Molecular Microbial Ecology Manual
Molecular Microbial Ecology Manual
Second Edition - Volume 1

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Contents

Foreword

SECTION 1: Isolation of Nucleic Acids

1.01 Simplified protocols for the preparation of genomic DNA from bacterial cultures
   Edward Moore, Angelika Arnscheidt, Annette Krüger, Carsten Strömpl and Margit Mau

1.02 Extraction of ribosomal RNA from microbial cultures
   Erko Stackebrandt and Naomi Ward

1.03 Extraction of microbial DNA from aquatic sources: Marine environments
   John H. Paul

1.04 Extraction of microbial DNA from aquatic sources: Freshwater
   Roger W. Pickup, Glenn Rhodes and Jon R. Saunders

1.05 Methods for extracting DNA from microbial mats and cultivated micro-organisms: high molecular weight DNA from French press lysis
   Mary M. Bateson and David M. Ward

1.06 Extraction of microbial DNA from aquatic sediments
   Elizabeth Wheeler Alm and David A. Stahl

1.07 Extraction of microbial RNA from aquatic sources: Marine environments
   Scott L. Pichard and John H. Paul
Extraction of total RNA and DNA from bacterioplankton
Stefan Eichler, Markus G. Weinbauer, Katja Dominik and Manfred G. Höfle

Methods for extracting RNA or ribosomes from microbial mats and cultivated microorganisms
David M. Ward, Alyson L. Ruff-Roberts and Roland Weller

Cell extraction method
Vigdis Torsvik

DNA and RNA extraction from soil
Robert I. Griffiths, Mike Manefield, Andrew S. Whiteley and Mark J. Bailey

Rapid simultaneous extraction of DNA and RNA from bulk and rhizosphere soil
Newton C.M. Gomes, Rodrigo Costa and Kornelia Smalla

Direct Extraction of Fungal DNA from Soil
Ross N. Nazar, E. Jane Robb and Tatiana Volossiouk

Purification of microbial genes from soil and rhizosphere by magnetic capture hybridization and subsequent amplification of target genes by PCR
Carsten S. Jacobsen

Direct ribosome isolation from soil
Andreas Felske, Horst Backhaus and Antoon D.L. Akkermans

DNA Extraction from Actinorhizal Nodules
Hugo Ramírez-Saad, Wilma M. Akkermans and Antoon D.L. Akkermans

SECTION 2: Detection of microbial nucleic acid sequences

Quantification of nucleic acids
Vigdis Torsvik

Quantification of nucleic acids from aquatic environments by using green-fluorescent dyes and microtiter plates
Markus G. Weinbauer and Manfred G. Höfle
2.03 Degradation and turnover of extracellular DNA in marine sediments
   Antonio Dell’anno and Cinzia Corinaldesi

2.04 Incorporation of thymidine into DNA of soil bacteria
   Erland Bååth

2.05 Preparation of radioactive probes
   Martin Cunningham

2.06 Detection of Nucleic Acids by Chemiluminescence
   Bronwen Harvey, Martin Cunningham and Martin Harris

2.07 Parameters of nucleic acid hybridization experiments
   Cindy H. Nakatsu and Larry J. Forney

2.08 Detection and quantification of microbial DNA sequences in soil by Southern- and dot/slot blot hybridization
   Carsten S. Jacobsen

2.09 Detection of microbial DNA sequences by colony hybridization
   Penny R. Hirsch

2.10 Polymerase chain reaction analysis of soil microbial DNA
   Jan Dirk van Elsas and Hidde Boersma

2.11 Detection of microbial nucleic acids by polymerase chain reaction in aquatic samples
   Asim K. Bej

2.12 Isolation and detection of bacterial DNA sequences in dairy products
   Lieve Herman and Nicolette Klijn

2.13 Quantitative PCR of environmental samples
   Janet K. Jansson and Thomas Leser

2.14 Molecular beacons for homogeneous real-time monitoring of amplification products
   Marianna Szemes, Cor D. Schoen and Jan M. Van der Wolf

2.15 Detection and enumeration of soil bacteria using the MPN-PCR technique
   Christine Picard, Xavier Nesme and Pascal Simonet
Detection of mRNA and rRNA via reverse transcription and PCR in soil
Sonja Selenska-Pobell

