

METHODS IN MOLECULAR BIOLOGY

Series Editor
John M. Walker
School of Life and Medical Sciences
University of Hertfordshire
Hatfield, Hertfordshire, AL10 9AB, UK

For further volumes:
<http://www.springer.com/series/7651>

Gene Essentiality

Methods and Protocols

Edited by

Long Jason Lu

Cincinnati Children's Hospital Medical Center, Cincinnati, OH, USA

 **Humana Press**

Editor

Long Jason Lu
Cincinnati Children's Hospital Medical Center
Cincinnati, OH, USA

ISSN 1064-3745 ISSN 1940-6029 (electronic)
Methods in Molecular Biology
ISBN 978-1-4939-2397-7 ISBN 978-1-4939-2398-4 (eBook)
DOI 10.1007/978-1-4939-2398-4

Library of Congress Control Number: 2014959295

Springer New York Heidelberg Dordrecht London
© Springer Science+Business Media New York 2015

This work is subject to copyright. All rights are reserved by the Publisher, whether the whole or part of the material is concerned, specifically the rights of translation, reprinting, reuse of illustrations, recitation, broadcasting, reproduction on microfilms or in any other physical way, and transmission or information storage and retrieval, electronic adaptation, computer software, or by similar or dissimilar methodology now known or hereafter developed.

The use of general descriptive names, registered names, trademarks, service marks, etc. in this publication does not imply, even in the absence of a specific statement, that such names are exempt from the relevant protective laws and regulations and therefore free for general use.

The publisher, the authors and the editors are safe to assume that the advice and information in this book are believed to be true and accurate at the date of publication. Neither the publisher nor the authors or the editors give a warranty, express or implied, with respect to the material contained herein or for any errors or omissions that may have been made.

Printed on acid-free paper

Humana Press is a brand of Springer
Springer Science+Business Media LLC New York is part of Springer Science+Business Media (www.springer.com)

Preface

This book is an update of the previously published book *Microbial Essential Genes* in this series. In the first eight chapters, we cover two main types of approaches that have been widely used to determine essential genes: single-gene knockouts and transposon mutagenesis, in both prokaryotes and *Candida albicans*. Since the last edition was published, we have seen significant advancement in the computational predictions of microbial essential genes. In the next seven chapters, we cover four main types of approaches: comparative genomics, supervised machine learning, constraint-based methods, and corrections of transposon mutagenesis data. We also present databases and servers that are often used in studying gene essentiality.

Finally, I would like to thank all the authors for the contributions. I would also like to thank Dr. John Walker. Without his encouragement and guidance, I would not have been able to complete this book.

Cincinnati, OH, USA

Long Jason Lu

Contents

<i>Preface</i>	<i>v</i>
<i>Contributors</i>	<i>ix</i>
1 Microarray Transposon Tracking for the Mapping of Conditionally Essential Genes in <i>Campylobacter jejuni</i> <i>Martin Stahl and Alain Stintzi</i>	1
2 Identifying Essential <i>Streptococcus sanguinis</i> Genes Using Genome-Wide Deletion Mutation <i>Lei Chen, Xiuchun Ge, and Ping Xu</i>	15
3 Defining Essential Genes and Identifying Virulence Factors of <i>Porphyromonas gingivalis</i> by Massively Parallel Sequencing of Transposon Libraries (Tn-seq) <i>Brian A. Klein, Margaret J. Duncan, and Linden T. Hu</i>	25
4 Identification of Essential Genes and Synthetic Lethal Gene Combinations in <i>Escherichia coli</i> K-12 <i>Hirotaada Mori, Tomoya Baba, Katsushi Yokoyama, Rikiya Takeuchi, Wataru Nomura, Kazuichi Makishi, Yuta Otsuka, Hitomi Dose, and Barry L. Wanner</i>	45
5 Identification of Genes Essential for Leptospirosis <i>Thanatchaporn Bartpho and Gerald L. Murray</i>	67
6 Identifying Essential Genes in <i>Mycobacterium tuberculosis</i> by Global Phenotypic Profiling <i>Jarukit E. Long, Michael DeJesus, Doyle Ward, Richard E. Baker, Thomas Ioerger, and Christopher M. Sassetti</i>	79
7 Essential Genes in the Infection Model of <i>Pseudomonas aeruginosa</i> -PCR-Based Signature-Tagged Mutagenesis <i>Irena Kukavica-Ibrulj and Roger C. Levesque</i>	97
8 Genome-Wide Synthetic Genetic Screening by Transposon Mutagenesis in <i>Candida albicans</i> <i>Brooke N. Horton and Anuj Kumar</i>	125
9 An Integrated Machine-Learning Model to Predict Prokaryotic Essential Genes <i>Jingyuan Deng</i>	137
10 A Statistical Framework for Improving Genomic Annotations of Transposon Mutagenesis (TM) Assigned Essential Genes <i>Jingyuan Deng</i>	153
11 A Proposed Essential Gene Discovery Pipeline: A <i>Campylobacter jejuni</i> Case Study <i>Mark Reuter, Duncan J.H. Gaskin, and Aline Metris</i>	167

