

## 6. Seznam použité literatury

- Amorim JH, Vidal RO, Lacerda-Junior GV, Dias JC, Brendel M, Rezende RP, Cascardo JC (2012) A simple boiling-based DNA extraction for RAPD profiling of landfarm soil to provide representative metagenomic content. *Genet Mol Res.*:11(1):182-9.
- Aneja MK, Sharma S, Munch JC, Schloter M (2004) RNA fingerprinting--a new method to screen for differences in plant litter degrading microbial communities. *J Microbiol Methods.* 59(2):223-31.
- Arbeli Z, Fuentes CL (2007) Improved purification and PCR amplification of DNA from environmental samples. *FEMS Microbiol Lett* 272:269–275.
- Ashelford KE, Day MJ, Fry JC (2003) Elevated abundance of bacteriophage infecting bacteria in soil. *Appl Environ Microbiol*: 69(1):285-9.
- Bahl A, Pfenninger M (1996) A rapid method of DNA isolation using laundry detergent. *Nucleic Acids Res.* 1996 Apr 15;24(8):1587-8.
- Bakken LR (1985) Separation and Purification of Bacteria from Soil. *Appl. Environ. Microbiol.*49(6):1482-1487.
- Baldari CT, Skaldi F (1976) DNA Reassociation Kinetics in Relation to Genome Size in Four Amphibian Species. *Chromosoma (Berl.)* 59: 13-22.
- Balkwill D L, Leach FR, Wilson JT, McNabb JF, White DC (1988) Equivalence of microbial biomass measures based on membrane lipid and cell-wall components, adenosine-triphosphate, and direct counts in subsurface aquifer sediments. *Microb. Ecol.* 16: 73–84.
- Bintrim SB, Donohue TJ, Handelsman J, Roberts GP, Goodman RM (1997) Molecular phylogeny of Archaea from soil. *Proc Natl Acad Sci U S A.*:94(1):277-82.
- Blaxter M., Floyd R (2003) Molecular taxonomy for biodiversity surveys: already a reality. *Trends Ecol. Evol.* 18, 268–269.
- Bodelier PL, Meima-Franke M, Zwart G, Laanbroek HJ (2005) New DGGE strategies for the analyses of methanotrophic microbial communities using different combinations of existing 16S rRNA-based primers. *FEMS Microbiol Ecol.* 52(2):163-74.
- Boschker HTS, Nold SC, Wellsbury P, Bos D, de Graf W, Pel R, Parkes RJ, Cappenberg TE (1998) Direct linking of microbial populations to specific biogeochemical processes by <sup>13</sup>C-labelling of biomarkers. *Nature* 392: 801-805.
- Boyle-Yarwood SA, Bottomley PJ, Myrold DD (2008) Community composition of ammonia-oxidizing bacteria and archaea in soils under stands of red alder and Douglas fir in Oregon. *Environ Microbiol.* 10(11):2956-65.

- Bruneau PMC, Ostle N, Davidson DA, Grieve I.C, Fallick AE (2002) Determination of rhizosphere  $^{13}\text{C}$  pulse signals in soil thin sections by laser ablation isotope ratio mass spectrometry. *Rapid Commun. Mass Spectrom.* 16, 2190–2194.
- Buckley DH, Graber JR, Schmidt TM (1998) Phylogenetic analysis of nonthermophilic members of the kingdom crenarchaeota and their diversity and abundance in soils. *Appl Environ Microbiol.* 64(11):4333-9.
- Campbell JH, Clark JS, Zak JC (2009) PCR-DGGE comparison of bacterial community structure in fresh and archived soils sampled along a Chihuahuan Desert elevational gradient. *Microb Ecol.* 57(2):261-6.
- Cho J-C a Tiedje JM (2001) Bacterial Species Determination from DNA-DNA Hybridization by Using Genome Fragments and DNA Microarrays. *Appl. Environ. Microbiol.* (67(8): 3677–3682.
- Chuah SY, Tan WF, Yap KH, Tai HE, Chow ST (1994) Analysis of the D1S80 locus by amplified fragment length polymorphism technique in the Chinese, Malays and Indians in Singapore. *Forensic Sci Int.* 68(3):169-80.
- Cole L, Dromph KM, Boaglio V, Bardgett RD (2004a). Effect of density and species richness of soil mesofauna on nutrient mineralization and plant growth. *Biol. Fertil. Soils* 39, 337–343.
- Cole L, Staddon PL, Sleep D, Bardgett RD (2004b) Soil animals influence microbial abundance, but not plant-microbial competition for soil organic nitrogen. *Funct. Ecol.* 18, 631–640.
- Cole L, Buckland SM, Bardgett RD (2005) Relating microarthropod community structure and diversity to soil fertility manipulations in temperate grassland. *Soil Biol. Biochem.* 37, 1707–1717.
- Collins MD, Goodfellow M, Minnikin DE (1979) Isoprenoid quinones in the classification of coryneform and related bacteria. *J Gen Microbiol.* 110(1):127-36.
- Courtois S, Frostegard A, Goransson P, Depret G, Jeannin P, Simonet P (2001) Quantification of bacterial subgroups in soil: comparison of DNA extracted directly from soil or from cells previously released by density gradient centrifugation. *Environ. Microbiol.* 3:431-439.
- Crombach WHJ (1972) DNA base composition of soil arthrobacters and other coryneforms from cheese and sea fish. *Antonie van Leewenhoek J. Microbiol.* 38, 105–120.
- Dar SA, Kuenen JG, Muyzer G (2005) Nested PCR-Denaturing Gradient Gel Electrophoresis Approach To Determine the Diversity of Sulfate-Reducing Bacteria in Complex Microbial Communities. *Appl Environ Microbiol.* 71(5): 2325–2330.

