

Index

A

- AAC. *See* Antibiotic-associated colitis
- AAD. *See* Antibiotic-associated diarrhea
- Abiotrophia*, 163
- Abortion, *Listeria*, 404
- ABP-118, *Lactobacillus*, 330
- Abscesses
- Bacillus*, 615
 - Enterococcus*, 169
 - Gemella*, 516
 - Leuconostoc*, 303
 - Pediococcus*, 254
 - Staphylococcus*, 59
 - Streptococcus*, 94
- Acaryochloris marina*, 1099
- Acetate production
- Bacillus larvae*, 576
 - Bacillus lentimorbus*, 569–70
 - Bacillus popilliae*, 569–70
 - Carnobacterium*, 376, 378
 - Clostridium*, 672–73
 - Clostridium perfringens*, 701
 - Coprococcus*, 804
 - Lactobacillus*, 365–66
 - Pediococcus*, 248
 - Sporomusa*, 997–98
- Acetate utilization, *Kurthia*, 525
- Acetivibrio*, 654
- Acetobacterium carbinolicum*, 998
- Acetohalobium arabaticum*, 810, 812, 815–20
- Acetoin production, *Pediococcus*, 247
- Acetonema*, 996
- Acetonema longum*, 996–97
- Acetyl CoA pathway, *Sporomusa*, 997–98
- Acholeplasma*, 836–37, 843, 845, 847, 852–55, 863, 869, 910
- Acholeplasma laidlawii*, 838–39, 845, 848, 853, 857, 860, 921, 926
- Acholeplasmataceae
- Acholeplasma*, 836–37
 - Anaeroplasma*, 836–37
 - Asteroleplasma*, 836–37
 - Phytoplasma*, 836–37
- Acidaminobacter*, 654
- Acidaminococcaceae, 1041
- Acidaminococcus*, 966, 968, 1022–23
- Acidaminococcus fermentans*, 965, 966, 1026
- Acidocin A, *Lactobacillus*, 330
- Acidocin B, *Lactobacillus*, 330
- Acidophile
- Megasphaera*, 970–71, 978
 - Pectinatus*, 970–71, 976–77
- Acidophilin, *Lactobacillus*, 369
- ActA, *Listeria*, 436–441
- Actin, *Listeria*, 425, 439
- Actin motility, *Listeria*, 417–19
- Actinobacteria, 823
- Actinobaculum*, 823
- Actinomyces*, 823, 1028
- Actinomyces israeli*, 1032, 1034
- Actinomyces naeslundii*, 1032, 1033, 1034
- Actinomyces odontolyticus*, 1024, 1032
- Actinomyces pyogenes*, 503
- Actinomyces viscosus*, 1031–32
- Actinomycin sensitivity, *Filibacter*, 645
- Acute streptococcal glomerulonephritis (ASGN), *Streptococcus pyogenes*, 122
- Adherence
- phytopathogenic spiroplasmas, 928
 - Veillonella*, 1031–35
- Adhesins
- Mycoplasma*, 841
 - phytopathogenic spiroplasmas, 928
 - Staphylococcus*, 48–49
 - Streptococcus agalactiae*, 134–35
 - Streptococcus pneumoniae*, 159
 - Streptococcus pyogenes*, 122–23
- Adult respiratory distress syndrome (ARDS), *Streptococcus*, 97
- Aerobe
- Brochothrix*, 483
 - Caryophanon*, 649
 - Erysipelothrix*, 492
 - Kurthia*, 519, 525
 - Marinococcus*, 644
 - Staphylococcus*, 24–27
 - Streptococcus*, 108
- Aerococcus*, 163, 229–56
- characteristics of, 230
- Aerococcus sanguinicola*, 229
- Aerococcus urinae*, 229
- Aerococcus urinaehominis*, 229
- Aerococcus viridans*, 229, 231, 247
- Aeromonas salmonicida*, 375–76
- Agar metabolism, *Bacillus*, 531
- Aggregation substance (AS), *Enterococcus*, 188, 194
- Agmatine metabolism, *Enterococcus*, 175–76, 180
- Agmenellum*, 1086
- Agmenellum quadruplicatum*, 1088
- Agmenellum quadruplicatum* PR-6, 1082
- Agr pheromones, *Staphylococcus*, 51–53
- Akinetes, 1068–70
- Aldolase
- Macrococcus*, 23
 - Staphylococcus*, 23
- Alicyclobacillus*, 520
- Alkaline environment
- Cyanobacteria, 1057, 1076
 - Heliobacteriaceae in, 956
- Alkaliphilus*, 654
- Alloiococcus*, 163, 229, 231
- Allophycocyanin (APC) genes, 1088
- American foulbrood, *Bacillus larvae*, 571–77
- Amikacin resistance/sensitivity
- Brochothrix*, 480
 - Gemella*, 515
- Amine production
- Leuconostoc*, 296
 - Oenococcus*, 296
 - Weissella*, 296
- Amino acid metabolism
- Clostridium*, 673
 - Enterococcus*, 175–76, 180
 - Lactococcus*, 220
- Aminoglycoside resistance
- Enterococcus*, 170–71, 189–90
 - Erysipelothrix*, 497
 - Gemella*, 511, 515
- Aminoglycoside sensitivity
- Bacillus*, 618
 - Listeria*, 408
 - Pediococcus*, 254
- Ammonia metabolism, *Selenomonas*, 988
- Ampicillin resistance/sensitivity
- Bacillus*, 618
 - Enterococcus*, 170
 - Listeria*, 408, 413–14
 - Pediococcus*, 254
- Anabaena*, 1069–70, 1082, 1086, 1088

- Anabaena* sp. PCC 7120, 1079–80, 1082–86, 1088
Anabaena sp. PCC 7937, 1080
Anabaena variabilis, 1078
Anacystis nidulans, 1079
Anaerobacter, 654–55
Anaerobacter polyendosporus, 655, 669
- Anaerobe
Brochothrix, 482
Leuconostoc, 267
Listeria, 408
Oenococcus, 267
Staphylococcus, 27–30
Weissella, 267
- Anaerobic cocci, 795–805
Anaerococcus, 795
Coprococcus, 795
Fingoldia, 795
Gallicola, 795
genera of, 800–2
habitats of, 795–96
identification of, 798, 799–805
isolation of, 796–97
Micromonas, 795
Peptococcus, 795
Peptoniphilus, 795
Peptostreptococcus, 795
phylogenetic tree of, 799
properties of, 800–4
Ruminococcus, 795
Sarcina, 795
- Anaerobic dark respiration,
Cyanobacteria, 1074, 1078
Anaerobranca, 665
Anaerococcus, 795–96, 798
Anaerococcus harei, 800
Anaerococcus hydrogenalis, 795, 803
Anaerococcus indolicus, 800
Anaerococcus lactolyticus, 803
Anaerococcus octavius, 803
Anaerococcus prevotii, 795, 803
Anaerococcus tetradius, 795, 803
Anaerococcus vaginalis, 795, 803
Anaeroplasma, 836–37, 843, 845, 847, 852–55, 863, 869, 910
Anaerovibrio, 965
- Animal feed
Enterococcus, 282
Lactobacillus, 320, 344, 347
Leuconostoc, 282
Pediococcus, 241–42, 255–56
Sporolactobacillus, 632
- Animal hosts
Bacillus anthracis, 610–14
Clostridiaceae, 659
Clostridium, 659
Clostridium difficile, 731–32
Clostridium perfringens, 713–15
Enterococcus, 169
Erysipelothrix, 494–97
Lactobacillus, 321–25, 327–28
Listeria, 450–53
Macrocooccus, 59
mollicutes, 874
mycoplasma pathogens in, 906–7
phytopathogenic spiroplasmas, 910, 914–15, 917
- Animal models
of adherence in oral cavity, 1034
Veillonella, 1024, 1029
- Anoxygenic photosynthesis. *See*
Photosynthesis
- Antarctica, Cyanobacteria in,
1056–57
- Anthrax
Bacillus anthracis, 609–14
history of, 609–10
treatment and prevention of,
612–13
types of, 610–12
vaccine for, 609
- Antibiotic production
Bacillus, 531, 554–55
Bacillus larvae, 572
- Antibiotic resistance
Clostridium perfringens, 755–56
Enterococcus, 169–71, 183–84, 186, 189–94
Lactococcus, 223–24
Leuconostoc, 302–3
Listeria, 408
Staphylococcus, 50
Streptococcus pneumoniae, 153–55
Veillonella, 1030
Weissella, 302–3
- Antibiotic sensitivity
anaerobic cocci, 804–5
Brochothrix, 480
Clostridium difficile disease, 730, 737
Clostridium difficile treatment,
741
Enterococcus, 170
Erysipelothrix, 497
Gemella, 515
mollicutes, 868
phytopathogenic spiroplasmas,
936–37
Streptococcus, 97–98
- Antibiotic-associated colitis (AAC),
730
- Antibiotic-associated diarrhea
(AAD), 730–31, 738, 741
- Antibodies
Megasphaera, 975–76
Pectinatus, 974
phytopathogenic spiroplasmas,
916, 937
- Antigens
Clostridium difficile, 732, 738–40
Mycoplasma, 873–78
Streptococcus agalactiae, 130
- Antimicrobial activities,
Lactobacillus, 367–69
- APC genes. *See* Allophycocyanin
genes
- Aphanotheca halophytica*, 1057,
1062, 1077, 1078
- Appendicitis, *Streptococcus*, 94
- Applications
Bacillus lentimorbus, 571
Bacillus popilliae, 571
Bacillus sphaericus, 596
Bacillus thuringiensis, 591–92
Butyrivibrio, 1011
Clostridiaceae, 674
Clostridium, 674
Clostridium perfringens, 730
Enterococcus, 171
Eubacterium, 831–32
Heliobacteriaceae, 962
Lactobacillus, 343–45
Lactococcus, 212–14
Leuconostoc, 303–5
Oenococcus, 305
Pediococcus, 238, 254–56
Selenomonas, 988
Sporolactobacillus, 635
Sporosarcina, 641
Staphylococcus, 61
Tetragenococcus, 254–56
Veillonella, 1030–31
Weissella, 304–5
- Aquifers, Syntrophomonadaceae,
1043
- Arabidopsis*, 935
- Arabinose metabolism
Carnobacterium, 380
Enterococcus, 176
- Arabitol metabolism, *Enterococcus*,
176
- Arcanobacterium haemolyticum*,
503
- ARDS. *See* Adult respiratory
distress syndrome
- Arginine metabolism
Enterococcus, 175–76, 180
Pediococcus, 244, 247
Tetragenococcus, 244
- Armoracea rusticana*. *See*
Horseradish brittle root
- Aromatic compound
demethoxylation, *Sporomusa*,
998
- Arsenate reduction
Desulfobacterium, 771
Desulfosporosinus, 771, 780–81
- Arthritis. *See also* Osteoarthritis;
Rheumatoid arthritis; Septic
arthritis
Pediococcus, 254
- Arthrospira*, 1068
- AS. *See* Aggregation substance
- ASGN. *See* Acute streptococcal
glomerulonephritis
- Asteroleplasma*, 836–37, 843, 854
Asteroleplasma anaerobium, 910
Atopobium fossor, 823, 828
Autolysins, *Listeria*, 442–45
Autolysis, Haloanaerobiales, 816
- Avoparcin resistance, *Enterococcus*,
171
- Axenic cultures, isolation of,
1045
- Azithromycin sensitivity, anaerobic
cocci, 805
- Azotobacter*, 1086
- B**
- Bacillaceae
Bacillus, 530
Caryophanon, 631–32
Filibacter, 631–32

- Planococcus*, 631–32
Sporolactobacillus, 631–32
Sporosarcina, 631–32
Bacillus, 404, 520, 843, 871, 953, 987
 bacteriophages of, 544, 546–48
 defective, 546–47
 lytic, 547
 pseudotemperate, 547–48
 temperate, 546
 characteristics of, 532, 624
 cultivation of, 532
 genetics of, 543–46
 plasmids, 544–46, 548–49
 transcriptional regulation, 549–51
 transduction, 544–45
 transformation, 543–44
 habitats of, 531
 identification of, 620–25
 key for, 534–35
 infections of, 609–19
 insect pathogens, 563–96
 isolation of, 532, 620–25
 life cycle of
 germination, 537–38
 sporulation, 538–42
 medical, 609–25
 morphology of, 530
 nonmedical, 530–55
 pathogenicity of, 619
 plasmids of, 544–46, 548–49
 species of, 531–35, 624
 taxonomy of, 530–37
 treatment of, 618–19
Bacillus acidocaldarius, 535
Bacillus alginolyticus, 533
Bacillus alvei, 542, 573, 618
Bacillus aminovorans, 536, 631
Bacillus amyloliquefaciens, 535, 545–46, 551
Bacillus amylolyticus, 571
Bacillus anthracis, 542, 544–45, 548–49, 581, 589, 609–14, 620–23, 625, 666
 epidemiology of, 612–13
 habitat and ecology of, 610–12
 vaccine for, 609, 612–13
 virulence factors of, 613–14
Bacillus azotofomans, 565
Bacillus badius, 536
Bacillus benzoovorans, 533
Bacillus brandenburgensis, 571
Bacillus brevis, 535, 542, 554, 609
Bacillus burri, 571
Bacillus caldotenax, 536
Bacillus cereus, 184, 433, 536, 539, 542–45, 580–81, 589, 594, 609, 614–19, 621–23, 640
Bacillus cereus subsp. *mycoides*, 526
Bacillus chondrotinus, 533
Bacillus circulans, 535, 542–43, 609, 618
Bacillus coagulans, 253, 535–36, 609, 634–35
Bacillus difficilis, 730
Bacillus eulomarahae, 566
Bacillus fastidiosus, 536, 542
Bacillus firmus, 536
Bacillus flexus, 533
Bacillus fibourgensis, 566
Bacillus fusiformis, 533
Bacillus globisporus, 536, 631
Bacillus gordonae, 533
Bacillus insolitus, 520, 536
Bacillus kaustophilus, 533
Bacillus larvae, 563, 565, 571–77
 ecophysiology of, 574–76
 genetics of, 576–77
 habitats of, 572
 identification of, 573–74
 isolation of, 572
 pathogenicity of, 574–75
 preservation of, 572
Bacillus laterosporus, 609
Bacillus lentimorbus, 563–71, 573, 575
 applications of, 571
 ecophysiology of, 567–70
 genetics of, 570–71
 habitats of, 563
 identification of, 565–67
 isolation of, 563–65
 morphology of, 566
 preservation of, 563–65
Bacillus lentimorbus var. *australis*, 566
Bacillus licheniformis, 535–36, 542–43, 550–52, 609, 618, 666
Bacillus macerans, 609
Bacillus macquariensis, 536
Bacillus macroides, 542
Bacillus megaterium, 531, 534–36, 539, 542, 544–45, 553, 589, 609, 618, 640
Bacillus mycoides, 542, 621–23, 625
Bacillus neidei, 520
Bacillus pasteurii, 536, 631, 640, 643, 646
Bacillus polymyxa, 543, 571
Bacillus popilliae, 563–71, 573, 575
 applications of, 571
 ecophysiology of, 567–70
 genetics of, 570–71
 habitats of, 563
 identification of, 565–67
 isolation of, 563–65
 morphology of, 566
 preservation of, 563–65
Bacillus popilliae subsp. *lentimorbus*, 566
Bacillus popilliae subsp. *popilliae*, 566–67, 569
Bacillus popilliae var. *holotrichia*, 566
Bacillus popilliae var. *melolontha*, 566, 568–69
Bacillus popilliae var. *rhopaea*, 567
Bacillus psychrophilus, 536, 542
Bacillus psychrosaccharolyticus, 533
Bacillus pulvifaciens, 533
Bacillus pumilus, 535–36, 542–43, 554, 609, 618, 640
Bacillus pycnus, 520
Bacillus schlegelii, 542
Bacillus silvestris, 520
Bacillus simplex, 534
Bacillus smithii, 533, 635
Bacillus sphaericus, 520, 535–36, 542, 563, 578, 592–96, 609, 616, 618, 625, 631, 646, 648
 applications of, 596
 ecophysiology of, 594–95
 genetics of, 595
 habitats of, 592–93
 identification of, 593–94
 pathogenicity of, 592
Bacillus stearothermophilus, 299, 535–36, 542–44, 553–54, 565, 625
Bacillus subtilis, 55–56, 181–82, 186–87, 530, 535–37, 539, 541, 543–55, 569, 575, 591, 595, 609, 618–19, 640, 666, 669, 702, 755, 758, 840, 862, 865, 872
Bacillus thermodenitrificans, 536
Bacillus thermoleovorans, 533
Bacillus thiaminolyticus, 534
Bacillus thuringiensis, 433, 539, 544–48, 563, 577–92, 594, 609, 616, 621–23, 625
 applications of, 591–92
 crystal toxin of, 581–88, 592
 biochemistry of, 584
 detection of, 622
 pathotype I, 584–85
 pathotype II, 587
 pathotype III, 587–88
 synthesis of, 588
 ecophysiology of, 581–88
 genetics of, 588–91
 habitats of, 577–78
 identification of, 580–81
 isolation and preservation of, 578–80
 morphology of, 577, 580
 pathogenicity of, 583–84
 physiology of, 580
Bacillus thuringiensis subsp. *aizawai*, 585
Bacillus thuringiensis subsp. *berliner*, 589
Bacillus thuringiensis subsp. *entomocidus*, 585
Bacillus thuringiensis subsp. *israelensis*, 578, 580–81, 584, 587–88, 591–92, 594–96
Bacillus thuringiensis subsp. *kurstaki*, 580–81, 585, 588, 590, 594
Bacillus thuringiensis subsp. *sandiego*, 588
Bacillus thuringiensis subsp. *tenebrionis*, 578, 584, 587–88
Bacillus thuringiensis subsp. *thuringiensis*, 583, 585, 590
Bacillus/Clostridium subphylum, 809
 Bacitracin resistance/sensitivity
 Gemella, 515
 Macrococcus, 12
 Staphylococcus, 5, 11
 Bacteremia
 Bacillus, 617
 Bacillus anthracis, 611
 Enterococcus, 169
 Lactobacillus, 334