SECTION 3: Identification and classification of microbes using DNA and RNA sequences

3.01 Amplification of ribosomal RNA sequences
Richard Devereux and Sherry S. Wilkinson

3.02 Cloning 16S rRNA genes and utilization to type bacterial communities
Andreas Felske and Roland Weller

3.03 SARST, Serial Analysis of Ribosomal Sequence Tags
Josh D. Neufeld, Zhongtang Yu, Wan Lam, William W. Mohn

3.04 Oligonucleotide Fingerprinting of Ribosomal RNA Genes (OFRG)

3.05 Genotyping of bacterial isolates from the environment using Low-Molecular-Weight RNA fingerprints
Manfred G. Höfle

3.06 Characterization of the diversity of ecologically important microbes by rep-PCR genomic fingerprinting
Jan L.W. Rademaker, Frank J. Louws, James Versalovic and Frans J. de Bruijn

3.07 Genomic Fingerprinting of Micro-organisms by AFLP™ and ERIC-anchor PCR
Henk J.M. Aarts, Angela H.A.M van Hoek and Jaap Keijer

3.08 The use of pulsed-field gel electrophoresis to study bacteria recovered from the environment
Julian J. Smith and Gerry S. Saddler

3.09 Easy individual strain and community typing by rDNA ITS1 analysis
X. Nesme, and P. Normand
3.10  *In situ* PCR methodologies for visualization of microscale genetic and taxonomic diversities of prokaryotic communities
   Wendy Dustman, Feng Chen, Mary Ann Moran and Robert E. Hodson

3.11 Sensitive multi-color fluorescence in situ hybridization for the identification of environmental microorganisms
   Annelie Pemthaler, Jakob Pemthaler and Rudolf Amann

3.12 Use of Cloned Artificial Targets for FISH (catFISH) for the optimization of oligonucleotide probe hybridization conditions with 16S rRNA clones for *in situ* quantification of uncultivated prokaryotic cells
   Cleber C. Ouerney, Gary C. Armitage and David A. Relman

3.13 Denaturing gradient gel electrophoresis (DGGE) in microbial ecology
   Gerard Muyzer, Thorsten Brinkhoff, Ulrich Nübel, Cecilia Santegoeds, Hendrik Schäfer and Cathrin Wawer

3.14 Fungal Community Analysis using PCR- Denaturing Gradient Gel Electrophoresis (DGGE)
   George Kowalchuk and Eric Srnit

3.15 The Analysis of Microbial Communities with Terminal Restriction Fragment Length Polymorphism (T-RFLP)
   Sang-Hoon Kim and Terence L. Marsh

3.16 Microbial community analysis by PCR-single-strand conformation polymorphism (PCR-SSCP)
   Anja B. Dohrmann and Christoph C. Tebbe

3.17 Isolation of high molecular weight genomic DNA from soil bacteria for genomic library construction
   Mark R. Liles, Lynn L. Williamson, Jo Handelsman and Robert M. Goodman

*SECTION 4: Detection, identification and classification of microbes using other methods*

4.01 Use of Biolog® for the Community Level Physiological Profiling (CLPP) of environmental samples
   Heribert Insam and Marta Gobena
4.02 Fluorescent staining of microbes for total direct counts
   Jaap Bloem and An Vos

4.03 Detection of microbes by Scanning Confocal Laser Microscopy (SCLM)
   Michael Schmid, Michael Rothballer, Berhard Åm;us,
   Peter Hutzler, John R. Lawrence, Michael Schloter and
   Anton Hartmann

4.04 Production of anti-microbial antibodies and their utilization in studies
   of microbial autecology by immunofluorescence microscopy and
   in situ CMEIAS image analysis
   Frank B. Dazzo

4.05 The slide immunoenzymatic assay (SIA): A simple and low cost
   system suitable for detecting water-borne microbes without the need
   for sophisticated technological infrastructure
   Everly Conway de Macario, Claire Jarmey-Swan, Alan R.
   Howgrave-Graham and Alberto J. L. Macario

4.06 In situ hybridization to detect microbial messenger RNA in plant
   tissues
   Katharina Pawlowski, Kirill Demchenko and Ton Bisseling