- Davidson AD, Bruneau PMC, Grieve IC, Young IM (2002) Impact of fauna on an upland grassland soil as determined by micromorphological analysis. *Appl. Soil Ecol.* 20, 133–143.
- Dawson LA, Grayston SJ, Murray PJ, Cook R, Gange AC, Ross JM, Pratt SM, Duff EI, Treonis A (2003) Influence of pasture management (nitrogen and lime addition and insecticide treatment) on soil organisms and pasture root system dynamics in the field. *Plant and Soil* 255: 121–130.
- Degrange V, Bardin R (1995) Detection and counting of *Nitrobacter* populations in soil by PCR. *Appl Environ Microbiol.*:61(6):2093-8.
- Dhillon SS, Rake AV, Miksche JP (1980) Reassociation Kinetics and Cytophotometric Characterization of Peanut (*Arachis hypogaea* L.) DNA. *Plant Physiol.* 65: 1121-1127.
- Dineen SM, Aranda R, Anders DL, Robertson JM (2010a) An evaluation of commercial DNA extraction kits for the isolation of bacterial spore DNA from soil. *J. Appl. Microbiol.* 109:1886–1896.
- Dineen SM, Aranda R, Dieta ME, Anders DL, Robertson JM (2010b) Evaluation of commercial RNA extraction kits for the isolation of viral MS2 RNA from soil. *J Virol. Methods* 168: 44–50
- Echt CS, Kidwell KK, Knapp SJ, Osborn TC, McCoy TJ (1994) Linkage mapping in diploid alfalfa (*Medicago sativa*). *Genome.*37(1):61-71.
- Ezaki T a Suzuki S (1982) Achromopeptidase for Lysis of Anaerobic Gram-Positive Cocci. *J. Cloníc. Microbiol.* 16(5): 844-846.
- Fægri A, Torsvik VL, GoksÖyr J (1977) Bacterial and fungal activities in soil: Separation of bacteria and fungi by a rapid fractionated centrifugation technique. *Soil Biol.Biochem.* 9 (2):105–112.
- Fernández-Guerra A, Buchan A, Mou X, Casamayor EO, González JM (2010) T-RFPred: a nucleotide sequence size prediction tool for microbial community description based on terminal-restriction fragment length polymorphism chromatograms. *BMC Microbiol.* 10:262 .
- Floyd R, Abebe E, Papert A, Blaxter M (2002) Molecular barcode for soil nematode identification. *Mol. Ecol.* 11, 839–850.
- Franklin RB, Taylor DR, Mills AL (1999) Characterization of microbial communities using randomly amplified polymorphic DNA (RAPD). *J Microbiol Methods.*: 35(3):225-35.
- Frostegård A, Courtois S, Ramisse V, Clerc S, Bernillon D, Le Gall D, Jeannin P, Nesme X, Simonet P (1999) Quantification of Bias Related to the Extraction of DNA Directly from Soils. *Appl Environ Microbiol.* 65(12): 5409–5420.

- Garland JL and Mills AL (1991) Classification and Characterization of Heterotrophic Microbial Communities on the Basis of Patterns of Community-Level Sole-Carbon-Source Utilization. *Appl. Environ. Microbiol.* 57(8):2351-2359.
- Gehron MJ, Davis JD, Smith GA, White DC (1984) Determination of the gram-positive bacterial content of soils and sediments by analysis of teichoic acid components. *J Microbiol Methods.* 2:165-76.
- Greene EA, Voordouw G (2003) Analysis of environmental microbial communities by reverse sample genome proviny. *J. Microbiol. Meth.* 53:211 – 219.
- Griffiths BS, Ritz K, Glover LA (1996) Broad-Scale Approaches to the Determination of Soil Microbial Community Structure: Application of the Community DNA Hybridization Technique. *Microb Ecol.* 31(3):269-80.
- Griffiths R, Whiteley A, O'Donnell AG, Bailey MJ (2000) Rapid Method for Coextraction of DNA and RNA from Natural Environments for Analysis of Ribosomal DNA and rRNA-Based Microbial Community Composition. *Appl. Environ. Microbiol.* 66(12): 5488–5491.
- Griffiths RI, Whiteley AS, O'Donnell AG, Bailey MJ (2003) Physiological and community responses of established grassland bacterial populations to water stress. *Appl. Environ. Microbiol.* 69, 6961–6968.
- Griffiths RI, Manefield M, Ostle N, McNamara N, O'Donnell AG, Bailey MJ, Whiteley AS (2004) <sup>13</sup>C<sub>2</sub> pulse labelling of plant in tandem with stable isotope probing: methodological considerations for examining microbial function in the rhizosphere. *J. Microbiol. Meth.* 58, 119–129.
- Handelsman J, Rondon MR, Brady SF, Clard J, Goodman RM (1998) Molecular biological access to the chemistry of unknown soil microbes: a new frontier for natural products. *Chemistry and Biology.* 5:R245-R249.
- He J, Xu Z, Hughes J (2005) Analyses of soil fungal communities in adjacent natural forest and hoop pine plantation ecosystems of subtropical Australia using molecular approaches based on 18S rRNA genes. *FEMS Microbiol Lett.* 247(1):91-100.
- Henne A, Daniel R, Schmitz RA, Gottschalk G (1999) Construction of environmental DNA libraries in *Escherichia coli* and screening for the presence of genes conferring utilization of 4-hydroxybutyrate. *Appl Environ Microbiol.* 65(9):3901-7.
- Henneberger R, Biich D, Bergquist P, Walter M, Anitori RP (2011) The fluorescent dyes TO-PRO-3 and TOTO-3 iodide allow detection of microbial cells in soil samples without interference from background fluorescence. *BioTechniques* 51(3):190–192.
- Heuer H, Krsek M, Baker P, Smalla K, Wellington EMH (1997) Analysis of actinomycete communities by specific amplification of genes encoding 16S rRNA and

