

# Foodborne and Waterborne Bacterial Pathogens

Epidemiology, Evolution and Molecular Biology

Edited by

Shah M. Faruque

Molecular Genetics Laboratory  
International Centre for Diarrhoeal Disease Research,  
Bangladesh;  
Department of Genetic Engineering and Biotechnology  
University of Dhaka  
Dhaka  
Bangladesh



Copyright © 2012

Caister Academic Press  
Norfolk, UK

[www.caister.com](http://www.caister.com)

British Library Cataloguing-in-Publication Data  
A catalogue record for this book is available from the British Library

ISBN: 978-1-908230-06-5

Description or mention of instrumentation, software, or other products in this book does not imply endorsement by the author or publisher. The author and publisher do not assume responsibility for the validity of any products or procedures mentioned or described in this book or for the consequences of their use.

All rights reserved. No part of this publication may be reproduced, stored in a retrieval system, or transmitted, in any form or by any means, electronic, mechanical, photocopying, recording or otherwise, without the prior permission of the publisher. No claim to original U.S. Government works.

Cover design adapted from Figure 10.3A

Printed and bound in Great Britain

# Contents

	<b>Contributors</b>	v
	<b>Preface</b>	ix
1	<b>Introduction</b> Shah M. Faruque	1
2	<b>Epidemiology, Pathogenesis and Genetics of Diarrhoeagenic <i>Escherichia coli</i> Infections</b> Thandavarayan Ramamurthy and M. John Albert	11
3	<b>Population Genetics and Molecular Epidemiology of <i>Shigella</i> Species</b> Kaisar Ali Talukder and Ishrat Jahan Azmi	63
4	<b>Molecular Pathogenesis, Epidemiology and Drug Resistance of <i>Shigella</i> species</b> Gururaja P. Pazhani and Thandavarayan Ramamurthy	77
5	<b>Salmonellae: Taxonomy, Genomics and Antimicrobial Resistance</b> Mahbubur Rahman	113
6	<b>Molecular Aspects of Pathogenesis and Drug Resistance in <i>Salmonella</i> Species</b> Indrani Karunasagar, Patit Paban Bhowmick and Deekshit Vijaya Kumar	121
7	<b>Epidemiology, Molecular Biology and Detection of Foodborne <i>Vibrio parahaemolyticus</i> Infections</b> Marie Yeung and Kathryn J. Boor	153
8	<b>Epidemiology and Genetics of the Pandemic Clone of <i>Vibrio parahaemolyticus</i></b> Indrani Karunasagar, Ballamoole Krishna Kumar and G. Balakrish Nair	185
9	<b>Epidemiology and Molecular Pathogenesis of <i>Vibrio vulnificus</i></b> Iddya Karunasagar and Anusha Rohit	197
10	<b>Epidemiology and Molecular Biology of <i>Vibrio cholerae</i></b> Shah M. Faruque and John J. Mekalanos	211

11	<b>Biology of <i>Campylobacter</i> Infection</b>	231
	Lieneke I. Bouwman and Jos P.M. van Putten	
12	<b>Epidemiology, Pathogenesis, Ecology and Genetics of <i>Listeria monocytogenes</i></b>	251
	Sangmi Lee, Robin M. Siletzky and Sophia Kathariou	
13	<b>Epidemiology, Virulence Genes, and Reservoirs of Enteropathogenic <i>Yersinia</i> Species</b>	269
	Riikka Laukkanen-Ninios and Maria Fredriksson-Ahomaa	
14	<b>Bacterial Factors Encoded by Mobile and Integrative Genetic Elements in Enteric Pathogens</b>	289
	E. Fidelma Boyd	
15	<b>Conclusion and Future Prospects</b>	305
	Shah M. Faruque	
	<b>Index</b>	313

# Preface

The developing scenario of global changes in climate with increasing frequency of natural disasters linked to the threat of enhanced epidemic spread of foodborne and waterborne diseases warrants an update of knowledge on these infectious diseases and the causative agents. Gastrointestinal diseases of which a substantial proportion are due to food- or waterborne bacterial pathogens is the second most common cause of morbidity throughout the world after acute respiratory tract illness. In children alone there may be between 3.5 and 18 million deaths per year worldwide from diarrhoeal diseases.

