



SELECTED PEER REVIEWED PUBLICATIONS: STUDIES UTILIZING THE PHYLOCHIP™ ASSAY

PhyloChip Technologies

1. High-density microarray of small-subunit ribosomal DNA probes. Wilson, K.H., *et al.*, Appl Environ Microbiol, 2002 68(5):2535-41.
2. Rapid quantification and taxonomic classification of environmental DNA from both prokaryotic and eukaryotic origins using a microarray. DeSantis, T.Z., *et al.*, FEMS Microbiol Lett, 2005 245(2): 271-8.
3. High-density universal 16S rRNA microarray analysis reveals broader diversity than typical clone library when sampling the environment. DeSantis, T.Z., *et al.*, Microb Ecol, 2007 53(3):371-83.
4. High quality draft sequences for prokaryotic genomes using a mix of new sequencing technologies. Aury, J.M., *et al.*, BMC Genomics, 2008 9:603.
5. Accurate determination of microbial diversity from 454 pyrosequencing data. Quince, C., *et al.*, Nat Methods, 2009 6(9):639-41.
6. Wrinkles in the rare biosphere: pyrosequencing errors can lead to artificial inflation of diversity estimates. Kunin, V., *et al.*, Environ Microbiol, 2010 12(1):118-23.
7. Fast UniFrac: facilitating high-throughput phylogenetic analyses of microbial communities including analysis of pyrosequencing and PhyloChip data. Hamady M., *et al.*, ISME J. 2010 Jan;4(1):17-27.

Environmental Applications

1. Characterization of coastal urban watershed bacterial communities leads to alternative community-based indicators. Wu C.H., *et al.*, PLoS One. 2010 Jun;5(6):e11285
2. Oligonucleotide microarray for 16S rRNA gene-based detection of all recognized lineages of sulfate-reducing prokaryotes in the environment. Loy A., *et al.*, Appl Environ Microbiol. 2002 Oct;68(10):5064-81.
3. Prokaryotic community profiles at different operational stages of a Greek solar saltern. Tsiamis G., *et al.*, Res Microbiol. 2008 Nov-Dec;159(9-10):609-27.
4. Comprehensive census of bacteria in clean rooms by using DNA microarray and cloning methods. La Duc M.T., *et al.*, Appl Environ Microbiol. 2009 Oct;75(20):6559-67.
5. Environmental microarray analyses of Antarctic soil microbial communities. Yergeau E., *et al.*, ISME J. 2009 Mar;3(3):340-51.
6. Selective progressive response of soil microbial community to wild oat roots. DeAngelis K. M., *et al.*, ISME J. 2009 Feb;3(2):168-78.
7. Application of Molecular Techniques to Elucidate the Influence of Cellulosic Waste on the Bacterial Community Structure at a Simulated Low Level Waste Site. Field E.K., *et al.*, Appl Environ Microbiol. 2010 May;76:3106-15.
8. Microbial diversity in uranium mining-impacted soils as revealed by high-density 16S microarray and clone library. Rastogi G., *et al.*, Microb Ecol. 2010 Jan;59(1):94-108.

Human Disease Research Applications

1. Comparative analysis of the bacterial microbiota of the human nostril and oropharynx. Lemon K.P., *et al.*, mBio.asm.org. 2010 Jul-Aug;1(3):e00129-10.
2. Loss of bacterial diversity during antibiotic treatment of intubated patients colonized with *Pseudomonas aeruginosa*. Flanagan J.L., *et al.*, J. J Clin Microbiol. 2007 Jun;45(6):1954-62.
3. A persistent and diverse airway microbiota present during chronic obstructive pulmonary disease exacerbations. Huang Y.J., *et al.*, OMICS. 2010 Feb;14(1):9-59.
4. *Lactobacillus casei* abundance is associated with profound shifts in the infant gut microbiome. Cox M.J., *et al.*, PLoS One. 2010 Jan;5(1):e8745.