Campylobacter
Third Edition
Campylobacter

Third Edition

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Cover: Scanning electron micrograph showing the apical surface of differentiated Caco-2 human intestinal epithelial cells containing typical, densely packed, microvillus extensions of the host plasma membrane, with knobs at their tips. Several spiral-shaped cells of Campylobacter jejuni 81-176 are tethered specifically to Caco-2 cell microvillus tips via interactions with the sides of bacterial flagella. These binding events cause the flagella to appear bent at angles greater than or equal to 90 degrees at point of contact. The early Campylobacter flagellum-host cell interactions are considered to be a major mechanism of adherence to intestinal cells in the gut lumen. This initial adherence event can sometimes lead to subsequent yet uncharacterized specific bacterial invasion ligand-host receptor binding, triggering host signal transduction events that cause host cell internalization of C. jejuni prior to bacterial transcytosis across the intestinal epithelial mucosa. Photo courtesy of Dennis J. Kopecko and Han Lu, Center for Biologics Evaluation and Research, Food and Drug Administration, Bethesda, Md.
CONTENTS

Contributors • ix
Preface • xv

I. The Organism

1. Taxonomy of the Family Campylobacteraceae • 3
   Lies Debruyne, Dirk Gevers, and Peter Vandamme

2. Population Biology of Campylobacter jejuni and Related Organisms • 27
   Martin C. J. Maiden and Kate E. Dingle

3. Complexity and Versatility in the Physiology and Metabolism of Campylobacter jejuni • 41
   David J. Kelly

4. Comparative Genomics of Campylobacter jejuni • 63
   Olivia L. Champion, Suaad Al-Jaberi, Richard A. Stabler, and Brendan W. Wren

5. Comparative Genomics of Campylobacter Species Other Than Campylobacter jejuni • 73
   William G. Miller

II. Clinical and Epidemiologic Aspects of Campylobacter Infections

6. Clinical Aspects of Campylobacter jejuni and Campylobacter coli Infections • 99
   Martin J. Blaser and Jørgen Engberg

7. Clinical Significance of Campylobacter and Related Species Other Than Campylobacter jejuni and Campylobacter coli • 123
   Albert J. Lastovica and Ban Mishu Allos

8. Burden of Illness of Campylobacteriosis and Sequelae • 151
   Kåre Mølbak and Arie Havelaar

9. Epidemiology of Campylobacter jejuni Infections in Industrialized Nations • 163
   Christine K. Olson, Steen Ethelberg, Wilfrid van Pelt, and Robert V. Tauxe

10. Molecular Epidemiology of Campylobacter Species • 191
    Stephen L. W. On, Noel McCarthy, William G. Miller, and Brent J. Gilpin

11. Isolation, Identification, Subspecies Differentiation, and Typing of Campylobacter fetus • 213
    Marcel A. P. van Bergen, Jos P. M. van Putten, Kate E. Dingle, Martin J. Blaser, and Jaap A. Wagenaar

12. Diagnosis and Antimicrobial Susceptibility of Campylobacter Species • 227
    Collette Fitzgerald, Jean Whichard, and Irving Nachamkin

13. Guillain-Barré Syndrome and Campylobacter Infection • 245
    Bart C. Jacobs, Alex van Belkum, and Hubert P. Endtz

14. Mechanisms of Antibiotic Resistance in Campylobacter • 263
    Qijing Zhang and Paul J. Plummer
15. National Molecular Subtyping Network for Food-Borne Bacterial Disease Surveillance in the United States • 277
Peter Gerner-Smidt, Steven G. Stroika, and Collette Fitzgerald

III. Pathogenesis and Immunity

16. Interaction of Campylobacter jejuni with Host Cells • 289
Robert O. Watson and Jorge E. Galán

17. Cell Biology of Human Host Cell Entry by Campylobacter jejuni • 297
Lan Hu and Dennis J. Kopecko

18. Campylobacter jejuni Secretes Proteins via the Flagellar Type III Secretion System That Contribute to Host Cell Invasion and Gastroenteritis • 315
Charles L. Larson, Jeffrey E. Christensen, Sophia A. Pacheco, Scott A. Minnich, and Michael E. Konkel

19. Innate Immunity in Campylobacter Infections • 333
Nicole M. Iovine

20. Chemosensory Signal Transduction Pathway of Campylobacter jejuni • 351
Victoria Korolik and Julian Ketley

21. Animal Models of Campylobacter jejuni Infections • 367
Linda S. Mansfield, David B. Schauer, and James G. Fox

22. Rabbit Model of Guillain-Barré Syndrome • 381
Nobuhiro Yuki

23. Pathogenesis of Campylobacter fetus • 401
Martin J. Blaser, Diane G. Newell, Stuart A. Thompson, and Ellen L. Zechner

24. Development of a Human Vaccine • 429
David R. Tribble, Shahida Baqar, and Stuart A. Thompson

IV. Glycobiology

25. N-Linked Protein Glycosylation in Campylobacter • 447
Harald Nothaft, Saba Amber, Markus Aebi, and Christine M. Seymansi

26. O-Linked Flagellar Glycosylation in Campylobacter • 471
Susan M. Logan, Ian C. Schoenhofen, and Patricia Guerry

27. Campylobacter jejuni Lipooligosaccharides: Structures and Biosynthesis • 483
Michel Gilbert, Craig T. Parker, and Anthony P. Moran

28. Campylobacter jejuni Capsular Polysaccharide • 505
Andrey V. Karlyshev, Brendan W. Wren, and Anthony P. Moran

29. Campylobacter Metabolomics • 523
Evelyn C. Soo, David J. McNally, Jean-Robert Brisson, and Christopher W. Reid

V. Genes and Gene Expression

30. Regulation of Flagellar Gene Expression and Assembly • 545
David R. Hendrixson

31. Natural Competence and Transformation in Campylobacter • 559
Rebecca S. Wiesner and Victor J. DiRita

32. Survival Strategies of Campylobacter jejuni: Stress Responses, the Viable but Nonculturable State, and Biofilms • 571
Sarah L. Svensson, Emilisa Ffridich, and Erin C. Gaynor

33. Iron Metabolism, Transport, and Regulation • 591
Alain Stintzi, Arnoud H. M. van Vliet, and Julian M. Ketley

34. Regulation of Genes in Campylobacter jejuni • 611
Marc M. S. M. Wösten, Andries van Mourik, and Jos P. M. van Putten
VI. Food Safety and Intervention

35. *Campylobacter* in the Food Supply
   Wilma Jacobs-Reitsma, Ulrike Lyhs, and Jaap Wagenaar
   • 627

36. Transmission of Antibiotic Resistance from Food Animals to Humans
   Frank M. Aarestrup, Patrick F. McDermott, and Henrik C. Wegener
   • 645

37. Poultry Colonization with *Campylobacter* and Its Control at the Primary Production Level
   Jaap A. Wagenaar, Wilma Jacobs-Reitsma, Merete Hofshagen, and Diane Newell
   • 667

38. Bacteriophage Therapy and *Campylobacter*
   Ian F. Connerton, Philippa L. Connerton, Paul Barrow, Bruce S. Seal, and Robert J. Atterbury
   • 679

Index • 695
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Our understanding of the clinical aspects, epidemiology, and pathogenesis of Campylobacter infection has increased dramatically since publication of the second edition of Campylobacter in 2000. As the number of species within the family has expanded, so has our knowledge of this group of organisms in terms of their physiology, population biology, and diversity. The ability to understand genomic diversity in Campylobacter is due in great part to improvements in technology that have advanced comparative analyses. The sequencing of the first C. jejuni strain in 2000 was a milestone in Campylobacter genetics and brought to light aspects of biology that previously could not have been identified. Since then, additional complete Campylobacter genome sequences have been published and have provided new insights about the genomic diversity of these organisms, which now is covered extensively in this new edition.

Campylobacter infections and their complications, such as Guillain-Barré syndrome, cause significant morbidity in specific populations. There is growing recognition of Campylobacter among clinicians as well as by the lay public. Antimicrobial resistance also continues to increase and poses new issues regarding therapies. Of particular note are the impact that researchers in our field have had on government regulation of antimicrobial agent use in food animals and how effecting change will ultimately improve human health.

Our understanding of the pathogenesis of Campylobacter infections has advanced greatly, especially in the area of signal transduction pathways and cell biology of the organism. The emerging field of Campylobacter glycobiology, which was pioneered by the late Gerald Aspinall, has provided a structural basis for important polysaccharides and glycolipids from the organism and great insight into glycosylation systems, which also are present in other prokaryotes and eukaryotes. This work, combined with an increased understanding of the molecular biology of gene expression in Campylobacter, is helping to form a more complete picture about the organism and its interaction with the host and environment.

Ultimately, research will help improve human health through understanding the immunology of campylobacter infection and the pertinent host defenses. These will lead to the development of strategies to reduce infection, through either effective vaccines or improved food safety. The ecology of food safety also has seen a dramatic increase in research, with emphasis on understanding the extent of campylobacter in the food supply, transmission of antibiotic resistant campylobacters from food animals to humans, and control of campylobacter at the food source.

The above advances have helped to form the nucleus for the 3rd edition of Campylobacter. We are grateful to the scientific groups from around the world that have contributed to the preparation of these outstanding chapters. These represent the generous sharing of our growing knowledge of these important zoonotic pathogens of humans. Finally, we especially thank Greg Payne at ASM Press for his help and guidance throughout the process of developing this volume.

