

MANUAL OF
ENVIRONMENTAL
MICROBIOLOGY

F O U R T H E D I T I O N

Editor in Chief Marylynn V. Yates

Editors

Cindy H. Nakatsu | Robert V. Miller | Suresh D. Pillai

MANUAL OF
**ENVIRONMENTAL
MICROBIOLOGY**
FOURTH EDITION

MANUAL OF ENVIRONMENTAL MICROBIOLOGY

F O U R T H E D I T I O N

Editor in Chief

Marylynn V. Yates

Department of Environmental Sciences
University of California
Riverside, California

Editors

Cindy H. Nakatsu

Department of Agronomy
Purdue University
West Lafayette, Indiana

Robert V. Miller

Department of Microbiology and Molecular Genetics
Oklahoma State University
Stillwater, Oklahoma

Suresh D. Pillai

National Center for Electron Beam Research
Departments of Poultry Science and Nutrition
and Food Science
Texas A&M University
College Station, Texas



Washington, DC

Copyright © 2016 American Society for Microbiology. All rights reserved. No part of this publication may be reproduced or transmitted in whole or in part or reused in any form or by any means, electronic or mechanical, including photocopying and recording, or by any information storage and retrieval system, without permission in writing from the publisher.

Disclaimer: To the best of the publisher's knowledge, this publication provides information concerning the subject matter covered that is accurate as of the date of publication. The publisher is not providing legal, medical, or other professional services. Any reference herein to any specific commercial products, procedures, or services by trade name, trademark, manufacturer, or otherwise does not constitute or imply endorsement, recommendation, or favored status by the American Society for Microbiology (ASM). The views and opinions of the author(s) expressed in this publication do not necessarily state or reflect those of ASM, and they shall not be used to advertise or endorse any product.

Library of Congress Cataloging-in-Publication Data

Names: Yates, M. V. (Marylynn V.), editor. | Nakatsu, Cindy H., editor. | Miller, Robert V. (Robert Verne), 1945- editor. | Pillai, Suresh D., 1962- editor.
Title: Manual of environmental microbiology / editor in chief, Marylynn V. Yates; editors, Cindy H. Nakatsu, Robert V. Miller, Suresh D. Pillai.
Description: Fourth edition. | Washington, DC : ASM Press, [2016] | Includes bibliographical references and index.
Identifiers: LCCN 2016014816 (print) | LCCN 2016016986 (ebook) | ISBN 9781555816025 (hardcover) | ISBN 9781555818821 ()
Subjects: LCSH: Microbial ecology--Laboratory manuals. | Sanitary microbiology--Laboratory manuals.
Classification: LCC QR100 .M36 2016 (print) | LCC QR100 (ebook) | DDC 577.8--dc23
LC record available at <https://lccn.loc.gov/2016014816>

All Rights Reserved

Printed in Canada

10 9 8 7 6 5 4 3 2 1

Address editorial correspondence to
ASM Press, 1752 N St., N.W.,
Washington, DC 20036-2904, USA

Send orders to ASM Press, P.O. Box 605, Herndon, VA 20172, USA
Phone: 800-546-2416; 703-661-1593
Fax: 703-661-1501
E-mail: books@asmusa.org
Online: <http://www.asmscience.org>

CONTENTS

Editorial Board ix

Contributors xi

1.1.1 Introduction / 1.1.1-1
MARYLYNN V. YATES

GENERAL METHODOLOGY

VOLUME EDITOR: SURESH D. PILLAI

SECTION EDITORS: YOICHI KAMAGATA,
CLEBER C. OUVENEY, DOUGLAS R. CALL,
STEFAN J. GREEN, YILDIZ T. CHAMBERS, AND
JOHN SCOTT MESCHKE

2.1 CULTURE-BASED AND PHYSIOLOGICAL
DETECTION

2.1.1 Detection of Specific Taxa Using
Chromogenic and Fluorogenic
Media / 2.1.1-1
MOHAMMAD MANAFI

2.1.2 Anaerobic Cultivation / 2.1.2-1
TAKASHI NARIHIRO AND YOICHI
KAMAGATA

2.1.3 New Devices for Cultivation / 2.1.3-1
YOSHITERU AOI AND SLAVA EPSTEIN

2.2 MICROSCOPIC METHODS

2.2.1 Gold-Based *In Situ* Hybridization for
Phylogenetic Single-Cell Detection of
Prokaryotes in Environmental
Samples / 2.2.1-1
THILO EICKHORST AND HANNES SCHMIDT

2.2.2 Assessment of Prokaryotic Biological Activity
at the Single-Cell Level by Combining
Microautoradiography and Fluorescence
in situ Hybridization / 2.2.2-1
CLEBER C. OUVENEY

2.3 TARGET-SPECIFIC DETECTION

2.3.1 Antibody-Based Technologies for
Environmental Biodetection / 2.3.1-1
CHERYL L. BAIRD AND SUSAN M. VARNUM

2.3.2 PCR, Real-Time PCR, Digital PCR, and
Isothermal Amplification / 2.3.2-1
RACHEL A. BARTHOLOMEW, JANINE
R. HUTCHISON, TIMOTHY M. STRAUB,
AND DOUGLAS R. CALL

2.3.3 Microarray-Based Environmental
Diagnostics / 2.3.3-1
DARRELL P. CHANDLER

2.3.4 Field Application of Pathogen Detection
Technologies / 2.3.4-1
TIMOTHY M. STRAUB, DOUGLAS
R. CALL, CINDY BRUCKNER-LEA,
HEATHER COLBURN, CHERYL L. BAIRD,
RACHEL A. BARTHOLOMEW,
RICHARD OZANICH, AND
KRISTIN JARMAN

2.4 MICROBIAL COMMUNITY ANALYSIS OF
ENVIRONMENTAL SAMPLES WITH
NEXT-GENERATION SEQUENCING

2.4.1 Introduction to Microbial
Community Analysis of Environmental
Samples with Next-Generation
Sequencing / 2.4.1-1
STEFAN J. GREEN AND JOSH D. NEUFELD

2.4.2 Microbial Community Analysis Using
High-Throughput Amplicon
Sequencing / 2.4.2-1
DANNY IONESCU, WILL A. OVERHOLT,
MICHAEL D. J. LYNCH, JOSH D. NEUFELD,
ANKUR NAQIB, AND STEFAN J. GREEN

2.4.3 Functional Metagenomics: Procedures and
Progress / 2.4.3-1
LAURA S. MORRIS AND JULIAN
R. MARCHESI

2.4.4 Metagenomics: Assigning Functional
Status to Community Gene
Content / 2.4.4-1
NASEER SANGWAN AND RUP LAL

2.4.5 Generation and Analysis of Microbial
Metatranscriptomes / 2.4.5-1
NEHA SARODE, DARREN J. PARRIS, SANGITA
GANESH, SHERRY L. SESTON, AND FRANK
J. STEWART

- 2.5 QA/QC IN ENVIRONMENTAL MICROBIOLOGY**
- 2.5.1 Introduction to Principles of Quality Assurance / 2.5.1-1**
KEVIN K. CONNELL
- 2.5.2 General Quality Control / 2.5.2-1**
ROBIN K. OSHIRO
- 2.5.3 Quality Control for Bacteriological Analyses / 2.5.3-1**
ELLEN BRAUN-HOWLAND
- 2.5.4 Quality Control for Virological Analyses / 2.5.4-1**
RICHARD E. DANIELSON
- 2.5.5 Quality Control for USEPA Method 1623 Protozoan Analysis and PCR Analyses / 2.5.5-1**
GEORGE D. DI GIOVANNI AND GREGORY D. STURBAUM
- 2.5.6 The Role of Statistical Thinking in Environmental Microbiology / 2.5.6-1**
J. VAUN MCARTHUR AND R. CARY TUCKFIELD
- 2.5.7 Study Design / 2.5.7-1**
YILDIZ T. CHAMBERS AND ROBIN K. OSHIRO
- 2.6 SAMPLING METHODS**
- 2.6.1 Water Sampling and Processing Techniques for Public Health-Related Microbes / 2.6.1-1**
VINCENT HILL
- 2.6.2 Surface Sampling / 2.6.2-1**
LAURA J. ROSE, JUDITH NOBLE-WANG, AND MATTHEW J. ARDUINO
- 2.6.3 Soil Sampling for Microbial Analyses / 2.6.3-1**
JOHN BROOKS
- 2.6.4 Microbiological Sampling of Wastewater and Biosolids / 2.6.4-1**
NICOLETTE A. ZHOU, ERIC C. THOMPSON, AND JOHN SCOTT MESCHKE

ENVIRONMENTAL PUBLIC HEALTH MICROBIOLOGY

VOLUME EDITOR: MARYLYNN V. YATES
SECTION EDITORS: GARY A. TORANZOS, MARK P. BUTTNER, ED TOPP, VALERIE J. HARWOOD, AND MARYLYNN V. YATES

3.1 WATER

- 3.1.1 Current and Developing Methods for the Detection of Microbial Indicators in Environmental Freshwaters and Drinking Waters / 3.1.1-1**
TASHA M. SANTIAGO-RODRIGUEZ, JULIE KINZELMAN, AND GARY A. TORANZOS

- 3.1.2 Best Practices for Cyanobacterial Harmful Algal Bloom Monitoring / 3.1.2-1**
TIMOTHY G. OTTEN AND HANS W. PAERL
- 3.1.3 Assessing the Efficiency of Wastewater Treatment / 3.1.3-1**
GRACIELA RAMÍREZ TORO AND HARVEY MINNIGH
- 3.1.4 Epidemiologic Aspects of Waterborne Infectious Disease / 3.1.4-1**
SAMUEL DOREVITCH
- 3.1.5 Waterborne Enteric Viruses: Diversity, Distribution, and Detection / 3.1.5-1**
MORTEZA ABBASZADEGAN AND ABSAR ALUM
- 3.1.6 Detection of Protozoa in Surface and Finished Waters / 3.1.6-1**
ABSAR ALUM, ERIC N. VILLEGAS, SCOTT P. KEELY, KELLY R. BRIGHT, LAURA Y. SIFUENTES, AND MORTEZA ABBASZADEGAN
- 3.1.7 Drinking Water Microbiology / 3.1.7-1**
MARYLYNN V. YATES
- 3.2 AIR**
- 3.2.1 Introduction to Aerobiology / 3.2.1-1**
PAULA KRAUTER AND LINDA D. STETZENBACH
- 3.2.2 Sampling for Airborne Microorganisms / 3.2.2-1**
SERGEY A. GRINSHPUN, MARK P. BUTTNER, GEDIMINAS MAINELIS, AND KLAUS WILLEKE
- 3.2.3 Analysis of Bioaerosol Samples / 3.2.3-1**
PATRICIA CRUZ AND MARK P. BUTTNER
- 3.2.4 Fate and Transport of Microorganisms in Air / 3.2.4-1**
GARY S. BROWN AND ALAN JEFF MOHR
- 3.2.5 Airborne Fungi and Mycotoxins / 3.2.5-1**
DE-WEI LI, ECKARDT JOHANNING, AND CHIN S. YANG
- 3.2.6 Airborne Bacteria, Archaea, and Endotoxin / 3.2.6-1**
PETER S. THORNE, CAROLINE DUCHAINE, AND PASCALE BLAIS LECOURS
- 3.2.7 Airborne Viruses / 3.2.7-1**
SYED A. SATTAR, NITIN BHARDWAJ, AND M. KHALID IJAZ
- 3.2.8 Aerobiology of Agricultural Pathogens / 3.2.8-1**
ESTELLE LEVETIN
- 3.2.9 Legionellae and Legionnaires' Disease / 3.2.9-1**
CLARESSA E. LUCAS AND BARRY S. FIELDS
- 3.3 SOIL**
- 3.3.1 Pathogenic Viruses and Protozoa Transmitted by Soil / 3.3.1-1**
PASCAL DELAQUIS, JULIE BRASSARD, AND ALVIN GAJADHAR

- 3.3.2 Natural Soil Reservoirs for Human Pathogenic and Fecal Indicator Bacteria / 3.3.2-1**
MARIA LAURA BOSCHIROLI, JOSEPH FALKINHAM, SABINE FAVRE-BONTÉ, SYLVIE NAZARET, PASCAL PIVETEAU, MICHAEL SADOWSKY, MURULEE BYAPPANAHALLI, PASCAL DELAQUIS, AND ALAIN HARTMANN
- 3.4 MICROBIAL SOURCE TRACKING**
- 3.4.1 The Evolving Science of Microbial Source Tracking / 3.4.1-1**
VALERIE J. HARWOOD, CHARLES HAGEDORN, AND MICHAEL SADOWSKY
- 3.4.2 Validation of Microbial Source Tracking Markers and Detection Protocols: Considerations for Effective Interpretation / 3.4.2-1**
ASJA KORAJKIC, DON STOECKEL, AND JOHN F. GRIFFITH
- 3.4.3 Overview of Microbial Source Tracking Methods Targeting Human Fecal Pollution Sources / 3.4.3-1**
ORIN C. SHANKS, HYATT GREEN, ASJA KORAJKIC, AND KATHARINE G. FIELD
- 3.4.4 Methods of Targeting Animal Sources of Fecal Pollution in Water / 3.4.4-1**
ANICET R. BLANCH, ELISENDA BALLESTÉ, JENNIFER WEIDHAAS, JORGE SANTO DOMINGO, AND HODON RYU
- 3.4.5 Microbial Source Tracking: Field Study Planning and Implementation / 3.4.5-1**
JULIE KINZELMAN AND WARISH AHMED
- 3.4.6 Fecal Indicator Organism Modeling and Microbial Source Tracking in Environmental Waters / 3.4.6-1**
MEREDITH B. NEVERS, MURULEEDHARA N. BYAPPANAHALLI, MANTHA S. PHANIKUMAR, AND RICHARD L. WHITMAN
- 3.5 MICROBIAL RISK ASSESSMENT**
- 3.5.1 Risk Assessment Framework / 3.5.1-1**
MARYLYNN V. YATES
- 3.5.2 Exposure Assessment / 3.5.2-1**
SUSAN R. PETTERSON AND NICHOLAS J. ASHBOLT
- 3.5.3 Dose-Response Modeling and Use: Challenges and Uncertainties in Environmental Exposure / 3.5.3-1**
MARK H. WEIR
- 4.1.1 Phylogenomic Networks of Microbial Genome Evolution / 4.1.1-1**
TAL DAGAN, OVIDIU POPA, THORSTEN KLÖSGES, AND GIDDY LANDAN
- 4.1.2 Evolutionary Ecology of Microorganisms: From the Tamed to the Wild / 4.1.2-1**
JAY T. LENNON AND VINCENT J. DENEFF
- 4.2 AQUATIC ENVIRONMENTS**
- 4.2.1 The Microbial Ecology of Benthic Environments / 4.2.1-1**
ROBERT H. FINDLAY AND TOM J. BATTIN
- 4.2.2 Heterotrophic Planktonic Microbes: Viruses, Bacteria, Archaea, and Protozoa / 4.2.2-1**
JED A. FUHRMAN AND DAVID A. CARON
- 4.2.3 Aquatic Biofilms: Development, Cultivation, Analyses, and Applications / 4.2.3-1**
JOHN R. LAWRENCE, THOMAS R. NEU, ARMELLE PAULE, DARREN R. KORBER, AND GIDEON M. WOLFAARDT
- 4.3 EXTREME ENVIRONMENTS**
- 4.3.1 The Microbiology of Extremely Acidic Environments / 4.3.1-1**
D. BARRIE JOHNSON AND ANGELES AGUILERA
- 4.3.2 Life in High Salinity Environments / 4.3.2-1**
AHARON OREN
- 4.3.3 Microbial Life in Extreme Low-Biomass Environments: A Molecular Approach / 4.3.3-1**
KASTHURI VENKATESWARAN, MYRON T. LA DUC, PARAG VAISHAMPAYAN, AND JAMES A. SPRY
- 4.3.4 Life in High-Temperature Environments / 4.3.4-1**
BRIAN P. HEDLUND, SCOTT C. THOMAS, JEREMY A. DODSWORTH, AND CHUANLUN L. ZHANG
- 4.4 ANIMAL-GUT MICROBIOMES**
- 4.4.1 Invertebrate Gut Associations / 4.4.1-1**
DANIELE DAFFONCHIO, ALBERTO ALMA, GUIDO FAVIA, LUCIANO SACCHI, AND CLAUDIO BANDI
- 4.4.2 Studying the Mammalian Intestinal Microbiome Using Animal Models / 4.4.2-1**
FLOOR HUGENHOLTZ, JING ZHANG, PAUL W. O'TOOLE, AND HAUKE SMIDT
- 4.4.3 Animal Gut Microbiomes / 4.4.3-1**
RICHARD J. ELLIS AND CHRISTOPHER S. MCSWEENEY