- Leuconostoc*, 303
Listeria, 410–11
Pediococcus, 254
Staphylococcus, 59–60
Streptococcus, 96
Streptococcus agalactiae, 132
Streptococcus dysgalactiae, 137
Streptococcus pneumoniae, 154–55, 159–60
- Bacterial vaginosis, *Lactobacillus*, 333–34
- Bacteriochlorophyll (Bchl) *g*, 951–52, 959
- Bacteriocins
Brochothrix, 485
Butyrivibrio, 1011
Clostridium perfringens, 754–55
Enterococcus, 171, 183
Lactobacillus, 330, 367–69
Lactococcus, 221–22
Leuconostoc, 299–301
Pediococcus, 249–53
Streptococcus pyogenes, 128–29
- Bacteriophage(s)
Bacillus, 544, 546–48, 625
Bacillus larvae, 573–74, 576–77
Bacillus sphaericus, 594
Brochothrix, 485
Clostridium, 673
 dairy fermentation problems with, 214–20
Lactobacillus, 370–72
Lactococcus, 216–20
Listeria, 411–12
Oenococcus, 301
Pediococcus, 249
 resistance to, 218–20
Streptococcus pyogenes, 128
Veillonella, 1034–35
- Bacteroidacea*, 987
Bacteroides, 741, 825, 978, 1025
Bacteroides halosphaerophilus, 809
- Baeocytes, Pleurocapsales, 1053, 1066–67
- Bchl *g*. *See* Bacteriochlorophyll *g*
- Bee. *See* Honey bee
- Beer
Lactobacillus, 341, 344, 348
Leuconostoc, 282
Megasphaera, 965, 970–71
Pectinatus, 965, 970–71
Pediococcus, 239, 242–43
 quality control of, 972
Weissella, 282
- Beer spoilage bacteria, 965–78
- Beggiatoa*, 1076
- Beverages, fermented. *See also* Beer; Wine
Lactobacillus, 340–42, 348
- Bifidobacterium*, 254, 327, 332, 345
- Bile salt hydrolases
Lactobacillus, 330–31
Listeria, 408
- Binary fission, Cyanobacteria, 1053–54, 1064–67
- Biochemical properties
Caryophanon, 649
Filibacter, 646
Planococcus, 643–44
Sporolactobacillus, 634–35
Sporosarcina, 640
- Biochemistry
Eubacterium, 830
Megasphaera, 978
Pectinatus, 976–78
 Syntrophomonadaceae, 1047–48
 butyrate metabolism, 1047–48
 crotonate metabolism, 1048
 long-chain fatty acid metabolism, 1048
Zymophilus, 978
- Biofilm. *See also* Cyanobacterial mats
 human oral flora, 1031–32
Listeria, 405
Staphylococcus, 43–45
- Biology, of *Listeria monocytogenes* infection, 415–18
- Biotechnology, Cyanobacteria, 1091
- Bird hosts. *See* Poultry hosts
- Blood environment
Erysipelothrix, 492, 502
Gemella, 515–16
Staphylococcus, 9
Streptococcus, 86, 95
Streptococcus pneumoniae, 150, 159
- Bog habitat, *Selenomonas*, 984
- BoNT. *See* Botulinum neurotoxin
- Botulinum neurotoxin (BoNT). *See also* Neurotoxins
 action of, 686–89
Clostridium, 679
 in food, 690–91
 for human therapy, 689
 structure of, 682–86
- Botulism
Clostridium perfringens, 753
 description of, 692–93
- Bovine gamma globulin, as
Clostridium difficile treatment, 741
- Bovine hosts. *See also* Ruminant hosts
Bacillus anthracis, 611–13
Clostridium perfringens, 714, 718, 720, 724, 726
Desulfotomaculum, 792
Enterococcus, 165
Erysipelothrix, 494
Lactococcus, 205–6, 224
Listeria, 405
- Bovine mastitis
Lactococcus, 205
Streptococcus agalactiae, 131
- Brackish habitat, *Sporomusa*, 993
- Bread production. *See* Food fermentation
- Brevibacillus*, 520
- Brewing, anaerobic genera isolated during, 968
- Brochocin, *Brochothrix*, 485
Brochothrix, 477–88, 520
 characteristics of, 481–85
 chemotaxonomy of, 478–79
 habitats of, 486–87
 identification of, 479–83
 isolation of, 487–88
 morphology of, 477, 479
 pathogenicity of, 477
 phylogenetic tree of, 478
 phylogeny and classification of, 477–78
 species of, 480–82
Brochothrix campestris, 477–88
Brochothrix thermosphacta, 477–88, 525
- Bronchitis, *Gemella*, 511
- Buccal mucosa, 1034
 intergeneric coaggregations of, 1032–33
Veillonella, 1024
- Bulgarian, *Lactobacillus*, 369
- Bulleidia extracta*, 493, 825, 828
- Butyrate metabolism
Butyrivibrio, 1009
 syntrophic, 1047–48
- Butyrate production
Butyrivibrio, 1007
Clostridium, 672–73
Clostridium perfringens, 701
Butyrivibrio, 1002–11
 applications of, 1011
 cultivation of, 1007
 ecology of, 1010–11
 genetics of, 1009–10
 groups of, 1002–4
 habitat of, 1004–5
 media for, 1008
 morphology of, 1002
 phylogenetic tree of, 1004
 phylogeny of, 1002–4
 physiology of, 1007–9
 preservation of, 1007
Butyrivibrio alactacidigens, 1007
Butyrivibrio crossotus, 1002, 1003
 identification of, 1007
 isolation of, 1005
Butyrivibrio fibrisolvens, 1002–4, 1008–11, 1013
 identification of, 1005–7
 isolation of, 1005
- C**
- C2 toxin, 735
- C5a peptidase (SCPA)
Streptococcus agalactiae, 135
Streptococcus dysgalactiae, 138
Streptococcus pyogenes, 115–16, 129
- Cadaverine, 1027
Selenomonas, 987
- Cadherin, *Listeria*, 424–26, 452
- Calcium transport, *Enterococcus*, 183
- Caloramator*, 654, 658, 671
Caloramator fervidum, 658
Caloramator fervidus, 1042
Caloranaerobacter, 654
Calothrix, 1070, 1076
Calothrix sp. PCC 7601, 1079, 1084, 1088, 1090
Camobacterium, phylogenetic tree of, 321

- Candida*, 1030
 Canine hosts
 Clostridium perfringens, 725
 Enterococcus, 165
 Erysipelothrix, 494
 Gemella, 512, 516
 Kurthia, 522
 Lactobacillus, 325
 Staphylococcus, 58
 Capsules
 Bacillus, 542
 Bacillus larvae, 574
 Clostridiaceae, 665–66
 Clostridium, 665–66
 Clostridium perfringens, 699
 Lactococcus, 222
 Streptococcus agalactiae, 130–31
 Streptococcus pneumoniae, 155
 Streptococcus pyogenes, 114–15
 Carbohydrate metabolism
 Bacillus larvae, 574
 Bacillus lentimorbis, 567
 Bacillus popilliae, 567
 Carnobacterium, 376, 380
 Clostridium perfringens, 701
 Coprococcus, 798
 Enterococcus, 175–77
 Erysipelothrix, 492–93, 500
 Lactobacillus, 327, 365–66
 Leuconostoc, 273, 289–90
 mollicutes, 861
 Oenococcus, 273, 290
 Pediococcus, 244, 247–49
 Ruminococcus, 798
 Sporolactobacillus, 635
 Tetragenococcus, 244, 247–48
 Weissella, 273, 290
 Carbohydrate transport,
 Enterococcus, 176–77
 Carbon catabolite repression,
 Staphylococcus, 23–25
 Carboxylic acid degradation,
 Syntrophomonadaceae,
 1042
 Carbuncles, *Staphylococcus*, 59
 Caries
 Eubacterium in, 831
 metabolic communication of,
 1029
 Carnivore hosts, *Staphylococcus*,
 58
Carnobacterium, 163, 229, 231, 240,
 246, 276, 293, 320, 372–80,
 482
 characteristics of, 323
 cultivation and preservation of,
 378
 habitats of, 373–76
 identification of, 378–79
 isolation of, 376–78
 phylogenetic tree of, 321, 373
 physiological properties of, 376
 species of, 379–80
Carnobacterium alterfunditum, 373,
 375–80
Carnobacterium divergens, 276, 320,
 373–80
Carnobacterium funditum, 373,
 375–80
Carnobacterium gallinarum, 373–74,
 376, 378–80
Carnobacterium inhibens, 373, 375,
 378–80
Carnobacterium mobilis, 373, 378–
 80
Carnobacterium piscicola, 276, 320,
 373–80
 α -Carotene, *Prochlorococcus*, 1103
 Carotenoids
 Heliobacteriaceae, 951–52
 Prochlorococcus, 1103
 Carrots
 Leuconostoc, 283–84, 302
 Weissella, 302
Caryophanon, 520, 631–32, 646–49
 cultivation of, 647
 genetics and phylogenetic
 relationships of, 648–49
 habitats of, 646–47
 identification of, 649
 isolation of, 647
 morphology of, 648
 preservation of, 648
 properties of, 649
Caryophanon latum, 536, 631,
 646–49
Caryophanon tenue, 646–49
 Catabolite regulation
 Bacillus, 551–52
 Staphylococcus, 22–24
Catenabacterium catenaforme, 327
 Catenin, *Listeria*, 424–25
 Cation transport, *Enterococcus*,
 182–83
 Ceca
 Roseburia, 1014, 1016
 Selenomonas, 982–84
 Cefotaxime resistance/sensitivity
 anaerobic cocci, 805
 Streptococcus pneumoniae, 155
 Cell division
 mollicutes, 842
 of phytopathogenic spiroplasmas,
 908
 Cell envelope
 Megasphaera, 968–69
 Pectinatus, 967
 Cell protein patterns
 Leuconostoc, 290
 Oenococcus, 290
 Weissella, 290
 Cell wall composition
 Bacillus, 536, 542–43
 Bacillus larvae, 573
 Brochothrix, 478–79
 Caryophanon, 648
 Desulfitobacterium, 772
 Desulfosporosinus, 772
 Erysipelothrix, 493, 498
 Eubacterium, 825
 Filibacter, 645
 Listeria, 438–42
 Macrocococcus, 5, 12–13
 Marinococcus, 644
 mollicutes, 859, 872
 Planococcus, 643
 Sporolactobacillus, 634
 Sporosarcina, 640
 Staphylococcus, 5, 12–13, 38–42
 Streptococcus pneumoniae,
 149–50, 155–56
 Streptococcus pyogenes, 114–15
 Weissella, 290
 Zymophilus, 969
 Cellobiose metabolism
 Brochothrix, 480
 Carnobacterium, 380
 Enterococcus, 176
 Pediococcus, 247
 Cellulitis, *Bacillus*, 616
 Cellulose metabolism
 Bacillus, 531
 Clostridium, 671
Centipeda, 984
 identification of, 985–86
Centipeda periodontii, 965, 969, 982,
 985, 987
 Central nervous system infection,
 Listeria, 411
 Cephalosporins resistance
 Bacillus, 619
 Enterococcus, 189
 Cephalosporins sensitivity
 anaerobic cocci, 805
 Bacillus, 618–19
 Erysipelothrix, 497
 Gemella, 515
 Cereals. *See* Food; Food
 fermentation
 Cerebritis, *Staphylococcus*, 59
 Cervicitis, *Staphylococcus*, 59
Chamaesiphon, 1065
 Cheese. *See also* Dairy environment;
 Food fermentation
 Carnobacterium, 375
 Lactobacillus, 339
 Listeria, 409
 Chemotaxonomy
 Brochothrix, 478–79
 Caryophanon, 648
 Desulfitobacterium, 777
 Filibacter, 645
 Planococcus, 643
 Sporolactobacillus, 634
 Sporosarcina, 639–40
 Chemotrophic growth,
 Heliobacteriaceae, 961
 Chickens. *See* Poultry hosts
 Chloramphenicol resistance
 Enterococcus, 187
 Listeria, 412–13
 Chloramphenicol sensitivity
 Bacillus, 618–19
 Clostridium perfringens, 717
 Gemella, 515
 Listeria, 408
 Pediococcus, 254
 Planococcus, 644
Chloroflexus auranticus, 1076
Chlorogloeopsis, 1070
Chlorogloeopsis fritschii
 CCAP1411/1b, 1086
 Chlorophyll *a*, 951–52
 Chlorophyll *a/b* light harvesting
 antennae, 1103–4
 Chlorophylls, *Prochlorococcus*,
 1102
 Chloroplast genes, Cyanobacteria,
 1083–84

- Cholesterol
 listeriolysin interaction with, 431
 mollicutes, 847, 855
- Cholesterol reduction, *Eubacterium coprostanoligenes*, 831
- Choline-binding proteins,
Streptococcus pneumoniae,
 157–58
- Chorioamnionitis, *Listeria*, 404,
 410
- Chromatic adaptation,
 Cyanobacteria, 1087–88
- Chromatium*, 1076
- Chroococcales, 1053–54
 genera and groups of, 1064–65
- Chroococcidiopsis*, 1056–57, 1066–67
- Ci. *See* Inorganic carbon
- Cider, *Lactobacillus*, 341, 347
- Ciprofloxacin sensitivity
Bacillus, 619
- Citrate metabolism
Enterococcus, 175, 178
Lactobacillus, 340–41
Lactococcus, 214
Leuconostoc, 279–80, 294–95,
 298–99
Oenococcus, 294–95
- Citrus stubborn, 905, 911–12
 control of, 935
 disease symptoms of, 930–31
 losses and impact of, 932
- Clam. *See* Shellfish hosts
- Clarithromycin sensitivity, anaerobic
 cocci, 805
- Clindafloxacin sensitivity
 anaerobic cocci, 805
- Clindamycin resistance/sensitivity
Bacillus, 618
Enterococcus, 189, 192
Erysipelothrix, 497
- Cloning
Butyrivibrio, 1010
 Cyanobacteria, 1083
 by phenotypic complementation,
 1083
- Clostridiaceae, 654–74
Acetivibrio, 654
Acidaminobacter, 654
Alkaliphilus, 654
Anaerobacter, 654
Caloramator, 654
Caloranaerobacter, 654
Clostridium, 654
Coprobacillus, 654
Dorea, 654
Natronincola, 654
Oxobacter, 654
Sarcina, 654
Sporobacter, 654
Thermobrachium, 654
Thermohalobacter, 654
Tindallia, 654
- Clostridiales, Peptococcaceae, 771
- Clostridium*, 338, 404, 493, 512, 530,
 620, 654–74, 741, 823, 825,
 843, 951, 953, 965, 966, 987,
 1022
 applications of, 674
 characteristics of, 679–80
 clusters of, 655–58, 679–80, 731,
 753–54, 991, 1002, 1012, 1014
 cultivation of, 659–63
 disease from, 699
 enterotoxic, 698–742
 genetics of, 673–74, 679–82
 habitats and ecology of, 658–59,
 689–90
 identification of, 663–73
 isolation of, 659–63
 morphology of, 664–70, 679–80
 neurotoxicogenic, 679–93
 action of, 686–89
 genetics of, 680–82
 structure of, 682–86
 phylogenetic tree of, 656, 754
 phylogeny of, 654–58
 species of, 655–57
 taxonomy of, 654–55
- Clostridium acetium*, 664
- Clostridium acetobutylicum*, 446,
 667–71, 673–74, 700, 702
- Clostridium acidisoli*, 671
- Clostridium acidurici*, 673
- Clostridium aerotolerans*, 660, 670
- Clostridium akagii*, 671
- Clostridium algidicarnis*, 671
- Clostridium algidixylanolyticum*, 671
- Clostridium aminophilum*, 671
- Clostridium aminovalericum*, 671
- Clostridium anthracis*, 665, 709
- Clostridium arcticum*, 664, 671
- Clostridium argentinense*, 681
- Clostridium baratii*, 680
- Clostridium barkeri*, 658, 665
- Clostridium beijerinckii*, 671
- Clostridium bifermentans*, 665,
 667–69, 732–33, 740
- Clostridium botulinum*, 658, 680–82,
 689–90, 692–93, 698, 709, 732,
 734, 735, 753–55
- Clostridium bryantii*, 658
- Clostridium butyricum*, 654–58, 664,
 667, 670, 672, 680, 683,
 689–90, 753
- Clostridium cadaveris*, 667
- Clostridium celecrecens*, 1012
- Clostridium celluloparum*, 664
- Clostridium chauvoei*, 669
- Clostridium clostridiforme*, 664–65,
 669
- Clostridium coccoides*, 667
- Clostridium cocleatum*, 320, 665, 667
- Clostridium difficile*, 709, 730–42,
 753–55
 diagnosis of, 738–39
 disease from, 737–41
 epidemiology of, 736–37
 habitat of, 731–32
 identification of, 732, 739
 isolation of, 732
 phylogeny of, 731
 physiology of, 733
 preservation of, 732–33
 prevention of, 741–42
 serogroups of, 736–37
 strains of
 atypical toxigenic, 735, 740
 nontoxigenic, 736
 taxonomy of, 731
 toxins of, 731, 733–36
 treatment of, 738, 741–42
- Clostridium disporicum*, 669
- Clostridium durum*, 658
- Clostridium estertheticum*, 671
- Clostridium fallax*, 759
- Clostridium felsineum*, 664
- Clostridium fervidum*, 658
- Clostridium formicaceticum*, 664,
 672
- Clostridium frididicarnis*, 671
- Clostridium gasigenes*, 671
- Clostridium glycolicum*, 664
- Clostridium haemolyticum*, 670
- Clostridium hastiforme*, 669
- Clostridium histolyticum*, 658, 753,
 759
- Clostridium homopropionicum*, 672
- Clostridium hydroxybenzoicum*, 658
- Clostridium indolus*, 664, 667
- Clostridium innocuum*, 837, 863
- Clostridium intestinale*, 670
- Clostridium kluyveri*, 669, 672, 825
- Clostridium lactatifermentans*, 672
- Clostridium laramiense*, 671
- Clostridium lentocellum*, 669
- Clostridium limosum*, 658
- Clostridium lituseburense*, 664, 669
- Clostridium lortetii*, 658
- Clostridium methoxybenzovorans*,
 673
- Clostridium methylpentosum*, 665
- Clostridium neopropionicum*, 672
- Clostridium nigrificans*, 787
- Clostridium novyi*, 670, 735, 753, 759
- Clostridium oceanicum*, 665, 669
- Clostridium oroticum*, 667
- Clostridium oxalicum*, 658
- Clostridium palmarium*, 665, 671
- Clostridium paradoxum*, 664, 669–70
- Clostridium paraputrificum*, 755
- Clostridium pasteurianum*, 671
- Clostridium perfringens*, 614, 659,
 665, 673–74, 698–730, 732,
 734–35, 753–65, 798, 829
 applications of, 730
 disease from, 698–700
 epidemiology of, 711–15, 759
 gastrointestinal disease of
 humans, 711–13
 veterinary enterotoxemia,
 713–15
 genetics of, 702–3, 753–58
 habitat and ecology of, 700
 isolation and identification of,
 700–1
 pathogenicity of, 760–62
 phylogeny of, 698, 753
 physiology of, 701–2
 preservation of, 701
 taxonomy of, 698–700
 toxins of, 702–11
 type A, 711, 713, 715–19, 726,
 728
 type B, 713, 719–20, 726–28
 type C, 712–13, 719–21, 726–28
 type D, 714, 721–24, 726–28
 type E, 714–15, 724, 726, 728

