Index

Note: Page numbers in *italics* refer to Figures; those in **bold** to Tables.

AFLP *see* amplified fragment length polymorphism (AFLP)

agarose gel electrophoresis
- average pore size, 32
- birefringence, 31
- *C. jejuni*, 191
- *C. perfringens*, 262

DNA electrophoresis, 32–3
- entanglements, 32
- gelation, 31
- *Salmonella*, 340, 342, 345
  - structure, 31–2

amplified fragment length polymorphism (AFLP)
- *B. cereus*, 171–4, **172**
- *C. botulinum*, 254–5
- *C. jejuni*, 190–191
- *C. perfringens*, 261
- discriminatory power, 7
- fluorescent (FAFLP), 7

*L. monocytogenes*
- combinations of enzymes, protocols, 309
- Experion™ automated microfluidic electrophoresis, 311
- fluorescence-labeled primers, 309
- foodborne listeriosis outbreaks, 310
- routes of contamination, 310
- subtyping approaches, 7, 309
- PCR primers, 6
- and pulsed-field gel electrophoresis (PFGE), 18
  - *Salmonella*, 341–2
  - AscI-PFGE, 305, 323
  - Association of Public Health Laboratories (APHL), 148
  - “atypical El Tor”, 362, 363, **369**

*Bacillus anthracis*
- anthrax disease, 166
- diagnostic microarray assay, 175
- Gegenees, 176–7
- MLVA and SNP analysis, 175
- polymerase chain reaction (PCR) systems, 170
- spores, US Postal System, 123

*Bacillus cereus*
- emesis and diarrhea, gastrointestinal diseases, 166–7
- MLST and AFLP, 171–4, **172**
- molecular differentiation, 170
- toxin gene profiling, 168, **169**

*Bacillus* genus
- food quality and safety, 165–6
- genome sequencing, 175–8
- microarrays, 175
- MLST and AFLP, 171–4
- PCR *see* polymerase chain reaction (PCR) methods
- pulsed-field gel electrophoresis (PFGE), 174–5
Bacillus thuringiensis, 166
Bacterial Isolate Genome Sequence
Database (BIGSdb), 69, 229, 238, 239
bacterial subtyping
housekeeping genes, 51
outbreaks source, 66
PFGE see pulsed-field gel
electrophoresis (PFGE)
PulseNet, 42
whole genome sequencing (WGS), 78
bacteriophage typing, Shiga
toxin-encoding, 290–291
band-based similarity metrics
gel electrophoresis patterns, 89
gel run normalization, 88
Jaccard, Dice, and simple matching
coefficients, 87, 87–8, 89
negative matches, 88
pulsed-field gel electrophoresis (PFGE), 88
Bioinformatics Resource Centers (BRCs), 124
biotyping, 66, 209, 221–2
birefringence phenomenon, 31
BOX-PCR system, 10, 18, 170–171, 222–3
CaliciNet see National Electronic Norovirus
Outbreak Network (CaliciNet)
campylobacteriosis, 185–6, 192–5
Campylobacter jejuni
amplified fragment length polymorphism
(AFLP), 190, 191
combination of techniques, 198–9
comparative genomic fingerprinting
(CGF), 197–8
differential characteristics, 186
DNA-based methods, 186, 187–9
multilocus sequence typing
(MLST), 190, 193–5
PCR amplification of repetitive elements
(REP and ERIC PCR), 196–7
polymerase chain reaction (PCR), 190
pulsed-field gel electrophoresis
(PFGE), 190, 192–3
pyrosequencing, 190
restriction fragment length polymorphism
of the flaA gene (flaA-RFLP), 191–2
ribotyping, 195
serotyping schemes, 186
CCs see clonal complexes (CCs)
CDC PulseNet program, 121, 346
Centers for Disease Control
and Prevention, 190
CGH see comparative genomic
hybridization (CGH)
cholera
Haitian cholera outbreak, 77
symptoms, 360
V. cholerae see Vibrio cholerae
chromosomal linkage map, 28
cladistics, 86
clonal complexes (CCs)
central genotypes, 229
clonal species, 101–2
C. sakazakii
multilocus sequence typing
(MLST) dataset, 234, 235
ST4, 237, 238
definition, 50, 53, 234
epidemic clones, 59
and epidemic clones, 56
evolution model, 52
multilocus sequence typing (MLST), 198
Clostridium botulinum
disease and organism characteristics, 251
DI, subtyping method, 257, 258
DNA-based subtyping method, 266, 267
strain subtyping
amplified fragment length
polymorphism (AFLP), 254–5
DI, 257, 258
DNA microarray, 256–7
multilocus sequence typing (MLST), 255–6
multilocus variable number tandem
repeat analysis (MLVA), 256
pulsed-field gel electrophoresis
(PFGE), 253–4
toxins and toxinotyping, 251–3
Clostridium difficile
disease and organism characteristics, 262–3
DNA-based subtyping methods, 266, 267
in foods, 250
infections, 266
isolation, 266
strain subtyping
multilocus sequence typing (MLST), 265
multilocus variable number tandem
repeat analysis (MLVA), 265–6
pulsed-field gel electrophoresis
(PFGE, 264
restriction endonuclease
analysis (REA), 264–5
ribotyping, 264
toxins and toxinotyping, 263–4
**Clostridium perfringens**