MICROBIAL ECOLOGY

VOLUME EDITOR: ROBERT V. MILLER
SECTION EDITORS: LARRY J. FORNEY, ROBERT H. FINDLAY, BRIAN P. HEDLUND, AND JULIAN R. MARCHESI

4.1 THEORY

BIODEGRADATION AND BIOTRANSFORMATION

VOLUME EDITOR: CINDY H. NAKATSU
SECTION EDITORS: CINDY H. NAKATSU AND CHRISTOPHER RENSING

5.1 BIODEGRADATION

5.1.1 Genomic Features and Genome-Wide Analysis of Dioxin-Like Compound Degradors / 5.1.1-1

MASAKI SHINTANI AND KAZUHIDE KIMBARA

5.1.2 Biodegradation of Organochlorine Pesticides / 5.1.2-1

YUJI NAGATA, MICHIO TABATA, YOSHIYUKI OHTSUBO, AND MASATAKA TSUDA

5.1.3 Anaerobic Degradation of Aromatic Compounds / 5.1.3-1

WEIMIN SUN, VALDIS KRUMINS, DONNA E. FENNELL, LEE J. KERKHOF, AND MAX M. HÄGGBLUM

5.1.4 Microbial Electrochemical Technologies Producing Electricity and Valuable Chemicals from Biodegradation of Waste Organic Matters / 5.1.4-1

TAEHO LEE, AKIHIRO OKAMOTO, SOKHEE JUNG, RYUHEI NAKAMURA, JUNG RAE KIM, KAZUYA WATANABE, AND KAZUHITO HASHIMOTO

5.1.5 A Basic Introduction to Aerobic Biodegradation of Petroleum Aromatic Compounds / 5.1.5-1

KENGO INOUE, ONRUTHAI PINYAKONG, KANO KASUGA, AND HIDEAKI NOJIRI

5.1.6 Environmental Systems Microbiology of Contaminated Environments / 5.1.6-1

TERRY C. HAZEN AND GARY S. SAYLER

5.2 BIOTRANSFORMATION

5.2.1 Breathing Iron: Molecular Mechanism of Microbial Iron Reduction by *Shewanella oneidensis* / 5.2.1-1

REBECCA E. COOPER, JENNIFER L. GOFF, BEN C. REED, RAMANAN SEKAR, AND THOMAS J. DICHRISTINA

5.2.2 Experimental Geomicrobiology: From Field to Laboratory / 5.2.2-1

TIMOTHY S. MAGNUSON AND RHESA N. LEDBETTER

5.2.3 Microbial Uses in the Remediation of Metal-Impacted Soils / 5.2.3-1

TIMBERLEY ROANE AND MUNIRA LANTZ

Index I-1

EDITORIAL BOARD

Mark P. Buttner Section 3.2

School of Community Health Sciences, University of Nevada, Las Vegas, Las Vegas, NV 89154

Douglas R. Call Section 2.3

Paul G. Allen School for Global Animal Health, Washington State University, Pullman, WA 99164

Yildiz T. Chambers Section 2.5

CSC Science, Engineering, and Mission Support, Alexandria, VA 22310

Robert H. Findlay Section 4.2

University of Alabama, Department of Biological Sciences, Tuscaloosa, AL 35487

Larry J. Forney Section 4.1

Department of Biological Sciences, University of Idaho, Moscow, ID 83844

Stefan J. Green Section 2.4

Research Resources Center, University of Illinois at Chicago, Chicago, IL 60612

Valerie J. Harwood Section 3.4

Department of Integrative Biology, University of South Florida, Tampa, FL 33620

Brian P. Hedlund Section 4.3

School of Life Sciences, Nevada Institute of Personalized Medicine, University of Nevada, Las Vegas, Las Vegas, NV 89154

Yoichi Kamagata Section 2.1

Bioproduction Research Institute, National Institute of Advanced Industrial Science and Technology (AIST), Tsukuba, Ibaraki 305-8566, Japan

Julian R. Marchesi Section 4.4

School of Biosciences, Cardiff University, Centre for Digestive and Gut Health, Imperial College London, Cardiff, Wales CF10 3AT, United Kingdom

John Scott Meschke Section 2.6

Department of Environmental and Occupational Health Sciences, University of Washington, Seattle, WA 98105

Cleber C. Ouverney Section 2.2

Department of Biological Sciences, San Jose State University, San Jose, CA 95192

Christopher Rensing Section 5.2

Department of Plant and Environmental Sciences, University of Copenhagen, Frederiksberg 1871, Denmark

Ed Topp Section 3.3

Agriculture and Agri-Food Canada, London, ON N5V 4T3, Canada

Gary A. Toranzos Section 3.1

Department of Biology, University of Puerto Rico, San Juan, PR 00932, Puerto Rico

CONTRIBUTORS

MORTEZA ABBASZADEGAN
Arizona State University, Tempe, AZ 85287

ANGELES AGUILERA
Centro de Astrobiología (INTA-CSIC), Madrid 28850, Spain

WARISH AHMED
CSIRO Land and Water Queensland Biosciences Precinct,
St. Lucia, Queensland 4067, Australia

ALBERTO ALMA
Department of Agriculture, Forestry and Food Sciences
DISAFA, University of Turin, Grugliasco I-10095, Italy

ABSAR ALUM
Arizona State University, Tempe, AZ, 85287

YOSHITERU AOI
Institute of Sustainable Sciences and Development, Hiroshima
University, Hiroshima 739-8529 Japan, and Northeastern
University, Boston, MA 02115

MATTHEW J. ARDUINO
Centers for Disease Control and Prevention, Division of
Healthcare Quality Promotion, Atlanta, GA 30329

NICHOLAS J. ASHBOLT
School of Public Health, University of Alberta, Edmonton, AB
T6G 2G7, Canada

CHERYL L. BAIRD
Pacific Northwest National Laboratory, Biochemistry and
Structural Biology, Fundamental and Computational Sciences
Division, Richland, WA 99352

ELISENDA BALLESTÉ
Department of Microbiology, University of Barcelona, Barcelona
08028, Spain

CLAUDIO BANDI
Department of Veterinary Sciences and Public Health,
University of Milan, Milan I-20133, Italy

RACHEL A. BARTHOLOMEW
Pacific Northwest National Laboratory, Chemical and Biological
Signature Sciences Group, National Security Directorate,
Richland, WA 99354

TOM J. BATTIN
Stream Biofilm and Ecosystem Research Laboratory, Ecole
Polytechnique Fédérale Lausanne, CH-1015 Lausanne,
Switzerland

NITIN BHARDWAJ
Advanced Medical Research Institute of Canada, Sudbury, ON
P3E 5J1, Canada

PASCALE BLAIS LECOURS
Centre deRecherché, University Institute of Cardiology and
Pulmonology of Québec, Université de Laval, Québec, QC
G1K7P4, Canada

ANICET R. BLANCH
Department of Microbiology, University of Barcelona, Barcelona
08028, Spain

MARIA LAURA BOSCHIROLI
ANSES French Agency for Food, Environmental &
Occupational Health Safety, Maisons-Alfort Animal Health
Laboratory, Bacterial Zoonoses Unit, Maisons-Alfort 94706,
France

JULIE BRASSARD
Agriculture and Agri-Food Canada, Food Research and
Development Centre, Saint-Hyacinthe, QC J2S 8E3, Canada

ELLEN BRAUN-HOWLAND
Laboratory of Environmental Biology, NYSDOH,
Wadsworth Center, Biggs Laboratory, Empire State Plaza ,
Albany, NY 12201

KELLY R. BRIGHT
University of Arizona, Tempe, AZ 85287

JOHN BROOKS
Genetics and Precision Agriculture Unit, USDA-ARS,
Mississippi State University, Mississippi State, MS 39762

GARY S. BROWN
Lockheed Martin Corporation, Scientific, Engineering,
Response, Analytical Services, Las Vegas, NV 89119

CINDY BRUCKNER-LEA
Pacific Northwest National Laboratory, Richland,
WA 99354

MARK P. BUTTNER

School of Community Health Sciences, University of Nevada,
Las Vegas, Las Vegas, NV 89154

MURULEE BYAPPANAHALLI

USGS Great Lakes Science Center, Ann Arbor, MI 48105

DOUGLAS R. CALL

Paul G. Allen School for Global Animal Health, Washington
State University, Pullman, WA 99164

DAVID A. CARON

Department of Biological Sciences, University of Southern
California, Los Angeles, CA 90089

YILDIZ T. CHAMBERS

CSC Science, Engineering, and Mission Support, Alexandria,
VA 22310

DARRELL P. CHANDLER

Akonni Biosystems, Inc., Frederick, MD 21701

HEATHER COLBURN

Pacific Northwest National Laboratory, Richland,
WA 99354

KEVIN K. CONNELL

Science & Engineering Line of Service, CSC, Alexandria, VA
22310

REBECCA E. COOPER

School of Biology, Georgia Institute of Technology, Atlanta,
GA 30332

PATRICIA CRUZ

School of Community Health Sciences, University of Nevada,
Las Vegas, Las Vegas, NV 89154

DANIELE DAFFONCHIO

Department of Food, Environmental and Nutritional, Sciences,
DeFENS, University of Milan, Milan I-20133, Italy

TAL DAGAN

Institute of Microbiology, Christian-Albrechts-University of
Kiel, Kiel 24118, Germany

RICHARD E. DANIELSON

BioVir Laboratories, Inc., Benicia, CA 94510

PASCAL DELAQUIS

Agriculture and Agri-Food Canada, Pacific Agri-Food Research
Centre, Summerland, BC V0H 1Z0, Canada

VINCENT J. DENEFF

Department of Ecology and Evolutionary Biology, University of
Michigan, Ann Arbor, MI 48109

GEORGE D. DI GIOVANNI

Environmental and Occupational Health Sciences, University of
Texas School of Public Health, El Paso Regional Campus, El
Paso, TX 79902

THOMAS J. DICHRISTINA

School of Biology, Georgia Institute of Technology, Atlanta,
GA 30332

JEREMY A. DODSWORTH

Department of Biology, California State University, San
Bernardino, CA 92407

SAMUEL DOREVITCH

U of Illinois at Chicago, School of Public Health, Chicago,
IL 60612

CAROLINE DUCHAINE

Department of Biochemistry and Microbiology, Université
Laval, Québec, QC G1K7P4, Canada

THILO EICKHORST

Soil Microbial Ecology, University of Bremen, Bremen 28359,
Germany

RICHARD J. ELLIS

Animal and Plant Health Agency, Specialist Scientific Support
Department, New Haw, Surrey KT15 3NB, United Kingdom

SLAVA EPSTEIN

Department of Biology, Northeastern University, Boston,
MA 02115

JOSEPH FALKINHAM

III, Department of Biological Sciences, Virginia Tech,
Blacksburg, VA 24061

GUIDO FAVIA

School of Biosciences and Biotechnology, University of
Camerino, Camerino I-62032, Italy

SABINE FAVRE-BONTÉ

Microbial Ecology Laboratory, UMR 5557, CNRS/University
Lyon I, Villeurbanne 69622, France

DONNA E. FENNELL

Department of Environmental Sciences, School of
Environmental and Biological Sciences, Rutgers, The State
University of New Jersey, New Brunswick, NJ 08901

KATHARINE G. FIELD

Oregon State University, Department of Microbiology,
Corvallis, OR 97331

BARRY S. FIELDS

Division of Global Disease Detection & Emergency Response,
Center for Global Health, Centers for Disease Control and
Prevention, Atlanta, GA 30333

ROBERT H. FINDLAY

University of Alabama, Department of Biological Sciences,
Tuscaloosa, AL 35487

JED A. FUHRMAN

Department of Biological Sciences, University of Southern
California, Los Angeles, CA 90089

ALVIN GAJADHAR

Canadian Food Inspection Agency, Centre for Foodborne and Animal Parasitology, Saskatoon, SK S7N 2R3, Canada

SANGITA GANESH

School of Biology, Georgia Institute of Technology, Atlanta, GA 30332

JENNIFER L. GOFF

School of Biology, Georgia Institute of Technology, Atlanta, GA 30332

HYATT GREEN

US EPA, Office of Research and Development, National Risk Management Research Laboratory, Cincinnati, OH 45268

STEFAN J. GREEN

Research Resources Center, University of Illinois at Chicago, Chicago, IL 60612

JOHN F. GRIFFITH

Southern California Coastal Water Research Program, Costa Mesa, CA 92626

SERGEY A. GRINSHPUN

University of Cincinnati, Center for Health-Related Aerosol Studies, Cincinnati, OH 45267

CHARLES HAGEDORN

Department of Crop and Soil Environmental Sciences, Virginia Tech, Blacksburg, VA 24061

MAX M. HÄGGBLUM

Department of Biochemistry and Microbiology, School of Environmental and Biological Sciences, Rutgers, The State University of New Jersey, New Brunswick, NJ 08901

ALAIN HARTMANN

Agroecology Unit, UMR 1347, INRA/University of Burgundy/AgroSup Dijon, Dijon 21065, France