The past 10–15 years have witnessed the unravelling of remarkable new insights on the biology of the pathogens that spread through water or contaminated foodstuff. These include the discovery of the filamentous phage that encodes cholera toxin in *Vibrio cholerae*, the existence of two chromosomes in *Vibrio* species and the whole genome sequencing of a number of these and related pathogens. The discovery of new mobile and integrative genetic elements, such as conjugative transposons, integrons, pathogenicity islands and phages, involved in horizontal transfer of virulence genes have provided new insights on the emergence of new pathogenic strains and their variants. Several foodborne and waterborne diseases have emerged in the past two decades as a consequence of changes in aetiological agents, hosts and the environment. Despite tremendous recent development in our understanding of the emergence, infectivity and spread of bacterial pathogens, such as *Vibrio cholerae*, pathogenic

*Escherichia coli*, *Salmonella*, *Shigella* and *Campylobacter* spp., updated compilations of this knowledge are rare. It is therefore, timely to compile a volume comprising the current status of research on the biology of these and related pathogens.

A tremendous amount of pioneering work in recent times and the voluminous information flow has provided the impetus for putting this book together. At this time a whole set of new research has been directed towards understanding how new pathogenic strains emerge, newly emerged strains replace old strains, their survival strategy and competition in the environment, the molecular mechanism of cell to cell communication, and biofilm formation, as well as the genetic determinants of epidemic and pandemic properties. In this book, we have attempted to capture the essence of this mighty deluge of information regarding bacterial pathogens that spread through food and water. The scope of this book, as emphasized by the publishers, is on the epidemiology and molecular biology of these pathogens. Leading experts in the fields have described various bacterial pathogens, their pathogenic properties, population genetics, virulence genes, epidemiology, identification and control strategies. Other topics include the molecular basis for enhanced transmissibility of waterborne pathogens, their mode of survival in the environment, and above all the evolution of the different species to attain increased fitness both as a pathogen and an environmental organism. I hope that the readers find this book interesting and comprehensive.

**A**

ADP-ribosylation 5, 25  
 Aminoglycoside 93, 95, 138, 139, 275  
 Amoebic dysentery 1  
 Amplified-fragment-length polymorphism (AFLP) 7,  
 20, 233, 273, 274  
 Antibiotic resistance 8, 70, 77, 93, 95–96, 113, 117,  
 136–139, 211–213, 217

**B**

Bacterial translocation 241–242  
 Bacterial virulence factors 292, 293, 296  
 Bacteriophage 11, 29, 44, 121, 127, 132, 136–137, 142,  
 212, 237. *See also* Phage  
*bfp* 12, 16  
 Biofilm 7, 8, 36, 37, 40, 41, 121, 134, 135, 170, 212,  
 221–225, 263, 308  
 -like 222, 224, 308  
 formation 18, 34, 35, 40, 41, 121, 131, 133, 135, 170,  
 221, 223  
 Bundle-forming pilus (BFP) 4, 6, 12, 14, 16

**C**

*Campylobacter coli* 232, 233, 234, 238, 239, 243  
*Campylobacter jejuni* 3, 173, 232–235, 239, 240  
 adhesion 239, 240, 250  
 bacterial translocation 241–242  
 capsule 237  
 cellular uptake 240  
 CheA 235  
 chemotaxis 235  
 CheY 235  
 colonization 239  
 -containing vacuole (CCV) 241  
 cytolethal distending toxin (CDT) 241  
 diversity 234  
 environmental adaptation 235  
 epidemiology 232  
*flaA* 235  
*flab* 235  
 flagellum 236  
 genome analysis 234  
 interaction with immune system 242–243  
 invasion antigens 241  
 lipooligosaccharide 237, 238

molecular typing 234  
 motility 235  
 N-glycosylation 238  
 O-glycosylation 238  
 phylogenetic tree 232  
 reservoirs 233  
 surface architecture 236  
 translocation 242  
 transmission 233  
 virulence factors 239, 241