disease and organism characteristics, 258–9
DNA-based subtyping methods, 266, 267
stool samples, 262
strain subtyping
  amplified fragment length polymorphism (AFLP), 261
  multilocus sequence typing (MLST), 261
  multilocus variable number tandem repeat analysis (MLVA), 262
  pulsed-field gel electrophoresis (PFGE), 260–261
toxins and toxinotyping, 259–60

Cloud Virtual Resource (CloVR), 75
cluster analysis
  boot strap resampling techniques, 97–8
  cluster cutoff value, 98
  cophenetic correlation coefficient (CCC), 96–7
dendrograms, 96, 97
description, 93–4
Dice similarity matrix, 89, 94
hierarchical and nonhierarchical, 93
iteration results, 95, 96
microbial typing, 98
single, average and complete linkage, 94–5, 95–7
clustered regularly interspaced short palindromic repeats (CRISPRs), 55, 59, 70–71, 191, 198

Cronobacter

genus
  biotyping, 221–2
DNA-based typing, 222–3
follow-on formula or follow-up formula, 220
goeBURST relationship analysis, 233–4
infections, 207
issues, 238–9
MLST, CDC in 2011, 235, 236, 237, 237–8
neonatal infections, issues, 205–6
PCR-based serotyping, 226–7
phenotyping and genotyping methods, 211, 212–14
phylogenetic analysis, 211, 215–18
powdered infant formula (PIF), 219–21
pubMLST.org/Cronobacter online database, 232, 232–3
pulsed-field gel electrophoresis analysis, 223–5
ribotyping Cronobacter strains, 226
taxonomic revisions, 208–11
virulence traits, 207–8