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INDEX

ABC transporters, 42–43, 451, 583, 594–596
Abdominal pain, Campylobacter enteritis, 101–104
Abortion
farm animals, 123, 126, 213–214, 401, 403, 423–424
human, 107, 127–128
Acetyl phosphate, 585
N-Acetylglucosamine-6-phosphate 2-epimerase, 488
Acetyltransferase, 494, 538–539
Acid stress, C. jejuni, 572, 576
AcrA protein, 450–452
Actin filaments, Campylobacter invasion of intestinal epithelium, 300–301, 320
Acute-phase response, 342–344
Adherence, bacterial
C. jejuni to intestinal epithelial cells, 298–299, 317, 319
capsular polysaccharide in, 512–514
N-linked protein glycosylation in, 456–457
ADP-L,D-Fep, 492
Aer receptors, 356–357
Aerobic stress
C. jejuni, 572, 574
long-term aerobic adaptation, 574
short-term, 574
short-term aerobic tolerance, 574
AFLP (amplified fragment length polymorphism), 192, 196–197
Arcobacter, 19, 203–204
C. concisus, 204
C. fetus, 203–204, 216–219, 222
C. helveticus, 204
C. jejuni, 251
C. lari, 203
C. upsaliensis, 203
differentiation of Campylobacter species, 16
epidemiologic typing, 232
fluorescent, 197
national subtyping network, 283
non-jejuni, non-coli Campylobacter, 203–204
Agar dilution method, antimicrobial susceptibility testing, 646
Age distribution, Campylobacter infections, 166–167, 170

Alkyl hydroperoxidase, 573, 599, 602, 604–605, 617
Alkyl peroxides, 598–600
Allelic profiles, 29
Alpha 1-antitrypsin, 343
AMAN (acute motor axonal neuropathy), 247, 249
immune attack on nerve root axons, 387–391
rabbit model, 381–399
treatment, 395–396
amiA gene, 579
Amino acid biosynthesis, 87–88
involvement of Pgl proteins, 458–459
Amino acid catabolism, 47–49
Amino acid identities, between Campylobacter proteomes, 76
Amino acid transport, 42–44, 583
involvement of Pgl proteins, 458–459
Aminoglycoside acetyltransferase, 268, 647–648
Aminoglycoside adenyltransferase, 268–269, 647–648
Aminoglycoside phosphotransferase, 268–269, 647–648
Aminoglycoside resistance, 267–269, 647–649
AMLPl element, 79–81
Amoxicillin resistance, 234, 648
Amoxicillin-clavulanic acid, clinical indications, 114
Amplified fragment length polymorphism, see AFLP
Ampicillin, clinical indications, 128
Ampicillin resistance, 234, 236, 648
Amyloid A, serum, 343–344
Amyloid P, serum, 343
Anaplerotic reactions, 44–46
Animal models, see also specific animals
C. fetus infections, 218, 423–424
C. jejuni infections, 367–379, 435–437
colonization modes, 369–370
defective for adaptive immunity or with altered flora, 372–373
disease models, 370–372
future goals, 375
major uses and desirable characteristics, 368
reagents and resources, 369
specific-pathogen-free status, 368–369
strain variations, 369
C. jejuni vaccine development, 373–374, 435–437
GBS, 254, 256, 381–399
ant(6)-la gene, 648–649
ant(3')-la gene, 648–649
Antianglioside antibodies, 381
GBS, 248–249, 252–254
serum, 252
Antigen [a], 409
Antigen sequence typing, C. jejuni, 36
Antimicrobial agents, see also specific drugs
C. fetus infections, 128
C. hyointestinalis infections, 133
C. lari infections, 134
C. upsaliensis infections, 131
Campylobacter enteritis, 111–114
enteric helicobacters, 140
Antimicrobial peptides/proteins, produced by neutrophils, 340
Antimicrobial resistance, 316, 618–619, see also specific drugs
association to antimicrobial use, 651–654
bacteria within biofilms, 581
consequences in human infections, 656–657
in different food animal reservoirs, 654–657
emergence, 651–654, 659
ecological observations, 652–654
epidemiological field studies, 652
experimental studies, 651–653
fitness cost for bacteria, 660
future aspects, 661
interventions to reduce occurrence, 659–661
mechanisms, 263–276, 647–651
plasmid-borne, 76–78
source attribution studies, 656, 658
surveillance, 182–183
transmission along food chain, 655–656
transmission from food animals to humans, 645–665
Antimicrobial resistance risk assessment, 657–659
Antimicrobial susceptibility testing, 230, 232–236
clinical breakpoints, 646–647
epidemiological cutoff values, 646–648
methods, 645–646
in vitro susceptibility profiles, 232–233
aphC gene, 618
Apoptosis, C. jejuni-induced, 308–309, 318
Appendicitis, 104
Aquatic environment, survival of campylobacters, 580
AraC protein, 612, 620
Arcobacter
AFLP, 19, 203–204
antimicrobial susceptibility, 235–236
characteristics of genus, 11, 17
differentiation of species, 19
isolation, 17
novel species, 18–19
species of genus, 17–18
taxonomy, 5
Arcobacter butzleri, 17–19
AMLP1, 81
antimicrobial susceptibility, 235–236
taxonomy, 5
Arcobacter butzleri infections, 125–127, 130, 137–139
Arcobacter cibarius, 18–19
Arcobacter cryaerophilus, 17–19
antimicrobial susceptibility, 235–236
Arcobacter cryaerophilus infections, 125–126, 137–139
Arcobacter halophilus, 18–19
Arcobacter infections, 137–139
classification of isolates, 138
clinical features, 126, 138
epidemiology, 126, 137–138
microbiology, 125, 137
pathogenesis, 138–139
Arcobacter nitrofigilis, 17
Arcobacter skirrowii, 5, 17–19
Arcobacter skirrowii infections, 126, 138
ArsR protein, 612, 620
Arthritis
reactive
burden of illness, 154–155
after Campylobacter enteritis, 109
vaccine-related, 432–433, 437
septic, 108, 127, 404
Asparaginase, 47
Aspartate transport, 42–43, 459
Aspartate/glutamate transaminase, 47
Aspartate:ammonia lyase, 47
asta A gene, 551
astP gene, 206
ATPase
F-type, 42
P-type, 42
Autoagglutination (AAG phenotype), 477–478, 583
Autoregulation, pgf genes, 457–458
Average nucleotide identity, 7–9
Azithromycin, clinical indications, 111
Azithromycin resistance, 265–266
Bacillosamine, 459
Bacillosamine phosphate, 450
Bacteremia
C. fetus, 124, 126–127
C. jejuni, 164
C. jejuni subsp. doylei, 135
C. lari, 133–134
C. upsaliensis, 128, 131
in Campylobacter enteritis, 105
enteric helicobacters, 139–140
Bacteriocins, 672
Bacterioferritin, 598, 600
Bacteriophage, 65
Campylobacter-specific, 681
C. jejuni response to phage predation, 689–690
non-jejuni Campylobacter, 81–82
phage characteristics, 681–682
resistant bacteria, 684
source, 682
strains of Campylobacter that populate chickens, 688–689
historical aspects, 680
structure, 680–681
taxonomy, 680–681
Bacteriophage Mu, 79–81, 682
Bacteriophage receptor, 514
Bacteriophage resistance, 684
Bacteriophage therapy
advantages and disadvantages, 682–683
elimination of *Campylobacter* from colonized flock, 679–693
elimination of *Campylobacter* from poultry
disinfection of meat, 687–688
proof of efficacy, 682–684
treatment of live chickens, 684–687
public acceptability, 688
regulatory issues, 688
Bacteriophage typing, 222, 232, 681
*Bacteroides gracilis*, 4
*Bacteroides ureolyticus*, 4–5, 20, 137
Barrett’s esophagus, 136
Basal body, 546, 548
Beef, 634–635
Beta-lactamases, 234, 269–270, 648
Bile, 272
Bile acids, defense against enteric pathogens, 334, 336, 344
Bile resistance, 271, 316, 336, 576–577, 615, 619
Biofilms
adaptation to environments encountered in vivo, 581
antimicrobial resistance of bacteria within, 581
autoagglutination, 583
*C. jejuni*, 580–585
formation, 478, 505–506, 514, 581, 584
AI-2-mediated quorum sensing, 585
conditions promoting, 584
cyclic di-GMP, 585
regulatory factors, 584–585
stringent control, 584–585
two-component regulatory systems, 585
iron metabolism and, 605
molecular themes underlying physiology, 583–584
structure and function, 581–583
survival in aquatic environments, 580
Biosecurity, poultry house, 670–672
general measures, 671
multispecies farming, 671–672
thinning, 672
Biotyping, 232
Blood, innate immune defenses, 334, 340–343
Blood samples, 228
Bottled water, 636
Bovine venereal campylobacteriosis, 401–402
Bovine vibriosis, 123
Breast milk
collostral antibodies, 429
oligosaccharides, 334–336, 344
Broth microdilution method, antimicrobial susceptibility
testing, 646
Buerger’s disease, 136
Burden of illness
definition, 151
measurement, 151–152
campylobacteriosis, 151–162
acute infections vs. postinfective complications, 157
ascertainment of outcomes, 154–155
disability weights, 156–157
immunity and, 155–156
industrialized countries, 171–172
integrating with risk assessment and economics, 157–160
perspectives and future research, 160–161
survival pyramid, 152–154
United States, 167–168
Bursitis, 108
Butter, 633
C4-dicarboxylate transport, 44
CadF protein, 91, 298, 309, 319–321, 407
Calcium ions
*Campylobacter* invasion of intestinal epithelium, 302–303, 305
intracellular, toxin effects, 307
*Campylobacter*
characteristics of genus, 11–12
chemotaxis pathway, 351–365
chickens, 157–160, 177, 180–182
colonization without disease, 432–433
culture, 229–230
differentiation of species, 15–16
evolution, 84–85
phage effects, 688–690
identification, 230–241
isolation, 4, 12
enrichment culture, 229, 628
filtration, 229
from food or water, 628–637
metabolomics, 523–542
phenotypic characteristics, 15–16
phylogenetic tree, 5–7, 30–32, 84–85
population studies, 27–40
PulseNet, 280–284
salt sensitivity, 575–576, 637
species of genus, 12–15
species tree, 5–7
taxonomy, 3–5, 227
thermophilic, 230, 403
thermotolerant, 627, 629, 637
typing systems
epidemiologic methods, 232
molecular methods, 232
phenotypic methods, 232
whole-genome taxonomy, 5–11
*Campylobacter bubulus*, 4
*Campylobacter canadensis*, 15
*Campylobacter coli*, see also Non-jejuni *Campylobacter*
antimicrobial susceptibility, 232–235
characteristics of species, 14–15
clonal complexes, 36
comparative genomics, 73–95
epidemiology, 37
evolution, 201–202
host species, 200
isolation, 229–230
MLST, 29–30, 36–38, 204
O-linked flagellar glycosylation, 530–534
INDEX

