

Contents

Preface	xiii
Contributors	xv
1. Introduction	1
<i>Frans J. de Bruijn</i>	
Part 1 Viral Genomes	
2. Viral Metagenomics	5
<i>Shannon J. Williamson</i>	
3. Methods in Viral Metagenomics	15
<i>Rebecca Vega Thurber</i>	
4. Metagenomic Contrasts of Viruses in Soil and Aquatic Environments	25
<i>K. Eric Wommack, Sharath Srinivasiah, Mark R. Liles, Jaysheel Bhavsar, Shellie Bench, Kurt E. Williamson, and Shawn W. Polson</i>	
5. Biodiversity and Biogeography of Phages in Modern Stromatolites and Thrombolites	37
<i>Christelle Desnues, Beltran Rodriguez-Brito, Steve Rayhawk, Scott Kelley, Tuong Tran, Matthew Haynes, Hong Liu, Mike Furlan, Linda Wegley, Betty Chau, Yijun Ruan, Dana Hall, Florent E. Angly, Robert A. Edwards, Linlin Li, Rebecca Vega Thurber, R. Pamela Reid, Janet Siefert, Valeria Souza, David L. Valentine, Brandon K. Swan, Mya Breitbart, and Forest Rohwer</i>	
6. Assembly of Viral Metagenomes from Yellowstone Hot Springs Reveals Phylogenetic Relationships and Host Co-Evolution	45
<i>Thomas W. Schoenfeld and David Mead</i>	

7. Next-Generation Sequencing and Metagenomic Analysis: A Universal Diagnostic Tool in Plant Pathology	63
<i>Ian P. Adams, Rachel H. Glover, Wendy A. Monger, Richard Thwaites, Rick Mumford, Elena Jackeviciene, Meletele Navalinskiene, Marija Samuitiene, and Neil Boonham</i>	
8. Direct Metagenomic Detection of Viral Pathogens in Human Specimens Using an Unbiased High-Throughput Sequencing Approach	73
<i>Takaaki Nakaya, Shota Nakamura, Yoshiko Okamoto, Yoshiyuki Nagai, Jun Kawai, Yoshihide Hayashizaki, Tetsuya Iida, and Toshihiro Horii</i>	
Part 2 The Soil Habitat	
9. Soil-Based Metagenomics	83
<i>Rolf Daniel</i>	
10. Methods in Metagenomic DNA, RNA, and Protein Isolation from Soil	93
<i>T. Rajesh, J. Rajendhran, P. Lavanya Pushpam, and P. Gunasekaran</i>	
11. Soil Microbial DNA Purification Strategies for Multiple Metagenomic Applications	109
<i>Larissa C. Parsley, Chengcang Wu, David Mead, Robert M. Goodman, and Mark R. Liles</i>	
12. Application of PCR-DGGE and Metagenome Walking to Retrieve Full-Length Functional Genes from Soil	117
<i>Sho Morimoto and Takeshi Fujii</i>	
13. Actinobacterial Diversity Associated with Antarctic Dry Valley Mineral Soils	125
<i>Bronwyn M. Kirby, Marilize Le Roes-Hill, S. Craig Cary, Stephanie G. Burton, I. Marla Tuffin, and Don A. Cowan</i>	
14. Targeting Major Soil-Borne Bacterial Lineages Using Large-Insert Metagenomic Approaches	135
<i>Anna M. Kielak and George A. Kowalchuk</i>	
15. Novelty and Uniqueness Patterns of Rare Members of the Soil Biosphere	143
<i>Mostafa S. Elshahed and Noha H. Youssef</i>	
16. Extensive Phylogenetic Analysis of a Soil Bacterial Community Illustrates Extreme Taxon Evenness and the Effects of Amplicon Length, Degree of Coverage, and DNA Fractionation on Classification and Ecological Parameters	151
<i>Sergio E. Morales, Theodore F. Cosart, Jesse V. Johnson, and William E. Holben</i>	
17. The Antibiotic Resistome: Origins, Diversity, and Future Prospects	165
<i>Erin L. Westman and Gerard D. Wright</i>	