CTX-1 (El Tor type CTX or CTX_{El Tor}), 360, 361, 362–4
CTX-2, 360, 364–6
CTX-3, 360, 366
CTX^{th} (classical type CTX), 360, 361, 362–4
data analysis methodologies, typing techniques
diversity measures
  comparison, 107, 109, 109
  confidence intervals, 105–7, 108
  indexes, 103–4, 104
  pairwise agreement measures, 104–5, 106
groupings, related isolates
  cluster analysis, 93–8
  graph theory methods, 98–103
  hierarchical and nonhierarchical clustering, 93
similarity metric
  allelic, 91–2
  band-based, 87–90
correlation coefficients, 90–91
  sequence similarity, 92–3
databases and internet applications
data repositories
ComBase, 125
Genomic Metadata for Infectious Agents (GEMINA), 124–5
Pathogen-Annotated Tracking Resource Network (PATRN), 125–6
Pathogen Tracker, 124
Pathosystem Resource Integration Center (PATRIC), The, 123–4
PulseNet and PulseNet International, 123
genome assembly/annotation, 126–7
genotypic and functional analysis, 127
genomeric identification, 129–30
global food safety, 115
global outbreak and surveillance
educational networks, 119–20
modernization, laboratory methods, 127–8
scientific networks and resources
Environmental Health Specialists Network (EHS-Ne), 122–3
Foodborne Disease Outbreak Surveillance (FDOS), 122
National Antimicrobial Resistance Monitoring System (NARMS), 121
National Electronic Norovirus Outbreak Network (CaliciNet), 121–2
standardized formats, annotation
and data exchange, 128–9
systems, 115, 116–18
de novo assemblers, 73, 74
discriminatory index (DI), 13, 198, 250, 257, 258
DiversiLab system, 344
DNA-based typing methods, 191, 194, 215, 222–3
DNA–DNA hybridization, 209
DNA fingerprinting
amplified fragment length polymorphism (AFLP), 279–80
multilocus variable-number tandem-repeat analysis (MLVA), 280–281
pulsed-field gel electrophoresis (PFGE), 278–9
random amplified polymorphic DNA (RAPD), 281
repetitive PCR (rep-PCR), 281–2
DNA microarray
*B. cereus*, 175
*C. botulinum*, 256–7
hybridization technology, 317–18
*L. monocytogenes*
comparative genomic hybridization, 317
macroarrays, 317–18
mixed-genome array, 317
pulsed-field gel electrophoresis (PFGE) and ribotyping data, 317
suspension microarray, 317
multigenome, 175
subtyping methods, 266, 267
DNA probes, *L. monocytogenes*
classification, 316
epidemic clones (ECs), 316–17
Southern blots and DNA arrays or microarrays, 316
DNA sequencing
subtyping methods
multilocus sequence typing (MLST), 319–21
prophage typing, 322
single nucleotide polymorphism (SNP), 323–5
whole-genome sequencing (WGS), 322–3
typing methods
multilocus sequence typing (MLST), 347
single nucleotide polymorphism (SNP), 347–9
whole-genome sequencing (WGS), 349–50
double-locus variants (DLVs), 92, 99–101, 103, 234
DPDx, 116, 120
eBURST algorithm
advantages, 99
allelic profiles analysis, 99
goeBURST algorithm, 100–103
EcoCyc database, 127
ECs see epidemic clones (ECs)
EHEC see enterohemorrhagic *E. coli* (EHEC)
EHS-Net see Environmental Health Specialists Network (EHS-Net)
electronic disease surveillance systems, 141, 141
electrophoresis device (ED), 36
El Tor biotype, 359, 361–3, 367, 369, 371, 375, 377