gel-electrophoretic separation in denaturing gradients. *Appl Environ Microbiol.* 63(8):3233-41.

Holben WE (1994) Isolation and purification of bacterial DNA from soil. in: R.W. Weaver (Ed.), *Methods of Soil Analysis, Part 2* Soil Science Society of America, Inc (1994), pp. 727–751.

Holben WE, Harris D (1995) DNA-based monitoring of total bacterial community structure in environmental samples. *Mol Ecol.* 4(5):627-31.

Holben WE, Jansson JK, Chrom BK, Tiedje JM (1988) DNA Probe Method for the Detection of Specific Microorganisms in the Soil Bacterial Community. *Appl. Environ. Microbiol.* 54(3): 703-711.

Holben WE, Feris KP, Kettunen A, Apajalahti JH (2004) GC fractionation enhances microbial community diversity assessment and detection of minority populations of bacteria by denaturing gradient gel electrophoresis. *Appl Environ Microbiol.* 70(4):2263-70.

Hopkins DW, Macnaughton SJ, O'Donnell AG (1991a) A dispersion and differential centrifugation technique for representatively sampling microorganisms from soil. *Soil Biol.Biochem.*23(3):217-225.

Hopkins DW, O'Donnell AG, Macnaughton SJ (1991b) Evaluation of a dispersion and elutriation technique for sampling microorganisms from soil. *Soil Biol. Biochem.* 23(3): 227-232.

Hopwood DA, Bibb MJ, Chater KF, Kieser T, Bruton CJ, Kieser HM, Lydiate DJ, Smith CP, Ward JM, Schrempf H (1985) *Genetic Manipulation of Streptomyces: A Laboratory Manual*, The John Innes Foundation, Norwich, England, pp. 124.

Howeler M, Ghiorse WC, Wolker LP (2003) A quantitative analysis of DNA extraction and purification from compost. *J Microbiol Methods.*:54(1):37-45.

Huang DL, Zeng GM, Feng CL, Hu S, Lai C, Zhao MH, Su FF, Tang L, Liu HL (2010) Changes of microbial population structure related to lignin degradation during lignocellulosic waste composting. *Bioresour Technol.* 101(11):4062-7.

Hugenholtz P, Goebel BM, Pace NR (1998) Impact of culture-independent studies on the emerging phylogenetic view of bacterial diversity. *J Bacteriol.* 180(18):4765-74.

Hurt RA, Qiu X, Wu L, Roh Y, Palubo AV, Tiedje JM, Zhou J (2001) Simultaneous Recovery of RNA and DNA from Soils and Sediments. *Appl. Environ. Microbiol.* 67(10): 4495–4503.

Ibekwe A, Kennedy AC (1998) Phospholipid fatty acid profiles and carbon utilization patterns for analysis of microbial community structure under field and greenhouse conditions *FEMS Microbiol. Exil.* 26: 151-163.

- Ibekwe AM, Kennedy AC (1999) Fatty acid methyl ester (FAME) profiles as a tool to investigate community structure of two agricultural soils. *Plant Soil* 206:151–161.
- Irvan HU (2006) Extraction of bacterial quinones from various different samples by usány supercritical CO<sub>2</sub>. *J Tekn Pros* 5(2):112-119.
- Johnson D, Leake JR, Ostle N, Ineson P, Read DJ (2002). In situ <sup>13</sup>CO<sub>2</sub> pulse-labelling of upland grassland demonstrates a rapid pathway of carbon flux from arbuscular mycorrhizal mycelia to the soil. *New Phytol.* 153, 327–334.
- Johnson D, Krsek M, Wellington EMH, Stott AW, Cole L, Bardgett RD, Read DJ, Leake JR (2005). Soil invertebrates disrupt carbon flow through fungal networks. *Science* 309, 1047.
- Kakirde KS, Parsley LC, Liles MR (2010) Size does matter: Application-driven approaches for soil metagenomics. *Soil Biol. Biochem.*42:1911-1923.
- Katayama A, Funasaka K, Fuji K (2001) Changes in the respiratory quinone profile of a soil treated with pesticides. *Biol Fertil Soils* 33:454–459
- Kauffmann IM, Schmitt J, Schmid RD (2004) DNA isolation from soil samples for cloning in different hosts. *Appl Microbiol Biotechnol* 64, 665–670.
- Khan M a Jithesh K (2012) Expression and purification of organic solvent stable lipase from soil metagenomic library. *World J Microbiol Biotechnol* 28:2417–2424.
- Kirk JL, Beaudette JA, Hart M, Moutoglis P, Klironomos JN, Lee H, Trevire JT (2004) Methods of studying soil microbial diversity. *J. Microbiol. Methods* 58:169– 188.
- Ko K-C, Rim S-O, Han Y, Shin BS, Kim G-J, Choi JH, Song JJ (2012) Identification and characterization of a novel cold-adapted esterase from a metagenomic library of mountain soil. *J Ind Microbiol Biotechnol* 39:681–689.
- Krsek M a Wellington EMH (1999) Comparison of different methods for the isolation and purification of total community DNA from soil. *J. Microbiol. Methods* 39: 1-16.
- Krsek M, Wellington EMH (2001) Comparison of different methods for the isolation and purification of total community DNA from soil *Antonie Van Leeuwenhoek.* 79(3-4):261-7.
- Krsek M, Wellington EMH (2001) Assessment of chitin decomposer diversity within an upland grassland. *Antonie Van Leeuwenhoek.* 79(3-4):261-7.
- Krsek, M., Wellington, E.M.H. (2006a) Studies of microbial community structure and function below ground in a managed upland grassland site at Sourhope Research Station. *Appl Soil Ecol.*33:127-136.
- Krsek, M., Wellington, E.M.H. (2006b) Nucleic acid extraction and metagenomic library construction from soil. In: Abstracts SGM 158th Meeting 3-6 April 2006, Univerzity of Warwick, p.14,