Part 3 The Digestive Tract

- | | |
|---|------------|
| 18. Functional Intestinal Metagenomics | 177 |
| <hr/> | |
| <i>Bartholomeus van den Bogert, Milkha M. Leimena, Willem M. de Vos, Erwin G. Zoetendal, and Michiel Kleerebezem</i> | |
| 19. Assessment and Improvement of Methods for Microbial DNA Preparation from Fecal Samples | 191 |
| <hr/> | |
| <i>Mariko Ueno, Mami Kikuchi, Kenshiro Oshima, Seok-won Kim, Hidetoshi Morita, and Masahira Hattori</i> | |
| 20. The Role of Dysbiosis in Inflammatory Bowel Diseases | 199 |
| <hr/> | |
| <i>Johan Dicksved and Ben Willing</i> | |
| 21. Culture-Independent Analysis of the Human Gut Microbiota and their Activities | 207 |
| <hr/> | |
| <i>Jonathan Swann, Selena E. Richards, Qing Shen, Elaine Holmes, Julian R. Marchesi, and Kieran Tuohy</i> | |
| 22. Complete Genome of an Uncultured Endosymbiont Coupling Nitrogen Fixation to Cellulolysis within Protist Cells in Termite Gut | 221 |
| <hr/> | |
| <i>Yuichi Hongoh</i> | |
| 23. Cloning and Identification of Genes Encoding Acidic Cellulases from the Metagenomes of Buffalo Rumen | 229 |
| <hr/> | |
| <i>Cheng-Jie Duan, Jun-Liang Liu, and Jia-Xun Feng</i> | |

Part 4 Marines and Lakes

- | | |
|--|------------|
| 24. Microbial Diversity in the Deep Sea and the Underexplored "Rare Biosphere" | 245 |
| <hr/> | |
| <i>David B. Mark Welch and Susan M. Huse</i> | |
| 25. Bacterial Community Structure and Dynamics in a Seasonally Anoxic Fjord: Saanich Inlet, British Columbia | 253 |
| <hr/> | |
| <i>David A. Walsh and Steven J. Hallam</i> | |
| 26. Adaptation to Nutrient Availability in Marine Microorganisms by Gene Gain and Loss | 269 |
| <hr/> | |
| <i>Adam C. Martiny, Ying Huang, and Weizhong Li</i> | |
| 27. Detection of Large Numbers of Novel Sequences in the Metatranscriptomes of Complex Marine Microbial Communities | 277 |
| <hr/> | |
| <i>Jack A. Gilbert, Dawn Field, Ying Huang, Robert A. Edwards, Weizhong Li, Paul Gilna, and Ian Joint</i> | |

28. Metagenomic Approach Studying the Taxonomic and Functional Diversity of the Bacterial Community in a Lacustrine Ecosystem	287
<i>Didier Debroas, François Enault, Isabelle Jouan-Dufournel, Gisèle Bronner, and Jean-François Humbert</i>	
29. Metagenomics of the Marine Subsurface: The First Glimpse from the Peru Margin, ODP Site 1229	295
<i>Jennifer F. Biddle</i>	
30. A Targeted Metagenomic Approach to Determine the “Population Genome” of Marine <i>Synechococcus</i>	301
<i>Sophie Mazard, Martin Ostrowski, Laurence Garczarek, and David J. Scanlan</i>	
31. Diversity and Role of Bacterial Integron/Gene Cassette Metagenome in Extreme Marine Environments	309
<i>Hosam Elsaied and Akihiko Maruyama</i>	
 Part 5 Other Habitats	
32. The <i>Olavius algarvensis</i> Metagenome Revisited: Lessons Learned from the Analysis of the Low-Diversity Microbial Consortium of a Gutless Marine Worm	321
<i>Manuel Kleiner, Tanja Woyke, Caroline Ruehland, and Nicole Dubilier</i>	
33. Microbiome Diversity in Human Saliva	335
<i>Ivan Nasidze and Mark Stoneking</i>	
34. Approaches to Understanding Population Level Functional Diversity in a Microbial Community	341
<i>Devaki Bhaya</i>	
35. A Functional Metagenomic Approach for Discovering Nickel Resistance Genes from the Rhizosphere of an Acid Mine Drainage Environment	355
<i>Salvador Mirete, Carolina G. de Figueras, and Jose E. González-Pastor</i>	
36. The Microbiome of Leaf-Cutter Ant Fungus Gardens	367
<i>Garret Suen, Jarrod J. Scott, Frank O. Aylward, and Cameron R. Currie</i>	
37. Diversity of Archaea in Terrestrial Hot Springs and Role in Ammonia Oxidation	381
<i>Chuanlun L. Zhang, Brian P. Hedlund, and Jun Meng</i>	
38. Colonization of Nascent, Deep-Sea Hydrothermal Vents by a Novel Archaeal and Nanoarchaeal Assemblage	395
<i>Thomas D. Niederberger, Elizabeth A. McCliment, and S. Craig Cary</i>	