enterobacterial repetitive intergenic consensus (ERIC) sequence
*Bacillus* spp. molecular typing, 170–171
description, 8
ERIC-PCR, 10–11, 196–7, 315, 315
and RAPD combination, 18
Rep-PCR, 350–351
enterohemorrhagic E. coli (EHEC)
LEE, 276
shiga toxins, 275–6
tropic elasticity, 30
tropic trapping, 32
Environmental Health Specialists
Network (EHS-Net), 122–3
epidemic clones (ECs)
and clonal complexes, 56
definition, 50
dissemination model, 58
evolution model, MLST data, 57
housekeeping gene sequences, 56
L. monocytogenes, 54, 59
virulence genes, 57
ERIC sequence see enterobacterial repetitive
intergenic consensus (ERIC) sequence
E. sakazakii Preceptrol™, 209
Escherichia coli
EcoCyc database, 121
enterohemorrhagic E. coli (EHEC), 77,
275–7, 277, 278, 286
enterotoxigenic E. coli (ETEC),
149, 277, 278, 360
multilocus variable-number
tandem-repeat analysis (MLVA), 13
O104:H4 outbreak, 77
O157:H7 outbreak, 41
pathotypes, 77
repetitive extragenic palindromic (REP)s, 8
Shigella, 42
STEC see Shiga toxin-producing
Escherichia coli (STEC)
European Food Safety Authority
(EFSA), 166, 304–5
extended MLST (eMLST), 194, 197
“farm-to-fork” approach, 113, 349
FDA Food Safety Modernization Act, 113
FDOS see Foodborne Disease Outbreak
Surveillance (FDOS)
Fight Bac!, 116, 119
fluorescent amplified fragment length polymor-
phism (FAFLP), 7, 209, 280, 341–2, 350
Food and Agriculture Organization
of the United Nations and the World
Health Organization (FAO/WHO),
206–7, 220
Foodborne Disease Coordinated
Outbreak Response Enhancement
(FoodCORE), 152
Foodborne Disease Outbreak Surveillance
(FDOS), 116, 122
Foodborne Diseases Active Surveillance
Network, 121
FoodCORE see Foodborne Disease
Coordinated Outbreak Response
Enhancement (FoodCORE)
FoodNet, 116, 121, 123, 128, 135
Food Safety Inspection Service of the US
Department of Agriculture
(FSIS/USDA), 122
Foodsafety.gov, 119
GEMINA see Genomic Metadata for
Infectious Agents (GEMINA)
GenBank, 75–7, 126, 211, 215, 230, 238, 364
gene amplification profiling, 343
GeneScan, 341
genetic map, 28
genome assembly/annotation, 73, 75, 76, 126–7
genome sequencing
Bacillus species, 176
Gegenees, 176–7, 177
population genomics, 177–8
Genomic Metadata for Infectious Agents
(GEMINA), 117, 124–5
genomic science, definition, 27
genomotyping, 175–8
GeoGenomic identification, 129–30
Global Foodborne Infections Network
(GFN) database, 116, 120
Global Incident Map, 116, 119–20
goeBURST algorithm
C. sakazakii MLST dataset, 234, 235
features, 100
hypothetical MLST data set, 100, 100, 101
MST, typing methodologies, 103
graph theory methods
eBURST and goeBURST algorithms,
93, 98–102
minimum spanning tree (MST), 102–3
Hamming distance, 92, 102
Hazard Analysis of Critical Control Points
(HACCP), 113, 174
HealthMap, 116, 119–20
hidden Markov models (HMMs), 73, 75
high-throughput sequencing
computational tools, WGS, 76
hypervariable markers, 70–71
MLST vs. WGS, 68–9
phenotypic markers vs. WGS, 71
single nucleotide polymorphism
(SNP), 69–70
subtyping methods, 66–7
technical process, WGS, 71–6
whole genome sequencing (WGS), 67–8