- Clostridium perfringens* enterotoxin (CPE toxin)
antitumor activity of, 730
Clostridium perfringens, 699–700, 702–7
cytotoxic effects of, 707
diseases from, 706–7, 711, 715–17, 724–25
genetics of, 703–4
mechanism of action, 704–6
structure and function of, 706–7
Clostridium pfennigii, 658, 673
Clostridium polysaccharolyticum, 664
Clostridium propionicum, 664, 672
Clostridium proteoclasticum, 1002
Clostridium proteolyticum, 658
Clostridium puniceum, 664
Clostridium purinolyticum, 673
Clostridium putrificum, 658
Clostridium quercicolum, 658, 664, 965
Clostridium ramosum, 320, 667, 837, 863
Clostridium scatologenes, 673, 733
Clostridium septicum, 753, 759
Clostridium sordellii, 669, 731–33, 735, 737, 740, 753, 759
Clostridium spiroforme, 320, 665, 709, 735
Clostridium sporogenes, 658, 667, 731–33
Clostridium stercorarium subsp. *thermolacticum*, 672
Clostridium sticklandii, 671, 673
Clostridium subterminale, 665
Clostridium tetani, 659, 664, 674, 679, 681, 689–90, 692, 734, 753–54
Clostridium tetanomorphum, 665, 667
Clostridium thermaceticum, 658, 666
Clostridium thermoalkaliphilum, 664
Clostridium thermobutyricum, 665–66, 671, 674
Clostridium thermocellum, 664–65, 667–69, 671
Clostridium thermocopriae, 658
Clostridium thermohydrosulfuricum, 658, 671
Clostridium thermosaccharolyticum, 658, 671
Clostridium thermosulfurigenes, 658
Clostridium ultunense, 670
Clostridium villosum, 658, 664
Clostridium vincetii, 671
Coaggregation, 1032–34
colonization sites, 1032–34
gnotobiotic animal model of, 1034
mechanisms, 1032
partners, 1028–29, 1032
Cobalt requirement, *Prochlorococcus*, 1105
Coccobacillus, 1032
Codons, Cyanobacteria, 1085–86
Coffee
Leuconostoc, 282
Weissella, 282
Colistin resistance, *Brochothrix*, 480
Colitis, *Clostridium perfringens*, 753
Collagen binding, *Streptococcus*, 77
Collinsella aerofaciens, 823, 825–28, 831
Colony morphology
Bacillus, 620, 622
Bacillus larvae, 573
Bacillus sphaericus, 593
Brochothrix, 479, 483
Carnobacterium, 377–78, 380
Caryophanon, 648
Clostridiaceae, 665
Clostridium, 665, 679–80
Clostridium perfringens, 699–700
Desulfotomaculum, 788
Erysipelothrix, 499, 502
Gemella, 513
Kurthia, 525
Lactobacillus, 329
Planococcus, 643
Streptococcus, 78–80, 108–9
Streptococcus pneumoniae, 151, 153, 159
Streptococcus pyogenes, 124
Comamonas testosteroni, 1028–29
Conjunctivitis
Bacillus, 615
Listeria, 411
Consortia
of human oral flora, 1028–29, 1031–34
for starch fermentation, 1031
Copper
in cyanobacteria media, 1060–61
Prochlorococcus sensitivity to, 1105
Copper transport, *Enterococcus*, 183
Coprobacillus, 320, 654
Coprococcus, 795, 798
differentiation of, 803–4
isolation of, 796–97
Corn stunt, 905, 911, 936
control of, 935
disease symptoms of, 930
losses and impact of, 931–32
Corrinoids, *Sporomusa*, 996
Corynebacterium, 620
Cow. *See* Bovine hosts
CPE toxin. *See* *Clostridium perfringens* enterotoxin
Crotonate metabolism, Syntrophomonadaceae, 1048
Cryptobacterium, 823
Cultivation
Bacillus, 532
Butyrivibrio, 1007
Carnobacterium, 378
Caryophanon, 647
Clostridiaceae, 659–63
Clostridium, 659–63
Desulfotomaculum, 790–91
Filibacter, 645
Heliobacteriaceae, 957–58
Lachnospira, 1013
Leuconostoc, 293–94
Marinococcus, 644
Megaspheara, 972
Oenococcus, 293–94
Pectinatus, 971–72
phytopathogenic spiroplasmas, 913–16
Planococcus, 643
Prochlorococcus, 1101–2
Roseburia, 1016
Selenomonas, 984–85
Sporolactobacillus, 633
Sporomusa, 993–96
Sporosarcina, 637–38
Streptococcus pneumoniae, 151
Syntrophomonadaceae, 1044–45
Weissella, 293–94
Zymophilus, 972–73
Cyanobacteria
applications of, 1091
biotechnology of, 1091
Chroococcales, 1064–65
collection of, 1057–58
cultivation of, 1062
differentiation in, 1088
ecology of, 1074–91
genetics of, 1074–91
groups of, 1053–54
growth conditions for, 1058–62
identification of, 1058, 1063–70
insect control, 1091
isolation of, 1057–58, 1063
maintenance of, 1063
mats of, 1075–76
media for, 1059–62
metabolism of, 1074, 1077–78, 1088–91
model systems with, 1091
Nostocales, 1068–70
orders of, 1064
Oscillatoriales, 1067–68
photosynthesis in, 1056, 1074, 1082–85, 1088–89
phylogenetic tree of, 1055
phylogeny of, 1054
physiology of, 1054–57, 1074–91
Pleurocapsales, 1066–67
purification of, 1057–58, 1063
rubisco in, 1089–90
Stigonematales, 1068–70
stress on, 1090–803
Cyanobacterial mats, 1075–76
Cyanophage
AS-1, 1080
N-1, 1080
Cyanophora, 1086
Cyanophora paradoxa, 1082, 1084–85, 1088
Cyanothece, 1065
Cylindrospermum, 1069–70
Cystitis, *Staphylococcus*, 59–60
Cytochrome profile
Brochothrix, 479, 483–84
Clostridium, 671
Lactococcus, 210
Staphylococcus, 5, 11, 26–27
Cytochrome synthesis,
Enterococcus, 175–76, 181–82
Cytolysin, *Enterococcus*, 170, 194
Cytotoxin. *See also* Toxin B
Streptococcus, 96

D

- Dacryocystitis, *Bacillus*, 615
Dactylococcopsis salina, 1078
Dairy environment
Bacillus cereus, 615
Brochothrix, 486
Carnobacterium, 375
Enterococcus, 171
Kurthia, 519, 523
Lactobacillus, 286–87, 338–39, 342–43, 346, 367
Lactococcus, 205–10, 212–14
Leuconostoc, 279–80, 286–87, 294, 302, 304
Listeria, 405
Pediococcus, 255, 286–87
Staphylococcus, 60
Weissella, 279–80, 302
Dairy fermentation
bacteriophage problems in, 214–20
Lactococcus, 212–14
DAPI, phytopathogenic spiroplasmas, 916
Decarboxylation phosphorylation, *Sporomusa*, 998
Dehalobacter, 772–73
properties of, 773
Deinococcus radiodurans, 553
Dendrosporobacter, 664
Dendrosporobacter quercicolus, 658, 997
Dental caries
Lactobacillus, 324–25
Streptococcus, 92–93
vaccine for, 94
virulence factors of, 93–94
Dental plaque, 1022, 1034
Gemella, 512
Kurthia, 522
Lactobacillus, 324–25
morphologies of bacteria in, 1033
Dermocarpa, 1066–67, 1076
Dermocarpella, 1066–67
Desemzia incerta, 375
Desemzia, phylogenetic tree of, 321
Desert
Cyanobacteria, 1057
Staphylococcus, 59
Desulfitobacterium, 771–80
habitats of, 774
identification of, 775
isolation of, 774–75
morphology of, 775–76
phylogenetic tree of, 772, 779
phylogeny of, 771–72
physiology and chemotaxonomy of, 777
preservation of, 779–80
properties of, 772–74, 776
Desulfitobacterium chlororespirans, 775–77, 779
Desulfitobacterium dehalogenens, 771–72, 774–77, 779, 953
Desulfitobacterium frappieri, 775, 777–79
Desulfitobacterium hafniense, 772, 775–79
Desulfitobacterium metallireducens, 775–76
Desulfosporosinus, 771–74, 780–85
habitats of, 780
identification of, 780–81
isolation of, 780
morphology of, 781–83
phylogenetic tree of, 772
phylogeny of, 771–72
preservation of, 784–85
properties of, 772–74, 782
Desulfosporosinus auripigmenti, 771, 780–81, 783
Desulfosporosinus idahoensis, 781, 783
Desulfosporosinus lacus, 781, 783
Desulfosporosinus meridiei, 781, 783
Desulfosporosinus orientis, 771–72, 780–81, 783, 785
Desulfosporosinus ruminis, 781
Desulfotomaculum, 530, 787–93
cultivation and media of, 790–91
habitats of, 787–89
morphology of, 788
phylogenetic tree of, 788
preservation of, 792
properties of, 789–90
taxonomy and identification of, 792–93
Desulfotomaculum acetoxidans, 788–89, 791–92
Desulfotomaculum geothermicum, 787
Desulfotomaculum guttoideum, 791
Desulfotomaculum kuznetsovii, 787
Desulfotomaculum nigrificans, 787–91
Desulfotomaculum orientis, 771, 787–88, 790, 792
Desulfotomaculum ruminis, 788–92
Desulfotomaculum sapomandens, 787
Desulfotomaculum thermoacetoxidans, 787
Desulfovibrio, 1044
Desulfovibrio orientis, 771
Desulfovibrio vulgaris, 1048
Detection
Megasphaera, 972
Pectinatus, 971–72
phytopathogenic spiroplasmas, 914–17
Zymophilus, 972–73
Dextran production
Leuconostoc, 295–96, 305
Weissella, 295–96
Dextranucrase, *Leuconostoc*, 295–96, 299, 305
Dextrin metabolism, *Pediococcus*, 247
Diacetyl production, *Lactococcus*, 214
Dialister pneumosintes, 965, 966
Differentiation, 1068–70
Cyanobacteria, 1056, 1088
Megasphaera, 968
Nostocales, 1054
Pectinatus, 966–67
Zymophilus, 969
Diplococcus morbillorum, 511
Disease
Clostridium difficile, 737–38
Clostridium perfringens, 698–730, 759–60
gastrointestinal disease in humans, 715–17
veterinary enterotoxemias, 717–30
Enterococcus, 169–71
Eubacterium, 831
Listeria, 408–11
mollicutes, 878
Pediococcus, 253–54
phytopathogenic spiroplasmas, 930–35
losses and impact of, 931–32
symptoms of, 930–31
Spiroplasma, 851
Streptococcus, 92–97
Streptococcus agalactiae, 131–35
Streptococcus pneumoniae, 155–60
Streptococcus pyogenes, 112–24
Tetragenococcus, 253–54
Veillonella, 1030
Disseminated infections, *Bacillus*, 617–18
Divinyl chlorophyll *a/b*-protein complexes, 1103
DNA, Cyanobacteria, 1078–83
DNA restriction/modification, of Cyanobacteria, 1079–80
DNA uptake, in Cyanobacteria, 1074–75
DNA-DNA hybridization
anaerobic cocci, 804
Bacillus, 531, 534–35, 625
Bacillus sphaericus, 593–94
Brochothrix, 478
Carnobacterium, 375
Caryophanon, 648
Desulfitobacterium, 775, 777
Desulfosporosinus, 781, 783
Enterococcus, 163
Erysipelothrix, 493, 504
Kurthia, 525
Lactobacillus, 333, 362–63, 372
Lactococcus, 216
Leuconostoc, 273, 276–77, 289–92, 303
Listeria, 455
Macrococcus, 5, 11
mollicutes, 844
Oenococcus, 273, 276, 289, 291–92
Pediococcus, 231–32, 244
Peptococcus, 803
Sporolactobacillus, 634
Sporosarcina, 640
Staphylococcus, 5, 11, 13, 57
Streptococcus, 81–82, 85, 89–91, 98
Streptococcus dysgalactiae, 136–37
Tetragenococcus, 231, 244
Weissella, 273, 276, 283, 289, 291–92
DNA-rRNA hybridization
Enterococcus, 163
Leuconostoc, 273
Oenococcus, 273

Dolosigranulum, 163
Dorea, 654, 823

E

Ecology

Bacillus anthracis, 610–11
Butyrivibrio, 1010–11
Clostridium perfringens, 700
 Cyanobacteria, 1074–91
 Haloanaerobiales, 818–20
 Heliobacteriaceae, 961–62
Lachnospira, 1014
Leuconostoc, 302
Macrococcus, 59
 mollicutes, 845, 848
Sporomusa, 998–99
Staphylococcus, 57–59
Veillonella, 1027–29
Weissella, 302

Ecophysiology

Bacillus larvae, 574–76
Bacillus lentimorbus, 567–70
Bacillus popilliae, 567–70
Bacillus sphaericus, 594–95
Bacillus thuringiensis, 581–88

Ectothiorhodospira halochloris, 1076

Eggerthella lenta, 823

Emden-Meyerhof-Parnas pathway

Bacillus larvae, 576
Bacillus lentimorbus, 570
Bacillus popilliae, 570
Clostridium, 672
Clostridium perfringens, 701
Enterococcus, 176, 179
Erysipelothrix, 499–500
Gemella, 514
Pediococcus, 244, 248
Tetragenococcus, 244

Empyema

Bacillus, 616
Streptococcus, 94

Encephalitis, *Listeria*, 404, 411

Endocarditis

Bacillus, 617–19
Enterococcus, 169–70
Erysipelothrix, 495–97
Gemella, 515–16
Lactobacillus, 334
Lactococcus, 205
Leuconostoc, 303
Listeria, 411
Staphylococcus, 59–60
Streptococcus, 96–97
Streptococcus dysgalactiae, 137

Endolysins, *Listeria*, 442–45

Endometritis, *Streptococcus agalactiae*, 132

Endophthalmitis, *Bacillus*, 616

Endospores

Bacillus, 530–31
Bacillus larvae, 573
Bacillus thuringiensis, 577, 580
 Clostridiaceae, 669–70
Clostridium, 669–70
Clostridium perfringens, 759
Desulfobacterium, 774
Desulfosporosinus, 780

Desulfotomaculum, 792–93
 Haloanaerobiales, 810, 812–16
 Heliobacteriaceae, 953, 956, 960
Sporolactobacillus, 632, 634
Sporomusa, 991, 993, 996–97
Sporosarcina, 639
 Endotoxin, *Veillonella*, 1027
 Energy metabolism
Enterococcus, 180–82
Leuconostoc, 294
 mollicutes, 862, 867
Oenococcus, 294
Ureaplasma, 862
Weissella, 294

Enrichment

Selenomonas, 984
Sporomusa, 993–94
 Syntrophomonadaceae, 1043

Entamoeba histolytica, 828

Enteritis necroticans, *Clostridium perfringens*, 712–13, 717

Enterococcus, 81, 163–71, 175–94, 229, 231, 240, 249, 276, 281, 404, 669, 983, 987

applications of, 171
 characterizations of, 167
 disease of, 169–71

epidemiology of, 168–69

hospital, 169
 transfer between host species, 168–69

genetics of, 183–89

habitats of, 165–66

identification of, 166–68

isolation of, 166

phylogenetic tree of, 321

phylogeny of, 163–64

physiology of, 175–83

species groups of, 163–64, 167–68

species of, 164–65, 167–68

Enterococcus asini, 167

Enterococcus avium, 164–66

Enterococcus casseliflavus, 164–68,

179–81, 190–92

Enterococcus cecorum, 163, 165, 168

Enterococcus columbae, 163, 165

Enterococcus dispar, 163, 179

Enterococcus durans, 164–66, 171, 181

Enterococcus faecalis, 163–66, 168–71, 175–88, 190–94, 208, 282, 337, 345, 366, 380, 446, 595, 864, 1031

Enterococcus faecium, 164–66, 168, 171, 175, 177, 179–83, 185–86, 190–94, 344–45, 380