*Campylobacter* species 1, 2, 3, 29, 157, 231, 232, 234,  
 305, 307  
 Ceftriaxone 92, 94, 99  
 Ciprofloxacin 31, 39, 67, 93, 95, 98, 99, 135, 217, 218  
 Cholera 1, 2, 31, 211, 212  
 Cholera toxin (CT) 5, 23, 25, 32, 133, 164, 211, 213,  
 218, 220, 295, 296  
 Conjugative transposon 290  
*Cryptosporidium parvum* 1  
*ctx* operon 218, 221, 290, 295, 298  
 CTX phage 190, 212, 213, 220  
 CVD432 33, 36, 38  
 Conditionally viable environmental cells (CVEC) 7,  
 156, 222–225, 308  
 CVEC-like cells 224  
 formation 7, 222, 224  
 genetics of 222–223, 224

**D**

Diarrhoea 1, 2, 3, 4, 11, 12, 14, 25, 38, 40, 164, 289, 299,  
 305  
 persistent 12, 14, 38, 40  
 travellers' 2, 26, 31, 32, 33, 36, 100  
 watery 11, 25, 41, 42  
 inflammatory 12, 36, 164, 289, 299  
 infantile 15, 22, 305  
 Diarrhoeagenic *E. coli* 2, 4, 11, 12, 13, 16  
 detection 16  
 serotype 13  
 EAEC *see* Enteraggregative *E. coli*  
 EHEC *see* Enterohaemorrhagic *E. coli*  
 EIEC *see* Enteroinvasive *E. coli*  
 EPEC *see* Enteropathogenic *E. coli*  
 ETEC *see* Enterotoxigenic *E. coli*

**E**

- EAF plasmid 6
- Emerging antibiotic resistance 307
- Enteroaggregative *E. coli* (EAEC) 2, 4, 11, 13, 14, 16, 29, 30, 33–41, 289
  - aafA 38
  - aap 37, 38, 40
  - aatA 38, 39, 40
  - afimbrial adhesins 34
  - aggA 38, 39
  - aggR 37, 39, 40
  - antibiotic resistance 39
  - astA 37
  - clinical manifestation 33
  - dispersin 34
  - EAST1 33, 35, 36
  - epidemiology 36
  - fimbrial adhesins 33–34
  - flagellin 36
  - fliC 36
  - in HIV-infected 38
  - molecular typing 39
  - outbreaks 39
  - pathogenesis 37
  - Pet 34, 35, 36
  - pet* 38
  - pic* gene 35, 36, 39
  - treatment 40
  - virulence gene distribution 38
  - virulence gene markers 36, 37
- Enterohaemorrhagic *E. coli* (EHEC) 289, 294
  - clinical manifestations 17
  - diagnosis 21
  - epidemiology 18–19
  - locus for enterocyte effacement (LEE) 294
  - molecular typing 20
  - non-O157:H7 19
  - O104:H4 17
  - O104:H4 44
  - O157:H7 17–18
  - pathogenesis 17
  - plasmid analysis 21
  - prevention 22
  - serotypes 13
  - type III secretion system (T3SS) 294
- Enteroinvasive *E. coli* (EIEC) 2, 4, 5, 11, 12, 13, 16, 29, 41–44, 72, 83, 84, 85, 90, 289, 307
  - clinical manifestations 41
  - detection 43
  - epidemiology 43–44
  - IpaB 41
  - IpaC 41
  - IpaD 41
  - IpaH 43
  - mxi* 41
  - pathogenesis 41–42
  - spa* 41
  - type III secretion system (T3SS) 42
  - treatment 43
  - VirF 41
  - VirG 41
  - VirR 41
  - virulence plasmid 41
- Enteropathogenic *E. coli* (EPEC) 2, 4, 5, 11–17, 24, 30, 31, 35, 38, 44, 83, 127, 289, 305, 307
  - actin-related protein 2/3 (ARP2/3) 13
  - attaching and effacing 12
  - atypical 14
  - clinical manifestation 12
  - cycle inhibiting factor (Cif) 13
  - diarrhoea antibiotic 17
  - DNA probe 16
  - eae* 16
  - enterobacterial repetitive intergenic consensus (ERIC)-PCR 16
  - epidemiology 15–16
  - EspA 13
  - EspB 13
  - EspD 13
  - EspF 13
  - EspH 13
  - intestinal serotonin transporter (SERT) 13
  - LEE-encoded regulator Ler 12
  - locus for enterocyte effacement (LEE) 12, 16
  - mitochondrial-associated protein (Map) 13
  - Nck 13
  - NF-κB 13
  - non-LEE encoded proteins 13
  - sodium d-glucose cotransporter (SGLT1) 13
  - Tir 13
  - Wiskott–Aldrich syndrome protein (N-WASP) 13
- Enterotoxigenic *E. coli* (ETEC) 2, 4, 11, 12, 13, 16, 22–32, 35, 37, 43, 48, 83, 289, 305, 307
  - breast feeding 31
  - case–control studies 28
  - colonization factor antigens 22
  - colonization factors 23–24
  - diagnosis 30
  - dual infection with EPEC 24
  - enterotoxins 23
    - heat liable (LT) 22, 23, 25
    - heat stable (ST) 22, 23, 26
  - epidemiology 26–28
  - genome analysis 29
  - heat-labile (LT)-encoding genes 29
  - pathogenesis 24–25
  - PCR 30
  - probiotics 31
  - source of infection 28
  - treatment 31
  - vaccines 32