Human Genome Project, 27, 30
hybridization-based methods, *L. monocytogenes*
DNA microarray-based methods, 317–18
DNA probes, 316–17
DNA sequence-based subtyping methods, 318
multilocus sequence typing (MLST), 319–21
prophage typing, 322
SNP-based subtyping, 323–6
whole-genome sequencing (WGS), 322–3

HyperCat, 174
hypervariable markers, 70–71

Illumina VeraCode technology, The, 287
infrequent restriction site PCR (IRS-PCR), 342
insertion sequence (IS)-RFLP, 340–341
Integrated Microbial Genomes system, The, 127
intergenic spacer (IGS) region, PCR, 308, 309
internal transcribed spacer (ITS) region, 210
International Commission on Microbiological Specifications for Foods (ICMSF), 219–20
IS200-PCR, 350–351

Kratky–Porod model, 30
Kyoto Encyclopedia of Genes and Genomes (KEGG) system, The, 118, 127

Laboratory Information Management Systems (LIMS), 128
lineage-specific polymorphism assay (LSPA), 283–4, 286, 288, 291, 292

*Listeria monocytogenes*
differential characteristics, 186
fragment-based methods, 304–7
hybridization-based methods
DNA probes, 316–17
DNA sequence-based subtyping methods, 318
multilocus sequence typing (MLST), 319–21
prophage typing, 322
SNP-based subtyping, 323–6
whole-genome sequencing (WGS), 322–3

outbreak, 42, 323
PCR-based subtyping methods
multiple-locus variable number tandem repeat analysis (MLVA), 311, 314
random amplified polymorphic DNA (RAPD), 307–8
repetitive element sequence-based PCR (REP-PCR), 314–16
ribosomal intergenic spacer region analysis (RISA), 308–9
listeriosis, 42, 76, 303–4, 307–8, 310, 314, 317–19, 321–3, 327

matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI TOF MS), 198, 211, 287, 293
MetaCyc database, 118, 127
metagenomics, 75, 127, 158, 159
minimum spanning tree (MST), 93, 102–3, 293, 346
MLEE see multilocus enzyme electrophoresis (MLEE)
MLST see multilocus sequence typing (MLST)
molecular epidemiology, foodborne disease
enzyme immunoassays (EIA), 157
metagenomic DNA extraction, 158
nucleic acid-based technologies (NAT), 156
outbreaks, 142–6
principles, 153–6
PulseNet see PulseNet
surveillance see surveillance, foodborne disease
molecular serotyping, 293–4
molecular subtyping
*C. botulinum see Clostridium botulinum
C. difficile see Clostridium difficile
C. perfringens see Clostridium perfringens
network, 39
PCR-based see polymerase chain reaction (PCR) methods
whole genome sequencing (WGS), 67–8, 78–9
multilocus enzyme electrophoresis (MLEE), 48–9, 49, 174, 222, 227–8, 228, 234, 284
multilocus sequence analysis (MLSA), 210, 218, 230–231
multilocus sequence typing (MLST)
advantages
clonal complexes, 52, 53
housekeeping genes, 49, 51
recombinational exchange, 51
sequence data, 49
terms, population genetics and molecular epidemiology, 49, 50–51

B. cereus group
AFLP-based approaches, 173
B. cereus sensu lato population structure, 172
database “SuperCAT”, 172–3
HyperCAT, 174
rpoB gene, 173
sporulation stage III AB gene (spoIIIAB), 173
BIGSdb, PubMLST database, 229
C. botulinum, 255–6
CDC in 2011, 235, 236, 237, 237–8
C. difficile, 265
centralized databases, 228–9
C. jejuni, 193, 195
clonal complexes, 56–9, 228
C. perfringens, 261
of Cronobacter spp., 230–231
databases, 48
description, 47
discriminatory power and epidemiologic concordance, 55–6
DNA sequence-based methods, 228
eBURST, 229
epidemic and outbreak clones, 56–9
extended MLST (eMLST), 188, 194, 197
housekeeping genes, 193
L. monocytogenes
clonal complexes (CCs), 319
housekeeping genes, 320–321
multi-virulence-locus sequence typing (MVLS), 321
REP-PCR results, 319
MLEE technique, 227
N. meningitidis scheme, 228
online databases, 91, 91
PubMLST database, 194
pulsed-field gel electrophoresis (PFGE), 229
ribosomal MLST (rMLST), 69, 194
Salmonella, 347, 348, 351
schemes, 171
sequence type analysis and recombinational tests (START) package, 229
sequence types (STs), 227–31
Shiga toxin-producing Escherichia coli (STEC), 284–5
SplitsTree, 229
types, schemes
epidemic clones, 54, 54, 55
MLST + strategies, 53
virulence genes, 53–4
virulence genes, 54
whole-genome multilocus sequence typing (wgMLST), 194

vs. whole genome sequencing (WGS), 68–9, 194–5
mutilocus variable number tandem repeat analysis (MLVA)
B. anthracis, 175
C. botulinum, 256
C. difficile, 265–6
C. perfringens, 262
description, 91
E. coli O157:H7 strains, 13
Euclidean distance, 92
foodborne pathogens subtyping, 13
L. monocytogenes
1989 listeriosis outbreak, 314
subtyping, 311, 312–13
tandem repeats (TRs), 311
online databases, 91, 91
Salmonella, 346
serovar-specific MLVA typing schemes, 13
stability, targets, 13
tandem repeats (TRs), 11, 12
V. cholerae O1 strains, 371–6, 375–6
multi-virulence-locus sequence typing (MVLS), 53, 54, 56, 57, 58, 59, 238, 321–3, 325, 347