PFGE, 282
population studies, 36–37
sequence types, 36–37
taxonomy, 4–5
transformation, 562
VBN C state, 577
Campylobacter coli infections, 99–121, 182, see also Enteritis, Campylobacter
clinical features, 127
diagnosis, 227–232
extraintestinal, 105–109
microbiology, 125
Campylobacter concisus, see also Non-jejuni Campylobacter
AFLP, 204
antimicrobial susceptibility, 236
characteristics of species, 13–14
comparative genomics, 73–95
PFGE, 202
RAPD, 204
taxonomy, 5
Campylobacter concisus infections, 135–137
clinical features, 126–127, 130
epidemiology, 126
microbiology, 125
Campylobacter cryaerophila, 5
Campylobacter curvus, see also Non-jejuni Campylobacter
characteristics of species, 13–14
comparative genomics, 73–95
taxonomy, 5
Campylobacter curvus infections, 135–137
clinical features, 127
microbiology, 125
Campylobacter fetus, 213–225
AFLP, 203–204, 216–219, 222
cell envelope proteins, 405
characteristics of species, 12
epidemiology, 403
genome plasticity, 405
genome sequence, 404–407
genome size, 404–406
genomic islands, 405
historic classification, 213–215
host associations, 214
isolation, 124, 126, 214–215
lipopolysaccharide, 407–408
metabolism, 404–406
MLST, 29–30, 37, 204, 216, 218–219, 222
molecular identification, 216
PCR methods, 216, 218
PFGE, 202, 222, 404–405
phenotypic identification, 215–216, 404–406
population studies, 37
RAPD, 218, 222
reptile strains, 221–222
16S rRNA, 222
sap genes, 415–417
sequence types, 37
serum-resistant strains, 409–410
S-layer, 409–412, 505
Campylobacter fetus subsp. fetus, 12, 37, 123–128, 213, 401, see also Non-jejuni Campylobacter
antimicrobial susceptibility, 235
comparative genomics, 73–95
subspecies differentiation, 216–222
Campylobacter fetus subsp. venerealis, 12, 37, 123–124, 213, 401–402
subspecies differentiation, 216–222
Campylobacter fetus subsp. venerealis biovar intermedius, 216, 220–221
Campylobacter gracilis, 5, 12, 14
Campylobacter gracilis infections, 135–137
Campylobacter helveticus, 15, 128
AFLP, 204
MLST, 29–30, 37–38, 204
Campylobacter hominis, 141, see also Non-jejuni Campylobacter
characteristics of species, 14
comparative genomics, 73–95
genomic reduction, 88
Campylobacter hyointestinalis
characteristics of species, 12–13
PFGE, 203
taxonomy, 5
Campylobacter hyointestinalis infections, 131–133
clinical features, 126–127, 130, 132–133
diagnosis, 131–132
epidemiology, 126, 132
microbiology, 125, 131–132
treatment, 132–133
Campylobacter hyointestinalis subsp. hyointestinalis
characteristics of species, 12–13
PFGE, 203
taxonomy, 5
Campylobacter hyointestinalis infections, 131–133
clinical features, 126–127, 130, 132–133
diagnosis, 131–132
epidemiology, 126, 132
microbiology, 125, 131–132
treatment, 132–133
Campylobacter hyointestinalis subsp. lawsonii, 12–13, 131
Campylobacter infections
animal models, 367–379
ascertainment of outcomes, 154–155
burden of illness, 151–162
children, 177, 429–430
common-source outbreaks, 172–174
developing countries, 156, 161, 430
diagnosis, 227–232
culture and isolation of campylobacters, 229–230
direct detection in stool samples, 228–229
identification of campylobacters, 230–241
specimen considerations, 227–228
disability weights, 156–157
epidemiology, 429
GBS, see Guillain-Barre syndrome
immune response, 155–156, 182, 432
immunocompromised patients, 163–164
incidence, 429
industrialized countries, 156, 161, 163–189, 430–431
innate immunity, 333–350
molecular epidemiology, 191–211, see also Molecular typing
morbidity, 152–154
protective factors, 182
serology, 429
age-related, 429
sporadic, 174–182
surveillance pyramid, 152–154, 167–168
United States, 164–168
Campylobacter insulaenigrae, 88, 141
characteristics of species, 15
MLST, 204
Campylobacter jejuni
acid stress, 572, 576
aerobic stress, 572, 574
AFLP, 251
amino acid catabolism, 47–49
amino acid transport, 42–44
anaplerotic reactions, 44–46
antigen sequence typing, 36
antimicrobial susceptibility, 232–235
bile stress, 572, 576–577
biofilms, 580–585
capsular polysaccharide, 66, 483, 505–521
central carbon metabolism, 44–47
characteristics of species, 14–15
chickens, 264–265, 298–299, 580
clonal complexes, 32–36
cold stress, 571
colonization, 41, 49
comparative genomics, 63–71
comparative phylogenomics, 68–69
competence, 563–565
electron transport, 48, 50–58
epidemiology, 36
evolution, 201–202
flagellar genes, 323, 550–553
flagellar type III secretion system, 315–332
GBS-related
gene characteristics, 251–252
gene-specific variation, 251
rarity of disease, 254–255
strains that cannot trigger GBS, 255–256
whole-genome polymorphisms, 250–251
gene gazing, 64–65
gene regulation, 611–624
gene sequencing, 65–66
geno-diversity, 63–64, 67, 560–561
genome sequences, 41, 63–71
rearrangements in response to phage, 689–690
genomics to phenomics, 66
gluconeogenesis, 44–46
heat stress, 571–573
homoplasy ratio, 560
host species, 199–200
isolation, 229–230
lipooligosaccharide, 66, 251–256, 381–382, 483–504, 507–508
lipopolysaccharide, 339
microaerophilic, 49–50
MLST, 29–30, 32–36, 38, 204
nitrogen assimilation, 47–49
nitrosative stress, 572, 576, 617–618
N-linked protein glycosylation, 66, 448–451, 537–539
O-linked flagellar glycosylation, 66, 524–530
organic acid transport, 44
oxidative stress, 572–574
pathogenesis, 64–66
pathogenicity islands, 65
PFGE, 195–196, 280–282
phase variation, 65–66
physiology and metabolism, 41–61
plasmids, 64–65
plasticity regions, 621
polysaccharide capsule, 439
polysaccharides, 514–515
population studies, 32–36, 559–561
pseudogenes, 65
pVir, 565–566
RAPD, 204
restriction/modification system, 64
sequence types, 32–34, 36
sigma factors, 612–614
solute transport, 41–44
starvation, 572, 574–575
stationary phase stress, 572, 574–575
stress response, 515, 571–577
surface glycostructures, 66
taxonomy, 4–5
under oxygen limitation, 54–58
VBNF state, 577–580
virulence factors/virulence phenotypes, 316–318
Campylobacter jejuni infections, 99–121, see also Enteritis, Campylobacter
adherence to intestinal epithelium, 298–299, 317, 319
animal models, 367–379, 435–437
clinical features, 127, 130
bovine venereal campylobacteriosis, 402
development, 429–444
animal models, 373–374, 435–437
human, 429–444, 517–518
candidate selection process, 433–437
epidemiological issues and strain diversity, 431–432
killed whole cell vaccines, 437–438, 517
live attenuated vaccines, 437, 517
outer membrane proteins and secreted proteins, 433–435
safety concerns, 432–433, 517
subunit vaccines, 439–440, 517
target populations, 430–431
veterinary, 517–518
Campylobacteraceae, characteristics of family, 11–12
Campylobacter-like organisms, 4–5, 108, 135, 139
“Candidatus Arcobacter sulfidicus,” 18
capA gene, 320
CapA protein, 319, 321, 514
Cape Town protocol, 128–129, 205
Capsular polysaccharide, 298–299
in adhesion, 512–514
bacterium-host interaction, 516–517
biochemistry, 507–512
biological role, 505–506, 512–514
biosynthesis, 491, 506–507
influence of growth conditions, 515
C. jejuni, 66, 483, 505–521
comparative genomics, 509
detached, 514–515
discovery of CPS production in campylobacters, 507–508
evidence from genome sequencing of C. jejuni, 508–509
gastroenteritis and, 516–517
 genetics, 506–512
group II, 506
group III, 506
immunogenicity, 513–514
in vitro models of infection, 512–513
phase variation, 515
phospholipid anchor, 510, 512
phosphorilamidate modification, 510
sorbofuranose modification, 510
stabilization with Alcian Blue, 510–513
structural analyses, 510–511, 515
subunit vaccines, 439
types, 506–507
Carbapenems, clinical indications, 128
Carbon dioxide, effect on transformation, 562
CARMA project, 157–160
Cary-Blair medium, modified, 228
Case-control method, 627
sporadic infections, 175–179
Caspases, 309
cat genes, 649–650
Catalase, 573–574, 599, 602, 604, 617
Cathelicidins, 334, 338, 344
Cattle
C. fetus infections, 214–215, 401–403
INDEX 701

C. jejuni infections, 199–200
drug-resistant Campylobacter, 657
Caveolae, Campylobacter invasion of intestinal epithelium, 303

CbrR gene, 336, 572, 585, 612
ChrR protein, 577, 615
econNOPQ genes, 87
cdt genes, 90–92, 308
Cefoperazone resistance, 270
Cell wall, VBNC state, 578–579
Cellulitis, 404
Central carbon metabolism, 44–47
Central genotypes, 32
Central nervous system infections, 127
Cephalosporin(s), clinical indications, 128
Cephalosporin resistance, 234, 236, 269–270, 648
Cet proteins, 356, 548
ceu genes, 595
ceuB gene, 594–595
ceuBCDE genes, 617–618
ceuC gene, 594–595
ceuD gene, 594–595
ceuE gene, 231, 594–596, 603
Ceu proteins, 604
CeuBCD protein, 594
CeuE protein, 596, 602
cfrA gene, 595, 603, 605, 617–618
CfrA protein, 594–595, 602
cft gene, 598, 603
Cft protein, 598, 600, 602
cgb gene, 572, 576, 619
Cgb protein, 576, 618
Cgp proteins, 448, 452, 493
cgt genes
cgtA gene, 488, 491, 494–495
cgtB gene, 488, 494–495
Cgt proteins
CgtA protein, 491, 493–494, 497–500
CgtB protein, 491, 494, 497–499
cbe genes, 355
Che proteins
CheA protein, 351–352, 355, 357–358, 548, 583
CheB protein, 359–360, 548
CheR protein, 359–360, 548
CheV protein, 358–359, 548
Che signaling cascade, 546, 548
CheA histidine kinase, 357–358
CheR protein, 359–360
CheW and CheV proteins, 358–359
CheY protein, 360–362
E. coli, 352–354
gene content of components, 355–357
group A receptors, 355–357
groups B, C, and Aer receptors, 356–357
model, 363
organization, 355–357
receptor specificity, 357
sensory receptor complex, 357
variations, 354
Chest wall abscess, 108
Chickens, see also Poultry
C. jejuni, 199–200, 264–265, 298–299, 580
Campylobacter, 157–160, 177, 180–182
Campylobacter-specific phages, 682
colonization, 513–514, 639
role of N-linked protein glycosylation, 457
drug-resistant Campylobacter, 654–656
vaccination, 673
Children, Campylobacter infections, 100–103, 177, 429–430
Chloramphenicol, clinical indications, 114
Chloramphenicol acetyltransferase, 650
Chloramphenicol resistance, 76, 236, 270
food-animal reservoirs, 655
mechanisms, 649–650
Chlorine disinfection, 581, 637–638
Cholangitis, 127
Cholecystitis, 106, 127, 336
Chorioamnionitis, 127
ChpA protein, 595
chu genes
chuA gene, 596, 604–605
chuABCD genes, 603, 617–618
chuB gene, 604
chuBCD genes, 596
Chu proteins
ChuA protein, 594, 598
ChuABCD protein, 602
ChuZ protein, 594, 596
Cia proteins, 329, 434
CiaB protein, 91–92, 309, 320–322, 326–327, 336, 407
recognition and export by type III secretion system, 323–325
Ciprofloxacin, clinical indications, 111–114
CIRCE element, 620
Citrate synthase, 87
Citric acid cycle, 44–45, 85–86, 406
with characteristics of anaerobes, 46–47
Gj1496c protein, 453–456
Cja proteins
CjaA protein, 43, 458–459
CjaC protein, 452
CJIE3 element, 82
CJIE4 element, 82
Clarithromycin, clinical indications, 111
Clarithromycin resistance, 265–266
CLIE1 element, 82
Clindamycin resistance, 233, 235–236