4.07 Fatty acid analysis in the identification, taxonomy and ecology of
   (plant pathogenic) bacteria
   Jaap D. Janse

4.08 Determination of microbial community structure using phospholipid
   fatty acid profiles
   Robert H. Findlay

4.09 Respiratory lipoquinones as biomarkers
   B.J. Tindall

4.10 Environmental Proteomics: Methods and Applications for Aquatic
   Ecosystems
   Oladele A. Ogunseitan and James F. Leblanc

SECTION 5: Detection of gene transfer in the environment

5.01 Natural transformation in aquatic environments
   John H. Paul and Haydn G. Williams
Natural transformation in soil: microcosm studies
Kaare Magne Nielsen, Jessica Louise Ray, Jan Dirk Van Elsas

Plasmid transfer in aquatic environments
Søren J. Sørensen, Gunnar Oregaard, Julia R. de Lipthay and Niels Kroer

Conjugation in the epilithon
Katja E. Hill, Julian R. Marchesi and John C. fry

Detection of bacterial conjugation in soil
Jan Dirk van Elsas, Hidde Boersma and Eric Smit

Transduction in the aquatic environment
Martin Day and Julian Marchesi

Phage ecology and genetic exchange in soil
Paul R. Herron

SECTION 6: Tracking of specific microbes in the environment

Lac as a marker gene to track microbes in the environment
Frans de Leij and Nigel Bainton

XylE as a marker gene for microorganisms
Roger W. Pickup, Jon R. Saunders, J. Alun Morgan, Craig Winstanley and Venetia A. Saunders

GUS as a marker to track microbes
Kate J. Wilson

The celB marker gene
Angela Sessitsch, Kate J. Wilson, Antoon D. L. Akkermans and Willem M. de Vos

Visualisation of microbes and their interactions in the rhizosphere using auto fluorescent proteins as markers
Guido V. Bloemberg, Anastasia Lagopodi, Frans J. de Bruijn and Janet K. Jansson

Identification of bacteria by their intrinsic sequences:
Probe design and testing of their specificity
Éva Tas and Kristina Lindström
6.07 Subtraction hybridization for the production of high specificity DNA probes
   A.J. Bjourson, W. Streit and J.E. Cooper

6.08 Considerations for the use of functional markers and field release of genetically engineered microorganisms to soils and plants
   Mark J. Bailey, Tracey M. Timms-Wilson and Andrew K. Lilley

SECTION 7: Statistical, computer-assisted and other analyses

7.01 Application of ecological diversity statistics in microbial ecology
   Jennifer B. Hughes and Brendan J.M. Bohannan

7.02 Sampling efficiency and interpretation of diversity in 16S rRNA gene libraries
   John Dunbar

7.03 LIBSHUFF Comparisons of 16S rRNA Gene Clone Libraries
   David R. Singleton, Steven L. Rathbun, Glen E. Dyszynski and William B. Whitman

7.04 Cluster analysis and statistical comparison of molecular community profile data
   Henk W. van Verseveld and Wilfred F. M. Röling

7.05 Computer-assisted analysis of molecular fingerprint profiles and database construction
   Jan L.W. Rademaker and Frans J. de Bruijn

7.06 Multivariate statistical methods and artificial neural networks for analysis of microbial community molecular fingerprints
   Sherry L. Dollhopf, Héctor L. Ayala-Del-Río, Syed A. Hashsham and James M. Tiedje

7.07 Quantitative fluorescence in situ hybridisation (FISH): statistical methods for valid cell counting
   Russell James Davenport and Thomas Peter Curtis

7.08 Oligonucleotide probe design for mixed microbial community microarrays and other applications and important considerations for data analysis
   Syed Hashsham, Stephen Callister and Marjolijn Tijdens
Design of microarrays for genome-wide expression profiling
Anke Becker

SECTION 8: Molecular tools to assess microbial activities

8.01 Assessment of the membrane potential, intracellular pH and respiration of bacteria employing fluorescence techniques
Pieter Breeuwer and Tjakko Abe

8.02 Use of microelectrodes to measure in situ microbial activities in biofilms, sediments, and microbial mats
Armin Gieseke, Dirk de Beer