- Lakay FM, Botha A, Prior BA (2006) Comparative analysis of environmental DNA extraction and purification methods from different humic acid-rich soils. *J. Appl Microbiol.* 102: 265–273.
- Lee LH, Cheah YK, Mohd Sidik S, Ab Mutalib NS, Tang YL, Lin HP, Hong K.(2012) Molecular characterization of Antarctic actinobacteria and screening for antimicrobial metabolite production. *World J Microbiol Biotechnol.* 28(5):2125-37.
- Leff LG, Dana JR, McArthur JV, Shimkets LJ (1995) Comparison of methods of DNA extraction from stream sediments. *Appl. Environ. Microbiol.* 61, 1141–1143.
- Leininger S, Urich T, Schloter M, Schwark L, Qi J, Nicol GW, Prosser JI, Schuster SC, Schleper C (2006) Archaea predominate among ammonia-oxidizing prokaryotes in soils. *Nature.*: 442(7104):806-9.
- Lindahl V, Bakken LR (1995) Evaluation of methods for extraction of bacteria from soil *FEMS Microbiol. Exil.* 16(2):135–142.
- Liu W, Marsh T, Cheng H, a Forney L (1997) Characterization of microbial diversity by determining terminal restriction fragment length polymorphisms of genes encoding 16S rRNA. *Appl. Environ. Microbiol.* 63: 4516-4522.
- Liles MR, Williamson LL, Rodbumrer J, Torsvik V, Goodman RM, Handelsman J (2008) Recovery, Purification, and Cloning of High-Molecular-Weight DNA from Soil Microorganisms. *Appl. Environ. Microbiol.* 74(10):3302–3305.
- Liu J, Li J, Feng L, Cao H, Cui Z (2010) An improved method for extracting bacteria from soil for high molecular weight DNA recovery and BAC library construction. *J Microbiol.* ;48(6):728-33.
- Macdonald RM (1986a) Sampling soil microfloras: Dispersion of soil by ion exchange and extraction of specific microorganisms from suspension by elutriation . *Soil Biol. Biochem.* 18(4):399–406.
- Macdonald RM (1986b) Sampling soil microfloras: Optimization of density gradient centrifugation in percoll to separate microorganisms from soil suspensions. *Soil Biol. Biochem.* 18(4):407-410.
- Macdonald RM (1986c) Sampling soil microfloras: problems in estimating concentration and activity of suspensions of mixed populations of soil microorganisms. *Soil Biol. Biochem.* 18(4): 411-416.
- MacNaughton SJ, Stephen JR, Venosa AD, Davis GA, Chang YJ, White DC (1999) Microbial population changes during bioremediation of an experimental oil spill. *Appl Environ Microbiol.* 65(8):3566-74.
- Mahmood S, Freitag TE, Prosser JI (2006) Comparison of PCR primer-based strategies for characterization of ammonia oxidizer communities in environmental samples. *FEMS Microbiol Ecol.* 56(3):482-93.

Manefield M, Whiteley AS, Griffiths RI, Bailey MJ (2002) RNA stable isotope probing, a novel means of linking microbial community function to phylogeny. *Appl Environ Microbiol.* 68(11):5367-73.

Margesin R, Jud M, Tscherko D, Schinner F (2009) Microbial communities and activities in alpine and subalpine soils. *FEMS Microbiol Ecol* 67:208–218.

Masschalck B, Van Houdt R, Van Haver ER (2001) Inactivation of Gram-Negative Bacteria by Lysozyme, Denatured Lysozyme, and Lysozyme-Derived Peptides under High Hydrostatic Pressure. *Appl. Environ. Microbiol.* 67(1): 339–344.

Mathioni SM, Beló A, Townsend JP, Donofrio NM (2011) Getting the most out of your fungal microarray data: two cost- and time-effective methods. *Methods Mol Biol.* 722:61-77.

McGarvey KM, Queitsch K, Fields S (2012) Wide variation in antibiotic resistance proteins identified by functional metagenomic screening of a soil DNA library. *Appl Environ Microbiol.* 78(6):1708-14.

Medlin LK, Metfies K, Mehl H, Wiltshire K, Valentin K (2006) Picoeukaryotic plankton diversity at the Helgoland time series site as assessed by three molecular methods. *Microb Ecol.* 52(1):53-71.