Enterococcus flavescens, 164

Enterococcus gallinarum, 164–66,

168, 181, 190–92

Enterococcus hirae, 164–66, 169, 175, 181, 183, 190

Enterococcus malodoratus, 165–66

Enterococcus mundtii, 165

Enterococcus pseudoavium, 165–66

Enterococcus raffinosus, 165–66

Enterococcus saccharolyticus, 163, 167

Enterococcus seriolicida, 164, 224

Enterococcus solitarius, 164, 233

Enterococcus sulfureus, 163

Enterocolitis, *Staphylococcus*, 59

Enterotoxemia. *See* Veterinary enterotoxemia

Enterotoxin. *See* Toxin A

Entner-Duodoroff pathway

Bacillus larvae, 576

Enterococcus, 176

Entomoplasma, 836–37, 843, 847, 851, 910–11

Entomoplasmataceae

Entomoplasma, 836–37

Mesoplasma, 831–32, 836–37, 843, 847, 851–52, 854–55, 869

Enzymes

Leuconostoc, 290

Oenococcus, 290

Weissella, 290

Eperythrozoon, 836–37, 845, 848

phylogenetic tree of, 848

Epidemiology

Bacillus anthracis, 612–13

Clostridium difficile, 736–37

Clostridium perfringens, 711–15, 759

gastrointestinal disease of humans, 711–13

veterinary enterotoxins, 713–15

Enterococcus, 168–69

Listeria, 408–10

mollicutes, 857

Pediococcus, 253–54

phytopathogenic spiroplasmas, 929–30

Streptococcus agalactiae, 131–35

Streptococcus pneumoniae, 155–60

Streptococcus pyogenes, 112–24

Tetragenococcus, 253–54

Veillonella, 1029–30

Erysipelas

Erysipelothrix, 492

Streptococcus pyogenes, 112

Erysipeloid, *Erysipelothrix*, 496

Erysipelothrichaceae, *Erysipelothrix*, 492–93

Erysipelothrix, 303, 482, 492–505, 620, 825

disease from, 495–97

genetics of, 504–5

habitats of, 494–95

isolation and identification of, 502–4

morphology of, 492–93

pathogenicity of, 497–98

phylogenetic tree of, 493, 499

properties of, 498–502

taxonomy and phylogeny of, 493–94

Erysipelothrix erysipeloides, 492

Erysipelothrix inopinata, 492, 494, 502, 504

Erysipelothrix insidiosa, 492

Erysipelothrix muriseptica, 492

Erysipelothrix porci, 492

Erysipelothrix rhusiopathiae, 492–504

Erysipelothrix tonsillarum, 492–94, 501–2, 504

Erysipelotrichaceae, 823

- Erythromycin resistance
Enterococcus, 183–84, 186, 188
Gemella, 515
Listeria, 414
Pediococcus, 249
Staphylococcus, 11
Streptococcus, 97
- Erythromycin sensitivity
 anaerobic cocci, 805
Bacillus, 618
Erysipelothrix, 497
Gemella, 515
Pediococcus, 254
Planococcus, 644
Staphylococcus, 5
- Escherichia coli*, 345, 367, 553, 843, 857, 987
 in Cyanobacteria gene studies, 1081–83, 1085–87, 1089
- Esterase isoenzymes, *Brochothrix*, 485
- Ethanol production
Bacillus lentimorbus, 569–70
Bacillus popilliae, 569–70
Brochothrix, 483
Carnobacterium, 376, 378
Clostridium perfringens, 701
Lactobacillus, 365
- Eubacterium*, 493, 655, 823–32, 1031
 applications of, 831–32
 biochemical characteristics of, 830
 habitat of, 825–29
 identification of, 829–31
 isolation of, 829
 phylogenetic tree of, 824–25
 phylogeny of, 823
 saccharolytic species of, 823–25
 taxonomy of, 823–25
- Eubacterium acidaminophilum*, 825, 828–29
Eubacterium aggregans, 823, 829
Eubacterium alactolyticum, 825
Eubacterium angustum, 825, 828
Eubacterium barkeri, 658, 823
Eubacterium bifforme, 823, 825, 828
Eubacterium brachy, 823, 825, 828, 831
Eubacterium budayi, 829
Eubacterium callanderi, 823, 825, 828, 831
Eubacterium cellulosolvans, 828
Eubacterium combesii, 825
Eubacterium contortum, 825–28
Eubacterium coprostanoligenes, 825, 829, 831
Eubacterium cylindroides, 823, 825–28
Eubacterium desmolans, 825, 829, 831
Eubacterium dolichum, 823, 828
Eubacterium eligens, 828
Eubacterium formicigenerans, 823, 828
Eubacterium hadrum, 828
Eubacterium hallii, 828
Eubacterium infirmum, 823
Eubacterium lenta, 825, 828, 831
Eubacterium limosum, 823, 825, 828, 832, 1014
- Eubacterium minutum*, 823
Eubacterium moniliforme, 655, 829
Eubacterium nitritogenes, 829
Eubacterium nodatum, 823, 825, 828, 831
Eubacterium oxidoreducens, 825, 828
Eubacterium plautii, 825, 828, 831
Eubacterium pyruvativorans, 825, 828
Eubacterium ramulus, 828
Eubacterium rectale, 828, 1007, 1012
Eubacterium ruminantium, 828
Eubacterium saburreum, 825, 828, 1028, 1032
Eubacterium saphenum, 823, 828
Eubacterium siraeum, 828
Eubacterium suis, 823, 825
Eubacterium sulci, 823, 825
Eubacterium tarantellae, 655, 828
Eubacterium tenue, 825
Eubacterium tortuosum, 823
Eubacterium uniformis, 828
Eubacterium ventriosum, 828–29
Eubacterium xylanophilum, 828
Eubacterium yurii, 828
Exiguobacterium, 520
 Exoenzymes, *Staphylococcus*, 47
 Exopolysaccharides
Lactococcus, 222
Leuconostoc, 302
Pediococcus, 247–48
 Exosporium, *Bacillus*, 539
 Exotoxins
Bacillus thuringiensis, 583–84
Streptococcus pneumoniae, 156
 Extrachromosomal DNA. *See also*
 Plasmids
 in phytopathogenic spiroplasmas, 923–25
- Eye infections, *Bacillus*, 615
- F**
- Facklamia*, 163
 Fatty acid metabolism
Desulfotomaculum, 787
 mollicutes, 859
 Syntrophomonadaceae, 1047–48
 Fatty acids
Bacillus, 535, 543
Brochothrix, 479
Carnobacterium, 379–80
Desulfitobacterium, 778
Desulfosporosinus, 782–83
Erysipelothrix, 493, 498–99
Filibacter, 645
Kurthia, 525, 527
Leuconostoc, 290–91
 of *Megasphaera*, 968–69
Oenococcus, 290–91
 of *Pectinatus*, 967
Sporolactobacillus, 634
Weissella, 290–91
 Feces environment
 anaerobic cocci, 795
Brochothrix, 486–87
Caryophanon, 646–47
 Clostridiaceae, 659
Clostridium, 659
Clostridium perfringens, 759
Desulfitobacterium, 774
Desulfotomaculum, 792
Erysipelothrix, 503
Kurthia, 519, 522
Lactobacillus, 325, 327–29, 332
Pediococcus, 236
Sporosarcina, 636
Streptococcus, 77
 Feline hosts
Enterococcus, 165
Kurthia, 519
Lactobacillus, 324–25, 328
 Fermentation
Butyrivibrio, 1009
Butyrivibrio fibrisolvens, 1006–7
 Cyanobacteria, 1078
Lachnospira, 1014
Roseburia, 1015–16
Selenomonas, 988
 Fermented food. *See* Food
 fermentation
 Fiber digestion, *Butyrivibrio*, 1011
 Fibrils, phytopathogenic
 spiroplasmas, 906
 Fibrin dissolving, *Streptococcus pyogenes*, 121
Fibroacter, 1011
Filibacter, 520, 631–32, 645–46
 habitats of, 645
 identification of, 646
 isolation of, 645
 morphology of, 645
 properties of, 645–46
Filibacter limicola, 536, 631, 645–46, 648
Filifactor villosus, 658
 Fimbriae, phytopathogenic
 spiroplasmas, 907, 933
Fingoldia, 795–96, 798
Fingoldia magna, 795, 803
Fischerella, 1070
 Fish hosts
Brochothrix, 486–87
Carnobacterium, 320, 374–77
Erysipelothrix, 494–95
Lactobacillus, 342
Lactococcus, 205, 224
Leuconostoc, 280
 mollicutes, 841, 843–44
Pediococcus, 236, 240
Tetragenococcus, 240, 243
Weissella, 267, 280
 Fish lactococcosis, *Lactococcus*, 205, 224
 Flagella
Bacillus, 542
Bacillus larvae, 573
Bacillus sphaericus, 594
 Clostridiaceae, 666
Clostridium, 666, 679
Desulfitobacterium, 772, 776
Desulfosporosinus, 772, 781
Kurthia, 525
Roseburia, 1016
Sporolactobacillus, 634

- Flesh-eating bacteria. *See* Toxic shock syndrome
- Fluorescence, *Veillonella*, 1023
- Fluoroquinolone resistance, *Enterococcus*, 193
- Fly hosts. *See also* Insect hosts
Staphylococcus, 59
- Food
Bacillus cereus, 615
BoNT in, 690–91
Cyanobacteria as, 1091
Enterococcus, 171
Leuconostoc, 280–84
Listeria, 405
mollicutes, 866
Oenococcus, 280–84
Pediococcus, 240, 254–56
Weissella, 280–84
- Food contamination, *Listeria*, 404
- Food fermentation
Lactobacillus, 279–80, 320, 332, 334, 336–44, 348
Leuconostoc, 273–81, 283–84, 304–5
Oenococcus, 281
Pediococcus, 236–40, 255–56, 280–81
Staphylococcus, 61
Tetragenococcus, 240–41
Weissella, 279–81, 304
- Food poisoning
Bacillus cereus, 614–15
Clostridium perfringens, 703, 711, 715–16
- Food spoilage, *Lactobacillus*, 339–40
- Formate production
Carnobacterium, 378
Coprococcus, 804
- Foulbrood. *See* American foulbrood
Fremyella, 1086
- Freshwater environment
Bacillus thuringiensis, 578
Clostridiaceae, 659
Clostridium, 659
Cyanobacteria, 1057, 1061
Desulfotobacterium, 774
Desulfosporosinus, 780
Desulfotomaculum, 789
Filibacter, 645
Heliobacteriaceae in, 956
Kurthia, 519, 523
Lactobacillus, 336
Listeria, 405
Sporomusa, 991
Staphylococcus, 59
- Fructan production,
Sporolactobacillus, 635
- Fructose metabolism
Bacillus larvae, 574
Bacillus popilliae, 567
Brochothrix, 480
Carnobacterium, 380
Enterococcus, 176
Leuconostoc, 294
mollicutes, 861
Oenococcus, 294
Pediococcus, 247
phytopathogenic spiroplasmas, 919, 934
Sporolactobacillus, 635
Weissella, 294
- Fruit
Lactobacillus, 336–37, 347
Leuconostoc, 280–84
Oenococcus, 280–84
Weissella, 280–84
- Fumarate reductase, *Enterococcus*, 182
- Furazolidone sensitivity
Macroccoccus, 12
Staphylococcus, 11
- Furuncles, *Staphylococcus*, 59
- Fusidic acid sensitivity, *Gemella*, 515
- Fusobacteria, 1033
Fusobacterium, 333, 825, 1025
Fusobacterium nucleatum, 1026–27, 1030, 1032–33
- G**
- Galactose metabolism
Bacillus larvae, 574
Bacillus lentimorbus, 567
Bacillus popilliae, 567
Carnobacterium, 380
Enterococcus, 176
Pediococcus, 247
Staphylococcus, 20–21
Gallicola, 795, 798
- Gas gangrene, *Clostridium perfringens*, 700, 753, 759–60
- Gastroenteritis
Bacillus cereus, 615
Listeria, 404
- Gastrointestinal environment
anaerobic cocci, 795
Clostridium perfringens, 698, 711–13
Coprococcus, 804
ecosystem of, 325–28
Lactobacillus, 325–33, 346, 369
Listeria, 405
mollicutes, 875
Pediococcus, 236
Streptococcus, 95
Streptococcus agalactiae, 131
- Gastrointestinal tract
Butyrivibrio in, 1004–5
Clostridium difficile in, 731
Eubacterium in, 825–28
Lachnospira in, 1012
Roseburia in, 1016
- GBS. *See* *Streptococcus agalactiae*
- G+C content
Acidaminococcus, 1023
anaerobic cocci, 795, 798
Bacillus, 532, 534
Bacillus larvae, 573
Bacillus sphaericus, 593
Brochothrix, 479, 482
Caryophanon, 648
Clostridiaceae, 654–55, 664
Clostridium difficile, 731
Clostridium perfringens, 702
Desulfotobacterium, 772
Desulfosporosinus, 772
Desulfotomaculum, 787, 792
Enterococcus, 163
Eubacterium, 823
Filibacter, 646
Gemella, 511, 515
Haloanaerobiales, 809
Kurthia, 520, 525
Lachnospira multipara, 1013
Lachnospira pectinoschiza, 1013
Lactobacillus, 350, 362–63
Lactococcus, 212, 220
Leuconostoc, 267, 274–75, 279
Listeria, 404
Macroccoccus, 5, 11–12
Megasphaera, 968, 1023
Microccoccus, 5
mollicutes, 864, 872
Oenococcus, 267, 274–75
Pectinatus, 967
Pediococcus, 231, 233
phytopathogenic spiroplasmas, 921–22
Planococcus, 641, 643
Prochlorococcus, 1106–7
Roseburia, 1015
Selenomonas, 983, 987
Sporolactobacillus, 634
Sporosarcina, 640
Staphylococcus, 5, 11
Streptococcus, 80–81, 90, 92
Synechococcus, 1065
Tetragenococcus, 231
Veillonella, 1023
Weissella, 267, 274–75, 278
Zymophilus, 969
- Gemella*, 493, 511–16
habitats of, 512
identification of, 513–15
isolation and maintenance of, 513
morphology of, 514
phylogenetic tree of, 512
Gemella bergeri, 511–12, 514–16
Gemella cuniculi, 511, 514
Gemella haemolysans, 511–15
Gemella morbillorum, 511–16, 799, 1032
Gemella palaticanis, 511, 514–15
Gemella sanguinis, 511–12, 514–16
- Gene families, Cyanobacteria, 1087
- Gene manipulation, *Clostridium perfringens*, 757–58
- Gene regulation
Listeria, 446–50
Staphylococcus, 50–51
- Gene transfer
Cyanobacteria, 1081–83
phytopathogenic spiroplasmas, 923
- Genetic conjugation
Bacillus sphaericus, 595
Enterococcus, 187–89
Listeria, 415
- Genetic mutagenesis
Clostridium, 673
phytopathogenic spiroplasmas, 923
Streptococcus agalactiae, 135–36
Streptococcus pyogenes, 126–28

- Genetic recombination,
Cyanobacterial DNA,
1080–81
- Genetic transfer systems
Bacillus thuringiensis, 590–91
Clostridium, 673
mollicutes, 843
- Genetics
Bacillus, 543–46
Bacillus larvae, 576–77
Bacillus lentimorbus, 570–71
Bacillus popilliae, 570–71
Bacillus sphaericus, 595
Bacillus thuringiensis, 588–91
Butyrivibrio, 1009–10
Caryophanon, 648–49
Clostridiaceae, 673–74
Clostridium, 673–74, 679–82
Clostridium difficile toxins, 733–34
Clostridium perfringens, 702–3,
753–58
Cyanobacteria, 1083–85
Enterococcus, 183–89
Erysipelothrix, 504–5
Filibacter, 646
Lactobacillus, 369–70
Lactococcus, 222–23
Leuconostoc, 296–302
Listeria, 411–15
Marinococcus, 644
mollicutes, 873
Oenococcus, 296–302
Pediococcus, 248–53
phytopathogenic spiroplasmas,
921–26
unique sequences in, 934
Planococcus, 643
Sporolactobacillus, 634
Sporosarcina, 640
Staphylococcus, 46–50
Streptococcus, 92
Streptococcus agalactiae, 135–36
Streptococcus pneumoniae, 151–53
Streptococcus pyogenes, 124–29
Tetragenococcus, 248–53
Veillonella, 1027
Weissella, 296–302
- Genetics transduction, *Bacillus*,
544–45
- Genetics transformation, *Bacillus*,
543–44
- Genitourinary tract, *Clostridium
difficile* in, 731
- Genome
Clostridium perfringens, 758–59
Lactococcus, 220
Listeria, 454–55
mollicutes, 837
phytopathogenic spiroplasmas,
917
Prochlorococcus, 1106–7
- Gentamycin resistance
Enterococcus, 186, 190
Gemella, 515
- Gentamycin sensitivity
Bacillus, 619
Brochothrix, 480
mollicutes, 873
Geobacillus, 520
- Gingival cavity
Carnobacterium, 324
ecological succession of
Veillonella in, 1028
Selenomonas, 982
- Gingivitis
Selenomonas, 982
Veillonella, 1028
- Globicatella*, 163
Gloecapsa, 1065
Gloeobacter, 1065
Gloeotheca, 1065
- Glomerulonephritis, *Streptococcus
pyogenes*, 112–13
- Gluconate metabolism
Brochothrix, 480
Carnobacterium, 380
Enterococcus, 176
Pediococcus, 247
- Gluconeogenesis
Staphylococcus, 24, 26
Veillonella, 1027
- Glucose metabolism
anaerobic cocci, 799
Bacillus larvae, 574–76
Bacillus lentimorbus, 567, 569–70
Bacillus popilliae, 567, 569–70
Brochothrix, 480, 483
Carnobacterium, 380
Enterococcus, 176
Erysipelothrix, 492–93, 499–500
Gemella, 514
Lactococcus, 211, 221
Leuconostoc, 211, 273, 289, 294
Oenococcus, 273, 289, 294
Pediococcus, 211, 229
phytopathogenic spiroplasmas,
919, 934
Sporolactobacillus, 635
Weissella, 273, 289, 294
- Glucosyltransferase, 1031–32
- Glycerol kinase, *Enterococcus*, 179
- Glycerol metabolism
Bacillus larvae, 574
Carnobacterium, 380
Enterococcus, 175–76, 179–80
Pediococcus, 247
- Glycerol oxidation,
Haloanaerobiales, 819
- Glycerol production
Bacillus lentimorbus, 569–70
Bacillus popilliae, 569–70
- Glycolytic pathway
Lactobacillus, 365
Lactococcus, 221
Staphylococcus, 20
- Glycopeptide resistance,
Enterococcus, 191–92
- Goat hosts. *See* Ruminant hosts
- Gram-negative, Clostridiaceae, 664
- Gram-positive
Bacillus, 620
Bacillus larvae, 573
Bacillus thuringiensis, 577
Carnobacterium, 378
Caryophanon, 648
Clostridiaceae, 654, 664
Desulfotobacterium, 771–72
Desulfosporosinus, 771–72
Erysipelothrix, 492–93
Gemella, 511, 514
Kurthia, 519–20, 524, 527
Lactobacillus, 320
Lactococcus, 210–11, 220
Leuconostoc, 267, 272
Listeria, 404, 408
Macrococcus, 12
Marinococcus, 644
Oenococcus, 267
Pediococcus, 229, 244
Planococcus, 643
Sporolactobacillus, 632–33
Staphylococcus, 5–61
Streptococcus, 80, 108
Streptococcus pneumoniae, 149–50
Streptococcus pyogenes, 112
Tetragenococcus, 229, 244
Weissella, 267
- Grass environment, *Brochothrix*,
487
- Grey Lung disease, mollicutes, 848
- Group B streptococcus. *See
Streptococcus agalactiae*
- Growth conditions
of beer spoilage bacteria, 970–71
for Cyanobacteria, 1058–62
- Gut environment. *See also
Gastrointestinal environment
Enterococcus*, 165
mollicutes, 875
- ## H
- Haemobartonella*, 836, 845–46, 848
phylogenetic tree of, 848
Haemophilus influenzae, 298, 864
Haemophilus parainfluenzae,
1028–29
Haloanaerobacter chitinovorans,
812, 815–16, 819
Haloanaerobacter lacunaris, 815, 818
Haloanaerobacter salinaris, 812,
815–16, 819
Haloanaerobiaceae, 809
properties of, 813–14
taxonomy of, 810
Haloanaerobiales, 809–20
ecology of, 818–20
habitat of, 810–11
identification of, 812–16
isolation of, 811–12
media for, 816–17
morphology of, 810–11
phylogenetic tree of, 810
phylogeny of, 809
physiology of, 817–18
preservation of, 816
taxonomy of, 809–10
Haloanaerobium, 814
Haloanaerobium acetobutylicum,
813
Haloanaerobium acetoethylicum,
814, 816, 818
Haloanaerobium alcaliphilum, 810,
813, 817–19
Haloanaerobium congolense, 813,
817–18