National Antimicrobial Resistance Monitoring System (NARMS), 116, 121, 140
National Center for Biotechnology Information gateway (NCBI), 75–6, 117, 126, 128
National Electronic Norovirus Outbreak Network (CaliciNet), 116, 121–2
National Hypothesis-Generating Questionnaire, 152
National Institute of Allergy and Infectious Diseases (NIAID), 123–4
National Notifiable Diseases Surveillance System, 135, 137
National Outbreak Reporting System (NORS), 116, 122, 140
National Voluntary Environmental Assessment Information System (NVEAIS), 122
neonatal intensive care units (NICUs), 205–8, 215, 219, 224
neurotoxigenic clostridia, 249
nucleic acid-based technologies (NAT), 156
nucleotides, 30
octamer-based genome scanning (OBGS), 282–3, 288, 291
Ogston sieving, 32
Outbreak Alert! database, 116, 120
OutbreakNet, 151, 152
Outbreaks
  case-control study, 144, 145
definition, 142
determination, case, 143
investigation steps, 142–3
odds ratio (OR) calculation, 144, 145, 146
PulseNet US regions and laboratories, 146, 147
relative risk (RR), 143–4, 144–5
“Outbreaks Near Me” mobile applications (app.), 119

“partial digest”, 29
Pathogen-Annnotated Tracking Resource Network (PATRN), 117, 125–6, 129
Pathogen Tracker, 117, 124, 128
Pathosystem Resource Integration Center (PATRIC), The, 123–4, 127
Pathway Tools, 127
PCR melting profile analysis (PCR-MP), 17
Pearson correlation coefficient, 90
PFGE see pulsed-field gel electrophoresis (PFGE)
phenetics, 86
phenotypic markers, 71
phylogenetic analysis
  advantages of MLSA, 218
  E. sakazakii strains, 215
  fusA gene sequences, 215, 217
  multilocus sequence typing (MLST) scheme, 215, 218
Ribosomal Database Project (RDBII), 211
16S rDNA sequencing, 211, 215, 216
16S rRNA gene sequence analysis, 211
PHYLOVIZ, 234, 235
plasmid analysis, 342–3
plasmid typing, 292, 343, 350
polymerase chain reaction (PCR) methods
  Bacillus
    molecular differentiation, 170
  REP-PCR, 171
  REP-, ERIC-, and BOX-PCR systems, 170–171
toxin gene profiling, 168–70, 169
RFLP
  PCR-ribotyping, 17
  virulence genes, 16
serotyping
  LPS structure, 227
  MboII, 226
  O-antigen (somatic antigen), 226
subtyping methods
  amplified fragment length polymorphism (AFLP), 6–7, 309–11
  comparison, methods, 14, 17–19
  multilocus variable number tandem repeat analysis (MLVA), 11–14, 311, 314
PCR melting profile analysis (PCR-MP), 17
PCR-restriction fragment length polymorphism (PCR-RFLP), 15–17
random amplified polymorphic DNA (RAPD), 3–6, 307–8
repetitive-sequence-based PCR (REP-PCR), 8–11, 314–16
ribosomal intergenic spacer region analysis (RISA), 308–9
typing methods, 343
polymer physics, DNA, 30–31
powdered infant formula (PIF)
  chromogenic agar, 221
  E. sakazakii, 219
  FAO/WHO risk assessment, 220
  prevalence, 219–20
  pulsed-field gel electrophoresis (PFGE), 219
  VRBG agar, 220
principal component analysis (PCA), 93, 198, 343
“production-chain” approach, 305
Program for Monitoring Emerging Diseases (ProMED), 116, 119
Prokaryotic Genome Automatic Annotation Pipeline (PGAAP), 75, 76
prophage typing, 322
PubMLST database, 48, 193, 194, 229, 232, 234
pulsed-field gel electrophoresis (PFGE)
  agarose gels structure, 31–2
B. cereus, 174
C. botulinum, 253–4
C. difficile, 264
Clostridium spp., 192–3
communication