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Clinical breakpoints, 646–647
Clonal complexes, 29, 198–201
C. coli, 36
C. jejuni, 32–36
Clonal population, 31, 560
ClonalFrame algorithm, 34–35
clp genes, 572–573
cme genes
cmeABC genes, 619
cmeB gene, 650
cmeDEF genes, 565
cmeR gene, 572, 612, 619
Cme proteins
CmeABC efflux pump, 263–267, 270–272, 336, 576–577, 619, 651
CmeDEF efflux pump, 270–271
CmeR protein, 271–272, 615, 619
Cmg proteins, 77
CMLP1 element, 79–81
CMP sugars, 475–476, 525
CMP-Kdo synthetase, 506–507
CMP-Leg5Ac7Ac, 532–534
CMP-Leg5Am7Ac, 533–534
CMP-Leg5AmNMe7Ac, 533
CMP-Neu5Ac, 493, 525–526, 533
CMP-Neu5Ac synthase, 488
CMP-Pse5Ac7Ac, 526, 533
CMP-Pse5Ac7Am, 530, 532–534
CMP-PseAm, 526, 530, see also CMP-Leg5Am7Ac
Cold stress, C. jejuni, 571
Colitis, 104–105
Collectins, 334, 343
Colonization
biofilm formation, 581
C. jejuni, 41, 49
capsular polysaccharide in, 513–514
without disease, 432–433
poultry, 513–514, 629–632, 639, 667–678
bacteriophage therapy, 679–693
eliminating Campylobacter from colonized flock, 674–675, 679–693
epidemiology of flock colonization, 668–669
lag phase, 668
phage effects, 688–689
prevalence rates between countries, 668–669
prevention of introduction of Campylobacter into flock, 670–674
risk factors, 669–670
role of N-linked protein glycosylation, 457
seasonal variation, 669–670
sources, 669–670
transcriptional profile of iron metabolism genes, 604–605
Colonization models, 369–370
Colonization potential, 668, 672
Colony morphology, 230
com genes
comABC genes, 572
comB3 gene, 566
Common-source outbreaks, 172–174, 627
evolution and, 201–202
industrialized countries, 173–174
molecular typing studies, 201–202
United States, 172–173
Comparative genomics, 7–9, 35–36
C. jejuni, 63–71
capsular polysaccharide, 509
DNA microarray analysis, 66–67
non-jejuni Campylobacter, 73–95
Comparative phylogenomics, 67
C. jejuni, 68–69
Competence
DNA discrimination, 562–563
evolution, 559
genetics, 563–565
molecular biology, 563–565
natural, 559–570
Competitive exclusion, prevention of colonization of poultry, 672
Complement inhibitors, 343
Complement system
complement factor C3, 410
complement-mediated nerve injury in GBS, 394–395
innate immune defenses, 334, 342–344
resistance of C. fetus, 410
Complex I, see NDH-1 complex
Conjugate vaccines, 439
Contingency (phase-variable) genes, non-jejuni Campylobacter, 78–79
CorA protein, 593–594
Cost of illness methodology, 152, 157–159
cps genes, 509
C-reactive protein, 342–344
CRISPR elements
HRM analysis, 194
non-jejuni Campylobacter, 82–83
Cross-contamination, during food preparation, 180, 638–639
Cross-reactive antibodies, to lipooligosaccharide and gangliosides, 253–255
Crp protein, 612, 617–618
Csp proteins, 323–324
csrA gene, 620–621
CsrA protein, 612, 620–621
cst-II/III gene, 251–252, 394, 488, 494–495
Cst-II/III protein, 493–494, 497–501
cts genes, 563–564, 566
Cts proteins
CtsD protein, 560, 563
CtsE protein, 560, 563
CtsF protein, 560, 563
CtsG protein, 560
CtsP protein, 560, 563–564
CtsT protein, 560
CtsW protein, 565
CtsX protein, 564
CURIE2 element, 82
Cutting boards, 180, 638
Cyanide-insensitive oxidase, 53
Cyanide-sensitive oxidase, 53
Cyclic di-GMP, 585
cydAB operon, 53, 87
Cysteine transport, 43, 458–459
cytC gene, 66
Cytochrome(s), 50–51
Cytochrome c, 52–53, 65
Cytochrome c nitrite reductase, 56
Cytochrome c oxidase, 87, 406
Cytochrome c peroxidase, 53–54
Cytochrome cp-oxidase, 53
Cytokines, Campylobacter-induced, 308, 318, 342
Cytolethal distending toxin, 90–91, 131, 307–309, 406
Cytoskeleton, Campylobacter invasion of intestinal epithelium, 299–301, 320
Cytotoxin, 307
Dairy cows, 633
Dairy products, 633–634
DALY (disability-adjusted life-year), 151–152
Dcc proteins, 614–616
dccR gene, 612
dcw genes, 44, 572, 574
Defensins, 334, 338, 344
Denaturing gradient gel electrophoresis, 194
Dendritic cells, 308, 318
innate immune defenses, 334, 342, 344
DeoR protein, 612, 619
Developed countries, see Industrialized countries
Developing countries, Campylobacter infections, 100, 156, 161, 430
dfr genes, 270, 649, 651
2,4-Diacetamide-bacillosamine biosynthetic pathway, 530
Diarrheal disease, 127, 429, see also Enteritis, Campylobacter
Arcobacter, 138
C. fetus, 124–125, 127, 403
C. jejuni subsp. doylei, 135
C. lari, 133–134
C. upsaliensis, 128, 130–131
enteric helicobacters, 139–140
hydrogen-requiring campylobacters, 136
toxins and, 307–308
Dicarboxylate/amino acid:cation symporter family, 44
Diffusion method, antimicrobial susceptibility testing, 645
Dihydrofolate reductase, 263, 651
Dihydroorotase, 84
Dihydropteroyl synthase, 651
Dilution method, antimicrobial susceptibility testing, 645
Disability weights, 156–157
Dish washing, 639
Disinfecting agents, 638
dmbA gene, 509
dmsA gene, 66
DMSO reductase, 56–58, 65, 87
DNA methylation, 562
transformation, see Transformation
DNA gyrase, 263–265, 650
DNA microarray, 194–195
comparative genomics, 66–67
species-specific, 231
DNA uptake sequence, 562–563
dna genes
dnaJ gene, 572
dnaK gene, 572–573, 620
DnaJ protein, 572, 615
Doc proteins, 548
Domestic animals, 126
dprA gene, 566
DprA protein, 560, 566
dps gene, 340, 572, 574, 598
Dps protein, 598, 600
Drinking water, 635–638
Drug efflux pumps, 263–267, 269, 336
multidrug pumps, 270–272, 336, 650
Dry Spot Campylobacter Test Kit, 231
Eggs, Campylobacter in food supply, 630–633
Electron acceptors, 50, 86–87, 406
alternative, 50, 54–58
fumarate, 55
hydrogen peroxide, 53–54
nitrate and nitrite, 55–56
S- or N-oxides, 56–58
Electron donors, 50–53, 406
hydrogen and formate, 51
organic acids, 52
sulfite, 52–53
Electron transport, 48, 50–58, 86–87
C. fetus, 406
iron in, 591
organization and assembly of electron transport chain, 50–51
oxygen-dependent respiration, 53
under oxygen limitation, 54–58
Electroporation, 562
Emden-Meyerhof-Parnas pathway, 44, 85
Empyema, 108, 127
Endocarditis, 127
Endoscopy, Campylobacter enteritis, 104, 110–111
Endosomes, intracellular movement of Campylobacter, 307
Endotoxin, 483
Enrichment culture, 229, 628
Enrofloxacin, 651, 653–654
Enrofloxacin resistance, 263–265
Enteritis, Campylobacter, 99–121, 126
abdominal pain, 101–104
bacteremia, 105
capsular polysaccharide and, 516–517
children, 100–103
clinical pathology, 99
developing countries, 100
diagnosis, 110–111, 227–232
diarrheal stage, 101–102
early infections, 316–318
extraintestinal infections, 105–109
hematology and biochemistry, 110
hepatobiliary infections, 105–107
immune response, 99–101
immunodeficient patient, 103
incubation period, 101–102
infective dose, 101, 316
intestinal complications, 103–105
late infection, 318–319
late-onset complications, 109–110
microbiology, 110
model, 315–318
morbidity, 102
neonatal infections, 103
onset and prodrome, 101
pathogenesis, 315–332
rashes, 103
recovery stage, 101–102
renal and urinary tract disease, 107–108
treatment, 111–114
Enterobactin, 594–597, 602
Enterobactin uptake permease, 604
Enteroxin, 307
Entner-Doudoroff pathway, 85, 406
Epidemiological cutoff values, 646–648
ERIC-PCR, 194
erm genes, 265
Erythema nodosum, 103
Erythromycin, clinical indications, 111, 128
Escherichia coli, chemotaxis pathway, 352–354
Evolution
Campylobacter, phage effects, 688–690
competence, 559
flagella, 327–328
outbreaks and, 201–202
type III secretion system, 327–328
exb genes, 597
exbB gene, 603
exbB1 gene, 618
exbB2 gene, 618
exbD gene, 603
Exb proteins
ExbB protein, 594, 602, 604
ExbD protein, 594, 602, 604
Extracellular-signal-regulated kinase, Campylobacter infections, 305, 308
Farm animals, sporadic infections and contact with animals, 181
Farm environment, 669–670
fdh genes, 51
fdxA gene, 572, 574
FdxA protein, 600
Fecal sample, 227–228
feo genes, 593
Feo proteins
FeoA protein, 592
FeoB protein, 458, 592, 594, 601
FeoC protein, 592
Ferredoxin, 574, 600
Ferret model, C. jejuni infections, 436
Ferrichrome, 594–595, 597
Ferritin, 592, 598, 600, 602
Fibronectin receptors, 298, 309, 318, 320
Filtration method, Campylobacter isolation, 229
fla genes, 323
flaA gene, 283, 323, 328–329, 459, 550
regulation by sigma-28, 552–553
flaB gene, 459, 550–551, 616
flaC gene, 584
fla typing, 192, 222
fla-RFLP, 192
fla-SVR sequencing, 192–193
recombination, 561
Fla proteins
FlaA protein, 317, 326–327, 546, 548, 550, 552, 583
glycosylation, 471–481
subunit vaccine, 439, 517
FlaB protein, 317, 326–327, 546, 548, 583
glycosylation, 471–481
FlaC protein, 326–327, 548, 583
vaccine target, 434
FlaG protein, 549
Flagellum assembly in campylobacters, 545, 614
comparisons to other bacteria, 554
flagellin glycosylation, 555–556
polar assembly, 554–555
regulation of flagellar number, 554–555
Campylobacter adherence to intestinal epithelium, 298, 319
Campylobacter invasion of intestinal epithelium, 305, 323
chemosensory signal transduction pathway, 351–365
evolution, 327–328
identification of flagellar proteins from genomic sequences, 546
motility
components involved, 545–547
phase variation, 553–554
requirements revealed by mutagenesis screens, 546–547
mutants, 323
O-linked glycosylation, see O-linked flagellar glycosylation
Flagellar export apparatus, 551–552
Flagellar genes
C. jejuni, 550–553
expression of early genes, 554
Pseudomonas, 550
regulation, 547–550
flaA by sigma-28, 552–553
Salmonella, 547–550
transcriptional regulatory cascade, 550–552
Vibrio, 550
Flagellar number, 551
regulation, 554–555
Flagellin, 317–318, 339, 546
biosynthesis, 459
glycosylation, see O-linked flagellar glycosylation
structure of glycoproteins, 471–472
INDEX 705