8.03 Application of whole-cell biosensors in soil
Søren Johannes Sørensen, Lars Hestbjerg Hansen, Mette Burmølle, Gunnar Oregaard and Pernille Hermansen

8.04 Detection of bacterial homoserine lactone quorum sensing signals
Scott A. Rice, Staffan Kjelleberg, Michael Givskov, Wietse de Boer and Leonid S. Chernin

8.05 BrdU Substrate Utilization Assay
Bei Yin, Alexandra J Scupham, Elizabeth Bent and James Borneman

8.06 Stable isotope probing of nucleic acids to identify active microbial populations
Stefan Radajewski, Ian R. Mcdonald and J. Colin Murrell

8.07 Linking microbial community structure and functioning: stable isotope (\textsuperscript{13}C) labeling in combination with PLFA analysis
H.T.S. Boschker

8.08 Correlating single-cell count with function in mixed natural microbial communities through STARFISH
Cleber C. Ouvemey and Jed A. Fuhrman

8.09 Differential display of mRNA
E.J. Kok, E.N.W. Van der Wal-Winnubst, A.M.A. Van Hoef and J. Keijer

8.10 Macro-arrays protocols for gene expression studies in bacteria
Frederic Ampe and Jacques Batut
8.11 Oligonucleotide-based functional gene arrays for analysis of microbial communities in the environment
   Sonia M. Tiquia, Song C. Chong, Matthew W. Fields and Jizhong Zhou

8.12 Proteomic Analysis of Bacterial Systems
   Barry G. Rolfe, Michael Djordjevic, Hancai Chen, Charles Hocart, Georg Weiller and Ulrike Mathesius
Contents

Foreword

SECTION 1: Isolation of Nucleic Acids

1.01 Simplified protocols for the preparation of genomic DNA from bacterial cultures
   Edward Moore, Angelika Arnscheidt, Annette Krüger, Carsten Strömpl and Margit Mau 3

1.02 Extraction of ribosomal RNA from microbial cultures
   Erko Stackebrandt and Naomi Ward 19

1.03 Extraction of microbial DNA from aquatic sources: Marine environments
   John H. Paul 29

1.04 Extraction of microbial DNA from aquatic sources: Freshwater
   Roger W. Pickup, Glenn Rhodes and Jon R. Saunders 41

1.05 Methods for extracting DNA from microbial mats and cultivated micro-organisms: high molecular weight DNA from French press lysis
   Mary M. Bateson and David M. Ward 53

1.06 Extraction of microbial DNA from aquatic sediments
   Elizabeth Wheeler Alm and David A. Stahl 61

1.07 Extraction of microbial RNA from aquatic sources: Marine environments
   Scott L. Pichard and John H. Paul 89
1.08 Extraction of total RNA and DNA from bacterioplankton
   Stefan Eichler, Markus G. Weinbauer, Katja Dominik and
   Manfred G. Höfle

1.09 Methods for extracting RNA or ribosomes from microbial
   mats and cultivated microorganisms
   David M. Ward, Alyson L. Ruff-Roberts and Roland
   Weller

1.10 Cell extraction method
   Vigdis Torsvik

1.11 DNA and RNA extraction from soil
   Robert I. Griffiths, Mike Manefield, Andrew S. Whiteley
   and Mark J. Bailey

1.12 Rapid simultaneous extraction of DNA and RNA from bulk and
   rhizosphere soil
   Newton C.M. Gomes, Rodrigo Costa and Kornelia Smalla

1.13 Direct Extraction of Fungal DNA from Soil
   Ross N. Nazar, E. Jane Robb and Tatiana Volossiouk

1.14 Purification of microbial genes from soil and rhizosphere by
   magnetic capture hybridization and subsequent amplification
   of target genes by PCR
   Carsten S. Jacobsen

1.15 Direct ribosome isolation from soil
   Andreas Felske, Horst Backhaus and Antoon D.L.
   Akkermans

1.16 DNA Extraction from Actinorhizal Nodules
   Hugo Ramírez-Saad, Wilma M. Akkermans and Antoon
   D.L. Akkermans

SECTION 2: Detection of microbial nucleic acid sequences

2.01 Quantification of nucleic acids
   Vigdis Torsvik

2.02 Quantification of nucleic acids from aquatic environments
   by using green-fluorescent dyes and microtiter plates
   Markus G. Weinbauer and Manfred G. Höfle
2.03 Degradation and turnover of extracellular DNA in marine sediments
   Antonio Dell’anno and Cinzia Corinaldesi 235