VALERIE J. HARWOOD

Department of Integrative Biology, University of South Florida, Tampa, FL 33620

KAZUHITO HASHIMOTO

Department of Applied Chemistry, School of Engineering, University of Tokyo, Tokyo 113-8656, Japan

TERRY C. HAZEN

Department of Civil & Environmental Engineering, University of Tennessee/Oak Ridge National Laboratory, Knoxville, TN 37996

BRIAN P. HEDLUND

School of Life Sciences, Nevada Institute of Personalized Medicine, University of Nevada, Las Vegas, Las Vegas, NV 89154

VINCENT HILL

Centers for Disease Control and Prevention, Atlanta, GA 30333

FLOOR HUGENHOLTZ

Wageningen University, Laboratory of Microbiology, TI Food and Nutrition, Netherlands Consortium for Systems Biology, University of Amsterdam, Wageningen 6703HB, The Netherlands

JANINE R. HUTCHISON

Pacific Northwest National Laboratory, Chemical and Biological Signature Sciences Group, National Security Directorate, Richland, WA 99354

M. KHALID IJAZ

R&D Surface Care and Germ Protection, Reckitt Benckiser LLC., Montvale, NJ 07645

KENGO INOUE

University of Miyazaki, Biochemistry and Applied Biosciences, Miyazaki 889-2192, Japan

DANNY IONESCU

Leibniz Institute for Freshwater Ecology and Inland Fisheries, Neuglobsow, Stechlin 16775, Germany

KRISTIN JARMAN

Pacific Northwest National Laboratory, Applied Statistics and Computational Modeling Group, Fundamental and Computational Sciences Directorate, Richland, WA 99354

ECKARDT JOHANNING

Occupational & Environmental Life Science, Fungal Research Group Foundation, Inc., Albany, NY 12203

D. BARRIE JOHNSON

College of Natural Sciences, Bangor University, Bangor LL57 2UW, United Kingdom

SOKHEE JUNG

School of Civil and Environmental Engineering, Yonsei University, Seoul 120-749, Korea

YOICHI KAMAGATA

Bioproduction Research Institute, National Institute of Advanced Industrial Science and Technology (AIST), Tsukuba, Ibaraki 305-8566, Japan

KANO KASUGA

Akita Prefectural University, Department of Biotechnology, Akita 010-0195, Japan

SCOTT P. KEELY

United States Environmental Protection Agency, Cincinnati, OH 45268

LEE J. KERKHOF

Department of Marine and Coastal Sciences, School of Environmental and Biological Sciences, Rutgers, The State University of New Jersey, New Brunswick, NJ 08901

JUNG RAE KIM

School of Chemical and Biomolecular Engineering, Pusan National University, Pusan 609-735, Korea

KAZUHIDE KIMBARA

Department of Applied Chemistry and Biochemical Engineering, Graduate School of Engineering, Shizuoka University, Hamamatsu, Shizuoka 432-8561, Japan

JULIE KINZELMAN

City of Racine Health Department, Racine, WI 53403

THORSTEN KLÖSGES

Institute of Molecular Evolution, Heinrich-Heine University Düsseldorf, Düsseldorf 40225, Germany

ASJA KORAJKIC

US Environmental Protection Agency, Cincinnati, OH 45268

DARREN R. KORBER

Department of Food and Bioproduct Science, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada

PAULA KRAUTER

Sandia National Laboratories (retired), Livermore, CA 94550

VALDIS KRUMINS

Department of Environmental Sciences, School of Environmental and Biological Sciences, Rutgers, The State University of New Jersey, New Brunswick, NJ 08901

MYRON T. LA DUC

Jet Propulsion Lab, California Institute of Technology, Pasadena, CA 91109

RUP LAL

Department of Zoology, University of Delhi, Delhi 110007, India

GIDDY LANDAN

Institute of Microbiology, Christian-Albrechts-University of Kiel, Kiel 24118, Germany

MUNIRA LANTZ

Department of Integrative Biology, University of Colorado, Denver, Denver, CO 80217

JOHN R. LAWRENCE

Environment Canada, Saskatoon, SK S7N3H5, Canada

RHESA N. LEDBETTER

Department of Chemistry and Biochemistry, Utah State University, Logan, UT 84322

TAEHO LEE

Department of Environmental Engineering, Pusan National University, Pusan 609-735, Korea

JAY T. LENNON

Department of Biology, Indiana University, Bloomington, IN 47405

ESTELLE LEVETIN

Department of Biological Science, The University of Tulsa, Tulsa, OK 74104

DE-WEI LI

Connecticut Agricultural Experiment Station Valley Laboratory, Windsor, CT 06095

CLARESSA E. LUCAS

Division of Bacterial Diseases, National Center for Infectious Disease, Centers for Disease Control and Prevention, Atlanta, GA 30333

MICHAEL D.J. LYNCH

Department of Biology, University of Waterloo, Waterloo, ON N2L 3G1, Canada

TIMOTHY S. MAGNUSON

Department of Biological Sciences, Idaho State University, Pocatello, ID 83209

GEDIMINAS MAINELIS

Rutgers University, New Brunswick, NJ 08901

MOHAMMAD MANAFI

Institute for Hygiene and Applied Immunology, Medical University of Vienna, Vienna 1090, Austria

JULIAN R. MARCHESI

School of Biosciences, Cardiff University, Centre for Digestive and Gut Health, Imperial College London, Cardiff, Wales CF10 3AT, United Kingdom

J. VAUN MCARTHUR

Savannah River Ecology Laboratory, Aiken, SC 29803

CHRISTOPHER S. MCSWEENEY

CSIRO Animal, Food and Health Services, Queensland Biosciences Precinct, St. Lucia, Queensland 4067, Australia

JOHN SCOTT MESCHKE

Department of Environmental and Occupational Health Sciences, University of Washington, Seattle, WA 98105

HARVEY MINNIGH

Gabriella and Paul Rosenbaum Foundation, Bryn Mawr, PA 19010

ALAN JEFF MOHR

Life Sciences Division, U.S. Army, Dugway Proving Ground, Dugway, UT 84022

LAURA S. MORRIS

School of Biosciences, Cardiff University, Cardiff, Wales CF10 3AT, United Kingdom

YUJI NAGATA

Department of Environmental Life Sciences, Graduate School of Life Sciences Tohoku University, Hatahira, Sendai 980-8577, Japan

RYUHEI NAKAMURA

Department of Applied Chemistry, School of Engineering, University of Tokyo, Tokyo 113-8656, Japan

ANKUR NAQIB
DNA Services Facility, University of Illinois at Chicago,
Chicago, IL, 60613

TAKASHI NARIHIRO
Bioproduction Research Institute, National Institute of
Advanced Industrial Science and Technology (AIST) Tsukuba
605-8566, Japan, and Department of Civil and Environmental
Engineering, University of Illinois at Urbana-Champaign,
Urbana, IL 61801

SYLVIE NAZARET
Microbial Ecology Laboratory, UMR 5557, CNRS/University
Lyon I, Villeurbanne 69622, France

THOMAS R. NEU
River Ecology, Helmholtz Centre for Environmental Research,
Magdeburg 39114, Germany

JOSH D. NEUFELD
Department of Biology, University of Waterloo, Waterloo, ON
NSL 3G1, Canada

MEREDITH B. NEVERS
U.S. Geological Survey, Great Lakes Science Center, Porter,
IN 46304

JUDITH NOBLE-WANG
Centers for Disease Control and Prevention, Division of
Healthcare Quality Promotion, Atlanta, GA 30329

HIDEAKI NOJIRI
The University of Tokyo, Biotechnology Research Center,
Tokyo 13-8657, Japan

YOSHIYUKI OHTSUBO
Department of Environmental Life Sciences, Graduate School of
Life Sciences Tohoku University, Hatahira, Sendai 980-8577,
Japan

AKIHIRO OKAMOTO
Department of Earth Sciences, University of Southern
California, Los Angeles, CA 90089

AHARON OREN
Department of Plant and Environmental Sciences, Institute of
Life Sciences, The Hebrew University of Jerusalem, Jerusalem
91904, Israel

ROBIN K. OSHIRO
Engineering and Analysis Division, USEPA Headquarters,
Washington, DC 20460

PAUL W. O'TOOLE
School of Microbiology & Alimentary Pharmabiotic Centre,
University College Cork, Cork T12 YN60, Ireland

TIMOTHY G. OTTEN
Department of Microbiology, Oregon State University,
Corvallis, OR 97331

CLEBER C. OUVERNEY
Department of Biological Sciences, San Jose State University,
San Jose, CA 95192

WILL A. OVERHOLT
School of Biology, Georgia Institute of Technology, Atlanta,
GA 30332

RICHARD OZANICH
Pacific Northwest National Laboratory, Richland,
WA 99355

HANS W. PAERL
Institute of Marine Sciences, University of North Carolina at
Chapel Hill, Morehead City, NC 28557

DARREN J. PARRIS
School of Biology, Georgia Institute of Technology, Atlanta,
GA 30332

ARMELLE PAULE
Global Institute for Water Security, Saskatoon, SK S7N3H5,
Canada

SUSAN R. PETTERSON
Water & Health Pty Ltd, Salamander Bay, NSW 2317,
Australia

MANTHA S. PHANIKUMAR
Michigan State University, Department of Civil and
Environmental Engineering, East Lansing, MI 48824

ONRUTHAI PINYAKONG
Chulalongkorn University, Department of Microbiology,
Bangkok 10330, Thailand

PASCAL PIVETEAU
Agroecology Unit, UMR 1347 INRA/University of Burgundy/
AgroSup Dijon, Dijon 21065, France

OVIDIU POPA
Institute of Microbiology, Christian-Albrechts-University of
Kiel, Kiel 24118, Germany

GRACIELA RAMÍREZ TORO
Centro de Educación, Conservación e Interpretación
Ambiental, Universidad Interamericana de Puerto Rico, San
Germán, PR 00683, Puerto Rico

BEN C. REED
School of Biology, Georgia Institute of Technology, Atlanta,
GA 30332

TIMBERLEY ROANE
Department of Integrative Biology, University of Colorado,
Denver, Denver, CO 80217

LAURA J. ROSE
Centers for Disease Control and Prevention, Division of
Healthcare Quality Promotion, Atlanta, GA 30329

HODON RYU
US EPA NRMRL/WSWRD/MCCB, Cincinnati, OH 45268

LUCIANO SACCHI
Department of Biology and Biotechnology "L. Spallanzani",
University of Pavia, Pavia I-27100, Italy

MICHAEL SADOWSKY
BioTechnology Institute, University of Minnesota, St. Paul,
MN 55108

NASEER SANGWAN
Department of Zoology, University of Delhi, Delhi 110007, India

TASHA M. SANTIAGO-RODRIGUEZ
Department of Biology, Center for Applications in
Biotechnology, California Polytechnic State University, San
Luis Obispo, CA 93407

JORGE SANTO DOMINGO
US EPA NRMRL/WSWRD/MCCB, Cincinnati, OH 45268

NEHA SARODE
School of Biology, Georgia Institute of Technology, Atlanta,
GA 30332

SYED A. SATTAR
Centre for Research on Environmental Microbiology, University
of Ottawa, Ottawa, ON K1H 8M5, Canada

GARY S. SAYLER
Department of Microbiology, University of Tennessee,
Knoxville, TN 37996

HANNES SCHMIDT
Soil Microbial Ecology, University of Bremen, Bremen 28359,
Germany

RAMANAN SEKAR
School of Biology, Georgia Institute of Technology, Atlanta, GA
30332

SHERRY L. SESTON
Department of Biology, Alverno College, Milwaukee,
WI 53234

ORIN C. SHANKS
US EPA, Office of Research and Development, National
Risk Management Research Laboratory, Cincinnati, OH 45268

MASAKI SHINTANI
Department of Applied Chemistry and Biochemical
Engineering, Graduate School of Engineering, Shizuoka
University, Hamamatsu, Shizuoka 432-8561, Japan

LAURA Y. SIFUENTES
University of Arizona, Tempe, AZ 85287

HAUKE SMIDT
Wageningen University, Laboratory of Microbiology, TI Food
and Nutrition, Netherlands Consortium for Systems Biology,

University of Amsterdam, Wageningen 6703HB, The
Netherlands

JAMES A. SPRY
Jet Propulsion Lab, California Institute of Technology, Pasadena,
CA 91109

LINDA D. STETZENBACH
University of Nevada, Las Vegas, Las Vegas, NV 89154

FRANK J. STEWART
School of Biology, Georgia Institute of Technology, Atlanta,
GA 30332

DON STOECKEL
Batelle Memorial Institute, Columbus, OH 43201

TIMOTHY M. STRAUB
Pacific Northwest National Laboratory, Chemical and Biological
Signature Sciences Group, National Security Directorate,
Richland, WA 99354

GREGORY D. STURBAUM
ALS Laboratory Group, Molecular Biology, Scoresby, VIC 3179,
Australia

WEIMIN SUN
Department of Biochemistry and Microbiology, Department
of Environmental Sciences, School of Environmental and
Biological Sciences, Rutgers, The State University of New Jersey,
New Brunswick, NJ 08901

MICHIRO TABATA
Department of Environmental Life Sciences, Graduate School of
Life Sciences Tohoku University, Hatahira, Sendai 980-8577,
Japan

SCOTT C. THOMAS
School of Life Sciences, University of Nevada Las Vegas, Las
Vegas, NV 89154

ERIC C. THOMPSON
King County Environmental Laboratory, Seattle,
WA 98119

PETER S. THORNE
Department of Occupational and Environmental Health,
The University of Iowa, College of Public Health, Iowa City,
IA 52246

GARY A. TORANZOS
Department of Biology, University of Puerto Rico, San Juan,
PR 00932, Puerto Rico

MASATAKA TSUDA
Department of Environmental Life Sciences, Graduate School of
Life Sciences, Tohoku University, Hatahira, Sendai 980-8577,
Japan

R. CARY TUCKFIELD
ECOSTATys LLC., Aiken, SC 29803

PARAG VAISHAMPAYAN

Jet Propulsion Lab, California Institute of Technology, Pasadena,
CA 91109

SUSAN M. VARNUM

Pacific Northwest National Laboratory, Biochemistry and
Structural Biology, Fundamental and Computational Sciences
Division, Richland, WA 99352

KASTHURI VENKATESWARAN

Jet Propulsion Lab, California Institute of Technology, Pasadena,
CA 91109

ERIC N. VILLEGAS

United States Environmental Protection Agency, Cincinnati,
OH 45268

KAZUYA WATANABE

School of Life Science, Tokyo University of Pharmacy and Life
Sciences, Tokyo 192-0392, Japan

JENNIFER WEIDHAAS

West Virginia University, Civil and Environmental Engineering,
Morgantown, WV 26506

MARK H. WEIR

Department of Public Health, Department of Civil and
Environmental Engineering, Temple University, Philadelphia,
PA 19122

RICHARD L. WHITMAN

U.S. Geological Survey, Great Lakes Science Center, Porter,
IN 46304

KLAUS WILLEKE

University of Cincinnati, Cincinnati, OH 45267

GIDEON M. WOLFAARDT

Department of Chemistry and Biology, Ryerson University,
Toronto, ON M5B2K3, Canada

CHIN S. YANG

Prestige EnviroMicrobiology, Voorhees, NJ 08043

MARYLYNN V. YATES

Department of Environmental Sciences, University of
California, Riverside, Riverside, CA 92521

CHUANLUN L. ZHANG

State Key Laboratory of Marine Geology School of Ocean and
Earth Sciences, Tongji University, Shanghai 201804, China

JING ZHANG

Wageningen University, Laboratory of Microbiology,
Wageningen 6703HB, The Netherlands

NICOLETTE A. ZHOU

Department of Environmental and Occupational Health
Sciences, University of Washington, Seattle, WA 98105

INTRODUCTION

MARYLYNN V. YATES

1.1.1

There are bred certain minute creatures which cannot be seen by the eyes, which float in the air and enter the body through the mouth and nose and there cause serious diseases.