- Haloanaerobium kushneri*, 813
Haloanaerobium lacusrosei, 811, 817, 819
Haloanaerobium lacusroseus, 813
Haloanaerobium praevalens, 809, 813, 818–20
Haloanaerobium saccharolyticum, 810, 814, 818–19
Haloanaerobium saccharolyticum subsp. *saccharolyticum*, 811, 813
Haloanaerobium saccharolyticum subsp. *senegalensis*, 811, 813
Haloanaerobium salsugensis, 813–14
Halobacteroidaceae, 809
 properties of, 815
 taxonomy of, 810
Halobacteroides, 814
Halobacteroides elegans, 815, 818
Halobacteroides halobius, 809–12, 815–16, 818, 820
Halocella cellulolytica, 814, 817, 819
Halophiles, Haloanaerobiales, 817–20
Halorhodospira, 819
Halothermothrix orenii, 809–11, 814, 818–19
Hamster, *Clostridium difficile* in, 732
Haplosiphon, 1070
Health, *Lactobacillus*, 331–32
Heat shock response, *Oenococcus*, 302
Heavy metal resistance, *Carnobacterium*, 380
Heliobacillus, 951
Heliobacillus mobilis, 955–56, 960
Heliobacteriaceae, 951–62
 applications of, 962
 ecology and habitats of, 956, 961–62
 identification of, 959–60
 isolation of, 956–58
 light absorption by, 951–52, 959
 media for, 957–58
 morphology of, 953–56, 959
 phylogenetic tree of, 953
 phylogeny of, 953
 physiology, 960–61
 preservation of, 960
 properties of, 954
 taxonomy of, 953
Heliobacterium, 951, 953
Heliobacterium chlorum, 951, 953, 955–56
Heliobacterium gestii, 953, 956, 960–61
Heliobacterium modesticaldum, 952, 955–56, 962
Heliophilum, 951, 953
Heliophilum fasciatum, 955–56
Heliorestis, 951
Heliorestis baculata, 956–58
Heliorestis daurensis, 953, 956–60
Helveticin, *Lactobacillus*, 369
Hemolysins
 Bacillus, 619
 Enterococcus, 183
 Streptococcus agalactiae, 135
 Streptococcus pneumoniae, 156–58
Hemolysis
 Bacillus, 622
 Erysipelothrix, 499
 Gemella, 513–14
 Listeria, 430
 α -Hemolysis, *Streptococcus*, 108, 149–71
 β -Hemolysis, *Streptococcus*, 108–38
Hemoptysis, *Bacillus*, 616
Herbicides resistance, *Cyanobacteria*, 1091
Heterocysts
 Cyanobacteria, 1056, 1068–70, 1077–79
 formation of, 1086, 1088
Heterologous hybridization, *Cyanobacteria*, 1083–84
Hexose metabolism
 Carnobacterium, 376
 Lactobacillus, 365
 Leuconostoc, 294
 Oenococcus, 294
 Weissella, 294
Hexose monophosphate pathway
 Enterococcus, 176
 Leuconostoc, 294
 Oenococcus, 294
 Weissella, 294
High light (HL) adapted ecotypes, 1106–7
 Prochlorococcus, 1100, 1102, 1104
Histotoxic disease, *Clostridium perfringens*, 759–60
HL adapted ecotypes. *See* High light (HL) adapted ecotypes
Holdemania filiformis, 493, 825
Homoacetogens
 Acetohalobium arabaticum, 817
 Natroniella acetigena, 817
 Sporomusa, 991–99
Honey bee, *Bacillus larvae*, 571–77
Hormogonia, *Cyanobacteria*, 1054, 1069–70
Horse hosts
 Clostridium perfringens, 718–21, 725
 Erysipelothrix, 494
 mollicutes, 849
 Staphylococcus, 58–59
Horseradish brittle root, 912
 control of, 935
 disease symptoms of, 931
 losses and impact of, 932
Host associations
 evolution of, 911
 of phytopathogenic spiroplasmas, 910
Hot spring
 Cyanobacteria in, 1057, 1076
 Heliobacteriaceae in, 956
Hot spring environment
 Clostridiaceae, 659
 Clostridium, 659
Human hosts
 Bacillus anthracis, 610–14
 Clostridium perfringens, 711–13
 Enterococcus, 165
 Erysipelothrix, 494–97
 Gemella, 512
Lactobacillus, 320–27, 329
Listeria, 408–11
 mollicutes, 850, 875, 878
 mycoplasma pathogens in, 906–7
 Pediococcus, 253–54
 Staphylococcus, 57–59
 Tetragenococcus, 253
Human oral flora, 1022
 adherence by, 1031–35
 disease of, 1030
 epidemiology of, 1030
 Eubacterium in, 825–28, 831
 in freshly cleaned mouth, 1034
 metabolic communication, 1028–29
 nichrome steel wire model of, 1031–32
 Selenomonas, 982
 Veillonella, 1023–24
Hyaluronidase, *Erysipelothrix*, 497
Hydrocarbon metabolism, *Bacillus*, 531
Hydrogen disulfide reduction, *Cyanobacteria*, 1077
Hydrogen peroxide production
 Bacillus popilliae, 569
 Streptococcus pneumoniae, 156
Hydrogen sulfide production
 Clostridium, 679–80
 Erysipelothrix, 501
 Kurthia, 525
Hydroxychlorophyll *a*, 951, 959
Hypersaline environment
 Cyanobacteria in, 1057, 1076
 Haloanaerobiales in, 809, 810–11, 818–20
- ## I
- Identification
 anaerobic cocci, 798, 799–805
 Bacillus, 534–35, 620–25
 Bacillus larvae, 573–74
 Bacillus lentimorbus, 565–67
 Bacillus popilliae, 565–67
 Bacillus sphaericus, 593–94
 Bacillus thuringiensis, 580–81
 Brochothrix, 479–83
 Butyrivibrio crossotus, 1007
 Butyrivibrio fibrisolvens, 1005–7
 Carnobacterium, 378–79
 Caryophanon, 649
 Centipeda, 985–86
 Clostridiaceae, 663–73
 Clostridium, 663–73
 Clostridium difficile, 732
 Clostridium perfringens, 700–1
 Cyanobacteria, 1058, 1063–70
 Desulfotobacterium, 775
 Desulfosporosinus, 780–81
 Desulfotomaculum, 792–93
 Enterococcus, 166–68
 Erysipelothrix, 502–4
 Eubacterium, 829–31
 Filibacter, 646
 Gemella, 513–15
 Haloanaerobiales, 812–16
 Heliobacteriaceae, 959–60

- Lachnospira*, 1012–13
Lactobacillus, 355–65
Lactococcus, 210–12
Leuconostoc, 289–93
Listeria, 405–8
Macrococcus, 11–17
Marinococcus, 644
Megasphaera, 975–76
mollicutes, 847–55
Oenococcus, 289–93
Pectinatus, 973–75, 985–86
Pediococcus, 244–46
phytopathogenic spiroplasmas,
914–17
Planococcus, 644
Roseburia, 1015–16
Selenomonas, 985–88
Sporolactobacillus, 635
Sporomusa, 996–97
Sporosarcina, 640
Staphylococcus, 11–17
Streptococcus, 91–92
Streptococcus agalactiae, 130–31
Streptococcus pneumoniae, 149–51
Streptococcus pyogenes, 110–12
Syntrophomonadaceae, 1045–47
Tetragenococcus, 244–46
Veillonella, 1025–26
Weissella, 289–93
Zymophilus, 976
- Impetigo
Staphylococcus, 59
Streptococcus pyogenes, 111
- Infection, *Eubacterium* in, 826–27,
831
- Inorganic carbon (Ci),
Cyanobacteria, 1090
- Inorganic carbon (Ci) pump,
Cyanobacteria, 1090
- Insect control
Cyanobacteria for, 1091
for managing phytopathogenic
spiroplasmas, 937
- Insect hosts
Bacillus, 563–96
Bacillus larvae, 571–77
Bacillus lentimorbus, 563–71
Bacillus popilliae, 563–71
Bacillus sphaericus, 592–96
Bacillus thuringiensis, 577–92
Clostridiaceae, 659
Clostridium, 659
Erysipelothrix, 494
Lactobacillus, 328
mollicutes, 848, 852, 863
phytopathogenic spiroplasmas in,
912–13, 926–29
spiroplasma pathogenicity to, 929
- Insect vectors
of phytopathogenic spiroplasmas,
906–7
- Insecticide
Bacillus larvae, 571–77
Bacillus lentimorbus, 563–71
Bacillus popilliae, 563–71
Bacillus sphaericus, 592–96
Bacillus thuringiensis, 577–92
- Insertion sequence elements
Bacillus thuringiensis, 589
Enterococcus, 186
Lactococcus, 220
Leuconostoc, 298
mollicutes, 874
Streptococcus agalactiae, 136
Streptococcus pyogenes, 128–29
Intermedilysin, *Streptococcus*, 96
Internalins, *Listeria*, 420–30, 452
Interspecies hydrogen transfer,
Sporomusa, 998–99
Intestinal environment. *See also*
Gastrointestinal environment
Clostridiaceae, 659
Clostridium, 659
Clostridium perfringens, 713, 759
Enterococcus, 165
Gemella, 512
Kurthia, 519, 521–22
Intracellular invasion
Bacillus popilliae, 567
Listeria, 416–18
Mycoplasma, 878
Streptococcus agalactiae, 135
Streptococcus pneumoniae, 158–59
Streptococcus pyogenes, 123–24
Inulin metabolism
Carnobacterium, 380
Enterococcus, 176
Pediococcus, 247
Iridocyclitis, *Bacillus*, 615
Iron limitation, Cyanobacteria,
1090
Iron metabolism, *Prochlorococcus*,
1105
Iron precipitation, *Bacillus*, 531
Iron transport, *Enterococcus*, 183
Iron uptake, *Staphylococcus*, 49
Isocaproic acid, 733
Isolation
anaerobic cocci, 796–97
Bacillus, 532, 620–25
Bacillus larvae, 572
Bacillus lentimorbus, 563–65
Bacillus popilliae, 563–65
Bacillus thuringiensis, 578–80
Brochothrix, 487–88
Butyrivibrio, 1005
Carnobacterium, 376–78
Caryophanon, 647
Clostridiaceae, 659–63
Clostridium, 659–63
Clostridium difficile, 732
Clostridium perfringens, 700–1
of cocultures, 1045
Cyanobacteria, 1057–58, 1063
Cyanobacterial genes, 1083–85
Desulfotobacterium, 774–75
Desulfosporosinus, 780
Desulfotomaculum, 792
Enterococcus, 166
Erysipelothrix, 502–4
Eubacterium, 829
Filibacter, 645
Gemella, 513
Haloanaerobiales, 811–12
Heliobacteriaceae, 956–58
Kurthia, 523–24, 524–27
Lachnospira multipara, 1012
Lachnospira pectinoschiza, 1012
Lactobacillus, 345–49
Lactococcus, 208–10
Leuconostoc, 284–89
Listeria, 405–8
Marinococcus, 644
Megasphaera, 972
mollicutes, 845–48, 854
cell cocultivation, 850, 854–55
media for, 852–54
Pectinatus, 971–72
Pediococcus, 241–44
phytopathogenic spiroplasmas,
914–16
Planococcus, 641
Prochlorococcus, 1101–2
Roseburia, 1015
Selenomonas, 984–85
Sporolactobacillus, 632–33
Sporomusa, 991–93
Sporosarcina, 636–37
Staphylococcus, 5–10
from clinical specimens, 8–10
from food, 5–8
from water, 10
Streptococcus, 77–80
Syntrophomonadaceae, 1043–45
Tetragenococcus, 241–44
Veillonella, 1024–25
Weissella, 284–89
Zymophilus, 972–73
- J**
Japanese beetle. *See also* Insect
hosts
Bacillus, 563–71
Jonesia, 527
- K**
Kanamycin resistance
Enterococcus, 190
Gemella, 515
Kawasaki disease, *Streptococcus*,
90
Keratitis, *Bacillus*, 615
 α -Keto acid metabolism,
Enterococcus, 178
Kineococcus, 665
Klebsiella, 1086
Klebsiella pneumoniae, 298, 330,
967, 1026
Kurthia, 482, 519–27, 620
characteristics of, 526–27
habitats of, 521–23
isolation of, 523–24, 524–27
morphology of, 519, 524–25, 527
phylogenetic tree of, 521
phylogeny of, 520–21
preservation of, 524
Kurthia bessonii, 519, 522
Kurthia catenaforma, 519
Kurthia gibsonii, 519–22, 524–26
Kurthia sibirica, 519, 521, 523, 525
Kurthia variabilis, 519, 522
Kurthia zenkeri, 519
Kurthia zopfii, 519–26

L

- Lachnospira*, 1011–14
 cultivation of, 1013
 ecology of, 1014
 habitat of, 1012
 media for, 1008
 morphology, 1011–12
 phylogenetic tree of, 1004
 phylogeny of, 1012
 physiology of, 1013–14
 preservation of, 1013
- Lachnospira multipara*, 1011–14
 identification of, 1012–13
 isolation of, 1012
- Lachnospira pectinoschiza*, 1011–12, 1014
 identification of, 1013
 isolation of, 1012
- Lachnospiraceae, 1002–16
Butyrivibrio, 1002–11
Lachnospira, 1011–14
Roseburia, 1014–16
- Lactacin, *Lactobacillus*, 330, 369
- β-Lactam resistance
Bacillus, 619
Enterococcus, 170, 186, 189–91
Streptococcus, 98
- Lactate dehydrogenase
Pediococcus, 229
Staphylococcus, 23
- Lactate metabolism
Clostridium, 672
Desulfotobacterium, 772
Desulfosporosinus, 772
Desulfotomaculum, 787
Enterococcus, 175–76, 180
Leuconostoc, 298–99
Selenomonas, 982–83
Veillonella, 1026
- Lactate production
 anaerobic cocci, 799
Bacillus lentimorbus, 569–70
Bacillus popilliae, 569–70
Brochothrix, 483
Carnobacterium, 376
Clostridium, 672–73
Coprococcus, 804
Lactobacillus, 321, 344, 365
Lactococcus, 213–14, 221
Leuconostoc, 267, 273, 279–80, 289, 294–95
Oenococcus, 267, 273, 289, 294, 305
Pediococcus, 229–30, 244, 247–48
Sporolactobacillus, 632–33, 635
Tetragenococcus, 244, 247–48
Weissella, 267, 273, 289, 294
- Lactic acid bacteria
Carnobacterium, 320, 372–80
Enterococcus, 175–94
 human influences of, 330–33
Lactobacillus, 320–72
Lactococcus, 205–24
Leuconostoc, 267–305
Oenococcus, 267–305
Pediococcus, 229–56
 phylogenetic tree of, 321
Streptococcus, 76–98, 108–38, 149–71
Tetragenococcus, 229–56
Weissella, 267–305
- Lactic acidosis, *Lactobacillus*, 328, 334–35
- Lactobacillaceae
Lactobacillus, 320
Pediococcus, 320
 phylogenetic tree of, 321
- Lactobacillus*, 231, 234, 239–41, 243, 246, 249, 254–55, 276, 280, 284, 289–90, 303–4, 320–72, 482, 632, 741, 843, 872, 983, 1029
 applications of, 343–45
 bacteriophages of, 370–72
 characteristics of, 323, 356–60
 genetics of, 369–70
 habitats of, 321–43
 human influences of, 330–33
 identification of, 355–65
 key for, 360–62
 isolation of, 345–49
 morphology of, 320, 355–56, 372
 pathogenicity of, 334–35
 phylogenetic tree of, 321, 350–54
 phylogeny of, 349–55, 477
 physiology of, 365–67
 preservation of, 348–49
 species of, 322–23, 326, 334, 351–54
- Lactobacillus acetotolerans*, 342
Lactobacillus acidipiscis, 354–55
Lactobacillus acidophilus, 324, 327–33, 335–36, 338–39, 342, 344–45, 355–56, 364, 366–70, 485
- Lactobacillus agilis*, 328, 336
Lactobacillus algidus, 374
Lactobacillus alimentarius, 339, 343
Lactobacillus amylovorus, 328, 344, 356
Lactobacillus animalis, 355, 363
Lactobacillus aviarius, 328
Lactobacillus aviarius subsp. *araffinosus*, 328
Lactobacillus aviarius subsp. *aviarius*, 328
Lactobacillus bavaricus, 343–44
Lactobacillus bif fermentans, 340, 350
Lactobacillus bilgardii, 246
Lactobacillus brevis, 244, 246, 281, 324, 327–28, 333, 336–44, 350, 356, 365–66, 369, 371
Lactobacillus brevis simile, 341
Lactobacillus buchneri, 324, 336–42, 349–52, 365–66, 369
Lactobacillus bulgaricus, 299, 328, 333, 342, 344, 367–69
Lactobacillus carnis, 373
Lactobacillus casei, 229, 231, 276, 305, 324–25, 328, 332–34, 338–45, 349–52, 364, 366–67, 370–72
Lactobacillus casei subsp. *casei*, 324
Lactobacillus casei subsp. *pseudoplan tarum*, 337
- Lactobacillus casei* subsp.
rhannosus, 333
Lactobacillus catenaformis, 320
Lactobacillus cellobiosus, 324, 328, 333, 342
Lactobacillus coleohominis, 333
Lactobacillus collinoides, 246
Lactobacillus confusus, 267, 342
Lactobacillus coprophilus, 338
Lactobacillus coryniformis, 246, 324, 336, 338, 341, 350
Lactobacillus crispatus, 327–29, 333, 371
Lactobacillus cucumeris, 337
Lactobacillus curvatus, 255, 276–78, 293, 304, 324, 327, 336–39, 341, 343, 345, 355–56, 364, 374
Lactobacillus cypriacaei, 355
Lactobacillus delbrueckii, 320, 327, 332, 333, 338, 340, 342–44, 349–50, 352, 356, 363–65, 371–72
Lactobacillus delbrueckii subsp. *bulgaricus*, 332, 338–39, 355–56, 364, 370, 372
Lactobacillus delbrueckii subsp. *delbrueckii*, 344, 364
Lactobacillus delbrueckii subsp. *lactis*, 339, 344, 364, 370, 372
Lactobacillus desidiosus, 340
Lactobacillus divergens, 373, 378
Lactobacillus durianis, 355, 363
Lactobacillus equi, 328
Lactobacillus eurydice, 328
Lactobacillus farciminis, 336, 338–39, 343, 355, 363, 366
Lactobacillus fermentum, 236, 324, 327, 333, 335–36, 342, 344, 365–66, 371
Lactobacillus fornicalis, 333
Lactobacillus fructivorans, 340, 342
Lactobacillus fructosus, 267
Lactobacillus fuchuensis, 354, 374
Lactobacillus gallinarum, 356
Lactobacillus gasseri, 327, 333, 356, 371–72
Lactobacillus graminis, 324, 338, 364
Lactobacillus halotolerans, 267, 343
Lactobacillus hamsteri, 324
Lactobacillus helveticus, 279, 298, 332, 339, 344–45, 356, 364, 367, 370
Lactobacillus hilgardii, 338, 340, 371
Lactobacillus homohiochii, 324, 338, 352
Lactobacillus iners, 333
Lactobacillus jensenii, 324, 333, 371
Lactobacillus johnsonii, 328, 330–31, 356, 361–62, 372
Lactobacillus kandleri, 267
Lactobacillus kefirifaciens, 339
Lactobacillus kefirii, 339, 356
Lactobacillus kimchii, 337, 355, 363
Lactobacillus lactis, 333, 336, 339, 342, 344–45, 366–67, 864
Lactobacillus lactis var. *maltigenes*, 369
Lactobacillus leichmanii, 333, 343, 366–67