2.04 Incorporation of thymidine into DNA of soil bacteria
   Erland Bååth 243

2.05 Preparation of radioactive probes
   Martin Cunningham 251

2.06 Detection of Nucleic Acids by Chemiluminescence
   Bronwen Harvey, Martin Cunningham and Martin Harris 289

2.07 Parameters of nucleic acid hybridization experiments
   Cindy H. Nakatsu and Larry J. Forney 321

2.08 Detection and quantification of microbial DNA sequences in soil by Southern- and dot/slot blot hybridization
   Carsten S. Jacobsen 333

2.09 Detection of microbial DNA sequences by colony hybridization
   Penny R. Hirsch 345

2.10 Polymerase chain reaction analysis of soil microbial DNA
   Jan Dirk van Elsas and Hidde Boersma 357

2.11 Detection of microbial nucleic acids by polymerase chain reaction in aquatic samples
   Asim K. Bej 369

2.12 Isolation and detection of bacterial DNA sequences in dairy products
   Lieve Herman and Nicolette Klijn 433

2.13 Quantitative PCR of environmental samples
   Janet K. Jansson and Thomas Leser 445

2.14 Molecular beacons for homogeneous real-time monitoring of amplification products
   Marianna Szemes, Cor D. Schoen and Jan M. Van der Wolf 465

2.15 Detection and enumeration of soil bacteria using the MPN-PCR technique
   Christine Picard, Xavier Nesme and Pascal Simonet 483
2.16 Detection of mRNA and rRNA via reverse transcription and PCR in soil
Sonja Selenska-Pobell

SECTION 3: Identification and classification of microbes using DNA and RNA sequences

3.01 Amplification of ribosomal RNA sequences
Richard Devereux and Sherry S. Wilkinson

3.02 Cloning 16S rRNA genes and utilization to type bacterial communities
Andreas Felske and Roland Weller

3.03 SARST, Serial Analysis of Ribosomal Sequence Tags
Josh D. Neufeld, Zhongtang Yu, Wan Lam, William W. Mohn

3.04 Oligonucleotide Fingerprinting of Ribosomal RNA Genes (OFRG)

3.05 Genotyping of bacterial isolates from the environment using Low-Molecular-Weight RNA fingerprints
Manfred G. Höfle

3.06 Characterization of the diversity of ecologically important microbes by rep-PCR genomic fingerprinting
Jan L.W. Rademaker, Frank J. Louws, James Versalovic and Frans J. de Bruijn

3.07 Genomic Fingerprinting of Micro-organisms by AFLP™ and ERIC-anchor PCR
Henk J.M. Aarts, Angela H.A.M van Hoek and Jaap Keijer

3.08 The use of pulsed-field gel electrophoresis to study bacteria recovered from the environment
Julian J. Smith and Gerry S. Saddler

3.09 Easy individual strain and community typing by rDNA ITS1 analysis
X. Nesme, and P. Normand
3.10 In situ PCR methodologies for visualization of microscale genetic and taxonomic diversities of prokaryotic communities
   Wendy Dustman, Feng Chen, Mary Ann Moran and Robert E. Hodson 689

3.11 Sensitive multi-color fluorescence in situ hybridization for the identification of environmental microorganisms
   Annelie Pernthaler, Jakob Pernthaler and Rudolf Amann 711

3.12 Use of Cloned Artificial Targets for FISH (catFISH) for the optimization of oligonucleotide probe hybridization conditions with 16S rRNA clones for in situ quantification of uncultivated prokaryotic cells
   Cleber C. Ouerney, Gary C. Armitage and David A. Relman 727

3.13 Denaturing gradient gel electrophoresis (DGGE) in microbial ecology
   Gerard Muyzer, Thorsten Brinkhoff, Ulrich Nübel, Cecilia Santegoeds, Hendrik Schäfer and Cathrin Wawer 743

3.14 Fungal Community Analysis using PCR- Denaturing Gradient Gel Electrophoresis (DGGE)
   George Kowalchuk and Eric Smit 771