— Marcus Terentius Varro, *De Re Rustica*
[On Agriculture], 37 BC

Environmental microbiology might be considered by some to be an ill-defined subject: Where does the environment begin, and where does it end? From Marcus Terentius Varro's observations regarding unseen “minute creatures” more than two millennia ago to Antonie van Leeuwenhoek's first glimpse of the “animalcula” beneath his lens, there is no place on Earth—from thermophilic, acidic springs to the air we breathe to the deepest subsurface locations we have yet been able to reach—where people have looked and *not* found microorganisms of some type. The domain of what may be considered environmental microbiology thus continues to expand beyond the textbook definition of “the study of microorganisms existing in natural and artificial environments.” At the same time, our knowledge of microorganisms is increasing at an ever-more rapid rate as the result of incredible improvements in analytical methodology, especially at the molecular level. When compiling a manual of this nature, therefore, how does one determine what to include and what to exclude? In the end, the editors decided to showcase as much information as possible on some of the most important areas of environmental microbiology, to provide a clear sense of the possibilities presented by the existence of microorganisms in various environments. Further and more detailed information can be found in the wealth of expertly chosen references within each chapter.

This edition of the *Manual of Environmental Microbiology* has been reorganized, with new and updated sections to provide recent information on topics of importance to the field. The General Methodology volume, beginning with Section 2.1, is devoted to methodologies—the “how” of environmental microbial studies from analytical detection to sample collection. The methods presented in this volume are the basis of how we understand the microbial world around us and are used across environmental microbial disciplines and applications. General Methodologies begins with tried-and-true culture-based and physiological detection methods, microscopy-based methods, and molecular target-specific detection

methods, before moving on to address the increasingly important study of microbes at the community level, thanks to the advent of next-generation sequencing technologies. This volume concludes with information on critical topics that are sometimes overlooked in environmental microbiology: quality assurance and quality control, which increase the usefulness and reliability of analytical data for downstream decision making.

The next volume, *Environmental Public Health Microbiology*, surveys the microorganisms in the water, air, or soil that can cause illness when humans are exposed to them. These potentially pathogenic microorganisms can take many avenues en route to their target host, ultimately leading to substantial health impacts and considerable negative economic and social consequences to the communities involved. The importance of understanding microbial distribution and detection for public health cannot be understated. This volume includes chapters describing the field of microbial source tracking; methods and approaches for determining predominant sources of fecal pollution of water, which has become a critical component of assessment; and determining ways to better protect water from microbial contamination. It culminates in a section on microbial risk assessment, integrating the information in the earlier sections and providing perspective for informed decision making and rational project design.

The *Microbial Ecology* volume addresses the various ways microorganisms can be classified and their interconnected relationships, with each other and with macroorganisms, and impacts on the environment. Some microorganisms are native to their environment and perform essential services, such as cycling nutrients or interacting with other organisms in ways that enable them to perform functions and/or inhabit environments where they would otherwise not exist. Other microorganisms may be introduced to a new environment, changing the overall ecosystem. This volume begins with an exploration of the theories behind microbial genome evolution and the evolutionary ecology of microorganisms. The subject matter then delves into more specific environments, including aquatic environments, environments with extreme conditions (extreme acidity, high salinity, low biomass, and high temperatures), and the unique environment inside the gastrointestinal tract of animals, an area of increasing study and data.

1.1.1-2 ■ INTRODUCTION

The final volume, Biodegradation and Biotransformation, focuses on the varied ways that microorganisms can transform or degrade nearly any natural or anthropogenic chemical compound. Since the earliest eras of the Industrial Revolution, study of microorganisms for these processes has been an active area of research. Microbial transformations of natural substances can make otherwise unavailable nutrients accessible by living organisms. Additionally, microorganisms can be used to degrade harmful contaminants, either by using the biochemical pathways naturally present or by employing genetic modification. These abilities have been exploited in numerous situations in which soil or water has been contaminated by organic or inorganic chemicals as well as for a variety of industrial and commercial uses.

Microorganisms play a critical role in the health and well-being of the planet and the human, animal, and plant life that dwells here. Our understanding of them is crucial for maintaining the environment. This fourth edition of the *Manual of Environmental Microbiology* builds on the solid foundation created by the previous three editions, and we are indebted to those who came before us. This edition is truly a collaborative triumph, and is the work of 19 editors and more than 180 contributing authors who generously gave their time, effort, and expertise. It is my hope that this reference serves as an informative and reliable source of information for current and future endeavors in environmental microbiology and inspires the next generation of researchers as they move along their path in this growing and important area.

Detection of Specific Taxa Using Chromogenic and Fluorogenic Media

MOHAMMAD MANAFI

2.1.1

OVERVIEW OF FLUOROGENIC AND CHROMOGENIC MEDIA IN ENVIRONMENTAL MICROBIOLOGY

Over the past 20 years, a number of selective chromogenic and fluorogenic media for detection and enumeration of most important bacteria and yeast in particular in food and water have been developed and marketed. Fluorogenic enzyme substrates generally consist of a specific substrate for the specific enzyme such as sugar or amino acid and a fluorogen such as 4-methylumbelliferone, being able to convert UV light (365 nm) to visible light. Chromogenic enzyme substrates are compounds that act as the substrate for specific enzymes and change color due to the action of the enzymes. Most commercially available chromogenic media have exploited indoxyl substrate. Indoxyl and its halogenated derivatives can be derivatized to form a range of esters. Halogenation of the indoxyl molecule has an effect on the color and intensity of the chromogen. 5-Bromo-4-chloro-indoxyl forms a green/blue dye, whereas 5-bromo-6-chloro-indoxyl forms a magenta dye. The incorporation of such substrates into a selective medium can eliminate the need for subculture and further biochemical tests to establish the identity of certain microorganisms. There have been some review papers dealing with the use of these substrates in environmental and clinical microbiology (1–3). A useful review describes the chemistry of chromogens and fluorogens in culture media (4). Some chromogenic or fluorogenic media (e.g., agar *Listeria* according to Ottaviani and Agosti [ALOA] and tryptone-bile-glucuronic [TBX] have therefore been taken up in the standardized ISO methods (ISO 11290-1/A1:2004 and ISO 16649:2001, respectively). This review describes some recent developments in chromogenic and fluorogenic culture media in microbiological diagnostic in particular in food and water microbiology.

GRAM-NEGATIVE BACTERIA

E. coli

E. coli is an important indicator of fecal contamination in samples from the food processing and water purification plants. The new enzymatic definition of *E. coli* is the possession of *uidA* gene coding for β -D-glucuronidase (GUD) as an indicator for *E. coli*. GUD is an enzyme that catalyzes the hydrolysis of β -D-glucopyranosiduronic acids into their

corresponding aglycons and D-glucuronic acid (5, 6). GUD activity is measured by using different chromogenic and fluorogenic substances such as 4-methylumbelliferyl- β -D-glucuronide (Fig. 1, MUG) or 5-bromo-4-chloro-3-indolyl- β -D-glucuronide. MUG has been incorporated into different media, including lauryl sulfate broth, lactose broth, m-Endo broth, EC broth, violet red bile agar, ECD agar, MacConkey agar and m-FC agar, and are described earlier (7). The disadvantage of incorporating MUG into solid media is that fluorescence diffuses rapidly from the colonies into the surrounding agar. The chromogenic substrate 5-bromo-4-chloro-3-indolyl- β -D-glucuronide (BCIG) is added into TBX agar. GUD cleaves BCIG, and the released chromophore causes distinct blue-green-colored colonies of *E. coli* and complies with the ISO/DIS Standard 16649 for the enumeration of *E. coli* in food and animal feeding stuffs.

Coliform

The new definition of coliforms, which is not method related, is the possession of *lacZ* gene coding for β -D-galactosidase which is responsible for the cleavage of lactose into glucose and galactose. The determination of β -D-galactosidase is accomplished by using substrates such as 6-bromo-3-indolyl- β -galactopyranoside (Salmon-Gal, red), 5-bromo-4-chloro-3-indolyl- β -D-galactopyranoside (Fig. 2, blue) or fluorogenic substrate 4-methylumbelliferyl- β -D-galactopyranoside (blue fluorescence under UV light). Attempts were made to enhance the coliform assay response by adding 1-isopropyl- β -D-thiogalactopyranoside (IPTG) to the media (8) increasing the β -D-galactosidase activity by improving the transfer of the substrate and/or enzyme across the outer membrane. IPTG molecule induces the *lac* operon but unlike the natural substrate it cannot be hydrolysed by β -galactosidase.

E. coli and Coliforms

Commercially available media have been developed which permit rapid simultaneous detection of *E. coli* and coliforms (Table 1) such as the Colilert system (IDEXX, Branford, CT), LMX broth, and ReadyCult coliforms (Merck, Germany). Other representative examples are MI agar (Becton-Dickinson, USA), CHROMagar CCA (CHROMagar, France), or Chromocult coliforms (Merck). Comparative studies have been done and are reviewed elsewhere (1). Schets et al. (47) compared Colilert with Dutch standard enumeration methods for *E. coli* and coliforms in water and

2.1.1-2 ■ CULTURE-BASED AND PHYSIOLOGICAL DETECTION

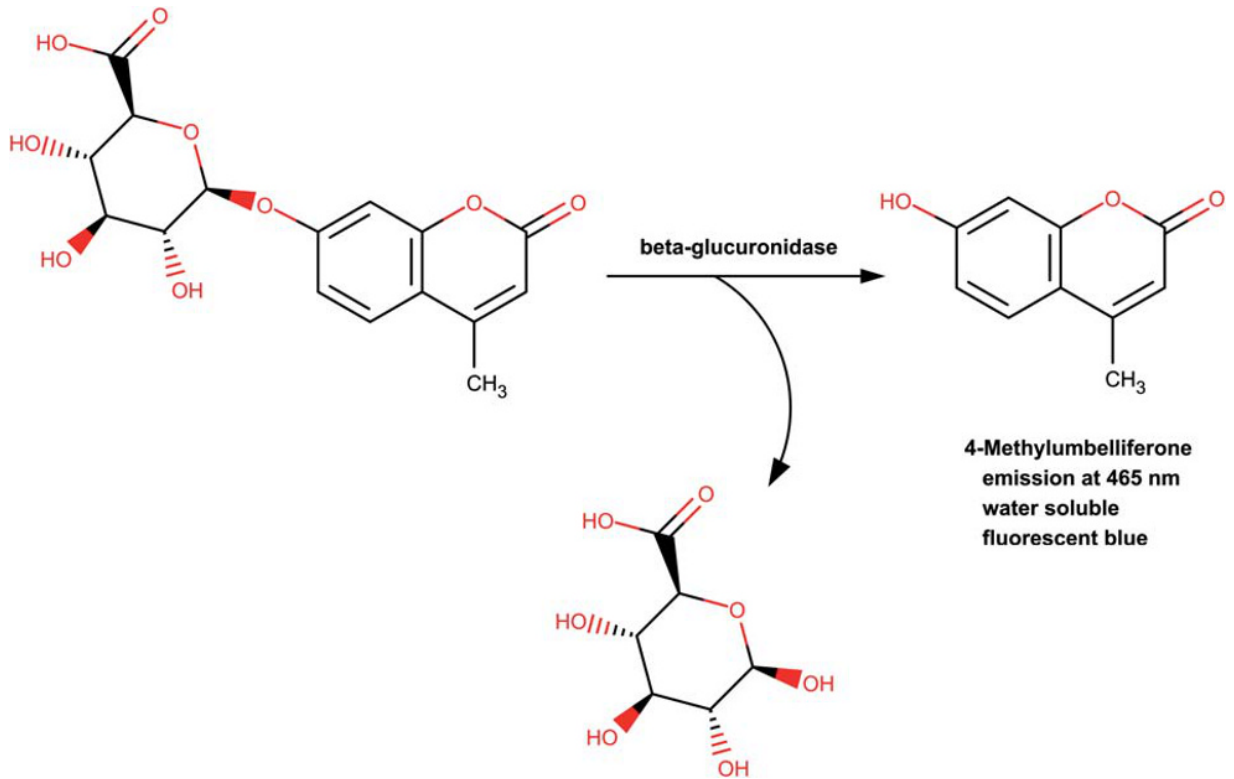


FIGURE 1 Structure of 4-Methylumbelliferyl-beta-D-glucuronide (MUG) for detection of *E. coli*. doi:10.1128/9781555818821.ch2.1.1.f1

found that Colilert gave false-negative results in samples with low numbers of *E. coli* or total coliforms. An evaluation of a number of presence/absence (P/A) tests for coliforms and *E. coli*, including LMX broth (Merck) and Colilert (IDEXX) has been published under the Department of the Environment series in the United Kingdom (48). The study concludes that there is no P/A test that is best at all locations for both coliforms and *E. coli*, and as there can be marked ecological differences between sources it is important that particular P/A tests are validated in each geographical area before use. The MI agar method (10) containing indoxyl- β -D-glucuronide and 4-methylumbelliferyl- β -D-galactopyranoside for the simultaneous detection of *E. coli* and total coliforms, was compared with the approved method by the use of wastewater-spiked tap water samples. Overall, weighted analysis of variance (significance level 0.05) showed that the MI

agar recoveries of total coliforms and *E. coli* were significantly higher than those of mEndo agar. MI agar method is approved for detecting total coliforms and *E. coli* under the total coliforms rule and for enumerating total coliforms under the surface water treatment rule in the United States. Byamukama et al. (49) described the quantification of *E. coli* contamination with Chromocult coliform agar from different polluted sites in a tropical environment. It proved to be efficient and feasible for determining fecal pollutions in the investigated area within 24 h. Blue coloration in the broth indicates the presence of total coliforms and/or *E. coli*.