- Lactobacillus lindneri*, 341
Lactobacillus mali, 246, 340–41, 366
Lactobacillus maltaromicus, 343, 373
Lactobacillus manihotivorans, 361–62
Lactobacillus mindensis, 355, 363
Lactobacillus minor, 267
Lactobacillus murinus, 324, 363
Lactobacillus nagelii, 354
Lactobacillus oris, 267, 324, 333
Lactobacillus panis, 327, 364
Lactobacillus pantheris, 327
Lactobacillus paracasei, 229, 246, 324–25, 327, 333–37, 352, 363–64
Lactobacillus paralimentarius, 337, 355, 363
Lactobacillus parapantarum, 352, 355, 363–64
Lactobacillus pastorianum, 342
Lactobacillus pentosaceus, 366
Lactobacillus pentosus, 324, 352, 363–66
Lactobacillus perolens, 231, 350
Lactobacillus piscicola, 373
Lactobacillus plantarum, 281–83, 324, 327, 331–45, 349–50, 352–53, 363–66, 369–72, 375, 634
Lactobacillus plantarum subsp. *rudensis*, 340
Lactobacillus pontis, 327, 363–64
Lactobacillus psittaci, 320
Lactobacillus reuteri, 327–28, 330, 332–33, 336, 349, 352–53, 355–56, 363, 369
Lactobacillus rhamnosus, 324–25, 327, 333–35, 344, 352, 364, 1028–29
Lactobacillus ruminis, 327, 333
Lactobacillus sakei, 255, 276–78, 293, 304, 324, 327, 336–37, 339, 343, 345, 350, 352, 354–56, 364–66, 374
Lactobacillus salivarius, 324, 327–28, 333, 335, 344–45, 349–50, 354–55, 365, 485
Lactobacillus salivarius subsp. *salivarius*, 330
Lactobacillus sanfranciscensis, 267, 338, 352
Lactobacillus sanfrancisco, 344
Lactobacillus sharpeae, 336
Lactobacillus suebicus, 267, 341, 366
Lactobacillus trichodes, 340
Lactobacillus vaccinostercus, 267, 336, 355, 363
Lactobacillus vaginalis, 333
Lactobacillus viridescens, 267, 328, 338, 343, 345, 366
Lactobacillus vitulinus, 320
Lactobacillus xylosus, 324
Lactobacillus yamanashiensis, 341
Lactobacillus zeae, 352
Lactocidin, *Lactobacillus*, 369
Lactocin B, *Lactobacillus*, 330
Lactocin, *Lactobacillus*, 369
Lactococcus, 81, 205–24, 229, 249, 255, 279, 296, 301, 304
application of, 212–14
genetics of, 222–23
habitats of, 205–8
identification of, 210–12
isolation of, 208–10
pathogenicity of, 224
phylogenetic tree of, 213, 321
plasmids of, 220–21
species characteristics of, 207–8, 212
taxonomy of, 205
Lactococcus cremoris, 366
Lactococcus delbrueckii subsp. *bulgaricus*, 210
Lactococcus garviae, 164, 205–6, 208, 224
Lactococcus lactis, 205–6, 211–12, 220–21, 253, 255, 286–87, 295
Lactococcus lactis biovar *diacetyllactis*, 205–6, 210–12, 214, 286
Lactococcus lactis subsp. *cremoris*, 206, 208, 210, 212, 214, 218, 221
Lactococcus lactis subsp. *lactis*, 205–6, 210–12, 214, 216, 218, 220–23, 375
Lactococcus piscium, 205–6, 224
Lactococcus plantarum, 205, 253
Lactococcus raffinolactis, 205–6
Lactose metabolism
Carnobacterium, 380
Enterococcus, 176
Gemella, 514
Lactobacillus, 366–67
Lactococcus, 213–14, 221
Pediococcus, 247
Staphylococcus, 20–21
Lamb hosts. *See* *Ovine* hosts
Larvae. *See* *Insect* hosts
Leafhoppers
feeding behavior of, 926–27
movement of, 929
phytopathogenic spiroplasmas in, 912–13, 927–29, 936
Leucocins, *Leuconostoc*, 299–301
Leuconostoc, 210–11, 229, 234, 240–41, 243, 246, 249, 255, 267–305, 336, 348, 364, 366, 375
applications of, 303–5
characteristics of, 268, 274–75
cultivation and preservation of, 293–94
ecology of, 302
genetics of, 296–302
habitats of, 273–84
identification of, 289–93
isolation of, 284–89
morphology of, 289
phylogenetic tree of, 269, 321, 350
phylogeny of, 267–71
physiology of, 267, 294–96
species of, 272, 289
taxonomy of, 271–73
Leuconostoc amelibiosum, 272, 276, 278–79
Leuconostoc argentinum, 269, 272, 302
Leuconostoc carnosum, 269, 272, 275–78, 289, 291–93, 300, 302, 304
Leuconostoc citreum, 269, 272, 276, 278–81, 283, 289, 292–93, 296, 303–4
Leuconostoc fallax, 269, 272, 292–93, 295
Leuconostoc gasicomitatum, 269, 271–72, 291, 302
Leuconostoc gelidum, 269, 272, 275–77, 281, 289, 291, 293, 296, 300, 302, 304, 337
Leuconostoc kimchii, 269, 272, 281, 337
Leuconostoc lactis, 269, 272, 279–80, 290, 293–94, 297–300, 303, 305
Leuconostoc mesenteroides, 246, 269, 271–72, 276, 279–82, 288, 290–93, 295–303, 305, 337, 340, 371
Leuconostoc mesenteroides subsp. *cremoris*, 269, 279–80, 293–98, 304
Leuconostoc mesenteroides subsp. *dextranicum*, 269, 279, 281–82, 293, 295–98, 304
Leuconostoc mesenteroides subsp. *mesenteroides*, 269, 275, 277–84, 291–96, 302, 305
Leuconostoc oenos, 267, 269, 271–73, 344. *See also* *Oenococcus oeni*
Leuconostoc paramesenteroides, 267, 269, 271–72
Leuconostoc pseudomesenteroides, 271–72, 283, 292–93, 296, 303–5
Leuconostoc sensu stricto, 269, 271–72, 289–90
Light
Cyanobacteria, 1056, 1062, 1086–180
Heliobacteriaceae absorption of, 951–52, 959
Prochlorococcus adaptation to, 1104
Lincomycin resistance/sensitivity
Enterococcus, 189, 192
Gemella, 515
Lincosamide resistance,
Enterococcus, 192
Linezolid resistance, *Enterococcus*, 193–94
Lipids, phytopathogenic
spiroplasmas, 920
Lipopolysaccharide composition
Clostridiaceae, 664
Pectinatus, 967–68
Veillonella, 1027
Lipoteichoic acid (LTA), 39–42
alanine esterification and
virulence, 41–42
biological functions of, 40–41
Listeria, 438, 440
properties of, 40
Streptococcus pneumoniae, 149, 155–56

Listeria, 404–56, 482, 493, 520, 527, 620, 669
 biology of infection of, 415–18
 characteristics of, 406
 classification of, 404–5
 comparative genetics of, 453–55
 concluding remarks on, 455–56
 disease from, 408–11
 epidemiology of, 408–10
 gene regulation in, 446–50
 genetics of, 411–15
 isolation and identification of, 405–8
 morphology of, 404
 pathogenicity of, 407–8
 phylogenetic tree of, 478
 physiology of, 408, 438–42
 stress resistance of, 445–46
 virulence factors of, 419–46
 ActA, 435–38
 internalins, 420–30
 listeriolysin, 430–33
 phospholipases and metalloproteases, 433–35
Listeria grayi, 405, 407, 453
Listeria innocua, 404–7, 424–25, 436, 444, 452–54, 478
Listeria ivanovii, 404–7, 430, 433, 478
Listeria ivanovii subsp. *ivanovii*, 404
Listeria ivanovii subsp. *londoniensis*, 404–5
Listeria monocytogenes, 224, 330, 338, 376, 404–56, 478, 484, 493, 503, 527, 1031
Listeria seeligeri, 405, 407, 453, 478
Listeria welshimeri, 405, 407, 453, 478
 Listeriolysin
 cholesterol interaction with, 431
 Listeria, 430–33
 pH dependence of, 431–32
 Listeriosis, *Listeria*, 404, 408–11, 415–18, 450–53
 Ljungdahl-Wood pathway,
 Clostridium, 672
 LL adapted ecotypes. *See* Low light adapted ecotypes
 Lotic environment, 1034
 Veillonella, 1022
 Low light (LL) adapted ecotypes,
 1106–7
 Prochlorococcus, 1100, 1102, 1104
 LPP group, 1067–68
 LTA. *See* Lipoteichoic acid
 Lungs. *See also* Respiratory tract
 mollicutes, 876, 878, 887
 Sporosarcina, 636
 Streptococcus pneumoniae, 159
 Lyngbya, 1068, 1076
 Lysine production, *Bacillus*, 534
 Lysogeny
 Bacillus sphaericus, 595
 Lactobacillus, 371
 Lysostaphin resistance/sensitivity
 Macrocooccus, 12
 Staphylococcus, 11
 Lysylphosphatidylglycerol,
 Staphylococcus, 45

M

M protein

Streptococcus dysgalactiae, 137–38
Streptococcus pyogenes, 110–13, 115–18, 120, 122, 124, 129
Macrocooccus, 5–61
 ecology of, 59
 identification of, 11–17
 phylogenetic tree of, 11–12
 phylogeny of, 11
 physiology of, 17–46
 species of, 6, 13, 16–17
Macrocooccus bovicus, 11, 13
Macrocooccus carouselicus, 11, 13
Macrocooccus caseolyticus, 5, 11, 13, 23, 26, 61
Macrocooccus equiperficus, 11, 13
 Macrofibers, *Bacillus*, 543
 Macrolide resistance/sensitivity
 Gemella, 515
 Listeria, 408
 mollicutes, 878
 Streptococcus pneumoniae, 155
 Malate metabolism
 Enterococcus, 175, 178
 Lactobacillus, 340–41, 344
 Leuconostoc, 294
 Oenococcus, 294, 305
 Malonate fermentation, *Sporomusa*, 998
 Maltose metabolism
 Bacillus lentimorbus, 567
 Bacillus popilliae, 567
 Brochothrix, 480
 Carnobacterium, 380
 Enterococcus, 176
 Erysipelothrix, 500
 Gemella, 514
 Pediococcus, 247
 Sporolactobacillus, 635
 Staphylococcus, 21–22
 Manganese oxidation/reduction
 Bacillus, 531, 533
 Mannitol metabolism
 Bacillus larvae, 573
 Brochothrix, 480
 Carnobacterium, 380
 Enterococcus, 176–77
 Gemella, 514–15
 Pediococcus, 247
 Staphylococcus, 21–22
 Mannose metabolism
 Bacillus larvae, 574
 Bacillus lentimorbus, 567
 Bacillus popilliae, 567
 Brochothrix, 480
 Carnobacterium, 380
 Enterococcus, 176
 Pediococcus, 247
 Sporolactobacillus, 635
 Manure. *See* Feces environment
 Marine environment
 Carnobacterium, 375–76
 Cyanobacteria in, 1056–57, 1060–61, 1076
 Heliobacteriaceae in, 956
 Marinococcus, 644
 Planococcus, 641

Prochlorococcus in, 1099–101
Sporomusa in, 993
Staphylococcus, 59
Marinococcus, 520, 644
 habitats of, 644
 properties of, 642, 644
Marinococcus albus, 644
Marinococcus hispanicus, 644
Mastigocladus laminosus, 1076
 Mastitis, *Staphylococcus*, 59–60
 Measles, *Gemella*, 511, 516
 Meat
 Bacillus cereus, 615
 Brochothrix, 477, 484–86
 Carnobacterium, 373–74, 377
 Clostridium perfringens, 711
 Erysipelothrix, 492
 Kurthia, 519, 521–22
 Lactobacillus, 286, 338–40, 343, 346–47
 Leuconostoc, 273–78, 286, 302–4
 Listeria, 409
 Pediococcus, 240, 255
 Petrigenococcus, 240
 Weissella, 278, 302
 Media
 Bacillus, 622–25
 Butyrivibrio, 1008
 Caryophanon, 647
 Clostridiaceae, 661–62
 Clostridium, 661–62
 Cyanobacteria, 1058–62
 Desulfotobacterium, 775
 Desulfosporosinus, 780
 Desulfotomaculum, 790–91
 Haloanaerobiales, 816–17
 Heliobacteriaceae, 957–58
 Lachnospira, 1008
 mollicutes, 852–54
 Prochlorococcus, 1100
 Roseburia, 1008
 Selenomonas, 984–85
 Sporolactobacillus, 632–34
 Sporomusa, 995–96
 Sporosarcina, 636–38
 Syntrophomonadaceae, 1044
 Mediastinitis, *Staphylococcus*, 60
Megasphaera, 664, 965–78, 982, 991, 1022–23
 characteristics of, 968, 978
 cultivation of, 972
 detection of, 972
 differentiation of, 968–69
 habitat of, 969–70
 identification of, 975–76
 isolation of, 972
 molecular biological methods for, 976
 morphology of, 975–76
 phylogeny of, 966
 physiology of, 978
 preservation of, 976
 serological characteristics of, 975–76
 taxonomy of, 968–69
Megasphaera cerevisiae, 965–66, 968–69, 971–72, 974–76, 978
Megasphaera elsdenii, 669, 825, 965–66, 968–69, 975, 978, 987

- Melissococcus*, phylogenetic tree of, 321
- Membranes, phytopathogenic spiroplasmas, 920
- Menaquinone pattern
- Bacillus*, 535, 543
 - Bacillus larvae*, 573
 - Bacillus popilliae*, 565
 - Brochothrix*, 479
 - Clostridium*, 671
 - Desulfobacterium*, 772
 - Desulfosporosinus*, 772
 - Filibacter*, 645
 - Kurthia*, 525
 - Lactococcus*, 212
 - Planococcus*, 643
 - Sporolactobacillus*, 634
 - Sporosarcina*, 640
 - Staphylococcus*, 5, 11, 26–27
- Meningitis
- Bacillus*, 617–19
 - Bacillus anthracis*, 611–12
 - Enterococcus*, 169
 - Leuconostoc*, 303
 - Listeria*, 404, 411
 - Pediococcus*, 254
 - Staphylococcus*, 59
 - Streptococcus*, 94, 97
 - Streptococcus agalactiae*, 132–33
 - Streptococcus pneumoniae*, 153–55, 159–60
- Mesentericin, *Leuconostoc*, 300–1
- Mesoplasma*, 836–37, 843, 847, 851–52, 854–55, 910–11
- Mesoplasma lactucae*, 868
- Metabolic communication, in human oral flora, 1028–29
- Metabolism
- Bacillus larvae*, 575–76
 - Bacillus lentimorbus*, 569–70
 - Bacillus popilliae*, 569–70
 - Brochothrix*, 483–84
 - Clostridiaceae, 672–73
 - Clostridium*, 672–73
 - Lactobacillus*, 365
 - Leuconostoc*, 294–95
 - mollicutes, 861–62
 - Oenococcus*, 294–95
 - Weissella*, 294–95
- Metalloprotease, *Listeria*, 433–35
- Methane production
- Cyanobacteria, 1075
- Methanobacterium thermautotrophicum*, 1044
- Methanogenesis, *Veillonella*, 1031
- Methanogenic environment, Syntrophomonadaceae, 1043
- Methanogens
- culturing of, 1044–45
 - Sporomusa* and, 994, 999
 - Syntrophomonadaceae and, 1041, 1043
- Methanol fermentation, *Sporomusa*, 998
- Methanol metabolism, *Bacillus*, 534
- Methanosarcina*, 665
- Methanosarcina barkeri*, 1048
- Methanospirillum hungatei*, 994, 1044
- Methicillin sensitivity, *Bacillus*, 618
- Methyl-malonyl-CoA decarboxylase, *Veillonella*, 1026
- Metronidazole resistance/sensitivity anaerobic cocci, 805
- Clostridium difficile*, 741
 - Clostridium perfringens*, 717
 - Microbacterium lacticum*, 477
- Microbacterium*, phylogeny of, 477
- Microbacterium thermosphactum*, 477
- Microbial mats. *See also* Cyanobacterial mats
- Heliobacteriaceae in, 956, 962
- Micrococcus*, 5, 643
- Microcoleus*, 1068
- Microcoleus chthonoplastes*, 1076–78
- Microcystis firma*, 1090
- Micromonas*, 795–96, 798
- Micromonas micros*, 795, 803
- Middle wall protein (MWP), *Bacillus*, 542
- Milk. *See* Dairy environment; Food fermentation
- Milky disease, *Bacillus*, 563, 565–66, 568
- Minocycline resistance, *Enterococcus*, 186, 193
- Mixed infections, *Bacillus*, 616–17
- Mixotrophy, Cyanobacteria, 1056
- M-like proteins
- Streptococcus dysgalactiae*, 137
 - Streptococcus pyogenes*, 117–18
- Mobiluncus*, 333
- Mogibacterium*, 823, 829
- Mogibacterium diversum*, 829
- Mogibacterium neglectum*, 829
- Mogibacterium timidum*, 823, 825, 828, 831
- Mogibacterium vescum*, 829
- Molecular genetics of Cyanobacteria, 1074–91
- for phytopathogenic spiroplasmas, 925–26
- Mollicutes
- Acholeplasmataceae, 836–37
 - conserved genes of, 845–47
 - Entomoplasmataceae, 836–37
 - epidemiology of, 857
 - adhesion to host cells, 882
 - prevention, 867–68, 876
 - transmission, 865–67, 875, 881
 - evolution of, 910–11
 - genetics of, 837, 856–65
 - DNA replication and repair, 870–71
 - extrachromosomal elements, 856–57, 864
 - genome, 837, 856–57
 - genome sequencing, 864
 - transcription and translation, 846, 867, 871, 888
 - habitats and ecology, 848
 - cell cultures, 849, 854, 858, 878, 881–82, 889
 - host and tissue specificity, 849
 - uncultured, 852
- identification of, 847, 855
- cultural properties of, 855
 - polymerase chain reaction, 845, 857
 - restriction endonuclease analysis, 856
 - serology, 855–56
 - isolation of, 849, 873
 - morphology of, 831, 836, 838, 845
 - motility and cytoskeletal elements, 836
- Mycoplasmataceae, 837
- pathogenicity of, 836, 851, 878, 882–83
- adhesion, 882
 - antigenic variation, 884–85
 - disease manifestations, 878
 - immune system modulation, 887
 - molecular basis of, 879
 - phylogenetic tree of, 843, 847
 - phylogeny of, 843, 872
 - physiology, 859, 882
 - cell membrane, 859–62, 864
 - metabolism, 861–62
 - preservation of, 859
 - spiroplasma position among, 910–11
- Spiroplasmataceae, 837
- taxonomy of, 843–47
 - cell division of, 841–42
 - intraspecies genetic heterogeneity, 846
 - metabolic and phenotypic markers, 846
 - taxonomy and phylogeny, 872
- Molybdopterin cofactor, *Staphylococcus*, 28–30
- Moorella*, 672, 1041
- Moorella glycerini*, 666, 1042
- Moorella thermacetica*, 658, 666, 669
- Moorella thermautotrophica*, 666
- Moorella thermoautotrophica*, 1042
- Morphology
- Bacillus*, 530, 620
 - Bacillus lentimorbus*, 566
 - Bacillus popilliae*, 566
 - Bacillus thuringiensis*, 577, 580
 - Brochothrix*, 477, 479
 - Butyrivibrio*, 1002
 - Butyrivibrio crossotus*, 1007
 - Butyrivibrio fibrisolvens*, 1005–6
 - Caryophanon*, 648
 - Clostridiaceae, 664–70
 - Clostridium*, 664–70, 679–80
 - Desulfobacterium*, 772–73, 775–76
 - Desulfosporosinus*, 772–73, 781–83
 - Desulfotomaculum*, 788
 - Erysipelothrix*, 492–93, 498–502
 - Filibacter*, 645
 - Gemella*, 514
 - Haloanaerobiales, 810–11
 - Heliobacteriaceae, 953–56, 959
 - intergeneric coaggregations in oral cavity, 1033
 - Kurthia*, 519, 524–25, 527
 - Lachnospira*, 1011–12
 - Lachnospira multipara*, 1012–13