**F**

- Future prospect 309
- Fimbriae 4, 16, 23, 24, 32, 33, 35, 122, 123, 131–133, 237
  - adherence 4, 16, 33, 35, 39
  - aggregative 122, 123
  - polar 122, 123
- Fimbrial adhesins 33–34
- Flagellin 36, 114, 128, 235, 238, 240, 242, 243

**G**

G-protein 5, 293  
 Genomic diversity 306  
 Genotyping 20, 213, 233, 258, 273  
 Global monitoring 310  
 GM1 ganglioside 25, 30, 238  
 Guillian-Barré syndrome (GBS) 3, 233

**H**

Haemolytic uraemic syndrome (HUS) 8, 12, 17, 19, 22, 39, 39, 64  
*Helicobacter pylori* 2, 165  
 Hog cholera 113  
 Horizontal gene transfer 5, 92, 93, 114, 115, 134, 136, 234, 256, 258, 289–306

**I**

Inflammatory diarrhea 12, 33, 36, 264, 289, 290, 291, 298, 299  
 Insertion sequence 29, 84, 274  
 IpaBCDA 41

**K**

Kanagawa phenomenon 153, 168–169, 299  
 Kanamycin 138, 217

**L**

*Legionella* species 1  
*Listeria monocytogenes* 1, 3, 6, 251, 310  
   epidemic clones 261–263  
   evolution 260, 262  
   listeriosis 3, 251, 252, 253, 254, 255, 257, 259, 262, 263  
   pathogenicity 251, 254, 261  
   pathogenicity islands 255–256, 258, 259  
   population structure 258–260  
   serotyping 258, 260  
   virulence genes 255, 260  
*Listeria* species 251, 255–258, 262  
   DNA array 259, 260  
   epidemiology 251–254  
   genome comparison 257, 258  
   phages 262, 263  
   phylogeny 257  
 Locus of enterocyte effacement (LEE) pathogenicity island 19, 294