***E. coli* O157:H7**

E. coli O157:H7 is an important foodborne pathogen and can cause diarrhea, hemorrhagic colitis, and hemolytic uremic syndrome. Several chromogenic media have been applied to

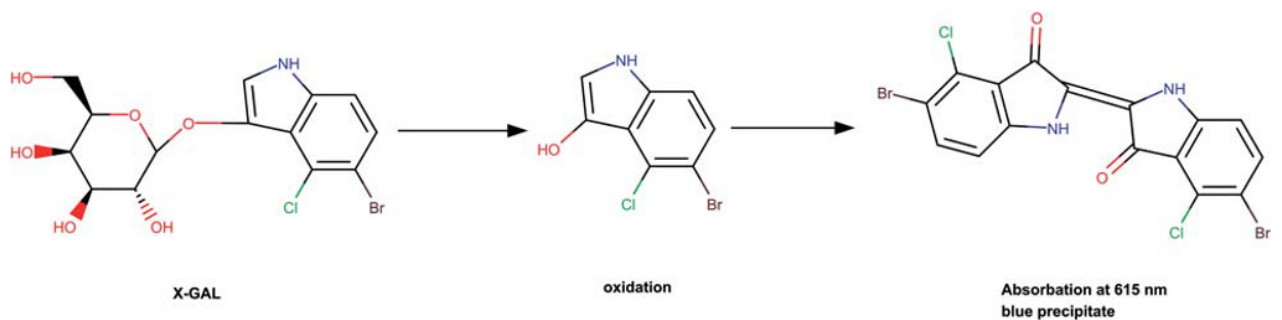


FIGURE 2 Structure of X-GAL (5-bromo-4-chloro-3-indolyl-beta-D-galactopyranoside) for detection of coliforms. doi:10.1128/9781555818821.ch2.1.1.f2

TABLE 1 Example of commercial chromogenic and fluorogenic culture media

Target	Medium/colony color	Company	Reference
<i>E. coli</i> /coliforms	ReadyCult (<i>E. coli</i> : blue fluorescence /coliforms blue green coloration)	Merck (Germany)	9
	MI-agar (<i>E. coli</i> : blue colonies/coliforms blue fluorescence)	BD (USA)	10
	LMX broth (<i>E. coli</i> : blue fluorescence /coliforms blue green coloration)	Merck (Germany)	11
	Chromocult (<i>E. coli</i> : blue colonies/coliforms red colonies)	Merck (Germany)	12
	Coli Complete (<i>E. coli</i> : blue fluorescence /coliforms blue green coloration)	Biocontrol (USA)	13
<i>E. coli</i> O157:H7	m-Colibblue (<i>E. coli</i> : blue colonies/coliforms red colonies)	Hach (USA)	14
	CHROMagar O157 (red)	CHROMagar (France)	15
<i>Salmonella</i> spp.	Rainbow agar O157 (black)	Biolog (USA)	16, 17
	BCM <i>E. coli</i> O157:H7 (blue-black)	Biosynth (Switzerland)	18
	SM ID medium and SM ID 2-medium (red)	BioMérieux (France)	19
	BBL CHROMagar <i>Salmonella</i> (mauve)	BD (USA)	20
	Harlequin <i>Salmonella</i> ABC (green)	lab m (England)	21
<i>Cronobacter sakazakii</i>	Rambach agar (red)	Merck (Germany)	22
	<i>Salmonella</i> -Chromogen-agar	Oxoid (England)	23
	DFI agar (blue)	Oxoid (England)	24
<i>Yersinia enterocolitica</i>	ESPM (blue)	R&F Laboratories	25
ESBL	CHROMagar <i>Yersinia</i> , pathogenic (mauve) and nonpathogenic (blue).	CHROMagar (France)	26
	ChromID ESBL	bioMérieux (France)	27
<i>Vibrio</i> sp.	Brilliance ESBL agar	Oxoid (England)	27
	CHROMagar <i>Vibrio</i>	CHROMagar (France)	28
<i>Staphylococcus aureus</i>	Bio-Chrome <i>Vibrio</i> medium	BioMedix, USA	29
	CHROMagar <i>Staph. aureus</i>	CHROMagar (France)	30
MRSA	<i>S. aureus</i> ID agar (SA ID)	BioMérieux (France)	31
	CHROMagar MRSA	CHROMagar (France)	32
<i>Listeria monocytogenes</i>	MRSASelect	Bio-Rad (USA)	32
	BCM <i>Listeria monocytogenes</i> plating medium	Biosynth (Switzerland)	33
	CHROMagar <i>Listeria</i>	CHROMagar (France)	34
	Oxoid Chromogenic <i>Listeria</i> agar (OCLA)	Oxoid (England)	34
	Rapid ⁺ L.mono	Sanofi (France)	34
<i>Bacillus</i> group	Agar <i>Listeria</i> (ALOA)	AES (France)	34
	BCM <i>Bacillus cereus</i> group	Biosynth (Switzerland)	35
	<i>B. cereus</i> / <i>B. thuringiensis</i> agar	R&F Laboratories (USA)	36
	Chromogenic <i>Bacillus Cereus</i> agar (CBC)	Oxoid (England)	37
<i>Enterococcus</i> spp	<i>Bacillus anthracis</i> agar	R&F Laboratories (USA)	38
	mEI agar (indoxyl- β -D-glucoside)	BD (USA)	39
	Chromocult Enterococci broth and ReadyCult/blue	Merck (Germany)	40
	Chromocult Enterococci agar/red	Merck (Germany)	41
VRE	Enterolert (4-methylumbelliferone - β -D-glucoside)/ blue fluorescence	Idexx (USA)	42
	ChromID VRE agar	bioMérieux (France)	43
<i>Clostridium perfringens</i>	CHROMagar VanRE	CHROMagar (France)	44
	Chromoselect CP/green	Sigma (Switzerland)	45
<i>Clostridium difficile</i>	ChromID <i>C. difficile</i> agar	BioMérieux (France)	46

the detection of *E. coli* O157:H7 from food samples. Most are based on similar principles, relying on nonfermentation of sorbitol and/or rhamnose and lack of β -glucuronidase activity (50). A second chromogenic substrate (for α - or β -galactosidase) may be used to highlight the presence of *E. coli* O157:H7 among nonreactive background flora. Some selective media increase the effectiveness of *E. coli* O157:H7 isolation, including Rainbow agar O157 (RB, Biolog, Hayward, USA), BCM O157:H7 (BCM, Biosynth AG, Staad, Switzerland), Fluorocult *E. coli* O157:H7 (H7, Merck), and CHROMagar O157 (Chromagar).

The performance of three chromogenic agars—Rainbow Agar O157, CHROMagar O157, and O157:H7 ID agar—with a large collection of verotoxigenic and nontoxigenic *E. coli* strains have been tested (15, 16). Another study

compared Rainbow Agar O157, BCM O157:H7, and Fluorocult HC with the conventional Sorbitol MacConkey have showed the clear advantage of the chromogenic media for the isolation of *E. coli* O157:H7 from raw ground beef and raw drinking milk (51). The behavior of *E. coli* O157:H7 was studied during the manufacture and ripening of raw goat milk lactic cheeses using O157:H7 ID (bioMérieux) and CT-SMAC agar (52). In conclusion, this new chromogenic media O157:H7 ID proved to be well suited and simplified many of the inherent problems associated with plate confirmation of *E. coli* O157:H7 using SMAC as subculture media.

Salmonella

The conventional media for the detection of *Salmonella* have a very poor specificity, creating an abundance of false

positives (such as *Citrobacter*, *Proteus*) among the rare real positive *Salmonella*. On Rambach agar, *Salmonella* strains gave red colonies because of their ability to acidify neutral red by fermentation of propylene glycol (22). This medium employs X-gal for β -D-galactosidase positive coliforms. However, the strains of *S. typhi* and *S. paratyphi* fail to produce acid from propylene glycol, resulting in colorless colonies on Rambach agar. Furthermore, the strains of *S. enterica* subspecies *S. arizona* show blue-violet colonies on this medium (53). On SM-ID agar (bioMérieux) *Salmonella* colonies are detected by their distinctive red coloration, while coliforms appear blue, violet, or colorless. A rare study in food microbiology using chromogenic media has been done by Schönerbrücher et al. (23). The draft ISO 6579:2002 was compared to the European gold standard (DIN EN 12824:1998), including the three chromogenic plating media AES *Salmonella* agar plate, Oxoid *Salmonella* chromogen media, and Miller-Mallinson agar. MUCAP-test (Biolife, Italy) is a confirmation test for *Salmonella* species based on the rapid detection of caprylate esterase, using fluorogenic 4-methylumbelliferyl-caprylate. In the presence of C_8 esterase the substrate is cleaved with the release of 4-methylumbelliferone. Strong bluish fluorescence indicates the presence of *Salmonella* spp. Since most of the false-positive strains are oxidase positive, the combination of MUCAP and the oxidase test is recommended (54). Other chromogenic media for detection of *Salmonella* spp. are listed in Table 1.

Shigella

The chromogenic *Shigella* spp. agar (R&F Laboratories, West Chicago, IL), offers intermediate selectivity using bile salts and antibiotic supplementation (55). Colony color enhancements created by the chromogenic *Shigella* spp. agar results from the lack of the *Shigella* to utilize the carbohydrates and metabolize the chromogens. Presumptive positive colonies of *Shigella* sp. appears as white/clear colonies 1.0–3.0 mm diameter with or without a clear ring after 22–28 h incubation, whereas the colonies of other members of the *Enterobacteriaceae* are variously colored. The second medium, xylose galactosidase medium contains bile salts, D-xylose and 5-bromo-4-chloro-3-indolyl- β -D-galactopyranoside and IPTG as biochemical marker (56). *S. sonnei* give green colonies (xylose negative and β -gal positive) and colorless colonies for other species of *Shigella* (xylose and β -gal negative).

Cronobacter (Enterobacter) sakazakii

C. sakazakii is a recently described genus that is composed of six genomospecies. *C. sakazakii* is an occasional contaminant of powdered infant formula that can cause rare but severe foodborne infections such as meningitis, necrotizing enterocolitis, bacteremia, and sepsis in infants. *C. sakazakii* possesses α -glucosidase activity and a number of selective, chromogenic agars for *C. sakazakii* are based on the detection of this enzyme (57, 58, 59). 5-Bromo-4-chloro-3-indolyl- α -D-glucopyranoside (X- α -Glc) is added to a basal medium to differentiate *C. sakazakii* strains from other members of the *Enterobacteriaceae*. The enzyme α -glucosidase hydrolyses X- α -Glc, giving blue-colored colonies on DFI agar (Oxoid, UK), ESIA agar (recommended by ISO/TS 22964, AES, France), Compas (Biokar, France), or Chromocult *E. sakazakii* (Merck), which are commercially available. Hi Chrome *E. sakazakii* agar (Sigma-Aldrich) also complies with the formulation recommended in ISO/TS 22964.

A dual chromogenic medium (ESPM) is available from R&F Laboratories (25), as well as from bioMérieux

(ChromID *Sakazakii*). A second substrate, 5-bromo-4-chloro-3-indolyl- β -cellobioside, is included in this medium. A mix of carbohydrates such as D-sorbitol, D-arabitol, and adonitol and antibiotics vancomycin and cefsulodin are added. *Cronobacter* colonies appear blue-black, with most other species appearing as colorless, yellow, or green colonies. 4-Methylumbelliferyl- α -D-glucoside, the fluorogenic substrate of α -D-glucosidase, was used as a selective marker to develop a differential medium for *C. sakazakii*. This bacterium showed strong fluorogenic characteristics clearly distinguishable from other microorganisms. On the basis of reducing background noise, an optimum basal medium and nitrogen source were selected. Incubation conditions were optimized (60, 61).

Extended-Spectrum β -lactamase (ESBL)

Rapid detection of extended-spectrum β -lactamase (ESBL)-producing Gram-negative bacilli in surveillance samples of high-risk patients allows early optimization of antimicrobial therapy and timely introduction of infection control procedures. BLSE (AES Chemunex), chromID ESBL (bioMérieux), and Brilliance ESBL agar (Oxoid) for rapid detection of ESBL-producing *Enterobacteriaceae* are the few available chromogenic media (27). A comprehensive study from Germany showing a high prevalence of TEM-, CTX-M-, and SHV-type ESBLs in *Enterobacteriaceae* isolated from retail chicken meat. The high rate of coresistance to different classes of antibiotics in the ESBL producers might reflect the common veterinary usage of these and related substances (62).

Yersinia enterocolitica

Weagant (63) described an agar, so-called YeCM, for detection of potentially virulent *Y. enterocolitica*. This agar contains cellobiose as the fermentable sugar, a chromogenic substrate, and selective inhibitors for suppression of colony formation by many competing bacteria. The strains of biotypes 1B, and biotypes 2–5 formed convex, red bull's-eye colonies on YeCM. *Y. enterocolitica* biotype 1A and other related *Yersinia* formed colonies that were purple/blue on YeCM while they formed typical red bull's-eye colonies on CIN agar. Commercially available CHROMagar *Yersinia* is a new chromogenic medium for the presumptive detection of virulent *Y. enterocolitica* in stools (26).

Campylobacter

R & F *Campylobacter jejuni*/C. coli is a new chromogenic plating medium. Presumptively positive colonies of *C. jejuni*/C. coli appear as dark salmon flat to convex colonies, 1.0–2.0 mm in diameter with and without a clear ring after 48 h at 41–42°C under microaerophilic conditions. Brilliance CampyCount Agar (Oxoid) is specifically designed for accurate, specific, and easy enumeration of *C. jejuni* and *C. coli* from poultry testing. It is a transparent medium on which *Campylobacter* produce distinct dark red colonies, making identification and counting of *Campylobacter* significantly easier than on traditional charcoal or blood-containing agar.

Vibrio

Vibrio parahaemolyticus has been one of the most important foodborne pathogens in Japan since the 1960s, and a large epidemic was caused by the pandemic serotype O3:K6 from 1997 to 2001. The traditional most-probable number (MPN) method using thiosulfate-citrate-bile-salts-sucrose medium (TCBS) for detecting *V. parahaemolyticus* cannot differentiate growth of *V. parahaemolyticus* from *Vibrio vulnificus*

or *Vibrio mimicus*. Suspicious colonies grown on TCBS need to be confirmed with lengthy biochemical tests. Recently, a chromogenic medium (Bio-Chrome *Vibrio* medium, Bio-Medix, USA) was developed for differentiating *V. parahaemolyticus* from other *Vibrio* species based on the formation of purple colonies by *V. parahaemolyticus* (29, 64). To distinguish *V. vulnificus* from other pathogens that cause necrotizing fasciitis, Nakashima et al. (65) have developed a selective isolation culture agar plate (Chromochecker *Vibrio* Agar) for use in environmental monitoring and the clinical setting. There are a few other chromogenic media for detection of *Vibrio* spp., which shows different color between *V. parahaemolyticus*, *V. cholera*, and *V. vulnificus* such as VVM (66), Chromagar *Vibrio* (28, 67, 68), and *Vibrio* ID (bioMérieux) and further evaluation studies are needed.