12	Computational Prediction of Essential Metabolic Genes Using Constraint-Based Approaches	183
	<i>Georg Basler</i>	
13	Three Computational Tools for Predicting Bacterial Essential Genes	205
	<i>Feng-Biao Guo, Yuan-Nong Ye, Lu-Wen Ning, and Wen Wei</i>	
14	Gene Essentiality Analysis Based on DEG 10, an Updated Database of Essential Genes	219
	<i>Feng Gao, Hao Luo, Chun-Ting Zhang, and Ren Zhang</i>	
15	Discovering Essential Domains in Essential Genes	235
	<i>Yulan Lu, Yao Lu, Jingyuan Deng, Hui Lu, and Long Jason Lu</i>	
	<i>Index</i>	247

Contributors

- TOMOYA BABA • *Transdisciplinary Research Integration Center, Shizuoka, Japan*
- RICHARD E. BAKER • *Department of Microbiology and Physiological Systems, University of Massachusetts Medical School, Worcester, MA, USA*
- THANATCHAPORN BARTPHO • *Department of Microbiology, Monash University, Clayton, VIC, Australia*
- GEORG BASLER • *Department of Environmental Protection, Estación Experimental del Zaidín, Consejo Superior de Investigaciones Científicas (CSIC), Granada, Spain*
- LEI CHEN • *Philips Institute, Virginia Commonwealth University, Richmond, VA, USA*
- MICHAEL DEJESUS • *Department of Computer Science, Texas A&M University, College Station, TX, USA*
- JINGYUAN DENG • *Division of Biomedical Informatics, Cincinnati Children's Hospital Medical Center, Cincinnati, OH, USA*
- HITOMI DOSE • *Graduate School of Biological Sciences, Nara Institute of Science and Technology, Nara, Japan*
- MARGARET J. DUNCAN • *Department of Microbiology, The Forsyth Institute, Cambridge, MA, USA*
- FENG GAO • *Department of Physics, Tianjin University, Tianjin, China*
- DUNCAN J.H. GASKIN • *Institute of Food Research, Norwich Research Park, Norwich, UK*
- XIUCHUN GE • *Philips Institute, Virginia Commonwealth University, Richmond, VA, USA*
- FENG-BIAO GUO • *Computational, Comparative, Evolutionary and Functional Genomics Group (CEFG), School of Life Science and Technology, University of Electronic Science and Technology of China, Chengdu, China*
- BROOKE N. HORTON • *Department of Molecular, Cellular, and Developmental Biology, University of Michigan, Ann Arbor, MI, USA*
- LINDEN T. HU • *Graduate Program of Molecular Microbiology, Tufts University School of Medicine, Boston, MA, USA; Department of Geographical Medicine and Infectious Disease, Tufts Medical Center, Boston, MA, USA*
- THOMAS IOERGER • *Department of Computer Science, Texas A&M University, College Station, TX, USA*
- BRIAN A. KLEIN • *Graduate Program of Molecular Microbiology, Tufts University School of Medicine, Boston, MA, USA*
- IRENA KUKAVICA-IBRULJ • *Institut de biologie intégrative et des systèmes (IBIS), Faculté de Médecine, Université Laval, Québec, QC, Canada*
- ANUJ KUMAR • *Department of Molecular, Cellular, and Developmental Biology, University of Michigan, Ann Arbor, MI, USA*
- ROGER C. LEVESQUE • *Institut de biologie intégrative et des systèmes (IBIS), Faculté de Médecine, Université Laval, Québec, QC, Canada*
- JARUKIT E. LONG • *Department of Microbiology and Physiological Systems, University of Massachusetts Medical School, Worcester, MA, USA*
- HUI LU • *Shanghai Institute of Medical Genetics, Children's Hospital of Shanghai, Shanghai Jiao Tong University, Shanghai, China; Department of Bioengineering, University of Illinois at Chicago, Chicago, IL, USA*

