis. *Environ. Microbiol.* **2**, 69-78.