Metcalf AC, Krsek M, Gooday GW, Prosser JI, Wellington EMH (2002a) Molecular analysis of a bacterial chitinolytic community in an upland pasture. *Appl Environ Microbiol.* 68(10): 5042-50.

Metcalf AC, Williamson N, Krsek M a Wellington EMH (2002b) Molecular Diversity within Chitinolytic Actinomycetes Determined by *In Situ* Analysis Actinomycetol. (2002) 17:18–22 VOL. 17, NO. 1

Mettel C, Kim Y, Shrestha PM, Liesack W (2010) Extraction of mRNA from Soil. *Appl. Environ. Microbiol.* 76(17):5995–6000

Miller DN, Bryant JE, Madsen EL, Ghiorse WC (1999) Evaluation and Optimization of DNA Extraction and Purification Procedures for Soil and Sediment Symplex. *Appl Environ. Microbiol.* 65(11):4715–4724.

Muyzer G, de Waal EC, Uitterlinden AG (1993) Profiling of complex microbial populations by denaturing gradient gel electrophoresis analysis of polymerase chain reaction-amplified genes coding for 16S rRNA. *Appl Environ Microbiol.* 59(3):695-700.

Muyzer G, Smalla K (1998) Application of denaturing gradient gel electrophoresis (DGGE) and temperature gradient gel electrophoresis (TGGE) in microbial ecology. *Antonie Van Leeuwenhoek.* 73(1):127-41.

Nacke H, Will C, Herzog S, Nowka B, Engelhaupt M, Daniel R (2011) Identification of novel lipolytic genes and gene families by screening of metagenomic libraries derived



from soil samples of the German Biodiversity Exploratories. *FEMS Microbiol Ecol* 78:188–201.

Nicol GW, Glover LA, Prosser JI (2003) Spatial analysis of archaeal community structure in grassland soil. *Appl Environ Microbiol.* 69(12):7420-9.

Nübel U, Engelen B, Felske A, Snaird J, Wieshuber A, Amann RI, Ludwig W & Backhaus H (1996) Sequence heterogeneities of genes encoding 16S rRNAs in *Paenibacillus polymyxa* detected by temperature gradient gel electrophoresis. *J Bacteriol.* 178:5636–5643.

Ogram A, Saylor GS, Barkay T (1987) The extraction and purification of microbial DNA from sediments. *J. Microbiol. Methods* 7, 57–66.

Ostle N, Whiteley AS, Bailey MJ, Sleep D, Ineson P, Manefield M (2003) Active microbial RNA turnover in grassland soil estimated using a <sup>13</sup>C<sub>2</sub> spike. *Soil Biol. Biochem.* 35, 877–885.

Overbeek R, Begley T, Hitler RM, Choudhuri JV, Chuang H-Y, Cohoon M, de Cre´cy-Lagard V, Diaz N, Disz T, Edwards R, Fonstein M, Frank EdD, Gerdes S, Glass EM, Goesmann A, Hanson A, Iwata-Reuyl D, Jensen R, Jamshidi N, Krause L, Kubal M, Larsen N, Linke B, McHardy AC, Meyer F, Neuweger H, Olsen G, Olson R, Osterman A, Podtnou V, Pusch GD, Rodionov DA, Rucmery Ch, Steiner J, Stevens R, Thiele I, Vassieva O, Ye Y, Zagnitko O, Vonstein V (2005) The Subsystems Approach to Genome Annotation and its Use in the Project to Annotate 1000 Genomes. *Nucleic Acids Res.* 33/17: 5691–5702.

Øvreås L a Torsvik V (1998) Microbial Diversity and Community Structure in Two Different Agricultural Soil Communities. *Microb Ecol* 36:303–315.

Øvreås L, Daae FL, Torsvik V, Rodríguez-Valera F (2003) Characterization of Microbial Diversity in Hypersaline Environments by Melting Profiles and Reassociation Kinetics in Combination with Terminal Restriction Fragment Length Polymorphism (T-RFLP) *Microbial Ecol.* 46(3):291-301.

Palojarvi A (2006): Phospholipid fatty acid (PLFA) analysis. From: *Microbiological Methods For Assessing Soil Duality*, Bloem J, Hopkána DV, Benedetti A (eds) CABI Publishing, CAB International 2006, Wallingford, Oxfordshire OX10 8DE, UK, 2006, pp. 204-211.

Pan Y, Bodrossy L, Frenzel P, Hestnes A, Krause S, Lu¨ke C, Meima-Franke M, Siljanen H, Svenning MM, Bodelier PLE (2010) Impacts of Inter- and Intralaboratory Variations on the Reproducibility of Microbial Community analyse. *Appl. Environ. Microbiol.* 76(22):7451–7458.

Parker JH, Smith GA, Fredrickson HL, Vestal JR, White DC (1982) Sensitive assay, based on hydroxy fatty acids from lipopolysaccharide lipid A, for Gram-negative bacteria in sediments. *Appl Environ Microbiol.* 44(5):1170-7.

Pathak GP, Gärtner W (2010) Detection and isolation of selected genes of interest from metagenomic libraries by a DNA microarray approach. *Methods Mol Biol.* 668:299-312.

Paul EA a Clark FE (1989) *Soil Microbiology and Biochemistry*, Academic Press, San Diego, Kalifornia, pp 50-58.