Flavodoxin, 602
Flavodoxin:quinone-reductase, 46–47, 602
fldA gene, 602–603
FldA protein, 602
flg genes
flgB gene, 323, 616
flgC gene, 323
flgD gene, 616
flgDE2 gene, 550–551, 554
flgE gene, 323, 554, 616
flgE2 gene, 616
flgG gene, 323, 554, 616
flgH gene, 323
flgI gene, 323
flgK gene, 323
flgL gene, 323
flgM gene, 323
flgP gene, 547
flgQ gene, 547
flgR gene, 551, 553–554, 574, 612, 617, 621
flgS gene, 551, 553
Flg proteins
FlgA protein, 548
FlgB protein, 548
FlgC protein, 548
FlgD protein, 548
FlgE protein, 548
FlgE2 protein, 548
FlgF protein, 548
FlgH protein, 548
FlgI protein, 548
FlgK protein, 548
FlgL protein, 548
FlgM protein, 548, 552–553
FlgP protein, 547–548
FlgQ protein, 547–548
FlgR protein, 548, 551–554, 615–616, 621
FlgS protein, 548, 551–553, 616–617
flh genes
flhA gene, 551, 553–554, 584
flhB gene, 323, 551
flhF gene, 551, 555
Flh proteins
FlhA protein, 548, 553
FlhB protein, 548
FlhC protein, 548
FlhE protein, 549, 551–552, 554–555
FlhG protein, 549
FlhX protein, 549
fli genes
fliA gene, 612–613
fliD gene, 616
fliP gene, 551
fliR gene, 551
fliS gene, 584
Fli proteins
FliA protein, 548, 611, 613
FliD protein, 548
FliE protein, 548
FliF protein, 548
FliG protein, 548
FliH protein, 548
FliI protein, 546, 548
FliK protein, 548
FliL protein, 549
FliM protein, 548
FliN protein, 548
FliO protein, 548
FliR protein, 548
FliS protein, 548
FliY protein, 548
Flies, transmission of Campylobacter, 670
Flippase, 451, 538–539
Fluoroquinolone(s)
for Campylobacter enteritis, 111–114
in poultry, 183
consequences in human infections, 656–657
in different food animal reservoirs, 654–655
emergence, 651–654
interventions to reduce, 660–661
mechanisms, 263–265, 649–650
source attribution studies, 656
Focal infections, 108
folP gene, 649
Food(s)
Campylobacter in, 627–644
cross-contamination during preparation, 638–639
detection of Campylobacter in, 628–637
survival of Campylobacter on, 637–638
Food additives, 688
Food animals, transmission of antimicrobial resistance to humans, 645–665
Food chain surveillance, 153
Food packaging, 638
Foodborne Disease Burden Epidemiology Reference Group, 160–161
Food-borne illness, 627–644
common-source outbreaks in industrialized countries, 172–174
identifying source, 283
molecular subtyping network, 277–285
prevention, 639–640
sporadic infections, 177–180
FoodNet, 279–280, 283
Foreign travel, see Travel-related infections
Formate, electron donor, 51
Formate dehydrogenase, 51
“Founders,” 32
FqrB protein, 602–603
frdCAB operon, 55
Frozen food, 637
Fructose bisphosphate aldolase, 85
FspA protein, 320, 326–327, 613
Fumarase, 86
Fumarate, electron acceptor, 55
Fumarate reductase, 52, 55, 87, 406
Fumarate respiration, 44
fur genes, 600–602, 612
Fur proteins, 458, 600–601, 612, 617–618
G protein-coupled receptors, Campylobacter invasion of intestinal epithelium, 302–305
G+C content, 74
galE gene, 394, 487, 566
Gallinacins, 338
Ganglioside(s), see also Antiganglioside antibodies
peripheral nerve, 252–253
Ganglioside mimicry, 381, 484–486, 508
C. jejuni-related GBS, 252–256
Gastric acid, 334–335, 576
GBS, see Guillain-Barré syndrome
GD1a-immunized rabbits, 382
Gene regulation, C. jejuni, 611–624
Genetic diversity, C. jejuni, 560–561
Genome diversity, C. jejuni, 63–64, 67
Genome sequence, 3, 27, see also Comparative genomics
C. fetus, 406–407
C. jejuni, identification of flagellar sequences, 546
non-jejuni Campylobacter, 79–84
Genomic colinearity, Campylobacter genomes, 79–81
Genomic islands
C. fetus, 405
non-jejuni Campylobacter, 82
Genomic reduction, 87–88
Genomotyping, 232
C. jejuni, 36
Gentamicin protection assay, 320
Gentamicin resistance, 648–649, 652
ggt gene, 49, 66
gluA gene, 206, 219
glyT gene, 45
Gluconate, electron donor, 52
Glucconeogenesis, 44–46
Glucosyltransferase, 493, 538–539
Glucuronic acid-enriched polysaccharides, 672
Glutamate transport, 42–43, 459
Glutamine synthase, 47, 49
Glutamine:2-oxoglutarate aminotransferase, 47, 49
Gluteal abscess, 127
glyA gene, 206
Glycan
free, 459
N-linked, see N-linked glycan
O-linked, see O-linked glycan
Glycomics, 447, 459
Glycoproteins, N-linked, 451–453
Glycosylation, see N-linked protein glycosylation;
O-linked flagellar glycosylation
Glycosyltransferase, 449–450, 488–489, 493–494
GM1, rabbit model of GBS, 381–399
gmb genes
gmbA gene, 487
gmbA2 gene, 509, 516
gmbD gene, 487
gne gene, 459, 509
Gne protein, 449
Gram stain, 228, 230, 578
groEL/groES gene, 9, 572–573, 620
GroEL/GroES protein, 583
Groundwater, 635–636
grpE gene, 572, 620
GTPase, Rho, 305
Guillain-Barré syndrome (GBS), 245–261
animal models, 254, 256
antecedent infections, 249–250
axonal forms, 247–248, 255
burden of illness, 154–155
C. jejuni-related, 109
bacterial gene characteristics, 251–252
gene-specific variation in C. jejuni, 251
rarity of disease, 254–255
whole-genome polymorphisms in C. jejuni, 250–251
clinical features, 245–246, 251–252
diagnostic criteria, 245–246
heterogeneity, 246–248, 251–252
immunoglobulin treatment, 395–396
immunopathology, 248–249
outcome, 256
pathogenesis, 484
rabbit model, 381–399
complement-mediated nerve injury, 394–395
ganglioside immunization model, 382–387
immune attack on nerve root axons, 387–391
lipooligosaccharide immunization model, 391–394
passive transfer model, 396–397
subgroups, 246–248
vaccine-related, 433, 437, 517
gyrA gene, 19, 231, 264–265, 649–650, 661
GyrA protein, 404
HcrA protein, 620
bdd genes, 509, 516
Heat stress
C. jejuni, 571–573
heat shock proteins, 572
novel and alternative heat stress responses, 573
regulatory genes in heat shock response, 573
Heat-labile toxin, E. coli, mucosal adjuvant, 438
bec genes, 92
Helicobacter, taxonomy, 4–5
Helicobacter canis, 140
Helicobacter cinaedi infections, 139–140
clinical features, 126–127, 130, 139–140
epidemiology, 126, 139–140
microbiology, 125, 139
pathogenesis, 140
strain characterization, 139
treatment, 140
Helicobacter fennelliae infections, 139–140
clinical features, 126–127, 130, 139–140
epidemiology, 126, 139–140
microbiology, 125, 139
pathogenesis, 140
strain characterization, 139
treatment, 140
Helicobacter pullorum, 140–141
Helicobacter pullorum infections, 125
Helicobacter pylori, VBNC state, 579
Helicobacter rappini, 141
Helicobacter rappini infections, 126–127
Helicobacter westmeadii, 141
Helix-turn-helix motif, 611
Hemagglutinin, filamentous, 92
Hematology, Campylobacter enteritis, 110
Heme, 592, 594–596
Heme oxygenase, 596
Hemoglobin, iron availability, 596
Hemolysin, 596
Hemolytic-uremic syndrome, 131
Hemopexin, 596
Hemophore, 595–596
Hepatitis, 105–106
Heptose biosynthesis, 509
Heptosyltransferase, 487, 492–493
Hfr strains, 84
Highly conserved signaling domain, 358
High-resolution melt analysis, 194
hipO gene, 230
Hippurate hydrolysis test, 230
HisJ protein, 452
Histidine kinase sensor, 351, 357–358, 406, 551, 585
Homoplasy ratio, 560
Homopolymeric tracts, 78–79, 494, 621
Horizontal gene transfer, 405, 561
Host associations
C. coli, 200
C. fetus, 214–215
C. jejuni, 199–200
MLST studies, 198–201
Host cell entry, 297–313, see also Adherence, bacterial;
Innate immune defenses; Invasion, bacterial
Host range, plasmids, 77
Housekeeping genes, 29
brcA gene, 572, 612, 620
HrcA protein, 612
bsd genes, 88–90
hslU gene, 572
bshR gene, 572, 574, 612
HspR protein, 573, 620
btr genes
btrA gene, 572, 574
btrB gene, 487, 492, 572–576
Hybrid-cluster proteins, 86
Hydrogen, electron donor, 51
Hydrogen peroxide, 50, 53, 573, 598–600
electron acceptor, 53–54
Hydrogenase, 51, 87
Hydrogen-requiring campylobacters, 135–137
clinical features, 136–137
epidemiology, 136–137
isolation, 229
microbiology, 125, 135–136
Hydroxysisourate hydrodase, 49
Hydroxyl radicals, 53, 599
Hygromycin resistance, 77
Hyperglycemic bug, 66
Hyperosmotic stress, 575–576
Hypogammaglobulinemia, 103, 128, 156
Hypo-osmotic stress, 575–576
IeIR protein, 612, 620
IgA1 protease, 92
ileostomy stoma ulceration, 105
Imipenem, 234
Immune evasion, 317–318
Immune response, see also Innate immunity
Campylobacter enteritis, 99–101
Campylobacter infections, 153–156, 182, 318, 432
flagellin as antigen, 478
GBS, 248–249
role of N-linked protein glycosylation, 456–457
systemic vs. mucosal antibodies, 432
Immunocompromised patient, 163–164
C. fetus, 127
C. hominis, 132
C. lari, 134
Campylobacter enteritis, 103
Incubation period, Campylobacter enteritis, 101–102
Industrialized countries, Campylobacter infections, 156,
161, 163–189, 430–431
age and sex distribution, 170
burden of illness, 171–172
common-source outbreaks, 173–174
comparisons of incidence between countries, 169–170
seasonality, 170–171
surveillance, 168
trends, 168–169
INDX Campy-JCL, 230–231
Infective dose, 101, 316
Inflammatory bowel disease, postinfectious, 154–155
Innate immunity
Campylobacter infections, 333–350
defense against enteric pathogens, 333–339
in gastrointestinal tract, 333–339
in intestinal submucosa, 334, 340–343
in systemic circulation, 334, 340–343
Interleukin-8, 308, 337–338
Internalization, see Invasion, bacterial
Intestinal biota, normal, 334, 339
Intestinal epithelial cells
adherence of C. jejuni, 298–299, 317, 319
Campylobacter translocation across mucosa, 305–307, 318
defense against enteric pathogens, 333–350
invasion by C. jejuni, 299–307, 315–332
Intestinal hemorrhage, 105
Intestinal mucosa
Campylobacter translocation across, 305–307, 318
innate immune defenses, 334, 340–343
Intestinal tract
innate immune defense, 333–339
iron availability, 592
Intranasal challenge model, murine, 374
Intraepithelial lymphocytes, treatment of GBS, 395–396
Invasion, bacterial
C. jejuni in intestinal epithelium, 299–307, 315–332
capsular polysaccharide in, 513
cytoskeleton in, 299–301
role of N-linked protein glycosylation, 456–457
signal transduction, 301–305
Invasion receptors, 305
Invasion studies, 320–321
Inversion event, sap genes in C. fetus, 417–420
Iron functions, 591
oxidative stress defense mechanisms, 573, 598–600, 604
Iron acquisition, 404, 406, 456, 592–598, 602, 617
ferrous iron, 592–594
heme compounds, 595–596
host iron-binding proteins, 343, 596–597
involvement of Pgl proteins, 458
siderophore-mediated, 594–595
TonB and associated genes, 597–598
Iron availability, 591, 617
intestinal tract, 592
transcriptional responses, 601–604
Iron metabolism, 591–610
biofilms, 605
transcriptional profile of iron metabolism genes, 604–605
Iron regulatory proteins, 600–601
Iron stimulon, 601–605
Iron storage, 598, 600
Iron stress, 598
Iron-binding proteins, host, 343, 596–597
Irradiated food, 638–639
Irritable bowel syndrome, postinfectious, 109–110
IS elements, 78
ISCeo1, 83–84
ISCjd1, 83
non-jejuni Campylobacter, 83–84
ISO method, detection of Campylobacter in food, 628–629
jlpA gene, 320
JlpA protein, 91, 298, 319
Kanamycin resistance, 76–78, 648–649, 652
katA gene, 340, 572–574, 583, 599, 603, 605, 617–618
KatA protein, 598–599, 601–602, 604
Kdo, 506
kdtA gene, 492
Killed whole cell vaccines, 437–438, 517
kps genes, 506–507, 512–513, 515
genetic markers for diagnosis and epidemiology, 516
genetic rearrangements within gene clusters, 515–516
kpsC gene, 508
kpsE gene, 513
kpsM gene, 508, 512–514
kpsS gene, 508
Kps proteins
KpsM protein, 508
KpsT protein, 508
Lactate dehydrogenase, 52
Lactoferrin, 592, 594, 597
Lamb, 634–635
Lateral gene exchange, lipooligosaccharide biosynthesis genes, 490–492
Lateral gene transfer (localized sex), 30, 206
Lauroyl acyltransferase, 573
Lawsonia intracellularis, 13
Laying hens, 630
Lectins, mannose-binding, 334, 343–344
Legionaminic acid and derivatives, 473–474, 555
biosynthesis, 534
Leg5Ac7Ac, 533–534
Leg5Am7Ac, 473–479, 532–534
Leg5AmNMe7Ac, 473, 477–479, 533
Levofloxacin resistance, 263–265
lic gene, 206
Lipid A, 407–408, 483
biosynthesis, 492
structure, 483–484
Lipid A acyltransferase, 487
Lipid rafts, Campylobacter invasion of intestinal epithelium, 303, 305, 309
Lipid-linked oligosaccharide (LLO), 449, 451, 459, 538–539
Lipooligosaccharide (LOS) biosynthesis loci
genetic variation, 486–490
phase variation, 494
recombination and lateral exchange between, 490–492
biosynthesis pathways
O-acetylation of terminal α-2,8 Neu5Ac, 498–499, 501
class A and B cores with nonsialylated inner Gal, 497–499
class A cores with sialylated inner Gal, 496–498
class B cores extended from Glc-β(1,2)-HepII, 498, 500
class C cores, 496–497
extensions from HepII in sialylated outer cores, 495–496
generating core region variation, 494
inner core, 492
lipid A, 492
outer core, 492–494
C. jejuni, 66, 251–256, 381–382, 483–504, 507–508
ganglioside mimicry, 484–486
outer core structure, 485–487
structure, 484–486
in transformation, 566
Lipopolysaccharide (LPS), 342, 483
C. fetus, 407–408
C. jejuni, 339
GBS in immunized rabbits, 391–394
structure, 483
Lipopolysaccharide-binding protein, 343
Live attenuated vaccines, 437, 517
LLO, see Lipid-linked oligosaccharide
lon gene, 572
LOS, see Lipooligosaccharide