3.15 The Analysis of Microbial Communities with Terminal Restriction Fragment Length Polymorphism (T-RFLP)
   Sang-Hoon Kim and Terence L. Marsh 789

3.16 Microbial community analysis by PCR-single-strand conformation polymorphism (PCR-SSCP)
   Anja B. Dohrmann and Christoph C. Tebbe 809

3.17 Isolation of high molecular weight genomic DNA from soil bacteria for genomic library construction
   Mark R. Liles, Lynn L. Williamson, Jo Handelsman and Robert M. Goodman 839

SECTION 4: Detection, identification and classification of microbes using other methods

4.01 Use of Biolog® for the Community Level Physiological Profiling (CLPP) of environmental samples
   Heribert Insam and Marta Goberna 853
4.02 Fluorescent staining of microbes for total direct counts
    Jaap Bloem and An Vos

4.03 Detection of microbes by Scanning Confocal Laser Microscopy (SCLM)
    Michael Schmid, Michael Rothballer, Berhard Aßmus,
    Peter Hutzler, John R. Lawrence, Michael Schloter and
    Anton Hartmann

4.04 Production of anti-microbial antibodies and their utilization in
    studies of microbial autecology by immunofluorescence
    microscopy and in situ CMEIAS image analysis
    Frank B. Dazzo

4.05 The slide immunoenzymatic assay (SIA): A simple and low cost
    system suitable for detecting water-borne microbes without the
    need for sophisticated technological infrastructure
    Everly Conway de Macario, Claire Jarmey-Swan, Alan R.
    Howgrave-Graham and Alberto J. L. Macario

4.06 In situ hybridization to detect microbial messenger RNA in
    plant tissues
    Katharina Pawlowski, Kirill Demchenko and Ton Bisseling

4.07 Fatty acid analysis in the identification, taxonomy and ecology
    of (plant pathogenic) bacteria
    Jaap D. Janse

4.08 Determination of microbial community structure using
    phospholipid fatty acid profiles
    Robert H. Findlay

4.09 Respiratory lipoquinones as biomarkers
    B.J. Tindall

4.10 Environmental Proteomics: Methods and Applications for
    Aquatic Ecosystems
    Oladele A. Ogunseitan and James F. Leblanc

SECTION 5: Detection of gene transfer in the environment

5.01 Natural transformation in aquatic environments
    John H. Paul and Haydn G. Williams
5.02 Natural transformation in soil: microcosm studies
Kaare Magne Nielsen, Jessica Louise Ray,
Jan Dirk Van Elsas

5.03 Plasmid transfer in aquatic environments
Søren J. Sørensen, Gunnar Oregaard, Julia R. de Lipthay
and Niels Kroer

5.04 Conjugation in the epilithon
Katja E. Hill, Julian R. Marchesi and John C. fry

5.05 Detection of bacterial conjugation in soil
Jan Dirk van Elsas, Hidde Boersma and Eric Smit

5.06 Transduction in the aquatic environment
Martin Day and Julian Marchesi

5.07 Phage ecology and genetic exchange in soil
Paul R. Herron

SECTION 6: Tracking of specific microbes in the environment

6.01 Lac as a marker gene to track microbes in the environment
Frans de Leij and Nigel Bainton

6.02 XylE as a marker gene for microorganisms
Roger W. Pickup, Jon R. Saunders, J. Alun Morgan, Craig
Winstanley and Venetia A. Saunders

6.03 GUS as a marker to track microbes
Kate J. Wilson

6.04 The celB marker gene
Angela Sessitsch, Kate J. Wilson, Antoon D. L. Akkermans
and Willem M. de Vos

6.05 Visualisation of microbes and their interactions in the
rhizosphere using auto fluorescent proteins as markers
Guido V. Bloemberg, Anastasia Lagopodi, Frans J. de
Bruijn and Janet K. Jansson