GRAM-POSITIVE BACTERIA

Enterococci

Enterococci are used as indicators of fecal contamination of water and food. On the basis of 16S rRNA cataloging, the genus *Streptococcus* was separated during the 1980s into the three genera *Enterococcus*, *Lactococcus*, and *Streptococcus*. Consequently, bacteria previously named *S. faecalis*, *S. faecium*, *S. avium*, and *S. gallinarum* were transferred to the revised genus *Enterococcus* as *E. faecalis*, *E. faecium*, *E. avium*, and *E. gallinarum*, respectively (69). More than 100 modifications of selective media have been described in the past for isolating fecal streptococci or enterococci from various specimens. In most literature, Slanetz-Bartley (70) agar is treated as a suitable MF medium to detect fecal enterococci from a water sample.

The use of chromogenic and fluorogenic substrates for detection of enterococci has received considerable attention (39, 71, 72). Substrates such as 5-bromo-4-chloro-3-indolyl- β -D-glucopyranoside (XGLU) and indoxyl- β -D-glucoside were already described for detection of β -D-glucosidase activity (40). Enterococci produce an insoluble indigo blue complex, which diffuses into the surrounding media, forming a blue halo around the colony. Chromocult *Enterococci* broth (Merck) and ReadyCult *Enterococci* (Merck) utilize the β -D-glucosidase reaction as an indicator for enterococci. XGLU is liberated and rapidly oxidized to bromochloroindigo, which produces blue color in Chromocult broth. Chromocult enterococci agar (EKA, Merck) uses a chromogenic mix in a selective agar; enterococci cleave chromogenic substrates in this medium and show red colonies on the plate. Nonenterococci produce colorless, blue/violet, or turquoise colonies (41).

4-Methylumbelliferyl- β -D-glucoside (MUD) has been proven useful to detect enterococci in water. This substrate, when hydrolyzed by enterococcal β -D-glucosidase, releases 4-methylumbelliferone, which exhibits fluorescence under a UV lamp (365 nm). Enterolert (IDEXX Laboratories), and a Microtiter plate MUST (Sanofi, France) utilize the nutrient indicator substrate MUD as a fluorogenic substrate detecting β -D-glucosidase. The MUD method tended to give slightly lower recoveries than the agar cultivation methods with some target species at 44°C, but recoveries were better than at 41°C (73). It has to be mentioned that there may be some problems with other glucosidase-positive bacteria such as *Aerococcus* spp., in particular in natural contaminated water samples.

Membrane-*Enterococcus* indoxyl- β -D-glucoside agar (mEI agar) is a selective culture medium used for the chromogenic

detection and enumeration of enterococci in water by the single-step membrane filtration technique. It conforms to the U.S. Environmental Protection Agency Approved Method 1600: Enterococci in Water by Membrane Filtration. Rhodes and Kator (74) evaluated mEI agar with respect to specificity and recovery of enterococci from environmental waters. Extending incubation from 24 to 48 h improved enterococci recovery, but 77% of the colonies classified as nontarget were confirmed as enterococci. Messer and Dufour (75) modified the medium by reducing the triphenyltetrazolium chloride from 0.15 to 0.02 g/liter and adding 0.75 g indoxyl β -D-glucoside per liter. The new MF medium, mEI medium, detected levels of enterococci in 24 h comparable to those detected by the original mE medium in 48 h, with the same level of statistical confidence.

Using XGLU Chromocult Enterococci broth (CEB) (Merck) and ReadyCult Enterococci (Merck) utilizes the β -D-glucosidase reaction as an indicator of the presence of enterococci. XGLU is liberated and rapidly oxidized to bromochloroindigo which produces blue color in Chromocult broth as well as blue colored enterococci colonies in Chromocult Enterococci agar. Other β -D-glucosidase-producing organisms were suppressed by the sodium azide content of the broth (40). The results obtained with pure cultures showed that 97% of the strains, which gave positive results, were identified as enterococci (*E. faecalis*, *E. faecium*, *E. durans*, *E. casseliflavus*, and *E. avium*). The false-positive strains (3%) were *Leuconostoc*, *Lactococcus lactis lactis*, and *Aerococcus* spp.

Clostridium perfringens

C. perfringens is an anaerobic, Gram-positive, spore-forming rod-shaped bacterium. They are widespread in the environment and also found in the digestive systems of humans and animals. *C. perfringens* is capable of surviving in soil and water for extended periods of time. Detection and enumeration of *C. perfringens* from food and environmental samples is usually based on cultivation on agar plates, but an MPN technique can also be applied. Several selective culture media for the detection and enumeration of *C. perfringens* are based on sulfite reduction as a differential characteristic and cycloserine as a selective agent. Selectivity of cultivation can be increased by using an elevated incubation temperature, since *C. perfringens* is able to grow rapidly at 45°C. The shortcoming of the selective culture and growth conditions is the poor recovery of injured vegetative cells of *C. perfringens*.

TSC-4-methylumbelliferyl phosphate (MUP) agar incorporates sodium metabisulfite and ferric ammonium citrate as an indicator for sulfite reduction and the disodium salt of MUP for detection of acid phosphatase. D-Cycloserine inhibits the accompanying bacterial flora and causes the colonies to remain smaller. All black colonies on this medium that emit light blue fluorescence when exposed to a UV lamp (365 nm) were counted as presumptive *C. perfringens*. The disadvantage of incorporating MUP into agar is that fluorescence diffuses rapidly from the colonies into the surrounding agar, and therefore the interpretation of the plates is difficult and confusing. The use of (MUP and ortho-nitrophenyl- β -d-galactopyranoside for the identification of *C. perfringens* was investigated (76). A liquid assay containing both compounds was a highly specific alternative method for *C. perfringens* confirmation, reducing incubation time from 48 to only 4 h. The new Chromoselect CP agar is now available, which can be used in the water microbiology (45). *C. perfringens* colonies give green-colored colonies, other

strains of clostridia give violet or blue colonies (Sigma, Switzerland).

Clostridium difficile

C. difficile is the major cause of colitis and pseudomembranous colitis associated with antibiotic treatment. ChromID *C. difficile* agar (bioMérieux) is a new chromogenic medium for isolation and identification of *C. difficile* in 24 h (46).

Listeria monocytogenes

L. monocytogenes is a human and animal pathogen that is widespread in nature. The organism is a transient constituent of the intestinal flora excreted by 1–10% of healthy humans. This organism can survive for many years in the cold in naturally infected sources. *L. monocytogenes* has been isolated from a wide variety of foods, including dairy products, meats, and fish. Although most of the foodborne listeriosis outbreaks have been linked to the consumption of dairy products, recent sporadic cases have been associated with meats as well as other foods. Several virulence genes have been identified in pathogenic *Listeria* spp. The lecithinase operon contains the gene *plcB*. *PlcB* encodes a lecithinase involved in cell-to-cell spread. The gene *plcA* encodes a phosphatidylinositol-specific phospholipase C (PI-PLC) that may contribute to the lysis of the phagosomal membrane. These virulence genes (*plcA*, *plcB*) occur in pathogenic *L. monocytogenes* and *L. ivanovii* (77, 78).

The detection of *L. monocytogenes* in food and environmental samples by cultivation includes enrichment step(s) for resuscitation of injured cells and concentration of the cells, followed by plating on selective media and confirmation of the tentative identifications of suspected colonies by biochemical tests. Current conventional culture techniques take approximately 1 week to complete. The recent methodology development has focused on the optimization of enrichment steps and the development of new differential culture media to obtain faster and more reliable detection of *L. monocytogenes*. Selective chromogenic *L. monocytogenes* plating media offer rapid economic detection and enumeration of pathogenic *Listeria* spp. within 24 or 48 h of incubation at $36 \pm 1^\circ\text{C}$.

Several studies have been done using chromogenic media for the detection of *L. monocytogenes* (34). Their advantages are direct detection and enumeration of pathogenic *Listeria* spp. utilizing cleavage of substrates by the virulence factor PI-PLC and by phosphatidylcholinphospholipase C (PC-PLC). There are two groups of such media: the first utilizes cleavage by PI-PLC of L-alpha-phosphatidyl-inositol, forming a white precipitation zone around the colony, combined with the chromogenic substrate 5-bromo-4-chloro-3-indoxyl-beta-D-glucopyranoside for detection of beta-D-glucosidase, which occurs in all *Listeria* spp. The typical colony morphology of *Listeria* spp. is reported to be turquoise blue (ALOA, CHROMagar *Listeria*). Pathogenic *Listeriae* are additionally surrounded by a translucent halo.

The second group of media such as BCM, Rapid' *L. mono*, and LIMONO-Ident-agar utilizes enzyme substrate 5-bromo-4-chloro-3-indoxyl-myo-inositol-1-phosphate (X-phos-Inositol, BIOSYNTH). Enzymatic cleavage of X-phos-Inositol leads to turquoise colonies of pathogenic *Listeria* spp. easy to enumerate (*L. monocytogenes* and *L. ivanovii*). Nonpathogenic *Listeria* spp. appears clearly distinguishable as white colonies. BCM *L. monocytogenes* Plating Medium II and LIMONO-Ident-Agar additionally combine the cleavage of X-phos-Inositol in forming turquoise colonies of pathogenic *Listeria* spp. with production of a white precipitate surrounding

these colonies. This precipitate is formed by addition of a selected lecithin–mixture (79, 80). For that reason, both virulence genes (*plcA* and *plcB*) may be involved in forming this precipitation zone (33). Rapid L'MONO agar (Sanofi, France) is based on the detection of phosphatidylinositol phospholipase C and xylose fermentation. In this way, the colonies of *L. ivanovii* appear blue surrounded by a yellow halo (xylose positive) whereas the colonies of *L. monocytogenes* are blue without the halo (xylose negative).

Stessel et al. (81) evaluated six chromogenic media similar to ALOA. Additionally, the ability of chromogenic agars to facilitate growth of stressed *L. monocytogenes* strains and mixed cultures with competitive non-*Listeria* strains was estimated. They have found that the competitive flora of food samples is able to overgrow low numbers of *L. monocytogenes*, especially in half-Fraser enrichment. This might lead to the underestimation of *L. monocytogenes* positive samples.

CHROMagar *Listeria* agar (CHROMagar), OCLA (Oxoid), Compass *L. mono* (Biokar), OAA (bioMérieux), and Chromoplate *Listeria* (Merck) are some of this kind of chromogenic media.

B. cereus, *B. thuringiensis*, and *B. anthracis* Group

Bacillus species is a group of ubiquitous facultative anaerobic spore-forming Gram-positive rods commonly found in soil. The spores frequently contaminate a variety of foods, including produce, meat, eggs, and dairy products. Several selective and nonselective culture media have been developed for the detection of *B. cereus* from foods. The enumeration of *B. cereus* in food and industrial samples is commonly based on a plate-counting culture technique, except for samples with low cell numbers (<10 CFU/g), for which the MPN method is preferred. BCM *Bacillus cereus* group Plating Medium (Biosynth) utilizes the production of the enzyme PI-PLC cleaving substrate 5-bromo-4-chloro-3-indoxyl myo-inositol-1-phosphate by members of the *B. cereus* group (except *B. anthracis*). Typical dull blue-turquoise colonies appear on this plating medium, easy to recognize and count (35). *B. anthracis* grows on BCM *Bacillus cereus* group plating medium in size and shape like *B. cereus*, but with white colonies.

B. anthracis chromogenic agar (ACA) has been evaluated by Juergensmeyer et al. (36). ACA contains the chromogenic substrate 5-bromo-4-chloro-3-indoxyl-choline phosphate that on hydrolysis yields blue green colonies indicating the presence of PC-PLC activity. Examination of colony morphology in 18 pure culture strains of *B. anthracis* required 48 h at 35–37°C for significant color production, whereas only 24 h was required for *B. cereus* and *B. thuringiensis*. This differential rate of PC-PLC synthesis in *B. anthracis* (due to the truncated *PlcR* gene and *PlcR* regulator in *B. anthracis*) allowed for the rapid differentiation on ACA of presumptive colonies of *B. anthracis* from *B. cereus* and *B. thuringiensis* in both pure and mixed cultures. The performance of two chromogenic plating media (CBC and BCM) was compared with two standard selective plating media (PEMBA and MYP) recommended by food authorities for isolation, identification, and enumeration of *B. cereus* (37). The Chromogenic *Bacillus Cereus* agar (CBC; Oxoid) contains 5-bromo-4-chloro-3-indolyl-beta-D-glucopyranoside that is cleaved by beta-D-glucosidase and results in white colonies with a blue-green center. Tallent et al. (82) evaluated the use of Bacara, a new chromogenic agar, as an efficient method to identify and enumerate *B. cereus* group from food matrixes, even in the presence of background flora.

Staphylococcus aureus

S. aureus is a major pathogenic bacterium found in clinical field and in food industry. Nosocomial infections due to *S. aureus* create an increasing number of problems, so it is becoming more important to detect *S. aureus* in foods and clinical microbiology. CHROMagar *S. aureus* is a selective agar medium that employs a combination of chromogenic enzyme substrates. *S. aureus* strains grow as typical pink-colored colonies on this medium, whereas most other staphylococci produce white or occasionally blue colonies (30). *S. aureus* ID (bioMérieux) is similar, and the colonies of *S. aureus* are distinctive green colonies because of production of α -glucosidase. Other staphylococci form white or occasionally pink colonies due to the hydrolysis of a substrate for β -glucosidase (31).

BIFIDOBACTERIA

The use of chromogenic X- α -D-galactoside for differential enumeration of *Bifidobacterium* spp. and lactic acid bacteria was described by Chevalier et al. (83). The X- α -D-galactoside-based medium is useful to identify *Bifidobacteria* among *Lactobacillus* or *Streptococcus* strains. *Bifidobacteria* show blue-colored colonies on the agar plate.

Methicillin-Resistant *S. aureus* (MRSA)

MRSA is a nosocomial pathogen of worldwide importance and an increasingly frequent cause of community-acquired infection. Rapid laboratory diagnosis is critical for treating, managing, and preventing MRSA infections. Different media are available (32) to detect MRSA such as Brilliance MRSA agar (Oxoid), ChromID (bioMérieux), MRSAselect (Bio-Rad), CHROMagar, Spectra MRSA (Remel, Lenexa, KS), and BBL-CHROMagar (BD Diagnostics).

Vancomycin-Resistant Enterococci (VRE)

Strains of enterococci are known to be nosocomial pathogens, which can be involved in infections of the urinary tract, surgical wounds, and the bloodstream. An increasing number of these infections are caused by enterococci that are resistant to vancomycin and to other antibiotics. Chromogenic media are available (43, 44) to detect VRE, such as chromID VRE agar (bioMérieux) and CHROMagar VanRE (BD Diagnostics).

CONCLUSIONS

Rapid detection and identification of microorganisms is of high importance in a diverse array of applied and research fields. Chromogenic and fluorogenic substrates have been used in diagnostic culture media for the past two decades. The incorporation of such substrates into a selective medium can eliminate the need for subculture and further biochemical tests to establish the identity of certain microorganisms.