LPS, see Lipopolysaccharide

lpx genes, 231, 492

Lung abscess, 127

luxS gene, 585

LysR protein, 612, 619

Macrolide resistance, 111–112
  emergence, 651–652
  interventions to reduce, 659–660
  mechanisms, 265–266, 649–651

Macrophages, 318
  innate immune defenses, 334, 340–341
  production of nitric oxide, 341
  production of reactive nitrogen species, 341

maf genes, 554

Malate oxidoreductase, 46, 52

MALDI-TOF MS, 16–17

mapA gene, 231

MarR protein, 620

Meat, red, 634–635, 638

MEDPeD (Murine Enteric Disease Phenome Database), 375–376

Megaplasmids, 76–78

Membrane attack complex, 394–395

Menaquinones, 12, 20, 47, 50

Meningitis, 126, 403

MerR protein, 612, 619–620

Metabolomics, 523–542
  future directions, 539–540
  in vitro analysis by NMR spectroscopy, 534–537

Methyl-accepting chemotaxis proteins, 352–355, 546, 548

Methylation, DNA, 562

Methyl-directed mismatch repair, 79

Methyltransferases, 267

C. upsaliensis, 90

mez gene, 46

Microaerophily, 44, 46, 49–50, 54–58, 562

Microfilaments, Campylobacter invasion of intestinal epithelium, 299–301, 320

Microtubules, Campylobacter invasion of intestinal epithelium, 299–301, 309, 320


Miller Fisher syndrome, 245–246, 250–251, 397, 484

Minimal inhibitory concentration, 645–646

Mismatch repair, non-jejuni Campylobacter, 78–79

Nitrogen-activated protein kinase pathway, 305, 308

MLST (multilocus sequence typing), 27–40, 192, 197–198
  C. coli, 29–30, 36–38, 204
  C. fetus, 29–30, 37, 204, 216, 218–219, 222
  C. helveticus, 29–30, 37–38, 204
  C. insulaenigrae, 204
  C. jejuni, 29–30, 32–36, 38, 204
  C. lari, 29–30, 37–38, 204
  C. upsaliensis, 29–30, 37–38, 204–206
  epidemiologic typing, 232
  host association studies, 198–201

national subtyping network, 283
  non-jejuni Campylobacter, 76
  non-jejuni, non-coli Campylobacter, 204–206

modE gene, 612

ModE protein, 619

Modified atmosphere packaging, 638

Molecular mimicry, see Ganglioside mimicry

Molecular typing, 191–211
  genotyping of non-jejuni, non-coli Campylobacter, 202–206
  methods, 192–198
  outbreak investigations, 201–202
  source tracking, 198–201

Molybdenum homeostasis, 619

Monkey model, C. jejuni infections, 436

Morbidity, 152–154

Motility
  bacteria within biofilms, 583
  Campylobacter adherence to intestinal epithelium, 298–299, 317, 319
  chemosensory signal transduction pathway, 351–365

flagellar
  components involved, 545–547
  phase variation, 553–554
  requirements revealed by mutagenesis screens, 546–547

Mouse model
  C. fetus infections, 410
  C. jejuni infections
    C3H SCID limited flora mice, 373
    C57BL/6 IL-10−/− mice, 370–371
    colonization models, 369–370
    diet effects, 374–375
    disease models, 370–372
    early studies, 368
    experimental design for mouse studies, 374
    future goals, 375
    immunocompetent mice refractory to C. jejuni, 369–370
    individual housing, 374
    NF-κB−/− mice, 371–372
    quantifying clinical signs of disease and pathology, 375
    screening immunodeficient mice for pathogen susceptibility, 372
    specific-pathogen-free status, 368–369
  C. jejuni vaccine development, 373–374, 436–437
  intranasal challenge model, 374
  MEDPeD, 375–376