39. Analysis of the Metagenome from a Biogas-Producing Microbial Community by Means of Bioinformatics Methods 403

Sebastian Jaenicke, Martha Zakrzewski, Sebastian Jünemann, Alfred Pühler, Alexander Goesmann, and Andreas Schlüter

40. Amplicon Pyrosequencing Analysis of Endosymbiont Population Structure 415

Frank J. Stewart and Colleen M. Cavanaugh

41. Investigating Bacterial Diversity Along Alkaline Hot-Spring Thermal Gradients by Barcoded Pyrosequencing 423

Scott R. Miller and Michael Weltzer

42. Genetic Characterization of Microbial Communities Living at the Surface of Building Stones 429

Maïté Berdoulay and Jean-Claude Salvado

Part 6 Biodegradation

43. Novel Aromatic Degradation Pathway Genes and their Organization as Revealed by Metagenomic Analysis 439

Kentaro Miyazaki

44. Functional Screening a Wide Host-Range Metagenomic Library from a Wastewater Treatment Plant Yields a Novel Alcohol/Aldehyde Dehydrogenase 451

Margaret Wexler, Philip L. Bond, David J. Richardson, and Andrew W. B. Johnston

45. Aromatic Hydrocarbon Degradation Genes from Chronically Polluted Subantarctic Marine Sediments 461

Hebe M. Dionisi, Mariana Lozada, Magalí S. Marcos, Walter D. Di Marzio, and Claudia L. Loviso

46. Isolation and Characterization of Alkane Hydroxylases from a Metagenomic Library of Pacific Deep-Sea Sediment 475

Fengping Wang, Meixiang Xu, and Xiang Xiao

Part 7 Biocatalysts and Natural Products

47. Emerging Fields in Functional Metagenomics and Its Industrial Relevance: Overcoming Limitations and Redirecting the Search for Novel Biocatalysts 483

Mirjam Perner, Nele Ilmberger, Hans Ulrich Köhler, Jennifer Chow, and Wolfgang R. Streit

48. Carboxylesterases and Lipases from Metagenomes 499

Jennifer Chow, Ulrich Krauss, Karl-Erich Jaeger, and Wolfgang R. Streit

49. Expanding Small-Molecule Functional Metagenomics through Parallel Screening of Broad Host-Range Cosmid Environmental DNA Libraries in Diverse <i>Proteobacteria</i>	507
<i>Jeffrey W. Craig and Sean F. Brady</i>	
50. Biomedicinals from the Microbial Metagenomes of Marine Invertebrates	517
<i>Walter C. Dunlap, Paul F. Long, and Marcel Jaspars</i>	
51. Molecular Characterization of TEM-Type Beta-Lactamases Identified in Cold-Seep Sediments of Edison Seamount (South of Lihir Island, Papua New Guinea)	545
<i>Sang Hee Lee and Jung-Hyun Lee</i>	
52. Identification of Novel Bioactive Compounds from the Metagenome of the Marine Sponge <i>Haliclona simulans</i>	553
<i>David P. H. Lejon, Jonathan Kennedy, and Alan D. W. Dobson</i>	
53. Functional Viral Metagenomics and the Development of New Enzymes for DNA and RNA Amplification and Sequencing	563
<i>Thomas W. Schoenfeld, Nick Hermersmann, Mike Moser, Darby Rennecker, Vinay Dhodda, and David Mead</i>	
Part 8 Summary	
54. Metagenomics: The Paths Forward	581
<i>C. Titus Brown and James M. Tiedje</i>	
55. Darwin in the Twenty-First Century: Natural Selection, Molecular Biology, and Species Concepts	589
<i>Francisco J. Ayala</i>	
Index	597