REFERENCES

1. Manafi M. 2000. New developments in chromogenic and fluorogenic culture media. *Int J Food Microbiol* **60**: 205–218.
2. Manafi M, Kneifel W, Bascomb S. 1991. Fluorogenic and chromogenic substrates used in bacterial diagnostics. *Microbiol Rev* **55**:335–348.
3. Orenga S, James AL, Manafi M, Perry JD, Pincus DH. 2009. Enzymatic substrates in microbiology. *J Microbiol Meth* **79**:139–155.
4. Druggan P. 2012. Chromogens, fluorogens, trojan horses and their use in culture media, p. 623–646. In Corry JEL, Curtis GDW, Baird RM (eds), *Handbook of Culture Media for Food and Water Microbiology*, 3rd ed. RSC Publishing, UK.
5. Bredie WL, de Boer E. 1992. Evaluation of the MPN, Anderson-Baird-Parker, Petrifilm *E. coli* and Fluorocult ECD method for enumeration of *E. coli* in foods of animal origin. *Int J Food Microbiol* **16**:197–208.
6. Hartman PA. 1989. The MUG glucuronidase test for *E. coli* in food and water, p. 290–308. In Turano A, (ed), *Rapid Methods and Automation in Microbiology and Immunology-Brixia* Academic Press, Brescia, Italy.
7. Frampton EW, Restaino L. 1993. Methods for *E. coli* identification in food, water and clinical samples based on β -glucuronidase detection. *J Appl Bacteriol* **74**:223–233.
8. Manafi M. 1995. New medium for the simultaneous detection of total coliforms and *E. coli* in water. Poster, 95th Meeting of the American Society for Microbiology. Washington, DC. Abstr. P-43, p. 389.
9. Manafi M, Rosmann H. 1998. Evaluation of Readycult presence-absence test for detection of total coliforms and *E. coli* in water. Poster, 98th Meeting of the American Society for Microbiology, Atlanta, GA. Abstr. Q-263, p. 464.
10. Brenner KP, Rankin CC, Roybal YR, Stelma GN, Scarpino PV, Dufour AP. 1993. New medium for simultaneous detection of total coliforms and *E. coli* in water. *Appl Environ Microbiol* **59**:3534–3544.
11. Hahn G, Wittrock E. 1991. Comparison of chromogenic and fluorogenic substances for differentiation of coliforms and *E. coli* in soft cheese. *Acta Microbiol Hung* **38**:265–271.
12. Alonso JL, Soriano K, Amoros I, Ferrus MA. 1998. Quantitative determination of *E. coli* and fecal coliforms in water using a chromogenic medium. *J Environ Sci Health* **33**: 1229–1248.
13. Feldsine PT, Falbo-Nelson MT, Hustead D. 1994. Coli-complete® substrate-supporting disc method for confirmed detection of total coliforms and *E. coli* in all foods, Comparative study. *J AOAC Int* **77**:58–63.
14. Grant MA. 1997. A new membrane filtration medium for simultaneous detection and enumeration of *E. coli* and total coliforms. *Appl Environ Microbiol* **63**:3526–3530.
15. Bettelheim KA. 1998. Reliability of CHROMagar O157 for the detection of enterohaemorrhagic *E. coli* EHEC O157 but not EHEC belonging to other serogroups. *Appl Environ Microbiol* **85**:425–428.
16. Bettelheim KA. 1998. Studies of *E. coli* cultured on Rainbow agar O157 with particular reference to enterohaemorrhagic *E. coli* (EHEC). *Microbiol Immunol* **42**:265–269.
17. Bochner BR. 1995. Rainbow Agar VTEC, a new chromogenic culture medium for detecting verotoxin-producing *E. coli*. Poster, Australian Society for Microbiology, Poster 2.1.
18. Restaino L, Frampton EW, Turner KM, Allison DR. 1999. A chromogenic plating medium for isolating *E. coli* O157: H7 from beef. *Lett Appl Microbiol* **29**:26–30.
19. Monnery I, Freydière AM, Baron C, Rousset AM, Tigaud S, Boude-Chevalier M, de Montclosand H, Gille Y. 1994. Evaluation of two new chromogenic media for detection of *Salmonella* in stools. *Eur J Clin Microbiol Infect Dis* **13**: 257–261.
20. Gaillot O, DiCamillo P, Berche P, Courcol R, Savage C. 1999. Comparison of CHROMagar *Salmonella* medium and Hektoen enteric agar for isolation of *Salmonellae* from stool samples. *J Clin Microbiol* **37**:762–765.
21. Perry JD, Ford M, Taylor J, Jones AL, Freeman R, Gould FK. 1999. ABC medium, a new chromogenic agar for the selective isolation of *Salmonella* spp. *J Clin Microbiol* **37**: 766–768.

22. Rambach A. 1990. New plate medium for facilitated differentiation of *Salmonella* spp. from *Proteus* spp. and other enteric bacteria. *Appl Environ Microbiol* **56**:301–303.
23. Schönenbrücher V, Mallinson ET, Bülte M. 2008. A comparison of standard cultural methods for the detection of foodborne *Salmonella* species including three new chromogenic plating media. *Int J Food Microbiol* **123**:61–66.
24. Song KY, Hyeon JY, Shin HC, Park CK, Choi IS, Seo KH. 2008. Evaluation of a chromogenic medium supplemented with glucose for detecting *Enterobacter sakazakii*. *J Microbiol Biotechnol* **18**:579–584.
25. Restaino L, Frampton EW, Lionberg WC, Becker RJA. 2006. Chromogenic plating medium for the isolation and identification of *Enterobacter sakazakii* from foods, food ingredients, and environmental sources. *J Food Prot* **69**:315–322.
26. Renaud N, Lecci L, Courcol RJ, Simonet M, Gaillot O. 2013. CHROMagar *Yersinia*, a new chromogenic agar for screening of potentially pathogenic *Yersinia enterocolitica* isolates in stools. *J Clin Microbiol* **51**:1184–1187.
27. Willems E, Cartuyvels R, Magerman K, Verhaegen J. 2013. Evaluation of 3 different agar media for rapid detection of extended-spectrum β -lactamase-producing *Enterobacteriaceae* from surveillance samples. *Diagn Microbiol Infect Dis* **76**:16–19.
28. Hara-Kudo Y, Nishina T, Nakagawa H, Konuma H, Hasegawa J, Kumugai S. 2001. Improved method for detection of *Vibrio parahaemolyticus* in seafood. *Appl Environ Microbiol* **67**:5819–5823.
29. Su YC, Duan J, Wu WH. 2005. Selectivity and specificity of a chromogenic medium for detecting *Vibrio parahaemolyticus*. *J Food Prot* **68**:1454–1456.
30. Gaillot O, Wetsch M, Fortineau N, Berche P. 2000. Evaluation of CHROMagar *S. aureus*, a new chromogenic medium, for isolation and presumptive identification of *Staphylococcus aureus* from human clinical specimens. *J Clin Microbiol* **38**:1587–1591.
31. Perry JD, Rennison C, Butterworth LA, Hopley AL, Gould FK. 2003. Evaluation of *S. aureus* ID, a new chromogenic agar medium for detection of *Staphylococcus aureus*. *J Clin Microbiol* **41**:5695–5698.
32. Denys GA, Renzi PB, Koch KM, Wissel CM. 2013. Three-way comparison of BBL CHROMagar MRSA II, MRSA Select, and spectra MRSA for detection of methicillin-resistant *Staphylococcus aureus* isolates in nasal surveillance cultures. *J Clin Microbiol* **51**:202–205.
33. Restaino L, Frampton EW, Irbe RM, Schabert G, Spitz H. 1999. Isolation and detection of *L. monocytogenes* using fluorogenic and chromogenic substrates for phosphatidylinositol-specific phospholipase C. *J Food Protect* **62**:244–251.
34. Reissbrodt R. 2004. New chromogenic plating media for detection and enumeration of pathogenic *Listeria* spp.-an overview. *Int J Food Microbiol* **95**:1–9.
35. Peng H, Ford V, Frampton EW, Restaino L, Shelef LA, Spitz H. 2001. Isolation and enumeration of *Bacillus cereus* from foods on a novel chromogenic plating medium. *Food Microbiol* **18**:231–238.
36. Juergensmeyer MA, Gingras BA, Restaino L, Frampton EW. 2006. A selective chromogenic agar that distinguishes *Bacillus anthracis* from *Bacillus cereus* and *Bacillus thuringiensis*. *J Food Prot* **69**:2002–2006.
37. Fricker M, Reissbrodt R, Ehling-Schulz M. 2008. Evaluation of standard and new chromogenic selective plating media for isolation and identification of *Bacillus cereus*. *Int J Food Microbiol* **121**:27–34.
38. Marston CK, Beesley C, Helsel L, Hoffmaster AR. 2008. Evaluation of two selective media for the isolation of *Bacillus anthracis*. *Lett Appl Microbiol* **47**:25–30.
39. Dufour AP. 1980. A 24-hour membrane filter procedure for enumerating enterococci. Abstract, 80th American Society for Microbiology, Washington, DC. Q-69, p. 205.
40. Manafi M, Windhager K. 1997. Rapid identification of enterococci in water with a new chromogenic assay. Poster, 97th Meeting of the American Society for Microbiology, Miami, FL. Abstr. P-107, p. 453.
41. Miranda JM, Franco CM, Vázquez BI, Fente CA, Barros-Velázquez J, Cepeda A. 2005. Evaluation of Chromocult enterococci agar for the isolation and selective enumeration of *Enterococcus* spp. in broilers. *Lett Appl Microbiol* **41**:153–156.
42. Budnick GE, Howard RT, Mayo DR. 1996. Evaluation of Enterolert for enumeration of enterococci in recreational waters. *Appl Environ Microbiol* **62**:3881–3884.
43. Cuzon G, Naas T, Fortineau N, Nordmann P. 2008. Novel chromogenic medium for detection of vancomycin-resistant *Enterococcus faecium* and *Enterococcus faecalis*. *J Clin Microbiol* **46**:2442–2444.
44. Stamper PD, Shulder S, Bekalo P, Manandhar D, Ross TL, Speser S, Kingery J, Carroll KC. 2010. Evaluation of BBL CHROMagar VanRE for detection of vancomycin-resistant Enterococci in rectal swab specimens. *J Clin Microbiol* **48**:4294–4297.
45. Manafi M, Waldherr K, Kundi M. 2013. Evaluation of CP Chromo Select Agar for the enumeration of *Clostridium perfringens* from water. *Int J Food Microbiol* **167**:92–95.
46. Eckert C, Burghoffer B, Lalande V, Barbut F. 2013. Evaluation of the chromogenic agar chromID C. difficile. *J Clin Microbiol* **51**:1002–1004.
47. Schets FM, Medema GJ, Havelaar AH. 1993. Comparison of Colilert with Dutch standard enumeration methods for *E. coli* and total coliforms in water. *Lett Appl Microbiol* **17**:17–19.
48. Lee JV, Lightfoot NF, Tillett HE. 1995. An evaluation of presence/absence tests for coliform organisms and *E. coli*. Int. Conf. on Coliforms and *E. coli*, Problem or Solution?, Leeds, UK.
49. Byamukama D, Kansime F, Mach RL, Farnleitner AH. 2000. Determination of *E. coli* contamination with chromocult coliform agar showed a high level of discrimination efficiency for differing fecal pollution levels in tropical waters of Kampala, Uganda. *Appl Environ Microbiol* **66**:864–868.
50. Rice EW, Allen MJ, Brenner DJ, Edberg SC. 1991. Assay for β -glucuronidase in species of the genus *Escherichia* and its application for drinking-water analysis. *Appl Environ Microbiol* **57**:592–593.
51. Manafi M, Kremsmair B. 2001. Comparative evaluation of different chromogenic/fluorogenic media for detecting *E. coli* O157H:7 in food. *Int J Food Microbiol* **71**:257–262.
52. Vernozy-Rozand C, Mazuy-Cruchaudet C, Bavai C, Montet MP, Bonin V, Dernburgand A, Richard Y. 2005. Growth and survival of *E. coli* O157:H7 during the manufacture and ripening of raw goat milk lactic cheeses. *Int J Food Microbiol* **105**:83–88.
53. Kühn H, Wonde B, Rabsch W, Reissbrodt R. 1994. Evaluation of Rambach agar for detection of *Salmonella* subspecies I to VI. *Appl Environ Microbiol* **60**:749–751.
54. Humbert F, Salvat G, Colin P, Lahellec C, Bennejean G. 1989. Rapid identification of *Salmonella* from poultry meat products by using “Mucap test”. *Int J Food Microbiol* **8**:79–83.
55. Warren BR, Parish ME, Schneider KR. 2005. Comparison of chromogenic *Shigella* spp. plating medium with standard media for the recovery of *Shigella boydii* and *Shigella sonnei* from tomato surfaces. *J Food Prot* **68**:621–624.
56. García-Aguayo JM, Ubeda P, Gobernado M. 1999. Evaluation of xylose-galactosidase medium, a new plate for the

