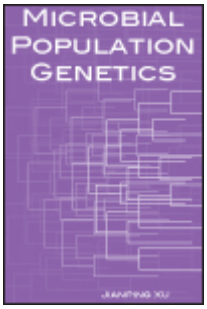
Microbial Population Genetics



Edited by: **Jianping Xu**
McMaster University, Hamilton, Ontario, Canada

Published: March 2010. **Pages:** viii + 214
Hardback: ISBN 978-1-904455-59-2 £159, $319
Published by: Caister Academic Press www.caister.com

Microbial population genetics is a rapidly advancing field of investigation with relevance to many areas of science. The subject encompasses theoretical issues such as the origins and evolution of species, sex and recombination. Population genetics lays the foundations for tracking the origin and evolution of antibiotic resistance and deadly infectious pathogens and is also an essential tool in the utilization of beneficial microbes.

Written by leading researchers in the field, this invaluable book details the major current advances in microbial population genetics and genomics. Distinguished international scientists introduce fundamental concepts, describe genetic tools and comprehensively review recent data from SNP surveys, whole-genome DNA sequences and microarray hybridizations. Chapters cover broad groups of microorganisms including viruses, bacteria, archaea, fungi, protozoa and algae. A major focus of the book is the application of molecular tools in the study of genetic variation. Topics covered include microbial systematics, comparative microbial genomics, horizontal gene transfer, pathogenic bacteria, nitrogen-fixing bacteria, cyanobacteria, microalgae, fungi, malaria parasites, viral pathogens and metagenomics.

An essential volume for everyone interested in population genetics and highly recommended reading for all microbiologists.

Chapter 1. Recent Advances in Understanding Microbial Systematics. *Radhey S. Gupta and Beile Gao*
Chapter 2. Comparative Microbial Genomics: Analytical Tools, Population Genetic Patterns and Evolutionary Implications. *Yingqin Luo, Kui Lin, Jianping Xu*
Chapter 3. Patterns of Horizontal Gene Transfer in Bacteria. *Weilong Hao and G. Brian Golding*
Chapter 4. Population Genetics of Human Pathogenic Bacteria: Implications for Source Tracking and Rapid Identification. *Ruifu Yang, Yujun Cui, Yanjun Li and Yanfeng Yan*
Chapter 5. Population Genetics of the Symbiotic Nitrogen-fixing Bacteria Rhizobia. *Bertrand D. Eardly and Jianping Xu*
Chapter 6. The Population Genetics of Cyanobacteria. *Scott R. Miller*
Chapter 7. Population Genetics of Microalgae. *Jim Provan*
Chapter 8. Population Genetics of Fungal Mutualists of Plants. *Teresa E. Pawlowska*
Chapter 9. Population Genetics of Pathogenic Fungi in Humans and Other Animals. *Thomas G. Mitchell*
Chapter 10. Population Genetics of Human Malaria Parasites. *Deirdre A. Joy*
Chapter 11. The Population Genetics and Epidemiology of Human Viral Pathogens. *Fernando González Candelas, Rafael Sanjuán*
Chapter 12. Population Genetics in the Age of Metagenomics: Impact on Investigations of Viral, Bacterial, Archaeal and Eukaryotic Microbial Communities. *Jianping Xu*

Order from:

Caister Academic Press, c/o Book Systems Plus http://www.caister.com/order

CURRENT BOOKS OF INTEREST www.caister.com

☞ **MALDI-TOF Mass Spectrometry in Microbiology**
Edited by: Markus Kostrzewa and Sören Schubert (Published: 2016)

☞ ***Aspergillus* and *Penicillium* in the Post-genomic Era**
Edited by: Ronald P. de Vries, Isabelle Benoit Gelber and Mikael Rørdam Andersen (Published: 2016)

☞ **The Bacteriocins: Current Knowledge and Future Prospects**
Edited by: Robert L. Dorit, Sandra M. Roy and Margaret A. Riley (Published: 2016)

☞ **Omics in Plant Disease Resistance**
Edited by: Vijai Bhadauria (Published: 2016)

☞ **Acidophiles: Life in Extremely Acidic Environments**
Edited by: Raquel Quatrini and D. Barrie Johnson (Published: 2016)

☞ **Climate Change and Microbial Ecology: Current Research and Future Trends**
Edited by: Jürgen Marxsen (Published: 2016)

☞ **Biofilms in Bioremediation: Current Research and Emerging Technologies**
Edited by: Gavin Lear (Published: 2016)

☞ **Microalgae: Current Research and Applications**
Edited by: Maria-Nefeli Tsaloglou (Published: 2016)

☞ **Gas Plasma Sterilization in Microbiology: Theory, Applications, Pitfalls and New Perspectives**
Edited by: Hideharu Shintani and Akikazu Sakudo (Published: 2016)

☞ **Virus Evolution: Current Research and Future Directions**
Edited by: Scott C. Weaver, Mark Denison, Marilyn Roossinck and Marco Vignuzzi (Published: 2016)

☞ **Arboviruses: Molecular Biology, Evolution and Control**
Edited by: Nikos Vasilakis and Duane J. Gubler (Published: 2016)

☞ ***Shigella*: Molecular and Cellular Biology**
Edited by: William D. Picking and Wendy L. Picking (Published: 2016)

☞ **Aquatic Biofilms: Ecology, Water Quality and Wastewater Treatment**
Edited by: Anna M. Romaní, Helena Guasch and M. Dolors Balaguer (Published: 2016)

☞ **Alphaviruses: Current Biology**
Edited by: Suresh Mahalingam, Lara Herrero and Belinda Herring (Published: 2016)

☞ **Thermophilic Microorganisms**
Edited by: Fu-Li Li (Published: 2015)

☞ **Flow Cytometry in Microbiology: Technology and Applications**
Edited by: Martin G. Wilkinson (Published: 2015)
"an impressive group of experts" (ProtoView)

☞ **Probiotics and Prebiotics: Current Research and Future Trends**
Edited by: Koen Venema and Ana Paula do Carmo (Published: 2015)

☞ **Epigenetics: Current Research and Emerging Trends**
Edited by: Brian P. Chadwick (Published: 2015)
"this is one text you don't want to miss" (Epigenie); "up-to-date information" (ChemMedChem)

☞ ***Corynebacterium glutamicum*: From Systems Biology to Biotechnological Applications**
Edited by: Andreas Burkovski (Published: 2015)
"Without question a valuable book" (BIOSpektrum)

☞ **Advanced Vaccine Research Methods for the Decade of Vaccines**
Edited by: Fabio Bagnoli and Rino Rappuoli (Published: 2015)

Population genetic simulations using population sizes between 10(3) and 10(7) suggest extremely high levels of microbial diversity in environments that sustain large populations. However, census and effective population sizes may differ considerably, and because we know nothing of the evolutionary history of environmental microbial populations, we also have no idea what N(e) of environmental populations is. On the one hand, this reflects our ignorance of the microbial world. We use the term â€œpopulationâ€ to describe an assemblage of co-existing microbial genomes in an environment that are similar enough to map to the context of the same reference genome. Cells within a population (i.e., all cells that would have classified as the same â€œspeciesâ€ or â€œstrainâ€ for whatever these terms mean to you) will share the vast majority of their genomes in the sequence space. Microbial population genetics is a rapidly advancing field of investigation with relevance to many areas of science. The subject encompasses theoretical issues such as the origins and evolution of species, sex and recombination. Population genetics lays the foundations for tracking the origin and evolution of antibiotic resistance and deadly infectious pathogens and is also an essential tool in the utilization of beneficial microbes.