Pearce, D.A., Newsham, K.K., Thorne, M.A., Calvo-Bado, L., Krsek, M., Laskaris, P., Hodson, A., Wellington, E.M. (2012) Metagenomic analysis of a southern maritime antarctic soil. *Front Microbiol.* 2012;3:403, 1-13.

Peters S, Koschinsky S, Schwieger F, Tebbe CC (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(3):930-6.

Peterson BJ, Fry B (1987) Stable isotopes in ecosystem studies. *Ann. Rev. Ecol. Syst.* 18:293-320.

Petrić I, Bru D, Udiković-Kolić N, Hršak D, Philippot L, Martin-Laurent F (2011a) Evidence for shifts in the structure and abundance of the microbial community in a long-term PCB-contaminated soil under bioremediation. *J Hazard Mater.*:195:254-60.

Petric I, Philippot L, Abbate C, Bispo A, Chesnot T, Hallin S, Laval K, Lebeau T, Lemanceau P, Leyval C, Lindström K, Pandard P, Romero E, Sarr A, Schloter M, Simonet P, Smalla K, Wilke BM, Martin-Laurent F (2011b) Inter-laboratory evaluation of the ISO standard 11063 "Soil quality - Method to directly extract DNA from soil samples". (2011b) *J Microbiol Methods.*:84(3):454-60.

Picard Ch, Ponsonnet C, Paget E, Nesme X, Simonet P (1992) Detection and enumeration of bacteria in soil by direct DNA extraction and polymerase chain reaction. *Appl. Environ, Microbiol.* 58, 2717–2722.

Palojarvi, A., 2006. "8.3 Phospholipid Fatty Acid (PLFA) Analyses" In: Bloem, J., Hopkins, D.W., and Benedetti, A. *Microbiological Methods for Assessing Soil Quality*. CABI Publishing. Cambridge, MA. pp 204-211.

Porteous LA, Armstrong JL (1991) Recovery of bulk DNA from soil by a rapid, small-scale extraction method. *Curr Microbiol* 22:345–348.

Radajewski S, Ineson P, Parekh NR, Murrell JC (2000) Stable-isotope probing as a tool in microbial ecology. *Nature* 403(6770):646-9.

Ramaiah N, Hill RT, Chun J, Ravel J, Matte MH, Straube WL, Colwell RR (2000) Use of a *chiA* probe for detection of chitinase genes in bacteria from the Chesapeake Bay. *FEMS Microbiol Exil* 34:63-71.

Rangel-Castro JI, Prosser JI, Ostle N, Scringour CM, Killham K, Meharg AA (2005a) Flux and turnover of fixed carbon in soil microbial biomass of limed and unlimed plots of an upland grassland ecosystem. *Environ. Microbiol.* 7, 544–552.

Rangel-Castro JI, Killham K, Ostle N, Nicol GW, Anderson IC, Scrimgeour CM, Ineson P, Meharg A, Prosser JI (2005b) Stable isotope probing analysis of the influence of lininy on root exudates utilization by soil microorganisms. *Environ. Microbiol.* 7, 828–838.

Ranjard L, Poly F, Lata JC, Mougel C, Thioulouse J, Nazaret S (2001) Characterization of bacterial and fungal soil communities by automated ribosomal intergenic spacer analysis fingerprints: biological and methodological variability. *Appl Environ Microbiol.* 67(10):4479-87.

Reid G a Wong P(2005) Soil bacteria. *Soil Biology Basics*  
[http://www.dpi.nsw.gov.au/\\_data/assets/pdf\\_file/0017/41642/Soil\\_bacteria.pdf](http://www.dpi.nsw.gov.au/_data/assets/pdf_file/0017/41642/Soil_bacteria.pdf)

Riesenfeld CS, Schloss PD, Handelsman J (2004). Metagenomics, genomic analysis of microbial communities. *Ann. Rev. Genetics* 38, 525-552.

Rickwood D, Ford T, Graham J (1982) Nycodenz: a new nonionic iodinated gradient medium. *Anal Biochem.* 123(1):23-31.

Rigby PW, Dieckmann M, Rhodes C, Berg P (1977) Labeling deoxyribonucleic acid to high specific activity in vitro by nick translation with DNA polymerase I. *J Mol Biol.*:113(1):237-51.

Ritchie NJ, Schutter ME, Dick RP, Myrold DD (2000) Use of length heterogeneity PCR and fatty acid methyl ester profiles to characterize microbial communities in soil. *Appl Environ Microbiol.*66(4):1668-75.

Ritz K, Griffiths BS, Torsvik VL, Hendriksen NB (1997) Analysis of soil and bacterioplankton community DNA by melting profiles and reassociation kinetice. *FEMS Microbiol. Lett.* 149(2):151–156.

Rondon MR, August PR, Bettermann AD, Brady SF, Grossman TH, Liles MR, Loiacono KA, Lynch BA, MacNeil IA, Minor C, Tiong CL, Gilman M, Osburne MS, Clardy J, Handelsman J, Goodman RM (2000) Cloning the soil metagenome: a strategy for accessing the genetic and functional diversity of uncultured microorganisms. *Appl Environ Microbiol.* 66(6):2541-2547.

Rousk J, Bååth E (2011) Growth of saprotrophic fungi and bacteria in soil. *FEMS Microbiol Ecol.* 78(1):17-30.

Sambrook J, Fritschi EF and Maniatis T (1989) *Molecular cloning: a laboratory manual*, Cold Spring Harbor Laboratory Press, New York.