Lachnospira pectinoschiza, 1013
Lactobacillus, 320, 355–56, 372
Lactococcus, 210, 217
Listeria, 404
Macrococcus, 12
Megasphaera, 975–76
 mollicutes, 831
Pectinatus, 973
Pediococcus, 233–34
 phytopathogenic spiroplasmas, 905–8, 914–15
Planococcus, 643
Prochlorococcus, 1099
Roseburia, 1014–15
Selenomonas, 985
Sporolactobacillus, 633–34
Sporomusa, 994, 996
Sporosarcina, 635–36, 638
Staphylococcus, 11
Tetragenococcus, 233–34
Veillonella, 1022–23, 1025–26
Weissella, 272
Zymophilus, 976
 Mosquito. *See also* Insect hosts
Bacillus sphaericus, 592–96
 Motility
Bacillus, 622
Bacillus larvae, 573
Butyrivibrio crossotus, 1007
Butyrivibrio fibrisolvens, 1005–6
Caryophanon, 648
Clostridium, 679
 Cyanobacteria, 1056
Desulfibacterium, 772
Desulfosporosinus, 772, 781
 Heliobacteriaceae, 959
Kurthia, 525
Lachnospira multipara, 1012–13
Lachnospira pectinoschiza, 1013
Listeria, 404, 417–19
 mollicutes, 836
Pectinatus, 973
 phytopathogenic spiroplasmas, 908
Planococcus, 641
Roseburia, 1014–16
Selenomonas, 985
Sporolactobacillus, 632, 634
Sporomusa, 996
Sporosarcina, 638
 Mouth. *See* Human oral flora
 Mucous membranes
Gemella, 512
 mollicutes, 842, 849, 866, 875
Staphylococcus, 57
Streptococcus, 77
Streptococcus agalactiae, 134
 Multiple fission, of Pleurocapsales, 1053, 1066–67
 MWP. *See* Middle wall protein
Mycoplasma, 333, 836, 843, 845, 847–48, 850, 853, 861, 863–64, 870, 872, 878–79, 910–11, 918
 phylogenetic tree of, 843
Mycoplasma agalactiae, 860–61, 885, 920, 928
Mycoplasma agassizi, 854
Mycoplasma alvi, 840
Mycoplasma arginini, 849

Mycoplasma arthritidis, 864, 873, 882, 884, 888–89
Mycoplasma bovigenitalium, 861
Mycoplasma bovis, 861, 884–86
Mycoplasma capricolum, 842, 857, 868–69, 871–72
Mycoplasma cavipharyngis, 848
Mycoplasma dispar, 887
Mycoplasma fastidiosum, 848
Mycoplasma fermentans, 849, 880
Mycoplasma gallisepticum, 838, 840, 848, 863, 866, 884
Mycoplasma genitalium, 839–40, 848, 879
Mycoplasma hominis, 841, 848, 879
Mycoplasma hyopneumoniae, 883
Mycoplasma hyorhinis, 849, 854, 860, 862, 870, 881, 885
Mycoplasma mobile, 836, 838, 840
Mycoplasma mycoides, 847, 910, 921
Mycoplasma mycoides subsp. *mycoides*, 842, 846, 848, 863–65, 874, 879
Mycoplasma orale, 849–50, 870
Mycoplasma penetrans, 848, 864, 867, 878, 880–81, 883, 888
Mycoplasma pirum, 850, 883
Mycoplasma pneumoniae, 836, 838–40, 848, 857, 866, 868, 875
Mycoplasma pulmonis, 838, 840
Mycoplasma ravigulmonis, 848
Mycoplasma salivarium, 850, 875
Mycoplasma synoviae, 848
Mycoplasma testudinis, 854
 Mycoplasmataceae
Mycoplasma, 836–37
Ureaplasma, 836–37, 842–43, 847, 855
 Myeloma, *Leuconostoc*, 303
 Myocarditis, *Staphylococcus*, 59
 Myosin, *Listeria*, 425–26
Myxosarcina, 1066–67

N

Nalidixic acid resistance,
Brochothrix, 480
Natroniella acetigena, 810, 812, 815–19
Natrononicola, 654
Natrononicola histidinovorans, 672
 Necrolysis, *Staphylococcus*, 59
Neisseria, 511, 1030, 1032
Neisseria haemolysins, 511
Neisseria subflava, 1028
 Neomycin resistance, *Gemella*, 515
 Neonatal infection, *Listeria*, 404, 408
 Neuraminidase, *Erysipelothrix*, 497
 Neurotoxins
 action of, 686–89
Clostridium, 679–93
 genetics of, 680–82
 structure of, 682–86
 Nichrome steel wire metal, 1031–32
 Nisin, *Lactococcus*, 221–23
 Nitrate reduction
Bacillus larvae, 573
Staphylococcus, 27–30

Nitrate utilization
Prochlorococcus, 1104, 1106–7
Veillonella, 1027
 Nitrite reduction
Gemella, 514
Staphylococcus, 27–30
 Nitrite utilization, *Prochlorococcus*, 1104, 1106–7
 Nitrofuran sensitivity,
Staphylococcus, 11
 Nitrogen fixation
Bacillus, 531
 Clostridiaceae, 659
Clostridium, 659
 Cyanobacteria, 1056, 1076–78, 1086–87
 Heliobacteriaceae, 961–62
 Nitrogen metabolism,
Prochlorococcus, 1104–5
Nodularia, 1069–70
Nostoc, 1070, 1082, 1090–91
Nostoc commune, 1090–91
Nostoc muscorum, 1077
Nostoc sp. PCC 7524, 1079
Nostoc sp. PCC 8009, 1085
 Nostocales, 1054
 genera of, 1068–70
 key to, 1069
 Novobiocin resistance/sensitivity
Brochothrix, 480
Erysipelothrix, 497
Gemella, 515
Planococcus, 644
 Nutritional requirements
Bacillus lentimorbus, 567
Bacillus popilliae, 567
Brochothrix, 483–84
Lactobacillus, 321, 365, 370
Leuconostoc, 295
Listeria, 408
Oenococcus, 295
Streptococcus, 77–78
Weissella, 295

O

Oenococcus, 239, 267–305
 applications of, 305
 characteristics of, 274–75
 cultivation and preservation of, 293–94
 genetics of, 296–302
 habitats of, 273–84
 identification of, 289–93
 morphology of, 289
 phylogenetic tree of, 269
 phylogeny of, 267–71
 physiology of, 267, 294–96
 taxonomy of, 271–73
Oenococcus oeni, 246, 267, 269, 271–73, 281–82, 287–92, 294–97, 301–2, 305, 371
Oerskovia, 527
 Oil environment,
Desulfotomaculum, 789
 Oligosaccharides, *Streptococcus agalactiae*, 130
Olsenella, 823

- Oral cavity
 anaerobic cocci, 795
Bacillus thuringiensis, 582
Gemella, 512, 516
Lactobacillus, 321–25, 346
Streptococcus, 77–78, 86, 90
Orenia marismortui, 810, 815–16, 818
- Organic acid decarboxylation,
Sporomusa, 998
- Oscillatoria*, 1067–68, 1076–77
Oscillatoria limnetica, 1076–78
Oscillatoria limosa, 1078
Oscillatoria terebriformis, 1076, 1078
- Oscillatoriales, 1054
 genera and groups of, 1067–68
 key to, 1067–68
- Osteoarthritis
Staphylococcus, 60
Streptococcus dysgalactiae, 137
- Osteomyelitis
Bacillus, 618
Staphylococcus, 59–60
Streptococcus dysgalactiae, 137
- Otitis media
 anaerobic cocci, 795
Streptococcus pneumoniae, 155
- Outer wall protein (OWP), *Bacillus*, 542
- Ovine hosts. *See also* Ruminant hosts
Clostridium perfringens, 714, 717–24, 726–27
Desulfotomaculum, 792
Erysipelothrix, 494
 mollicutes, 849
- OWP. *See* Outer wall protein
- Oxacillin resistance, *Brochothrix*, 480
- Oxalophagus oxalicus*, 658
- Oxidative damage, *Mycoplasma*, 879
- Oxidative pentose phosphate cycle
 Cyanobacteria, 1089
Staphylococcus, 24–25
- Oxidative phosphorylation,
Enterococcus, 181
- Oxobacter*, 654, 658
Oxobacter pfennigii, 658
- Oxygen metabolism, *Enterococcus*, 183
- Oxygen tolerance, *Sporomusa*, 999
- Oxygenic photosynthesis. *See* Photosynthesis
- P**
- Paenibacillus*, 520
Paenibacillus durus, 658
- Panophthalmitis, *Bacillus*, 615–16
- Paralactobacillus*, 320
 phylogenetic tree of, 350
- Paralactobacillus selangorensis*, 231
- Pathogenicity
Bacillus, 619
Bacillus larvae, 574–75
Bacillus sphaericus, 592
Bacillus thuringiensis, 583–84
Brochothrix, 477
Clostridium difficile, 730–42
Clostridium perfringens, 715, 760–62
Enterococcus, 169–70
Erysipelothrix, 497–98
 evolution of, 910–11
Gemella, 515–16
Lactobacillus, 334–35
Lactococcus, 224
Listeria, 407–8
 mollicutes, 836, 851, 878, 882–83
 spiroplasma, 929
Staphylococcus, 52–53, 59–61
Streptococcus, 95–96
Streptococcus agalactiae, 133
Streptococcus dysgalactiae, 137–38
Streptococcus pneumoniae, 159–60
Streptococcus pyogenes, 114
- Pathogenicity islet, of toxins A and B, 733
- Pathogenicity tests, for
 phytopathogenic
 spiroplasmas, 917
- PDH. *See* Pyruvate dehydrogenase
- Peat bogs, Cyanobacteria, 1057
- Pectin degradation, *Lachnospira*, 1013–14
- Pectinatus*, 965–78, 969
 characteristics of, 968, 976–78
 cultivation of, 971–72
 detection of, 971–72
 differentiation of, 966–67
 habitat of, 969–70
 identification of, 973–75, 985–86
 isolation of, 971–72
 metabolism of, 977–78
 molecular biological methods for, 974–75
 morphology of, 973
 phylogeny of, 965–66
 physiology of, 976–78
 preservation of, 976
 serological characteristics of, 974
 taxonomy of, 966–68
- Pectinatus cerevisiophilus*, 965–67, 969, 973, 974–77, 982, 985, 987
- Pectinatus frisingensis*, 965–67, 969, 973–78
- Pediocins, *Pediococcus*, 249–53
Pediococcus, 211, 229–56, 267, 276, 284, 303, 320, 336, 349–50
 applications of, 238, 254–56
 characteristics of, 230, 235, 245–46
 epidemiology and disease of, 253–54
 genetics of, 248–53
 habitats of, 234–41
 identification of, 244–46
 isolation of, 241–44
 morphology of, 233–34
 phylogenetic tree of, 321, 350
 phylogeny of, 231–33
 physiology of, 247–49
 preservation of, 246–47
 species of, 234, 245–46
 taxonomy of, 233–34
- Pediococcus acidilactici*, 229, 231, 233–34, 236, 239–40, 243–44, 246–47, 249, 251, 253–56, 344
Pediococcus cerevisiae, 234, 240, 280, 337
Pediococcus cerevisiae subsp. *mevalovorius*, 234
Pediococcus citrovorum, 234
Pediococcus claussenii, 229–30, 233–34, 236, 239, 244, 247
Pediococcus damnosus, 229–34, 236, 239, 243–44, 247–48, 341
Pediococcus dextrinicus, 229, 231, 233, 236, 239, 244, 247
Pediococcus halophilus, 229, 231, 233, 243, 249. *See also* *Tetragenococcus halophilus*
Pediococcus hennebergi, 234
Pediococcus inopinatus, 229, 231, 233–34, 236, 239, 247
Pediococcus lindneri, 234
Pediococcus mevalovorius, 234
Pediococcus odoris mellisimilis, 234
Pediococcus parvulus, 229, 231, 233–34, 236, 239, 246–49
Pediococcus pentosaceus, 229, 231, 233–34, 236, 239–40, 243–44, 246–49, 251, 254–56, 280–81
Pediococcus pentosaceus subsp. *intermedius*, 229
Pediococcus pentosaceus subsp. *pentosaceus*, 229
Pediococcus pernicius, 234
Pediococcus sarcinaeformis, 234
Pediococcus urinae-equi, 229, 231, 233, 247, 254
Pediococcus viscosus, 234
Pelospora, 1041, 1045–46
Pelospora glutarica, 1041–43, 1045
- Penicillin resistance
Bacillus, 619
Bacillus thuringiensis, 578
Enterococcus, 186, 190–91
Streptococcus pneumoniae, 149, 153–54
- Penicillin sensitivity
 anaerobic cocci, 805
Bacillus, 618–19, 621
Bacillus anthracis, 612
Clostridium perfringens, 717, 760
Enterococcus, 170, 189
Erysipelothrix, 497
Gemella, 511, 515
Listeria, 408
Pediococcus, 254
Planococcus, 644
Streptococcus, 97
- Pentose phosphate pathway
Bacillus larvae, 576
Bacillus lentimorbus, 570
Bacillus popilliae, 570
- Peptidases, *Lactobacillus*, 367
- Peptidoglycan
 antibiotics influencing synthesis of, 36–38
Bacillus, 542, 552
Bacillus larvae, 573
Bacillus lentimorbus, 565
 biological activity of, 36
 biosynthesis of, 30–35
Butyrivibrio fibrisolvens, 1006
Carnobacterium, 378

- Caryophanon*, 648
 Clostridiaceae, 664
Desulfotobacterium, 771
Desulfosporosinus, 771
Erysipelothrix, 493, 498
Eubacterium, 825
Kurthia, 520, 525
Lachnospira multipara, 1013
Lactobacillus, 350–52, 356
Listeria, 438–42
Megasphaera, 969
Pectinatus, 967
Staphylococcus, 12–13, 30–36, 40
Streptococcus pneumoniae, 149
Veillonella, 1027
Weissella, 290
- Peptococcaceae
Coprococcus, 795
Dendrosporobacter, 664
Desulfotobacterium, 771
Desulfosporosinus, 771
Peptococcus, 795
Peptostreptococcus, 795
Ruminococcus, 795
Sarcina, 795
Peptococcus, 795, 798
Peptococcus asaccharolyticus, 800
Peptococcus harei, 803
Peptococcus indolicus, 800
Peptococcus ivorii, 803
Peptococcus lacrimalis, 800, 803
Peptococcus niger, 795, 798, 803, 825
Peptoniphilus, 795–96, 798
Peptoniphilus asaccharolyticus, 795, 800
Peptoniphilus hydrogenalis, 800
Peptostreptococcus, 333, 795–96, 798, 1031
Peptostreptococcus anaerobius, 732, 795, 798, 803, 1030
Peptostreptococcus heliotrinreducens, 795, 798
Peptostreptococcus morbillorum, 511
Peptostreptococcus productus, 804
- Perfringolysin O
Clostridium perfringens, 699–700, 702, 761, 764–65
 structure-function relationship, 764–65
- Pericarditis
Bacillus, 616
Staphylococcus, 59
- Periodontal disease
Eubacterium, 831
Selenomonas, 982
Veillonella, 1028, 1030
- Peritonitis
Enterococcus, 169
Leuconostoc, 303
Staphylococcus, 60
Streptococcus, 94
- Permeaplasts, 1082
- PFL. *See* Pyruvate format lyase
- pH tolerance
Brochothrix, 483–84
Clostridium, 670–72
Erysipelothrix, 492
Listeria, 408
- Phage replication forms (RF), 921, 924–25
- Phagocytosis
Bacillus larvae, 574
Bacillus popilliae, 567
Listeria, 429
 mollicutes, 879
Streptococcus agalactiae, 135
Streptococcus dysgalactiae, 138
- Pharyngitis
Streptococcus, 85, 94
Streptococcus pyogenes, 111–12
- Phenotypic properties
Selenomonas, 985–87
Sporomusa, 992
- Pheromones, *Enterococcus*, 185–86, 188
- Phloem
 phytopathogenic spiroplasmas, 926–27, 932
 plant reaction to colonization of, 934–35
- Phormidium*, 1076
- Phosphate metabolism,
Prochlorococcus, 1105
- Phosphate regulation, in
 Cyanobacteria, 1090
- Phosphoketolase pathway
Leuconostoc, 294
Oenococcus, 294
Weissella, 294
- Phospholipases, *Listeria*, 433–35
- Phospholipids, *Bacillus*, 543
- Phosphotransferase system (PTS)
Bacillus lentimorbus, 570
Bacillus popilliae, 570
Enterococcus, 176–77
Lactobacillus, 366–67
Lactococcus, 221
 mollicutes, 863
Pediococcus, 248
Staphylococcus, 17–19
- Photoautotrophic growth,
 Heliobacteriaceae, 960–61
- Photosynthesis. *See also*
 Photosynthetic apparatus;
 Photosynthetic genes
 Cyanobacteria, 1054, 1074
 anoxygenic, 1074–77
 oxygenic, 1074
 Heliobacteriaceae, 951–52, 960–61
 in *Prochlorococcus*, 1099, 1102–4
- Photosynthetic apparatus, 1087–88
 Cyanobacteria, 1082–85
 Heliobacteriaceae, 951–52
Prochlorococcus, 1099
- Photosynthetic genes, in
 Cyanobacteria, 1088–89
- Photosystem I (PSI),
Prochlorococcus, 1103–4
- Photosystem II (PSII),
Prochlorococcus, 1103
- Phycobilins, Cyanobacteria, 1087–88
- Phycobiliproteins
 Cyanobacteria, 1086, 1087–88
Prochlorococcus, 1102–3
- Phycobilisomes, Cyanobacteria,
 1087–88
- Phycocyanins, 1090
- Phycoerythrin III, 1102–3
 Phycoerythrin, *Prochlorococcus*, 1102
- Phylogenetic tree
 anaerobic cocci, 799
Brochothrix, 478
Butyrivibrio, 1004
Camobacterium, 321
Carnobacterium, 321, 373
 Clostridiaceae, 656
Clostridium, 656, 754
 Cyanobacteria, 1055
Desemzia, 321
Desulfotobacterium, 772, 779
Desulfosporosinus, 772
Desulfotomaculum, 788
Enterococcus, 321
Eperythrozoon, 848
Erysipelothrix, 493, 499
Eubacterium, 824–25
Gemella, 512
Haemobartonella, 842
 Haloanaerobiales, 810
 Heliobacteriaceae, 953
Kurthia, 521
Lachnospira, 1004
 Lactic acid bacteria, 321
 Lactobacillaceae, 321
Lactobacillus, 230, 321, 350–54
Lactococcus, 213, 321
Leuconostoc, 269, 321, 350
Listeria, 478
Macrococcus, 11–12
Melissococcus, 321
 mollicutes, 837–38, 843, 847
Mycoplasma, 843
Oenococcus, 269
Paralactobacillus, 350
Pediococcus, 230, 321, 350
Roseburia, 1004
Salinicoccus, 11
Selenomonas, 983, 988
Sporolactobacillus, 478
Staphylococcus, 11–12
Streptococcus, 109, 321
 Syntrophomonadaceae, 1042
Tetragenococcus, 230, 321
Trichococcus, 321
Vagococcus, 321
Weissella, 269, 321, 350
- Phylogeny
Brochothrix, 477–78
Butyrivibrio, 1002–4
Caryophanon, 648–49
 Clostridiaceae, 654–58
Clostridium difficile, 731
Clostridium perfringens, 753
 Cyanobacteria, 1054
Desulfotobacterium, 771–72
Desulfosporosinus, 771–72
Enterococcus, 163–64
Erysipelothrix, 493–94
Eubacterium, 823
Filibacter, 646
 Haloanaerobiales, 809
 Heliobacteriaceae, 953
Lachnospira, 1012
Lactobacillus, 349–55
Leuconostoc, 267–71