Escherichia coli, 41
Listeria monocytogenes, 42
PulseNet, 41
Salmonella, 42
Shigella, 42
C. perfringens, 260–261
decentralization of testing, 40
dendrogram analysis, C. sakazakii, 224, 224
electric field shape and strength, 35
electrophoresis of DNA, agarose gels, 32–3
epidemiological applications
bacterial cells, 38
food-and waterborne pathogens, 38–9
typing bacterial strains, 37
gel concentration, 35
instrumentation
contour-clamped homogeneous electric field (CHEF), 36–7
electrophoresis device (ED), 36
pulse-oriented electrophoresis (POE), 36, 37
life science, 29
L. monocytogenes
Ascl-PFGE, 305
listeriosis, 304–5, 307
multilocus sequence typing (MLST), 225
powdered infant formula (PIF), 224
polymer physics, DNA, 30–31
“production-chain” approach, 305
pulsed-field effect, 33–4
PulseNet, 223
PulseNet International, 123, 174, 267, 279
pulse-oriented electrophoresis (POE), 36, 37
random amplified polymorphic DNA (RAPD)
annealing, arbitrary primers, 3–4, 4
cross-contamination, 4
discriminatory power, 4–5
E. coli O157:H7 strains, 5
foodborne pathogens subtyping, 4
L. monocytogenes
amplification reactions, 307
food and environment contamination, 307–8
intra- and interlaboratory reproducibility, 308
listeriosis, 308
strains, 5
PCR system, 171, 350
reproducibility, 5–6
Salmonella, 345
RAPD technique see random amplified polymorphic DNA (RAPD)
Rapid Annotation using Subsystem Technology (RAST), 75, 117, 126
time PCR, 168, 170, 210, 343, 349
repetitive extragenic palindromic (REP) sequences
L. monocytogenes
amplification reactions, 314
contamination pathways, 316
GTG5 primer sets, 315
PFGE and MLEE, 314
polymerase chain reaction (PCR)
avtomated REP-PCR system, 10
BOX sequences, 9
enterobacterial repetitive intergenic consensus (ERIC) sequence, 8, 10–11
fluorescently labeled primers, 10
L. monocytogenes strains, 9–10, 314–15
random amplified polymorphic DNA PCR (RAPD-PCR), 345
repetitive element PCR (Rep-PCR), 344
restriction analysis-based genotyping, 338
restriction fragment length polymorphismPCR (RFLP-PCR), 344–5
ribotyping, 339–40
single nucleotide polymorphism (SNP), 347–9
two-class testing plan, PIF, 206
whole-genome sequencing (WGS), 349–50
sequence type analysis and recombinational
tests (START) package, 229
sequence types (STs), 60, 171, 193, 227, 319, 368
Shannon’s diversity index, 104
Shiga toxin-producing Escherichia coli (STEC)
DNA fingerprinting see DNA fingerprinting
sequence-based genotyping
comparative genomic hybridization (CGH), 285–6
lineage-specific polymorphism assay (LSPA), 283–4
multilocus sequence typing (MLST), 284–5
octamer-based genome scanning (OBGS), 282–3
single nucleotide polymorphism (SNP), 287–8
whole genome sequencing (WGS), 288
virotyping
molecular serotyping, 293–4
plasmid typing, 292
screening, informative SNPs, 291–2
shiga toxin-encoding bacteriophage
typing, 290–291
and virulence gene profiling, 289–90
Shigella outbreak, 42, 149
similarity
allelic similarity metrics
Euclidean distance, 92
Hamming distance, 92
MLST and MLVA online databases, 91, 91
band-based similarity metrics see band-
based similarity metrics
correlation coefficients
curve-based coefficients, 90
Pearson correlation coefficient, 90, 91
ranked Pearson correlation coefficient, 90
Spearman’s rank-order correlation, 90
INDEX