- isolation of *Salmonella*, *Shigella*, *Yersinia* and *Aeromonas* species. *Eur J Clin Microbiol Infect Dis* **18**:77–78.
57. Druggan P, Iversen C. 2009. Culture media for the isolation of *Cronobacter* spp. *Inter J Food Microbiol* **136**:169–178.
 58. Iversen C, Forsythe SJ. 2007. Comparison of media for the isolation of *Enterobacter sakazakii*. *Appl Environ Microbiol* **73**:48–52.
 59. Lehner A, Nitzsche S, Breeuwer P, Diep B, Thelen K, Stephan R. 2006. Comparison of two chromogenic media and evaluation of two molecular based identification systems for *Enterobacter sakazakii* detection. *BMC Microbiol* **6**:15.
 60. Leuschner RG, Bew J. 2004. A medium for the presumptive detection of *Enterobacter sakazakii* in infant formula: interlaboratory study. *J AOAC Int* **87**:604–613.
 61. Oh SW, Kang DH. 2004. Fluorogenic selective and differential medium for isolation of *Enterobacter sakazakii*. *Appl Environ Microbiol* **70**:5692–5694.
 62. Kola A, Kohler C, Pfeifer Y, Schwab F, Kühn K, Schulz K, Balau V, Breitbach K, Bast A, Witte W, Gastmeier P, Steinmetz I. 2012. High prevalence of extended-spectrum- β -lactamase-producing *Enterobacteriaceae* in organic and conventional retail chicken meat, Germany. *J ntimicrob Chemother* **67**:2631–2634.
 63. Weagant SD. 2008. A new chromogenic agar medium for detection of potentially virulent *Yersinia enterocolitica*. *J Microbiol Meth* **72**:185–190.
 64. Duan J, Su YC. 2005. Comparison of a chromogenic medium with thiosulfate-citrate-bile salts-sucrose agar for detecting *Vibrio parahaemolyticus*. *J Food Sci* **70**:125–128.
 65. Nakashima Y, Oho M, Kusaba K, Nagasawa Z, Komatsu O, Manome I, Araki K, Oishi H, Nakashima M. 2007. A chromogenic substrate culture plate for early identification of *Vibrio vulnificus* and isolation of other marine *Vibrios*. *Ann Clin Lab Sci* **37**:330–334.
 66. Cerdà-Céllular M, Jofr J, Blanch AR. 2000. A selective media and a specific probe for detection of *V. vulnificus*. *Appl Environ Microbiol* **66**:855–859.
 67. Blanco-Abad V, Ansede-Bermejo J, Rodriguez-Castro A, Martinez-Urtaza J. 2009. Evaluation of different procedures for the optimized detection of *Vibrio parahaemolyticus* in mussels and environmental samples. *Int J Food Microbiol* **129**:229–236.
 68. Rosec JP, Causse V, Cruz B, Rauzier J, Carnat L. 2012. The international standard ISO/TS 21872–1 to study the occurrence of total and pathogenic *Vibrio parahaemolyticus* and *Vibrio cholerae* in seafood: ITS improvement by use of a chromogenic medium and PCR. *Int J Food Microbiol* **157**:189–194.
 69. Schleifer KH, Killper-Bälz R. 1984. Transfer of *Streptococcus faecalis* and *Streptococcus faecium* to the genus *Enterococcus* nom. rev. as *Enterococcus faecalis* comb. nov. and *Enterococcus faecium* comb. nov. *Int J Syst Bacteriol* **34**:31–34.
 70. Slanetz LW, Bartley CH. 1957. Numbers of enterococci in water, sewage, and feces determined by the membrane filter technique with an improved medium. *J Bacteriol* **74**:591–595.
 71. Hernandez JF, Pourcher AM, Delattre JM, Oger C, Loeuillard JL. 1993. MPN miniaturized procedure for the enumeration of faecal enterococci in fresh and marine waters, the MUST procedure. *Wat Res* **27**:597–606.
 72. Littel K, Hartman PA. 1983. Fluorogenic selective and differential medium for isolation of faecal streptococci. *Appl Environ Microbiol* **45**:622–627.
 73. Niemi RM, Ahtiainen J. 1995. Enumeration of intestinal enterococci and interfering organisms with Slanetz-Bartley agar, KF streptococcus agar and the MUST method. *Lett Appl Microbiol* **20**:92–97.
 74. Rhodes MW, Kator H. 1997. Enumeration of enterococcus sp. using a modified mE method. *J Appl Microbiol* **83**:120–126.
 75. Messer W, Dufour A. 1998. A rapid, specific membrane filtration procedure for enumeration of enterococci in recreational water. *Appl Environ Microbiol* **62**:3881–3884.
 76. Adcock PW, Saint CP. 2001. Rapid confirmation of *C. perfringens* by using chromogenic and fluorogenic substrates. *Appl Environ Microbiol* **67**:4382–4384.
 77. Camilli A, Goldfine H, Portnoy DA. 1991. *L. monocytogenes* mutants lacking phosphatidylinositol-specific phospholipase C are avirulent. *J Exp Med* **173**:751–754.
 78. Gouin E, Mengaud J, Cossart P. 1994. The virulence gene cluster of *L. monocytogenes* is also present in *Listeria ivanovii*, an animal pathogen, and *Listeria seeligeri*, a non-pathogenic species. *Infect Immun* **62**:3550–3553.
 79. Hechelmann H, Albert T, Reissbrodt R. 2002. *Characterization of new chromogenic plating media for detection and enumeration of L. monocytogenes*. Poster, “Food Micro,” Lillehammer, Norway.
 80. Roczen D, Knödlseder M, Friedrich K, Schabert G, Spitz H, Müller R, Reissbrodt R. 2003. Development of a new chromogenic *L. monocytogenes* plating medium and comparison with three other chromogenic plating media. Poster, Meeting of the American Society for Microbiology, Washington DC, Poster O-48.
 81. Stessl B, Luf W, Wagner M, Schoder D. 2009. Performance testing of six chromogenic ALOA-type media for the detection of *L. monocytogenes*. *J Appl Microbiol* **106**:651–659.
 82. Tallent SM, Kotewicz KM, Strain EA, Bennett RW. 2012. Efficient isolation and identification of *Bacillus cereus* group. *J AOAC Int* **95**:446–451.
 83. Chevalier P, Royand D, Savoie L. 1991. X- α -Gal-based medium for simultaneous enumeration of bifidobacteria and lactic acid bacteria in milk. *J Microbiol Meth* **13**:75–83.

Anaerobic Cultivation

TAKASHI NARIHIRO AND YOICHI KAMAGATA

2.1.2

Anaerobes are key players in global cycles of elements and nutrition in natural and anthropogenic ecosystems and are also causative agents of human and veterinary diseases. Numerous studies have sought to develop culturing techniques for anaerobes to enable the elucidation of their basic physiology, pathogenic mechanisms, and ecological functions. This chapter describes a brief history of the development of anaerobic culturing techniques from the historical Hungate technique to techniques and apparatuses commonly used in modern laboratories. In addition, recent progress in anaerobic culturing techniques (e.g., single-cell manipulation and isolation, the six-well plating method, the coculture method, bioreactor-based enrichment, and *in situ/in vivo* cultivation) are described, with several examples of the application of these techniques for the isolation of anaerobes from natural and artificial ecosystems.

Anaerobic microorganisms (hereafter designated anaerobes) are key players in global cycles of elements (e.g., carbon, nitrogen, sulfur, and iron) in natural and anthropogenic ecosystems, including aquifer/groundwater (1), animal/insect guts (2, 3), rice paddy fields (4), rumen (5), terrestrial/oceanic subsurfaces (6, 7), wetlands (8), biodiesel production processes (9), food production processes (10), and wastewater treatment processes (11). In these anoxic ecosystems, various metabolic groups of anaerobes play roles in specific biochemical reactions, such as fermentation (12, 13), anaerobic ammonium oxidation (anammox) (14), sulfate reduction (15), iron reduction (16), syntrophic substrate oxidation (17), and methanogenesis (18). In addition to these metabolic groups, anaerobes include human and animal pathogens, which were the main focus in the earliest era of modern microbiology. The challenges of cultivating, characterizing, and controlling these anaerobic pathogens spurred the establishment of modernized microbiology (19–23).

A crucial difference between aerobic and anaerobic culturing techniques is that creating and maintaining an anoxic (O_2 -free) condition is a prerequisite for the growth of anaerobes. This prerequisite long hindered the cultivation of pure cultures. However, a number of researchers have successfully isolated anaerobes using various means through a trial-and-error process. This chapter describes the early history and current status of anaerobic culturing techniques. The chapter comprises four sections: (a) a brief history of anaerobic culturing techniques, tracing a path through the development of the gold standard Hungate technique; (b)

apparatuses (e.g., gassing manifold, anaerobic chamber, and jar-type container) and reducing agents currently used in common laboratories; (c) successful examples using the Hungate technique, specifically those involving the isolation of anaerobes that had long been refractory to isolation, referred to as yet-uncultured organisms; and (d) novel techniques for culturing anaerobic microorganisms.

EARLY HISTORY OF ANAEROBIC CULTURING TECHNIQUES AND THE DEVELOPMENT OF THE HUNGATE TECHNIQUE

Anaerobic cultivation was first described by Pasteur in 1861 (24), who observed the growth of microorganisms involved in butyric fermentation under anoxic conditions produced by a vacuum pump, while no growth was observed in the presence of air. Forty years later, more than 50 primitive but creative methods for culturing anaerobes had been developed and were compiled by Hunziker in a review article in 1902 (25). In this 100-year-old seminal review, anaerobic culturing techniques were categorized on the basis of six concepts: (a) formation of a vacuum; (n) replacement of air by inert anoxic gases; (c) absorption of oxygen; (d) reduction of oxygen; (e) exclusion of atmospheric oxygen by means of various physical principles and mechanical devices; and (f) the combined application of any two or more of the foregoing principles. Surprisingly, these concepts still underlie current techniques. By the mid-20th century, anaerobic culturing techniques had become varied and disorganized: for example, there were reports of the use of pyrogallol, potassium hydroxide, phosphorous, cysteine, and thioglycollate to remove oxygen (26–28), whereas other studies used an inert gas-filled jar without reducing agents (29–31) or petri dishes combined with reducing agents (32, 33). In addition to these approaches, Esmarch (34) developed the roll tube technique in 1886; however, this technique did not become popular because it was laborious and time-consuming compared with the petri dish method (33, 35). Despite these difficulties, Wilson (36) implemented the roll tube technique for viable cell counting, and various types of mechanical devices for producing a roll tube with a uniform distribution of solidified medium were developed (35, 37–39). These enormous efforts were eventually integrated by Hungate to establish a sophisticated culturing technique for fastidious anaerobes, the so-called Hungate roll tube technique (40). The major

principles of the Hungate technique are (a) removal of oxygen from the medium; (b) mimicking the conditions in which the microbes were found (e.g., composition of the medium, pH buffering, and redox potential); (c) minimization of oxygen exposure during inoculation; and (d) rapid solidification of agar with cold water either in a mechanical device or manually (41). This technique was initially used for the isolation of anaerobic cellulose-degrading bacteria from ruminal environments (40, 41). By the end of the 1970s, the Hungate technique had been further improved by using pre-reduced anaerobically sterilized (PRAS) media (42), plugging the tube with butyl rubber stoppers (43), sealing with crimp-closure aluminum seals (44) or screw caps (45), inoculating with syringes and needles (46), and using pressurized (e.g., 2–3 atm) tubes or serum bottles (47) (Fig. 1). The improved Hungate technique has now become a mainstream methodology for the culturing of anaerobic microbes, including methanogens (48, 49), syntrophic bacteria (50, 51), fermentative bacteria (52), and anaerobic fungi (53).

BASIC APPARATUSES AND REAGENTS FOR ANAEROBIC CULTIVATION

Gassing Manifold

In terms of routine preparation for anaerobic cultivation, preparing many bottles/tubes of PRAS media is a time-consuming process. To overcome this problem, Balch and Wolfe (47) introduced a multichannel gassing manifold in 1976. This type of gassing manifold, including the Deoxygenized Gas Pressure Injector types IP-8 and GR-8 (Sanshin Industrial, Yokohama, Japan), is now commercially available from several manufacturers (Fig. 1c). In these systems, high-pressure gas cylinders are connected to a reactor containing a copper-based catalyst. The anoxic gas passes over the heated (approximately 220°C) copper reactor. The manifold is equipped with a three-way valve, which is connected to the gas injection, a vacuum pump, and eight valves connected to injection/vacuum needles. The gas pressure in the manifold is maintained using an ordinary two-stage regulator connected to the anoxic gas cylinder. Such gassing manifolds permit the preparation of large quantities of PRAS bottles/tubes with an appropriate gas composition and pressure and are compatible with the Hungate technique. More recently, Wolfe and Metcalf (54) developed a vacuum-vortex technique for the preparation of PRAS media with the gassing manifold. This simple technique is applicable for small-volume (approximately 50 ml) test tubes or serum bottles and combines the strong mixing of the vortex machine and the negative pressure produced by the gassing manifold. The liquid cultures prepared by this technique yielded a greater cell density of the methanogenic archaea *Methanosarcina barkeri* strain Fusaro Δhpt-WWM85 compared to the Hungate technique modified by Balch et al. (49).

Anaerobic Chamber (Glove Box) and Anaerobic Incubator

An anaerobic chamber (or glove box) provides sufficient workspace for traditional surface cultivation on Petri dishes under anaerobic conditions. The use of anaerobic chambers for cultivation was first described in the 1960s (55–58). In 1969, Aranki et al. (59) developed a glove box with clear flexible vinyl plastic to cover the chamber. They used this glove box for the isolation of anaerobic bacteria from human gingiva and mouse cecum and found that the cultures prepared in the glove box provided adequate recovery of the anaerobic

bacterial colonies from the samples compared with anaerobic jar-based cultivation. Typical vinyl-type anaerobic chambers are now available from COY Laboratory Products (Grass Lake, MI, USA) (Fig. 1j), and the detailed configuration of the anaerobic chambers was described in a review article by Speers (60). Subsequently, Balish et al. (61) have introduced a transparent plastic incubator for culturing anaerobes within the anaerobic glove box, in effect making the anaerobic glove box a tool for incubation. In addition, Metcalf et al. (62) have demonstrated the suitability of an anaerobic intrachamber incubator outfitted with a vacuum line, two gas-mixture supply lines, and a rectangular air lock for culturing *Methanosarcina* spp.

Jar-Type Apparatuses and Compact Gas Generators

The archetype of jar-type apparatuses for culturing anaerobes was invented by Novy in 1893 (63), with the development of derivatives until the early 20th century (25, 28, 31, 64). The prototypic Novy jar was connected to a vacuum pump and hydrogen gas tank via tubes, and a reducing agent (e.g., pyrogallol) solution was placed in the bottom of the jar. Although the combination of vacuum pump, hydrogen gas, and reducing agent permitted the effective formation of anoxic conditions, the entire system was relatively complicated, and it was difficult to maintain the anaerobic condition during the incubation period. As an alternative to this complex system, several researchers have developed methods of generating anoxic gas based on a simple chemical reaction and a metallic catalyst. Brewer et al. (65) used sodium borohydride and cobalt chloride to produce hydrogen gas and also tested the usability of a mixture of magnesium metal, zinc chloride, and sodium chloride for this purpose (66). They subsequently developed an improved, safe jar-type anaerobic system that employs sodium borohydride, a palladium catalyst, and a carbon dioxide tablet (containing sodium bicarbonate and citric acid) to generate anoxic conditions, with an anaerobic indicator based on the methylene blue–hydrogen reaction (67, 68). These studies resulted in the development of commercial disposable anoxic gas generators, such as GasPak (BD, Franklin Lakes, NJ, USA) (69–71), GasKit (Don Whitley Scientific, West Yorkshire, UK) (72), AnaeroGen (Oxoid, Hampshire, UK) (73), Anaerocult (Merck, Darmstadt, Germany) (74), and AnaeroPack (Mitsubishi Gas Chemical, Tokyo, Japan) (75, 76) (some of which are no longer available). The combination of a jar-type apparatus with gas-generating envelopes is widely used to culture anaerobic microorganisms on petri dishes (77). In addition, the Anoxomat, an automatic evacuation-replacement system that provides anaerobic conditions in a jar, was developed in 1989 (78). This easy-to-operate apparatus enables the cultivation of obligate anaerobic bacterial strains belonging to the genera *Bacteroides*, *Clostridium*, *Fusobacterium*, *Prevotella*, *Porphyromonas*, and *Peptostreptococcus* (79, 80). The Anoxomat Mark II is currently available from Mart Microbiology (Drachten, the Netherlands).

Bicarbonate–Carbon Dioxide Buffering System

Bicarbonate–carbon dioxide is the most popular buffering system for anaerobic culture media. In this system, carbonic acid (H_2CO_3) is formed by the reaction of carbon dioxide (CO_2) with water (H_2O), then produced carbonic acid is immediately dissociated into proton (H^+) and bicarbonate (HCO_3^-):