**M**

Mecillinam 67  
 Microarray 21, 31, 216, 219, 222, 233  
 Mobile and integrative genetic elements (MIGEs) 289–291, 299–300  
 Molecular typing 15, 16, 20, 29, 39, 117, 201, 233, 272, 306  
   amplified-fragment-length polymorphism (AFLP) 7, 20, 233, 273, 274  
   *Campylobacter* 233  
   enterohaemorrhagic *E. coli* (EHEC) 20  
   enterotoxigenic *E. coli* (ETEC) 29  
   enteroaggregative *E. coli* (EAEC) 39

  multilocus sequence typing (MLST) 7, 16, 20, 29, 39, 69, 73, 171, 186, 192–193, 233–234, 244, 248, 260, 263  
   multilocus variable-number tandem-repeat analysis (MLVA) 7, 20, 21, 261, 263, 273  
   PCR 7, 16, 20–22, 30–31, 38–40, 166–169, 175, 185, 189, 197, 233, 256, 279, 306  
   pulse-field gel electrophoresis (PFGE) 7, 20, 21, 66, 69–72, 171, 186, 187, 192, 233, 261, 272–273, 280  
   randomly amplified polymorphic DNA (RAPD) 20, 171, 273  
   ribotyping 7, 16, 20, 66, 69–72, 171, 192, 213, 216, 261, 273, 274  
   *Yersinia* species 272, 273  
 Most probable number (MPN) 154–155, 166, 172–173, 203–205, 278  
 Multilocus enzyme electrophoresis (MEE) 16

**N**

Neomycin 17, 135  
 Neonatal 31, 173, 289  
   claves 173  
   meningitis 289

**O**

Octamer-based genome scanning (OBGS) 21  
 Optical mapping 21, 29  
 Oral rehydration 17, 31, 40, 157. *See also* ORS  
 Oral vaccine 32  
 ORS 44

**P**

Pathogen evolution 306  
 Pathogenicity island (PAI) 4, 5, 11, 12, 14, 18, 79, 84, 97, 115, 190, 191, 290, 291  
 Phage 8, 21, 115, 117, 127, 131, 132. *See also* bacteriophage 293  
 Pivmecillinam 92, 99  
 pO157 18, 20  
 Prevention strategies 309

**Q**

Quorum sensing 7, 12, 18, 121, 133, 164, 172, 201, 220–223  
   AI-2 133  
   biofilm formation 222  
   conditionally viable environmental cells (CVEC) 223  
   LuxR 211  
   LuxS 18, 133, 211  
   circuit 223  
   in *V. Cholerae* 221–223, 225  
   in *Salmonella* 133, 134  
   mutants 222

**R**

Randomly amplified polymorphic DNA (RAPD) 20, 171, 273  
 Randomly amplified polymorphic DNA (RAPD)-PCR 171



Ribotyping 7, 16, 20, 66, 69–72, 171, 192, 213, 216, 261, 273, 274  
rRNA superfamily VI 2

## S

*Salmonella bongori* 3, 114, 121, 291, 293  
*Salmonella boydii* 1, 2, 6, 63, 77  
*Salmonella dysenteriae* 1, 2, 5, 64, 66, 67, 68, 69, 71, 72, 86–92, 94–98  
atypical strain 68  
novel serovar 71  
*Salmonella enterica* 3, 5, 113–116, 121, 127, 290–292, 294, 297  
chromosome 115, 122, 131, 132, 140, 291–294  
prophage in 137, 292  
*Salmonella* Enteritidis 3, 115, 116, 117, 129, 132, 136, 308  
*Salmonella flexneri* 1, 2, 6, 63, 77  
E1037 antigen 69  
pulse-field gel electrophoresis (PFGE) types 69, 70  
provisional serotypes 69  
*Salmonella sonnei* 1, 2, 6, 63, 77  
*Salmonella* species 1, 2, 113  
antibiotic resistance 117, 121, 135–136, 141–142  
antibiotic resistance mechanisms 138–141  
bacteriophages 136–137  
biofilm production 134  
bongori 291  
classification 113  
evolution 116  
genomics 114–115  
integrons 137  
MDR strain 117  
nomenclature 113, 114  
non-typhoidal 121  
pathogenesis 123–132  
pathogenicity island SPI 121, 123–132  
plasmid 136  
salmonellosis 1  
subspecies 3  
toxins 133  
transposons 137  
type III secretion system (T3SS) 293  
Typhi 117  
Typhimurium 203  
typhoidal 121  
virulence factors 122  
virulence genes 132–133  
virulence plasmid 133  
*Salmonella subterranea* 3  
*Salmonella* Typhimurium ST313 117, 118  
quorum sensing 133, 134  
*Salmonella* pathogenicity island 115, 116, 123, 124, 127–132  
sub-Saharan Africa 117, 118  
Secretory diarrhea 164, 289, 294, 298  
ShET1 33, 35  
*Shigella* species 2, 63–73, 77, 83, 84, 85, 94–100, 305, 307  
autophagy 77, 81, 82, 163, 164