Mucins, 336–337

Mucosal translocation, 305–307, 318

Multidrug efflux pump, 270–272, 336, 650

Multidrug resistance, 234–236, 270–272

Multilocus sequence analysis, 3, 9–11

Multilocus sequence typing, see MLST

Multispecies farming, 671–672

Murine model, see Mouse model

Mushrooms, 637
MviN protein, 91–92
Myocarditis, 108
NAD(P)H oxidation, 51–52
Nalidixic acid resistance, 233, 235–236, 404, 650, 652, 654
nap genes, 55, 85, 231, 574, 603–605
NARMS (National Antimicrobial Resistance Monitoring System), 279–281, 283
NARTC group (nalidixic acid-resistant thermophilic campylobacters), 15
NASC strains (nalidixic acid-susceptible strains), 15
Natural killer cells, Siglecs, 341–342
NDH-1 complex, 47, 51–52, 87, 406
Neomycin resistance, 649
Neonatal infections, 103
Nephritis, 107
Nerve root axons, immune attack in AMAN, 387–391
Neu proteins, 493
Neutrophil(s)
innate immune defenses, 334, 340
production of antimicrobial peptides/proteins, 340
production of reactive oxygen species, 340
Neutrophil-activating protein, 598
Nf-κB, 337, 339
Nf-κB/− mice, 371–372
NfrA protein, 617
Nitraten
electron acceptor, 55–56
salivary, 334–335, 344
Nitrareductase, 55, 85–86, 335, 357, 604
Nitric oxide, 576
antimicrobial property, 335
produced by macrophages, 341
Nitric oxide detoxification, 55
Nitric oxide reductase, 86
Nitric oxide synthase, 335, 339, 341
Nitrite, electron acceptor, 55–56
Nitrite reductase, 55–56, 86, 604
Nitrogen metabolism, 47–49, 86–87
Nitrosative stress, 572, 576, 600, 617–618
Nitrous oxide reductase, 86
NJ C, see Non-jejuni Campylobacter
NK-κB, 308
N-linked glycan, 567
biological effects of disrupting N-glycan pathway, 456–457
C. jejuni, 66, 448–451, 537–539
in chicken colonization, 457
effect on protein structure and function, 453–456
in immune response, 456–457
in invasion, 456–457
pathways in Proteobacteria, 464–466
transformation and, 567
NMR spectroscopy, in vitro metabolomics, 534–547
NOD proteins, defense against enteric pathogens, 334, 338–339, 344
Nodes of Ranvier, 394–395
Nonclonal population, 31–32
Nonhuman primate models, C. jejuni infections, 436
Non-jejuni Campylobacter (NJ C) bacteriophage, 81–82
bacteriophage Mu, 79–81
comparative genomics, 73–95
contingency genes, 78–79
CRISPR elements, 82–83
features of genomes, 74–76
genome structure, 79–84
genomic islands, 82
genomic reduction, 87–88
homopolymeric tracts, 78–79
IS elements, 83–84
metabolism, 85–86
mismatch repair, 78–79
MLST, 76
plasmids, 76–78, 82
proteomes, 74–76
pseudogenes, 78–79
respiration, 86–87
restriction/modification systems, 88–90
transposons, 83–84
virulence and pathogenicity, 90–92
Novobiocin resistance, 270
N-oxides, electron acceptors, 56–57
ndd genes, 87
O-antigen, 407–408
Oligosaccharides, breast milk, 334–336, 344
Oligosaccharyltransferase, 448, 451, 459, 538
O-linked flagellar glycosylation, 447, 459, 471–481, 553
C. coli, 530–534
C. fetus, 406
C. jejuni, 66, 524–530
flagellar pathway elucidation, 475–477
glycan structure, 472–474
glycosylation locus, 474–475
mechanism of glycosylation, 477
structure of flagellin glycoproteins, 471–472
Phosphoglucose isomerase, 85
Phosphoinositol-3 kinase, 304–305
Phospholipase, 514–515, 596
Phos proteins, 614–616
phosR gene, 612
Phylogenic tree, 5–7, 30–32, 84–85
Pili, type IV, 564
Pilins, 560, 564
Piperacillin resistance, 234, 648
Planktonic bacteria, 583
Plasmids, 434, 651
C. jejuni, 64–65
cryptic, 76–77
drug resistance, 267, 270
host range, 77
incompatibility groups, 77
integrated, 82
megaplasmids, 76–78
non-jejuni Campylobacter, 76–78, 82
pVir, 565–567
Plasticity regions, 621
pldA gene, 515, 596
PldA protein, 515, 596
Pleuritis, 404
Polyphosphate, 575–576, 584
Polysaccharides
C. jejuni, 514–515
capsular, see Capsular polysaccharide
cwitterinonic, 516
neutral, 514
Polysulfide reductase, 87
Population studies, 191–192
C. coli, 36–37
C. fetus, 37
C. jejuni, 32–36, 559–561
Campylobacter, 27–40
analysis of populations, 28–29
variation within genus, 28–38
interpretation of biological variation, 28
measuring variation, 27–28
sampling the population, 27
porA gene, 320
PorA protein, 319
Porins, 269, 319, 405
Pork, 634–635
Poultry, 627, see also Chickens
colonization, 629–632, 667–678
bacteriophage therapy, 679–693
broilers, 667–669
eliminating Campylobacter from colonized flock, 674–675, 679–693
epidemiology of flock colonization, 668–669
lag phase, 668
phage effects, 688–689
prevalence rates between countries, 668–669
prevention of introduction of Campylobacter into flock, 670–674
risk factors, 669–670
seasonal variation, 669–670
sources, 669–670
drug-resistant Campylobacter, 654–656
emergence, 651–654
genetic resistance to Campylobacter, 673–674
sporadic infections and, 177, 180
Poultry house, biosecurity, 670–672
Poultry meat, 629–632
fresh products, 629
marinated, 630
retail level, 630, 632
slaughterhouse level, 630–631
ppk1 gene, 572, 575–576, 584
Prepilin, 560, 564
Prepilin peptidase, 565
Probiotics, 672
Proctitis, 132, 139
Prodrome, Campylobacter enteritis, 101
Proinflammatory factors, C. jejuni-induced, 308
Proline dehydrogenase, 47
Promoters, 611
pgl operon, 457
ProSpecT Campylobacter immunoassay, 228
Prostatitis, 108
Prosthetic hip sepsis, 108, 127
Protein glycosylation, see N-linked protein glycosylation; O-linked flagellar glycosylation
Protein kinase, Campylobacter invasion of host cells, 304
Protein kinase C, 303, 305, 307
Protein secretion
Campylobacter invasion of host cells, 315–332
identification of secreted proteins, 325–326
Proteobacteria, N-glycosylation pathways, 464–466
Proteomes, non-jejuni Campylobacter, 74–76
Protozoa, Campylobacter survival in, 516–517, 581
pse genes, 555
pseA gene, 474–475, 477–478, 527, 534
pseB gene, 475, 477, 526, 534
pseC gene, 475, 477, 527–530
pseD gene, 475, 477
pseE gene, 475, 554
pseF gene, 526
pseI gene, 526
Pse proteins
PseA protein, 549
PseB protein, 449, 459, 476–477, 535–536, 549
PseC protein, 459, 476, 535, 549
PseD protein, 549
PseE protein, 549, 554
PseF protein, 475, 535, 549
PseG protein, 476, 535, 549
PseH protein, 476, 535, 549
PseI protein, 476, 535, 549
Pseudaminic acid and derivatives, 449, 459, 473–474, 555
biosynthesis, 524–525, 530, 534–535
PseS7Ac, 474–479, 524–525, 530, 533
PseS7Am, 473–475, 533
PseAm, 530, 555
Pseudogenes
C. jejuni, 65
non-jejuni Campylobacter, 78–79
Pseudomonas, flagellar genes, 550
Pseudopilins, 563–564
PstC proteins, 563–564
Pst genes, 477, 530, 532–534
PstM gene, 474–475
PstB gene, 474–475
PstC gene, 475
PstD gene, 475, 477, 534
PstE gene, 475
PstF gene, 475
PstG gene, 533–534
ptmA gene, 474–475
ptmB gene, 474–475
ptmC gene, 475
ptmD gene, 475
ptmE gene, 475
ptmF gene, 475
ptmG gene, 533–534
PulMLST website, 30, 36
Pulsed-field gel electrophoresis, see PFGE
PulseNet, 277–285
Campylobacter, 280–284
next-generation subtyping methods, 279
partnerships, 279–280
PFGE subtyping methods, 277–285
PulseNet International, 279–280
PulseNet USA, 277–279
Purine/pyrimidine phosphoribosyltransferase, 565
pyc genes, 45–46
pyk gene, 44–45
pyrC gene, 84
Pyruvate carboxylase, 45–46
Pyruvate dehydrogenase, 86
Pyruvate kinase, 44–45
Pyruvate:acceptor oxidoreductase, 46–47
Pyruvate:flavodoxin oxidoreductase, 86
QacR transcriptional factor, 271
QALY (quality-adjusted life-year), 152
D-QuinAc4NAc, 528–530, 535–536
Quinol dehydrogenase, 55
Quinol oxidase, 53
Quorum sensing, AI-2-mediated, 585
Rabbit model
C. jejuni infections, 436
Guillain-Barré syndrome, 381–399
complement-mediated nerve injury, 394–395
ganglioside immunization model, 382–387
immune attack on nerve root axons, 387–391
immunoglobulin treatment, 395–396
lipooligosaccharide immunization model, 391–394
passive transfer model, 396–397
rac genes
racR gene, 572, 612, 615
racS gene, 572, 615
Rac proteins
RacR protein, 573, 614–615
RacS protein, 615
Radiography, in Campylobacter enteritis, 110–111
RAPD (random amplification of polymorphic DNA), 193–194
C. concisus, 204
C. fetus, 218, 222
C. jejuni, 204
non-jejuni, non-coli Campylobacter, 204
Rash, Campylobacter enteritis, 103
Reactive nitrogen species
  gastrointestinal, 334–335, 339
  produced by macrophages, 341
Reactive oxygen species, 50, 572–574, 591, 598–600
  gastric, 334
  produced by neutrophils, 340
recA gene, 566
RecA protein, 566
Recombination, 688
DprA-mediated, 566
flagellin genes, 561
intergenomic, 561
interspecies, 561
interstrain, 621
intragenomic, 561, 621
lipooligosaccharide biosynthesis genes, 490–492
sap genes in C. fetus, 418–419
Rectal swab, 227
Refrigeration, 637
Regulons, 611
Reiter’s syndrome, 109
Removable intestinal tie adult rabbit diarrhea, 436
Renal disease, with Campylobacter enteritis, 107–108
Rep-PCR, 194
Reptiles, C. fetus, 221–222
Respiration, non-jejuni Campylobacter, 86–87
Response regulatory protein, 351, 355, 358–362, 406,
  551, 614–617
Restriction/modification systems, 562
C. jejuni, 64
  non-jejuni Campylobacter, 88–90
type I, 88–90
type II/III, 90
RFLP, Fla-RFLP, 192
Rhodotorulic acid, 594, 602
Ribonucleoside-diphosphate reductase, 87
Riboprinting, 193
Ribosomal protection protein, 266–267
Ribosomal proteins, 265, 650
Ribotyping, 193
Ribosomal protection protein, 266–267
Ribosomal proteins, 265, 650
Ribotyping, 193, 232
Ridascreen Campylobacter, 228
Rifampicin resistance, 621
Rifampin resistance, 270
Risk assessment, antimicrobial resistance, 657–659
rml genes, 491
RNA polymerase, 611, 621
rpmA gene, 603–604
RpmA protein, 604
rpo genes
rpoB gene, 9
rpoD gene, 612
rpoN gene, 550–551, 553, 612, 617
Rpo proteins
RpoD protein, 611–613
RpoN protein, 548, 611, 614, 616–617
Rfl2 protein, 612, 620
rRNA methylases, 265, 267
Ruminants
C. fetus, 214–215
C. jejuni, 199–200