- LONG JASON LU • *Division of Biomedical Informatics, Cincinnati Children's Hospital Medical Center, Cincinnati, OH, USA; Division of Biostatistics and Epidemiology, Cincinnati Children's Hospital Medical Center, Cincinnati, OH, USA; Department of Computer Science, University of Cincinnati, Cincinnati, OH, USA; Department of Environmental Health, University of Cincinnati, Cincinnati, OH, USA*
- YAO LU • *Shanghai Institute of Medical Genetics, Children's Hospital of Shanghai, Shanghai Jiao Tong University, Shanghai, China*
- YULAN LU • *State Key Laboratory of Genetic Engineering, Institute of Biostatistics, School of Life Science, Fudan University, Shanghai, China*
- HAO LUO • *Department of Physics, Tianjin University, Tianjin, China*
- KAZUICHI MAKISHI • *Graduate School of Biological Sciences, Nara Institute of Science and Technology, Nara, Japan*
- ALINE METRIS • *Institute of Food Research, Norwich Research Park, Norwich, UK*
- HIROTADA MORI • *Graduate School of Biological Sciences, Nara Institute of Science and Technology, Nara, Japan*
- GERALD L. MURRAY • *Department of Microbiology, Monash University, Clayton, VIC, Australia*
- LU-WEN NING • *Computational, Comparative, Evolutionary and Functional Genomics Group (CEFG), School of Life Science and Technology, University of Electronic Science and Technology of China, Chengdu, China*
- WATARU NOMURA • *Graduate School of Biological Sciences, Nara Institute of Science and Technology, Nara, Japan*
- YUTA OTSUKA • *Graduate School of Biological Sciences, Nara Institute of Science and Technology, Nara, Japan*
- MARK REUTER • *Institute of Food Research, Norwich Research Park, Norwich, UK*
- CHRISTOPHER M. SASSETTI • *Department of Microbiology and Physiological Systems, University of Massachusetts Medical School, Worcester, MA, USA; Howard Hughes Medical Institute, Chevy Chase, MD, USA*
- MARTIN STAHL • *Division of Gastroenterology, BC's Children's Hospital, the Child and Family Research Institute and the University of British Columbia, Vancouver, BC, Canada; Department of Biochemistry, Microbiology and Immunology, Faculty of Medicine, Ottawa Institute of Systems Biology, University of Ottawa, Ottawa, ON, Canada*
- ALAIN STINTZI • *Department of Biochemistry, Microbiology and Immunology, Faculty of Medicine, Ottawa Institute of Systems Biology, University of Ottawa, Ottawa, ON, Canada*
- RIKIYA TAKEUCHI • *Graduate School of Biological Sciences, Nara Institute of Science and Technology, Nara, Japan*
- BARRY L. WANNER • *Department of Microbiology and Immunobiology, Harvard Medical School, Boston, MA, USA*
- DOYLE WARD • *Broad Institute, Cambridge, MA, USA*
- WEN WEI • *Computational, Comparative, Evolutionary and Functional Genomics Group (CEFG), School of Life Science and Technology, University of Electronic Science and Technology of China, Chengdu, China*
- PING XU • *The Philips Institute for Oral Health Research, Virginia Commonwealth University, Richmond, VA, USA*

YUAN-NONG YE • *Computational, Comparative, Evolutionary and Functional Genomics Group (CEFG), School of Life Science and Technology, University of Electronic Science and Technology of China, Chengdu, China*

KATSUSHI YOKOYAMA • *Graduate School of Biological Sciences, Nara Institute of Science and Technology, Nara, Japan*

CHUN-TING ZHANG • *Department of Physics, Tianjin University, Tianjin, China*

REN ZHANG • *Center for Molecular Medicine and Genetics, School of Medicine, Wayne State University, Detroit, MI, USA*