biochemical characteristics 64  
cellular translocation 80  
drug resistance 92–93  
chromosomally mediated 98  
efflux mediated 98–99  
transfer of 93  
epidemiology 66–67, 85  
evolution 83–85  
inflammatory response 81  
-like organism 71  
macrophage cell death 92  
multilocus sequence typing (MLST) analysis 72–73  
pathogenesis 77–80  
phylogenetic analysis 72–73, 84  
plasmid profiles 69, 70–71  
plasmids 93  
risk groups 89  
seasonal variation 85  
serotype 64–65  
Shiga toxin (STX) 72  
toxins 72  
transmission 2  
transposons and integrons 95–96  
virulence associated proteins 79–80  
Shiga toxin 4, 14, 16, 17, 72, 159. *See also* Verotoxin  
Shiga toxin-producing *E. coli* (STEC) 18. *See also* Enterohaemorrhagic *E. coli*  
Shigellosis 1  
clinical management 99–100  
worldwide incidence 90–92  
Single nucleotide polymorphism (SNP) 21, 38, 263  
Staphylococcus 1  
Stx 8, 17, 18, 19, 22, 72  
*stx* 15, 16, 72  
SXT element 217, 219

## T

Type III secretion system (T3SS) 4, 6, 12–13, 42, 77–81, 122–128, 153, 159, 162, 164, 191, 291, 297  
EspB 5  
EspD 5  
invA 123  
invC 123  
in *Vibrio* pathogenicity island (VPI)-2 298, 299  
*Salmonella* pathogenicity island (SPI) 121, 123–132  
Tir 5  
VopQ 300  
VopR 300  
VopS 300  
Type VI secretion system (T6SS) 33, 40, 131, 132  
TCP pathogenicity island 5, 218, 219. *See also* *Vibrio* pathogenicity island  
Thermostable direct haemolysin (TDH) 5, 153, 159–162, 164, 299  
*tdh* 154, 159, 160–162, 166, 167, 169, 185, 186  
TDH-related protein (TRH) 5, 153, 299  
*trh* 159, 166, 167, 174  
Transposon 4, 96, 97, 137, 138, 217, 219, 290  
Travellers' diarrhoea 2, 26, 31, 32, 33, 36, 100  
Toxin coregulated pilus (TCP) 5, 211, 218–220

**U**

Uropathogenic *E. coli* 289

**V**

Variable-number tandem repeats (VNTR) 20, 21, 273  
 Verocytotoxin producing *E. coli* 1  
 Verotoxin 17  
 Viable but non-culturable (VBNC) 7, 154, 156, 168, 204  
*Vibrio cholerae* 1, 2, 211  
   AI-2 223  
   antibiotic resistance 217  
   biofilm formation 224  
   CAI-1 223  
   cholera toxin (CT) 211, 295  
   conditionally viable environmental cells (CVEC) 222  
   cqsA 223  
   cqsS 223  
   CTX phage 218, 220  
   epidemiology 213–215  
   evolution 218  
   gene regulation 220–222  
   genome analysis 216, 218  
   genomic variation 219–220  
   Haiti 216, 218  
   HapR 221, 223  
   hybrid biotypes 213  
   hyperinfectious 222  
   LuxO 223  
   LuxQ 223  
   LuxU 223  
   mannose sensitive haemagglutinin (MSHA) 211  
   model for transmissibility 225  
   molecular ecology 222, 225  
   molecular epidemiology 216  
   multiple antibiotic-resistant (MAR) 217  
   nomenclature 212  
   non-O1, non-O139 220, 295  
     inflammatory diarrhea 295, 298  
     pathogenesis 295  
   NqR 221  
   O1 294  
   O139 215, 216  
   pathogenesis 295  
   quorum sensing 223  
   recent outbreaks 215  
   single nucleotide variations (SNVs) 220  
   SXT element 217, 219  
   type III secretion system (T3SS) 295, 298  
   TCP/ACF 219  
   TcpH 221  
   TcpP 221  
   toxin coregulated pilus (TCP) 211  
   transmissibility 225  
   *Vibrio* pathogenicity island (VPI) 5, 219, 296  
   *Vibrio* pathogenicity island (VPI)-2 296, 297  
   *Vibrio* seventh pandemic island (VSP)-1 216  
   *Vibrio* seventh pandemic island (VSP)-2 216  
   virulence genes 218  
   Zimbabwe 215, 218  
*Vibrio mimicus* 299