SYBR® Green, 168
syndrome surveillance systems, 139

TaqMan®, 168, 210, 294
Team Diarrhea, 152
tension/electrophoretic blobs, 33
toxin gene profiling
anthrax toxin genes, 170
B. cereus, molecular systems, 168, 169
conventional PCR systems, 168
multiplex PCR systems, 168–9
real-time PCR, 168
toxin-linked cryptic (TLC) element, 367–8
triple-locus variants (TLVs), 234

UniProt Consortium (2012), The, 127
unweighted pair group method with arithmetic mean (UPGMA) clustering, 19, 198, 256, 280

V. cholerae

O1 strains
CTX phages, 360
multilocus variable number tandem repeat analysis (MLVA)
classical biotype strains, 369, 371, 375
El Tor strains containing CTX-2, 375
loci characteristics and alleles, 370
profiles, 372–4
prototype El Tor biotype strains, 369, 371, 375
strains containing CTX-3, 375–6

Vibrio cholerae

CTX-1 (El Tor type CTX or CTXEl Tor), 362–4
CTX-2, 364–6
CTX-3, 366
CTX and RS1 array, 362, 365, 365
ctxB typing, 367
CTXcl (classical type CTX), 362–4
CTX phage, 362, 365
El Tor biotype, 359
genotyping, 368–71
O1 serogroup strains, 359
TLC element, 367–8
whole genome sequencing (WGS), 77

virotyping, STEC
molecular serotyping, 293–4
plasmid typing, 292
screening, informative SNPs, 291–2

definition, 87
sequence similarity, 92–3

Simpson’s index of diversity
(SID), 103–4, 106, 107
single-locus variant (SLV), 234
single-nucleotide polymorphisms (SNPs)
ctxA gene and CTX phages, 361
ctxB gene and CTX phages, 361
of rstA gene, 364

subtyping
advantages, 325
ECV, 325, 326
minisequencing (SNapshot technology”), 324
multilocus genotyping (MLGT), 324
PMSCs, 325
targeted multilocus genotyping (TMLGT) assay, 324
vs. whole genome sequencing (WGS), 69–70

Spearman’s rank-order correlation, 90

SplitsTree, 229

SSH see suppression subtractive hybridization (SSH)

STEC see Shiga toxin–producing Escherichia coli (STEC)

subtyping methods see also molecular subtyping categories, 250
discriminatory index (DI), 250
MLEE, 48, 49, 284
MLST see multilocus sequence typing (MLST)
PCR-based see polymerase chain reaction (PCR) methods
standardized, 39, 123

SuperCAT database, 172, 174

suppression subtractive hybridization (SSH), 286

surveillance, foodborne disease
active, 134–5
complaint-based, 139–40
electronic disease, 141, 141
illness pyramid-reported cases vs. all cases, 137, 138
information sources, public health, 140, 140
limitation, 140
molecular subtyping, 138
passive, 135–7, 140, 142
pathogen-specific passive, 136, 137
patient information, 135
syndrome, 139
voluntary, 141
virotyping, STEC (cont’d)
  shiga toxin-encoding bacteriophage typing, 290–291
  and virulence gene profiling, 289–90
  Voges–Proskauer test, 208, 221, 359
  voluntary surveillance systems, 141
whole-genome multilocus sequence typing (wgMLST), 194
whole-genome sequencing (WGS)  
  C. jejuni, 194–5
  computational tools, 76
  de novo assemblers, 73, 74
draft genomes, 73
  feature annotation, 75
  feature prediction, 73, 75
  foodborne outbreak investigations, 76–8
  genome annotation, 75
  genome assembly, 73
  Listeria monocytogenes, 322, 323
  molecular subtyping, 78–9
  pangenome microarrays, 114
  platforms, 71, 72
  Salmonella, 349–50
  stages, 71, 72