6.06 Identification of bacteria by their intrinsic sequences:
Probe design and testing of their specificity
Éva Tas and Kristina Lindström
<table>
<thead>
<tr>
<th>Section</th>
<th>Title</th>
<th>Authors</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>6.07</td>
<td>Subtraction hybridization for the production of high specificity DNA probes</td>
<td>A.J. Bjourson, W. Streit and J.E. Cooper</td>
<td>1291</td>
</tr>
<tr>
<td>6.08</td>
<td>Considerations for the use of functional markers and field release of genetically engineered microorganisms to soils and plants</td>
<td>Mark J. Bailey, Tracey. M. Timms-Wilson and Andrew K. Lilley</td>
<td>1305</td>
</tr>
<tr>
<td>7.01</td>
<td>Application of ecological diversity statistics in microbial ecology</td>
<td>Jennifer B. Hughes and Brendan J.M. Bohannan</td>
<td>1321</td>
</tr>
<tr>
<td>7.02</td>
<td>Sampling efficiency and interpretation of diversity in 16S rRNA gene libraries</td>
<td>John Dunbar</td>
<td>1345</td>
</tr>
<tr>
<td>7.03</td>
<td>LIBSHUFF Comparisons of 16S rRNA Gene Clone Libraries</td>
<td>David R. Singleton, Steven L. Rathbun, Glen E. Dyszynski and William B. Whitman</td>
<td>1361</td>
</tr>
<tr>
<td>7.04</td>
<td>Cluster analysis and statistical comparison of molecular community profile data</td>
<td>Henk W. van Verseveld and Wilfred F. M. Röling</td>
<td>1373</td>
</tr>
<tr>
<td>7.05</td>
<td>Computer-assisted analysis of molecular fingerprint profiles and database construction</td>
<td>Jan L.W. Rademaker and Frans J. de Bruijn</td>
<td>1397</td>
</tr>
<tr>
<td>7.06</td>
<td>Multivariate statistical methods and artificial neural networks for analysis of microbial community molecular fingerprints</td>
<td>Sherry L. Dollhopf, Héctor L. Ayala-Del-Río, Syed A. Hashsham and James M. Tiedje</td>
<td>1447</td>
</tr>
<tr>
<td>7.07</td>
<td>Quantitative fluorescence in situ hybridisation (FISH): statistical methods for valid cell counting</td>
<td>Russell James Davenport and Thomas Peter Curtis</td>
<td>1487</td>
</tr>
<tr>
<td>7.08</td>
<td>Oligonucleotide probe design for mixed microbial community microarrays and other applications and important considerations for data analysis</td>
<td>Syed Hashsham, Stephen Callister and Marjolijn Tijdens</td>
<td>1517</td>
</tr>
</tbody>
</table>
### 7.09 Design of microarrays for genome-wide expression profiling
Anke Becker

**SECTION 8: Molecular tools to assess microbial activities**

<table>
<thead>
<tr>
<th>8.01</th>
<th>Assessment of the membrane potential, intracellular pH and respiration of bacteria employing fluorescence techniques</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Pieter Breeuwer and Tjakko Abee</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>8.02</th>
<th>Use of microelectrodes to measure <em>in situ</em> microbial activities in biofilms, sediments, and microbial mats</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Armin Gieseke, Dirk de Beer</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>8.03</th>
<th>Application of whole-cell biosensors in soil</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Søren Johannes Sørensen, Lars Hestbjerg Hansen, Mette Burmølle, Gunnar Oregaard and Pernille Hermansen</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>8.04</th>
<th>Detection of bacterial homoserine lactone quorum sensing signals</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Scott A. Rice, Staffan Kjelleberg, Michael Givskov, Wietse de Boer and Leonid S. Chernin</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>8.05</th>
<th>BrdU Substrate Utilization Assay</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Bei Yin, Alexandra J Scupham, Elizabeth Bent and James Borneman</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>8.06</th>
<th>Stable isotope probing of nucleic acids to identify active microbial populations</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Stefan Radajewski, Ian R. Mcdonald and J. Colin Murrell</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>8.07</th>
<th>Linking microbial community structure and functioning: stable isotope ($^{13}$C) labeling in combination with PLFA analysis</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>H.T.S. Boschker</td>
</tr>
</tbody>
</table>