16S rRNA
Arcobacter, 19
C. fetus, 222
Campylobacter, 4–7, 16
Sulfurospirillum, 20
16S/23S RNA, 231, 265
antimicrobial resistance, 650–651
Salad vegetables, 636
Salmonella, flagellar genes, 547–550
Salt tolerance, 575–576, 637
Sanitizer resistance, 581
sap genes
C. fetus, 411–415
gene expression, 415–417
genetic organization (clustering), 413–414, 421
sap island, 416
sapA gene, 412–414, 416–417
sapB gene, 413–414
sapCDDEF genes, 420
sap typing, 222
Sarafloxacin, 651
sat4 gene, 649
Scheduled slaughtering, 674–675
sda genes
sdaA gene, 47–49
sdaC gene, 43–44
sdh genes, 85, 572, 574, 603–604
Seafood, 627, 635–636
Seasonality
Campylobacter infections, 167, 170–171, 198
poultry colonization, 669–670
Secondary transmission, 181
Secreted proteins
S-layer proteins of C. fetus, 419–423
vaccine target, 433–435
Secretins, 560, 563
Sedoheptulose-7-phosphate isomerase, 487
Sensor kinase, 319, 614, see also Histidine kinase sensor
Sensory receptors, E. coli, 352
Septicemia, 126
Sequence types, 29, 204–205
C. coli, 36–37, 200
C. fetus, 37
C. jejuni, 32–34, 36, 199–200
Serine dehydratase, 47–48
Serine hydratase, 406
Serine protease, 92
Serine transport, 43–44
Seroepidemiology, 153–154
Serotyping, 191, 222, 232
Sessile bacteria, 583
Sex distribution, Campylobacter infections, 166–167, 170
Sheep, 634–635
C. fetus infections, 214–215, 403, 423–424
C. jejuni infections, 199–200
Shellfish, 636
Short variable regions, fla-SVR sequencing, 192–193
Sialic acid synthase, 488, 493
Sialic acid transferase, 251
Sialylated O-acetyltransferase, 498–499, 501
Sialyltransferase, 488, 493–494, 498
Siderophore(s), 592, 594–595
Siderophore piracy, 594
Siglec, 341–342
Sigma factors, 611
C. jejuni, 612–614
FliA, 611, 613
RpoD, 611–613
RpoN, 611, 614, 616–617
sigma-28, 550, 552, 613
regulation of flaA, 552–553
sigma-54, 554, 614
sigma-54 dependent flagellar genes, 550–553
sigma-70, 612–613
Signal transduction
Campylobacter invasion of intestinal epithelium, 301–305
chemosensory signal transduction pathway, 351–365
Slaughtering process, 629–630, 634, 638–639, 674–675
S-layer proteins, C. fetus, 409–412, 414–415
antigenic diversity in ovine immune responses, 423–424
antigenic variation, 415–419
in ovine abortion, 423–424
regulation of production, 422
sap genes, 411–415
secretion, 419–423
Slipped-strand mispairing, 621
SNP (single nucleotide polymorphism) binary typing, 194–195
sodB gene, 340, 572–574, 599
SodB protein, 598–599
Sodium channels, 394–395
Solute transport, 41–44
Source tracking, molecular methods, 198–201
S-oxides, electron acceptors, 56–58
Speciation, bacterial, 30
Species tree, 5–7
Spectinomycin resistance, 649
Spices, 637
Splenic rupture, 108–109
Sporadic infections, 627
cross-contamination and, 181
industrialized countries, 174–182
poultry and, 177, 180
raw milk and, 180
secondary transmission, 181
travel-associated, 182
waterborne, 180–181
spoT gene, 572, 574–575, 579, 584, 621
Starvation, 573–575
detriment and possible benefits, 575
resistance, 575
Stationary phase stress, C. jejuni, 572, 574–575
Statutory disease, 401
Stool antigen tests, 228
Streptomycin resistance, 648–649, 654–657
Streptothricin resistance, 648–649
Stress response, C. jejuni, 515, 571–577
Stringent response, 575, 584–585, 621
Subunit vaccines, 439–440, 517
Succinate dehydrogenase, 52, 85–86, 604–605
Sulfite, electron donor, 52–53
Sulfonamide resistance, 649, 651
Sulfurospirillum, 5, 19–20
Sulfurospirillum arcachonense, 19
Sulfurospirillum arsenophilum, 19
Sulfurospirillum barnesii, 19
Sulfurospirillum cavolei, 19
Sulfurospirillum deleyianum, 19–20
Sulfurospirillum halorespirans, 19
Sulfurospirillum multivorans, 19
Superoxide dismutase, 573–574, 599
Superoxide radicals, 50, 53, 573, 598–600
Superoxide stress defense, 599
Surface recognition, 514
Surface water, 635–636
Surveillance
Campylobacter infections
industrialized countries, 168
United States, 164
emerging antimicrobial resistance, 182–183
Surveillance pyramid, 152–154, 167–168
Swine, 634
drug-resistant Campylobacter, 656
piglet model, C. jejuni infections, 436
TAT signal peptides, 51, 56
Taxonomy
bacteriophage, 680–681
C. fetus, 401
Campylobacteraceae, 3–25
MLSA approach, 9–11
taxonomic history, 3–5, 213–215
whole-genome, 5–11
Tbp proteins, 597
Telithromycin resistance, 265–266
tet(O) gene, 649, 651
Tet(O) protein, 266–267
TetR family, 271, 612, 618–619
Tetracycline(s), clinical indications, 114
tetracycline(s), clinical indications, 114
Tetracycline resistance, 76–78, 183, 234–235, 404, 649,
651–652, 654–657, 661
mechanisms, 266–267
Thinning, poultry, 672
Thiol peroxidase, 604–605
Thioredoxin, 602, 604
Thioredoxin reductase, 599, 602
Ticarcillin resistance, 305–307, 318
Tight junctions, 306–307, 318
tkt gene, 206
Tlp proteins, 352, 355
group A receptors, 355–357
groups B, C, and Aer receptors, 356–357
TMAO reductase, 56–58, 86–87
Toll-like receptors, 478
defense against enteric pathogens, 334, 339
tonB gene, 595, 597–598, 603, 618
TonB protein, 594, 596–598, 602, 604
Topoisomerase, 263–265, 650
Toxic megacolon, 104–105
Toxins, host damage caused by, 307–308, 319
tpx gene, 603
Tpx protein, 583, 604–605
Transamination, 47
Transcription, 611
Transcription factors, 611, 614–621
Transcriptional profiling
iron metabolism genes, 604–605
pgl genes, 457–458, 460–463
Transcriptional regulation, flagellar genes, 550–552
Transcriptional repressors, 618–619
Transferrin, 592, 594, 596–597
Transformation, 77, 319, 406, 453, 559–570
candidate gene analyses to identify proteins, 566
conserved proteins associated with, 560
DNA discrimination, 562–563
N-linked protein glycosylation and, 567
physiology, 562
type IV secretion system, 565–566
Translocation, Campylobacter across intestinal mucosa,
305–307, 318
Transport media, 228
Transposon(s), non-jejuni Campylobacter, 83–84
Transposon mutagenesis, 546–547, 551
Traveler’s diarrhea, 429, 431
Travel-related infections, 111–113, 182, 430–431, 658
Trimethoprim resistance, 270, 649, 651
Trimethoprim-sulfamethoxazole resistance, 236
trc genes
trxA gene, 603
trxB gene, 583, 599, 603, 618
Trx proteins
TrxA protein, 602
TrxB protein, 599, 601–602, 604
“Twin arginine” translocation system, see TAT signal
peptides
Tylosin, 652, 659–660
Type I secretion system, 615
C. fetus, 420–421
Type II secretion system, 563–564
Type III secretion system, 546
C. jejuni, 315–322
evolution, 327–328
recognition and export of CiaB, 323–325
Type IV secretion system, 434, 453, 456, 563
pVir-encoded, 565–567
Tyrosine protein kinase, 304
UDP sugars, 525
UDP-6-deoxy-β-L-altNac4N, 526
UDP-diacetamido-trideoxyhexose, 525–526, 538
UDP-GlcNAc, 449
UDP-GlcNAc dehydratase, 449
UDP-GlcNAc/Glc-4-epimerase, 487
UDP-GlcNAc3N, 492
UDP-monoacetamido-trideoxyhexose, 525–526
UDP-α-D-QuinAc4NAc, 528–530
Undecaprenol, 450
Undecaprenylpyrophosphate, 449, 538
Undecaprenylpyrophosphate-heptasaccharide, 538
United States, *Campylobacter* infections
  age and sex distribution, 166–167
  burden of illness, 167–168
  common-source outbreaks, 172–173
  regional differences in incidence, 166
  seasonality, 167
  sporadic, 175–177
  surveillance, 164
  trends, 164–166
UPTC strains (urease-producing), 15, 133–134
Urinary tract infections, 107–108
Vaccine
  *Campylobacter*, see *Campylobacter* vaccine
  chickens, 673
Vacuum packaging, 638
Vaginosis, 403
Vascular disease, 127, 136, 404
VBNC state, see Viable but nonculturable state
Vegetable food types, 636–637
VetNet, 279, 283
Viability count, 577
Viable but nonculturable (VBNC) state, 571, 577–580
  resuscitation, 579–580
  VBNC formation
    changes in cell wall, 578–579
    morphology and viability changes, 577–578
  *Vibrio*, flagellar genes, 550
  *Vibrio fecalis*, 13
  VirB10 protein, 453
  Virulence factors/virulence phenotypes
    *C. jejuni*, 316–318
    non-jejuni *Campylobacter*, 90–92
  *waa* genes
    *waaC* gene, 487, 492–493
    *waaD* gene, 583
    *waaF* gene, 487–488, 493
Waterborne illness, 627, 635–636
  common-source outbreaks in United States, 172–173
  sporadic infections, 180–181
White cells, fecal, 228
Whole-genome sequence, see Genome sequence
Wild birds, 181, 199, 630, 635–636
Wildlife animals, 630, 636
*Wolinella*, 5
XylS protein, 612, 620
YLD (years lived with disability), 151–152
YLL (years of life lost to premature death), 151–152