*Vibrio* pathogenicity island (VPI)-2 299  
*Vibrio* pathogenicity island (VPI)-2V 299  
*Vibrio parahaemolyticus* 1, 2, 5, 6, 153, 299  
   acid sensitivity 170  
   associated foods 157  
   clinical manifestation 157  
   epidemiology 156–159  
   genome and evolution 191  
   haemolysins 159–161  
   identification Kanagawa test 168–169  
   identification PCR primers 167  
   inflammatory diarrhea 299  
   isolation and identification 166–169  
   metal resistance 170  
   molecular analysis 191–193  
   molecular fingerprinting 171  
     group-specific (GS)-PCR 171  
     pulse-field gel electrophoresis (PFGE) 171  
     randomly amplified polymorphic DNA (RAPD)-PCR 171  
   O3:K6 158, 162, 185–190  
     global spread 187–189  
     epidemiology 186  
   O4:K12 158  
   outbreak patterns 158  
   pandemic strains 185, 191  
   serotyping 171  
   siderophore production 170  
   susceptible population 157  
   swarming 165  
   *tdh* 169  
   thermolabile haemolysin (TLH) 159  
   thermostable direct haemolysin (TDH) 153, 159  
   *tlh* 159  
   TDH-related protein (TRH) 153, 161  
   *trh* 169  
   type III secretion system (T3SS) 159, 162, 164  
   virulence factors 159–165  
   virulence genes 159–165  
   world-wide distribution 154–156  
*Vibrio* pathogenicity island (VPI) 5, 296  
*Vibrio* pathogenicity island (VPI)-2 296–297  
*Vibrio vulnificus* 1, 2, 6, 197–206  
   control 205  
   detection 201–203  
   epidemiology 199  
   growth in seafood 204  
   loop-mediated isothermal amplification (LAMP) 203  
   pathogenesis 200–202  
   PCR 203  
   risk assessment 205  
   viable but non-culturable (VBNC) 204  
   virulence genes 200–202  
*Vibrio* seventh pandemic island (VSP)-1 298  
*Vibrio* seventh pandemic island (VSP)-2 298  
*virG* 6

**Y**

*Yersinia enterocolitica* 3, 6, 24, 270  
 clinical manifestation 274

- epidemiology 274
- high-pathogenicity island (HPI) 24
- typing 273
- Y. pseudotuberculosis* 6, 270
  - clinical manifestation 274
  - epidemiology 274
  - typing 273
- Yersinia* species 1, 269
  - enterocolitica* 3, 24, 134, 269
  - enteropathogenic 269
    - in animals 275–276
    - in environment 278
    - in foods 278, 279
  - identification 272
  - mucoïd *Yersinia* factor (Myf) 6
  - pathogenesis 271–272
  - pYV 6
  - taxonomy 269
  - thermostable enterotoxin (Yst) 6
  - transmission 278
  - type III secretion system (T3SS) 6
  - virulence genes 271–272
  - YadA 6
  - Yersiniosis 274
  - Yops 6
  - Ysc 6