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<th>Correlating single-cell count with function in mixed natural microbial communities through STARFISH</th>
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<td>Cleber C. Ouvemey and Jed A. Fuhrman</td>
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<td>E.J. Kok, E.N.W. Van der Wal-Winnubst, A.M.A. Van Hoef and J. Keijer</td>
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<th>Macro-arrays protocols for gene expression studies in bacteria</th>
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8.11 Oligonucleotide-based functional gene arrays for analysis of microbial communities in the environment
   Sonia M. Tiquia, Song C. Chong, Matthew W. Fields and Jizhong Zhou

8.12 Proteomic Analysis of Bacterial Systems
   Barry G. Rolfe, Michael Djordjevic, Hancai Chen, Charles Hocart, Georg Weiller and Ulrike Mathesius
Foreword

The field of microbial ecology is evolving rapidly. Critical to this evolution is the proper application of the ever-expanding toolbox of molecular microbiological methods. The first edition of the Molecular Microbial Ecology Manual (MMEM) served to provide access to key methods in this dynamic field and its loose-leaf format allowed for expansion with new methods. However, with replacement of older methods and rapid development of new ones, it became untenable to simply add on to MMEM-I. It was clear that a major overhaul was necessary to keep pace with recent developments, and provide a format for the future. Hence MMEM-II.

Carrying on in the tradition of MMEM-I, MMEM-II chapters provide detailed and user-friendly descriptions of the methods that have made recent advances in microbial ecology possible. However, MMEM-II is not simply an update, but a complete reassessment of the field, composed of mostly new and revamped chapters. A minority of chapters, describing basic technologies in the field, has been retained from MMEM-I.

The content of MMEM-II now reflects the major advances and trends in microbial ecology. For instance, many of the methods for nucleic acid extraction and quantification (sections 1 and 2), although still of practical value, have been surpassed by more efficient or, particularly, quicker methods. These sections have, therefore, been abridged and modified to reflect the most important, relevant and widely-used methods. Many of the methods for microbial detection and identification (sections 3 and 4) have undergone significant changes, and the vast majority of the chapters within these sections have been considerably modified to reflect these advances. Also, a number of chapters describing recently developed methods of nucleic acid-based microbial detection have been introduced. Similarly, the chapters for the detection of gene transfer (section 5) and detection of specific target organisms (section 6) have been updated to a considerable extent, to reflect recent advances in these areas of research.

Microbial ecology has advanced from a field of surveying and “stamp collecting” to one that seeks to quantify findings, discern underlying mechanisms and determine the functional importance of micro-organisms in their environment. This focus directed towards a more fundamental understanding of the life of micro-organisms in their natural settings is apparent in the explosion of chapters in the
manual’s sections dedicated to quantitative assessments of data (section 7), and methods that attempt to couple microbial identity and function (section 8). The many new chapters in section 7 seek to help researchers determine the significance of molecular data pertaining to patterns of microbial diversity, allowing one to go beyond the simple detection of populations, to the quantitative determination if the data are significant. The chapters of section 8 provide methods to go beyond the question of “who is there?” to the more important problem of “what are they doing?”

As in MMEM-I, the state-of-the-art methods described in MMEM-II have not only been provided by experts in the field, but in most cases by the laboratories that actually first developed and applied the methods, and authors have included their own first-hand tips and insight. Also, the new on-line format available for MMEM-II should add to the utility of the manual by allowing users to search for key topics throughout the manual and jump between interrelated chapters. Lastly, we expect the field of microbial ecology to continue, or even accelerate, its rapid advance, and the on-line format of MMEM-II allows for the timely inclusion of new chapters dedicated to emerging methodological developments, as well as amendments to existing chapters.

The editors wish to thank all of the authors who have contributed to MMEM-II. Without their efforts, both in the lab and behind the PC, we would not be able to profit from the methods described in this manual. We also thank numerous reviewers for their time and dedication to help ensure the accuracy and appearance of the work presented.

In brief, we hope that MMEM-II will be used as it was intended, as a true manual, but one with insight behind the theory and application of the best and newest methods in microbial ecology. MMEM-II seeks to provide not only the steps in important protocols, but also the ‘why’ behind the steps and insight into how to apply the methods described. We look forward to adding and amending MMEM-II to allow it to grow along with the field of microbial ecology.

Best wishes,

George Kowalchuk
Frans de Bruijn
Ian Head
Antoon Akkermans
Jan Dirk van Elsas