Sandaa R-A, Torsvik V, Enger O, Daae FL, Castberg T, Hahn D (1999) Analysis of bacterial communities in heavy metal-contaminated soils at dijerent levels of resolution. *FEMS Microbiol. Exil.*30: 237-251.

- Sang SL, Li G, Hu XP, Liu YH (2011) Molecular Cloning, Overexpression and Characterization of a Novel Feruloyl Esterase from a Soil Metagenomic Library. *J Mol Microbiol Biotechnol* 20:196–203.
- Schmidt TM, DeLong EF, Pace NR (1991) Analysis of a marine picoplankton community by 16S rRNA gene cloning and sequencing. *J Bacteriol.*:173(14): 4371–4378.
- Schwieger F, Tebbe CC (1998) A new approach to utilize PCR-single-strand-conformation polymorphism for 16S rRNA gene-based microbial community analysis. *Appl Environ Microbiol.* 64(12):4870-6.
- Scouw KM (2000) Soil microbiology. In: Lederberg J (ed. in chief) *Encyclopedia of Microbiology*, Vol. 4, 321-335, Academic Press, San Diego.
- Simon HM, Jahn CE, Bergerud LT, Sliwinski MK, Weimer PJ, Willis DK, Goodman RM (2005) Cultivation of mesophilic soil crenarchaeotes in enrichment cultures from plant roots. *J. Ecol.* :71(8):4751-60.
- Sims PL a Singh JS (1978) The structure and function of ten western North American grasslands II Intra-seasonal dynamics in primary producer compartments. *J. Ecol.* 66, 547–572.
- Small J, Call DR, Brockman FJ, Straub TM, Chandler DP (2001) Direct detection of 16S rRNA in soil extracts by using oligonucleotide microarrays. *Appl Environ Microbiol.* : 67(10):4708-16.
- Smalla K, Creswell N, Mendonca-Hagler LC, Wolters A, van Elsas JD (1993) Rapid DNA extraction protocol from soil for polymerase chain reaction-mediated amplification. *J. Appl. Bacteriol.* 74, 78–85.
- Sosio M, Giusino F, Cappellano C, Bossi E, Puglia AM, Donadio S (2000) Artificial chromosomes for antibiotic-producing actinomycetes. *Nat Biotechnol.* 18(3):343-5.
- Spits C, Le Caignec C, De Rycke M, Van Haute L, Van Steirteghem A, Liebaers I, Sermon K (2006) Whole-genome multiple displacement amplification from single cells. *Nature protocols* 1 (4): 1965–70.
- Srinivasiah S, Bhavsar J, Thapar K, Liles M, Schoenfeld T, Wommack KE (2008) Phages across the biosphere: contrasts of viruses in soil and aquatic environments. *Res Microbiol.* 159(5):349-57.
- Staddon PL, Ostle N, Dawson LA, Fitter AH (2003) The speed of soil carbon throughput in an upland grassland is increased by liming. *J Exp Bot.* 54(386):1461-9.
- Steffan RJ, Goksøyr J, Bej AK, Atlas RM (1988) Recovery of DNA from soils and sediments. *Appl. Environ. Microbiol.* 54(12):29085-2915.
- Stepanauskas R.(2012) Single cell genomics: an individual look at microbes. *Curr. Opin. Microbiol.* 15: 613-620.

- Straub TM, Proper IL, Gerba CP (1994) Detection of naturally occurring enteroviruses and hepatitis A virus in undigested and anaerobically digested sludge using the polymerase chain reaction. *Can. J. Microbiol.* 40(10): 884-888.
- Sudini H, Liles MR, Arias CR, Bowen KL, Huettel RN (2011) Exploring soil bacterial communities in different peanut-cropping sequences using multiple molecular approaches: 101(7):819-27.
- Taubert M, Vogt C, Wubet T, Kleinsteuber S, Tarkka MT, Harms H, Buscot F, Richnow HH, von Bergen M, Seifert J (2012) Protein-SIP enables time-resolved analysis of the carbon flux in a sulfate-reducing, benzene-degrading microbial consortium. *ISME J.* 6: 2291-2301.
- Teske A, Wawer C, Muyzer G, Ramsing NB (1996) Distribution of sulfate-reducing bacteria in a stratified fjord (Mariager Fjord, Denmark) as evaluated by most-probable-number counts and denaturing gradient gel electrophoresis of PCR-amplified ribosomal DNA fragments. *Appl Environ Microbiol.* 62(4):1405-15.
- Theron J, Cloete TE (2000) Molecular techniques for determining microbial diversity and community structure in natural environments. *Crit Rev Microbiol.* 26(1):37-57.
- Thomas-Cavallin M, Ait-Ahmed O (1988) The random primer labeling technique applied to in situ hybridization on tissue sections. *J Histochem Cytochem.* 36(10):1335-40.
- Tonn SJ a Gander JE (1979) Biosynthesis of Polysaccharides by Prokaryotes. *Ann. Rev. Microbiol.* 33: 169-199.
- Torsvik VL (1980) Isolation of bacterial DNA from soil. *Soil Biology & Biochemistry* 12: 15-21.
- Torsvik V, Goksoyr J, Daae FL (1990a) High Diversity in DNA of Soil Bakteria. *Appl. Environ. Microbiol.* 56(3): 782-787
- Torsvik V, Salte K, Sorheim R, Goksoyr J (1990b) Comparison of Phenotypic Diversity and DNA Heterogeneity in a Population of Soil bacteria. *Appl. Environ. Microbiol.* 56(3):776-781.
- Torsvik V a Øvreås L (2002) Microbial diversity and function in soil: from genes to ecosystems. *Curr. Opin. Microbiol.* 5:240-245.
- Töwe S, Wallisch S, Bannert A, Fischer D, Hai B, Haesler F, Kleineidam K, Schloter M (2011) Improved protocol for the simultaneous extraction and column-based separation of DNA and RNA from different soils. *J Microbiol Methods.* 84(3):406-12.
- Umene K, Yoshida M (1994) Preparation of herpes simplex virus type 1 genomic markers to differentiate strains of predominant genotypes. *Arch Virol.* 138(1-2):55-69.

- van Elsas JD, Mañtynen V, Wolters AC (1997) Soil DNA extraction and assessment of the fate of *Mycobacterium chlorophenicum* strain PCP-1 in different soils by 16s ribosomal RNA gene sequence based most-probable-number PCR and immunofluorescence. *Biol. Fertil. Soils.* 24, 188–195.
- Volossiuk T, Robb EJ, Nazar RN (1995) Direct DNA Extraction for PCR-Mediated Assays of Soil Organisms. *Appl. Environ. Microbiol.* 61(11): 3972–3976.
- Walker-Jonah A, Dolan SA, Gwadz RW, Panton LJ, Wellems TE (1992) An RFLP map of the *Plasmodium falciparum* genome, recombination rates and favored linkage groups in a genetic cross. *Mol Biochem Parasitol.* 51(2):313-20.
- Wang D a Bodovitz S (2010) Single cell analysis: the new frontier in 'omics'. *Trends. Biotechnol.* 28: 281-290.
- Wawer C, Ruggenberg H, Meyer G, Muyzer G (1995) A simple and rapid electrophoresis method to detect sequence variation in PCR-amplified DNA fragments. *Nucleic Acids Res.* 23: 4928-4929.
- Weinbauer MG, Rassoulzadegan F (2004) Are viruses driving microbial diversification and diversity? *Environ. Microbiol.* 6 (1): 1–11.
- Wellington, E.M.H., Berry, A., and Krsek, M. (2003) Resolving functional diversity in relation to microbial community structure in soil: exploiting genomics and stable isotope probing. *Curr. Opin. Microbiol.* 6: 295-301.
- Whiteley AS, Griffiths RI, Bailey MJ (2003) Analysis of the microbial functional diversity within water-stressed soil communities by flow cytometric analysis and CTC + cell sorting. *J.Microbiol. Meth.* 54, 257–267.
- Whitman WB, Coleman DC a Webe WJ (1998) Prokaryotes: the unseen majority. *Proc. Natl. Acad. Sci. U.S.A.* 94:6578-6583.
- Williamson KE, Wommack KE, Radosevich M (2003) Sampling Natural Viral Communities from Soil for Culture-Independent Analyse. *Appl. Environ. Microbiol.:* 69(11): 6628–6633.
- Williamson KE, Radosevich M, Smith DW, Wommack KE (2007) Incidence of lysogeny within temperate and extreme soil environments. *Environ Microbiol.:* 9(10):2563-74.
- Williamson KE, Schnitker JB, Radosevich M, Smith DW, Wommack KE (2008) Cultivation-Based Assessment of Lysogeny Among Soil Bacteria *Microb Exil:* 56:437–447.
- Williamson N, Brian P, Wellington EM (2000) Molecular detection of bacterial and streptomycete chitinases in the environment. *Antonie Van Leeuwenhoek* 78(3-4):315-21.

- Wipat A, Wellington EMH, Saunders VA (1994) Monoclonal antibodies for *Streptomyces lividans* and their use for immunomagnetic capture of spores from soil. *Microbiol.*140: 2067-2076.
- Wu QL, Chatzinotas A, Wang J, Boenigk J (2009) Genetic diversity of eukaryotic plankton assemblages in Eastern Tibetan Lakes differing by their salinity and altitude. *Microb Ecol.* 58(3):569-81.
- Xia W, Zhang C, Zeng X, Feng Y, Weng J, Lin X, Zhu J, Xiong Z, Xu J, Cai Z, Jia Z (2011) Autotrophic growth of nitrifying community in an agricultural soil. *ISME J.* 5(7):1226-36.
- Yarwood SA, Bottomley PJ, Myrold DD (2010) Soil microbial communities associated with Douglas-fir and red alder stands at high- and low-productivity forest sites in Oregon, USA. *Microb Ecol.* 60(3):606-17.
- Young CC, Burghoff RL, Keim LG, Minak-Bernero V, Lute JR, Hinton SM (1993) Polyvinylpyrrolidone-Agarose Gel Electrophoresis Purification of Polymerase Chain Reaction-Amplifiable DNA from Soils. *Appl Environ. Microbiol.* 59(6): 1972-1974.
- Zhang D-C, Mörtelmaier C, Margesin R (2012) Characterization of the bacterial archaeal diversity in hydrocarbon-contaminated soil. *Sci. Total Environ.* 421–422:184–196.
- Zhang L a Xu Z (2008) Assessing bacterial diversity in soil. *J Soils Sediments* 8:379–388.
- Zhou J, Bruns MA, Tiedje JM (1996) DNA Recovery from Soils of Diverse Composition. *Appl. Environ. Microbiol.* 62(2): 316–322.