- Macrococcus*, 11
Marinococcus, 644
Megasphaera, 966
 mollicutes, 843, 872
Oenococcus, 267–71
Pectinatus, 965–66
Pediococcus, 231–33
 phytopathogenic spiroplasmas, 909–11
Planococcus, 643
Roseburia, 1014
Selenomonas, 987–88
Sporolactobacillus, 634
Sporomusa, 991
Sporosarcina, 640
Staphylococcus, 11
Streptococcus, 80
Streptococcus pneumoniae, 149
 Syntrophomonadaceae, 1041–43
Tetragenococcus, 231–33
Veillonella, 1022
Weissella, 267–71
Zymophilus, 966
- Physiology**
Bacillus thuringiensis, 580
Butyrivibrio, 1007–9
Carnobacterium, 376
Caryophanon, 649
 Clostridiaceae, 670–73
Clostridium, 670–73
Clostridium difficile, 733
Clostridium perfringens, 701–2
 Cyanobacteria, 1054–57, 1074–91
Desulfotobacterium, 777
Enterococcus, 175–83
Filibacter, 646
 Haloanaerobiales, 817–18
 Heliobacteriaceae, 960–61
Lachnospira, 1013–14
Lactobacillus, 365–67
Leuconostoc, 267, 294–96
Listeria, 408
Macrococcus, 17–46
Megasphaera, 978
 mollicutes, 859, 882
Oenococcus, 267, 294–96
Pectinatus, 976–78
Pediococcus, 247–49
 phytopathogenic spiroplasmas, 918–21
Planococcus, 643–44
Roseburia, 1016
Selenomonas, 988
Sporolactobacillus, 634–35
Sporomusa, 997–98
Sporosarcina, 640
Staphylococcus, 17–46
 Syntrophomonadaceae, 1047–48
Tetragenococcus, 247–49
Veillonella, 1026–27
Weissella, 267, 294–96
Zymophilus, 978
- Phytopathogens**
 Spiroplasmas, 905–37
 unique gene sequences in, 934
 Phytoplasma, 836–37, 843, 845, 849–50, 852–53, 855, 858–60, 863–65, 869, 872, 875, 877, 880, 882
Phytoplasma aurantifolia, 935
Pigment
 Clostridiaceae, 670
 Clostridium, 670
 Clostridium perfringens, 700
 Prochlorococcus, 1102–4
 Streptococcus, 78–79
Pigment-protein complexes, *Prochlorococcus*, 1103–4
Pili, phytopathogenic spiroplasmas, 907, 933
Pitching yeast, *Zymophilus* in, 969–70
Planococcus, 520, 536, 631–32, 641–44
 cultivation of, 643
 genetic and phylogenetic relations of, 643
 habitats of, 641
 identification of, 644
 isolation of, 641
 morphology of, 643
 preservation of, 643
 properties of, 642–43, 643–44
Planococcus citreus, 536, 631, 641–44, 646, 648
Planococcus halophilus, 641
Planococcus kocurii, 641–44
Plant environment
 Enterococcus, 165
 Lactobacillus, 335–36, 370
 Lactococcus, 205–6, 208–9, 285–86
 Leuconostoc, 284–86, 302
 Listeria, 405
 mollicutes, 848, 878
 Pediococcus, 236–40, 285–86
 Staphylococcus, 59
 Streptococcus, 285–86
 Weissella, 302
Plant hosts
 phytopathogenic spiroplasmas, 905–37
 association with, 910
 chemical imbalances in, 932–33
 inoculation of, 926–27
 isolation from, 914–15
 phloem dysfunction in, 932
 plantibodies in, 937
 proteins secreted in, 933
 resistance in, 935–36
 reactions of, 934–35
 Plantacin, *Lactobacillus*, 369
 Plantaricin, *Pediococcus*, 253
Plantibodies, against
 phytopathogenic spiroplasmas, 937
Plasmalogen, *Veillonella*, 1027
Plasmids
 Bacillus, 544–46, 548–49
 Bacillus anthracis, 614
 Bacillus sphaericus, 595
 Bacillus thuringiensis, 578, 580–81, 588–89
 Brochothrix, 485
 Clostridium, 673, 754–56
 Clostridium perfringens, 702
 Cyanobacteria, 1078–79
 Enterococcus, 183–88, 194
 Kurthia, 525
 Lactobacillus, 356, 369
 Lactococcus, 213, 220–23
 Leuconostoc, 297, 300–1
 Listeria, 412–15
 mollicutes, 857, 864
 Oenococcus, 297
 Pediococcus, 248, 253
 phytopathogenic spiroplasmas, 923–24
 Streptococcus, 109
 Veillonella, 1034–35
 Weissella, 297
Plasmid transformation
 Butyrivibrio, 1009–10
 Cyanobacteria, 1075, 1081–83
 phytopathogenic spiroplasmas, 926
Plasminogen-binding, *Streptococcus pyogenes*, 118
PLC-A, *Listeria*, 433–35
PLC-B, *Listeria*, 433–35
Pleurocapsa, 1076
Pleurocapsa group, 1066–67
Pleurocapsales, 1053–54
 genera and groups of, 1066–67
 key to, 1066–67
PMC. See Pseudomembranous colitis
Pneumococci. See *Streptococcus pneumoniae*
Pneumolysin, *Streptococcus pneumoniae*, 156
Pneumonia
 Bacillus, 616, 618
 Leuconostoc, 303
 Pediococcus, 254
 Staphylococcus, 59
 Streptococcus agalactiae, 132–33
 Streptococcus pneumoniae, 149, 154–55, 159–60
Polar lipids, *Kurthia*, 525
Polymyxin resistance
 Bacillus thuringiensis, 578
 Erysipelothrix, 497
 Gemella, 511
Polysaccharide degradation, *Butyrivibrio*, 1010
Porphyromonas, 333
Potassium transport, *Enterococcus*, 182–83
Poultry hosts
 Brochothrix, 486
 Carnobacterium, 373–74, 377
 Clostridium perfringens, 711, 719, 726
 Enterococcus, 165
 Erysipelothrix, 494–95
 Kurthia, 519, 522
 Lactobacillus, 325, 328
 Pediococcus, 236
 Staphylococcus, 57–58, 58
Pregnancy, *Listeria*, 411
Preservation
 anaerobic cocci, 797–98
 Bacillus larvae, 572
 Bacillus lentimorbus, 563–65
 Bacillus popilliae, 563–65
 Bacillus thuringiensis, 578–80

- Brochothrix*, 488
Butyrivibrio, 1007
Carnobacterium, 378
Caryophanon, 648
Clostridium difficile, 732–33
Clostridium perfringens, 701
Cyanobacteria, 1063
Desulfotobacterium, 779–80
Desulfosporosinus, 784–85
Desulfotomaculum, 792
Enterococcus, 168
Erysipelothrix, 502
Gemella, 513
Haloanaerobiales, 816
Heliobacteriaceae, 960
Kurthia, 524
Lachnospira, 1013
Lactobacillus, 348–49
Lactococcus, 214
Leuconostoc, 293–94
Marinococcus, 644
Megasphaera, 976
mollicutes, 859
Oenococcus, 293–94
Pectinatus, 976
Pediococcus, 246–47
phytopathogenic spiroplasmas, 918
Planococcus, 643
Roseburia, 1016
Selenomonas, 985
Sporolactobacillus, 633
Sporomusa, 997
Sporosarcina, 638
Syntrophomonadaceae, 1045
Tetragenococcus, 246–47
Veillonella, 1026
Weissella, 293–94
Zymophilus, 976
Prevotella, 333
Prevotella loescheii, 1032
Prevotella melaninogenica, 1027
Prevotella ruminicola, 1005, 1009, 1011
Probiotics
for *Clostridium difficile* treatment, 741
Lactobacillus, 329, 332, 334, 344–45
Pediococcus, 256
Prochlorococcus, 1099–107
cultivation of, 1101–2
genomics of, 1106–7
habitats of, 1099–100
HL adapted ecotypes, 1100, 1102, 1104, 1106–7
isolation of, 1101–2
LL adapted ecotypes, 1100, 1102, 1104, 1106–7
media for, 1100
morphology, 1099
nutrient metabolism and acquisition by, 1104–5
iron, 1105
nitrogen, 1104–5
phosphate, 1105
trace metals, 1105
photosynthesis in, 1102–4
phycobiliproteins in, 1102–3
phycoerythrin in, 1102
pigments in, 1102–4
strains of, 1100–1
Prochlorococcus CCMP 1375, 1102–3
Prochlorococcus CCMP 1378, 1099, 1103
Prochlorococcus marinus, 1099
Prochlorococcus MED4, 1103–7
Prochlorococcus MIT9312, 1106
Prochlorococcus MIT9313, 1103–7
Prochlorococcus NATL2A, 1106
Prochlorococcus PCC9511, 1105
Prochlorococcus SS120, 1104–7
Prochloron, 1102–3
Prochloron didemni, 1099, 1103
Prochlorothrix, 1102–3
Prochlorothrix hollandica, 1099, 1103–4
Progesterone, from *Eubacterium*, 831
Propanediol production, *Clostridium*, 672
Propionate production, *Veillonella* in, 1030–31
Propionibacterium, 527, 977–78, 1027
Propionibacterium acnes, 1032
Propionic acid synthesis, *Pectinatus*, 977–78
Propionispora vibrioides, 997
Prostatitis, *Staphylococcus*, 59
Protein metabolism
Bacillus, 531
Lactococcus, 220
Protein secretion
Bacillus, 555
Staphylococcus, 45–46
Proteolysis
Butyrivibrio, 1009, 1011
Butyrivibrio fibrisolvens, 1006–7
Pseudanabaena, 1067–68
Pseudoanabaena, 1076
Pseudobutyrvibrio ruminis, 1002, 1004
Pseudolysogens, *Bacillus*, 547–48
Pseudomembranous colitis (PMC), 730–31, 738
Pseudomonas aeruginosa, 330, 369, 446–47
Pseudoramibacter alactolyticus, 825
PSI. *See* Photosystem I
PSII. *See* Photosystem II
PTS. *See* Phosphotransferase system
Purification, Cyanobacteria, 1057–58, 1063
Purine fermentation, *Veillonella*, 1027
Purulent infections, *Streptococcus*, 94–95
Putrescine, 1027
Selenomonas, 987
Pyelonephritis
Bacillus, 616
Gemella, 516
Staphylococcus, 60
Pyoarthritis, *Staphylococcus*, 60
Pyrogenic exotoxins. *See* Superantigens
Pyruvate decarboxylase, *Lactobacillus*, 366
Pyruvate dehydrogenase (PDH), *Enterococcus*, 177–78
Pyruvate format lyase (PFL), *Enterococcus*, 177–78
Pyruvate metabolism
Enterococcus, 177–78
Heliobacteriaceae, 960–61
Pyruvate oxidase, *Lactobacillus*, 366
Pyruvate production
Bacillus lentimorbus, 570
Bacillus popilliae, 570
- ## Q
- Quellung reaction, *Streptococcus pneumoniae*, 150–51
Quinolone resistance, *Pediococcus*, 254
Quorum sensing, *Staphylococcus*, 51–52
- ## R
- 16S rDNA
anaerobic cocci, 804
Butyrivibrio, 1002
Clostridium, 753
Enterococcus, 164
Lactobacillus, 365
Leuconostoc, 293, 302
mollicutes, 845, 847, 858
Oenococcus, 267, 291
Pediococcus, 231, 233, 246
*Streptococcus*2, 80–81
Syntrophomonadaceae, 1041–43
Tetragenococcus, 243, 246
23S rDNA
Clostridium, 654
Oenococcus, 267
Regulatory network, *Staphylococcus*, 50–57
Respiratory chain, *Staphylococcus*, 26–27
Respiratory pathways, phytopathogenic spiroplasmas, 918–19
Respiratory tract
anaerobic cocci, 795
Gemella, 512, 516
mollicutes, 849, 875, 878
Sporosarcina, 636
Streptococcus, 77, 95
Streptococcus pneumoniae, 149–50, 159
Restriction endonucleases, Cyanobacterial DNA cleavage by, 1079–80
Reuterin, *Lactobacillus*, 330
Reuterin, *Lactobacillus*, 330, 369
RF. *See* Phage replication forms
Rhamnose metabolism, *Pediococcus*, 247
Rheumatic fever, *Streptococcus pyogenes*, 111–14, 129

- Rheumatoid arthritis, *Erysipelothrix*, 498
- Rhizosphere
Desulfotomaculum, 787
Sporolactobacillus, 632
- Rhodococcus equi*, 406
- Rhodopseudomonas*, 1086
- Rhodospirillum rubrum*, 1089
- Ribose metabolism
Bacillus larvae, 574
Brochothrix, 480
Carnobacterium, 380
Enterococcus, 176
Staphylococcus, 21–22
- Rice. *See* Food
- Rickettsia conorii*, 417–18
- Rifampin resistance, *Bacillus*, 548
- Ristocetin sensitivity, *Gemella*, 515
- RNA-DNA hybridization, for isolation of Cyanobacterial DNA, 1085
- Rodent hosts
Bacillus, 619
Bacillus anthracis, 610–14
Clostridium perfringens, 724
Erysipelothrix, 492, 494, 503
Gemella, 512, 516
Lactobacillus, 324–25, 328, 331
Listeria, 450–53
Staphylococcus, 58–59
- Roseburia*, 1014–16
cultivation of, 1016
habitat of, 1014
identification of, 1015–16
isolation of, 1015
media for, 1008
morphology of, 1014
phylogenetic tree of, 1004
phylogeny of, 1014
physiology of, 1016
preservation of, 1016
- Roseburia cecicola*, 1012, 1014–16
- Rothia*, 527, 620
- Rothia dentocariosa*, 1032
- 5S rRNA
Leuconostoc, 297–98
mollicutes, 850, 863
Oenococcus, 297–98
Sporosarcina, 640
- 16S rRNA
Aerococcus, 229
anaerobic cocci, 795
Anaerococcus, 803
Bacillaceae, 631
Bacillus, 536
Brochothrix, 478, 480–81
Butyrivibrio, 1002–4
Carnobacterium, 373, 375, 378–79
Clostridiaceae, 654–55, 658–59, 663–64
Clostridium, 654–55, 658–59, 672
Clostridium difficile, 731
Cyanobacteria, 1054–55
Desulfibacterium, 771–72, 774–75, 777–79
Desulfosporosinus, 771–72, 781, 783
Desulfotomaculum, 787, 792
Enterococcus, 163–64, 166, 175
Erysipelothrix, 493–94, 504
Eubacterium, 823–25, 829
Gemella, 511, 513
Haloanaerobiaceae, 812
Haloanaerobiales, 809, 811
Halobacteroidaceae, 812
Kurthia, 520, 525, 527
Lachnospira, 1012
Lactobacillaceae, 320
Lactobacillus, 267, 320, 349–54, 363–64
Lactococcus, 206, 208, 212–13
Leuconostoc, 267, 269–71, 291, 293, 297–98
Listeria, 404
Macrocooccus, 5, 11
Megasphaera, 966
mollicutes, 843, 845–48, 857–58
Oenococcus, 267, 271, 291, 297–98
Pectinatus, 965–66
Pediococcus, 231, 233, 236, 244, 246
Peptococcus, 803
Planococcus, 643
Roseburia, 1014
Selenomonas, 987–88
Sporolactobacillus, 634
Sporomusa, 991
Sporosarcina, 640
Staphylococcus, 5, 11
Streptococcus, 80, 89–90, 98
Tetragenococcus, 229, 231, 233, 244, 246
Veillonella, 1023, 1026
Weissella, 267, 269–71, 291
Zymophilus, 966
- 23S rRNA
Clostridium, 654, 679–80
Enterococcus, 164, 192, 194
Kurthia, 527
Lactobacillus, 267, 320, 349–50, 363
Lactococcus, 206, 208, 212
Leuconostoc, 267, 297–98
mollicutes, 845–46
Oenococcus, 267, 271, 297–98
Pediococcus, 231, 233
Tetragenococcus, 231
Veillonella, 1023
Weissella, 267, 269
- Rubisco
Cyanobacteria, 1089–90
Heliobacteriaceae, 960–61
model systems of, 1091
- Rumen
Butyrivibrio in, 1004–5, 1010–11
Eubacterium in, 827–28
Lachnospira in, 1012, 1014
Selenomonas in, 982
- Rumen hosts
Clostridium, 658–59
Desulfotomaculum, 789
Lactobacillus, 328
mollicutes, 837, 849, 854
- Ruminant hosts
Bacillus anthracis, 610–13
Clostridium perfringens, 713
Desulfotomaculum, 789
Erysipelothrix, 494
Lactobacillus, 328
Listeria, 409
Macrocooccus, 61
Staphylococcus, 57–60
Ruminobacter amylophilus, 1009, 1011
Ruminococcus, 795–98, 1011
differentiation of, 803–4
isolation of, 796–97
Ruminococcus bromii, 795
Ruminococcus flavefaciens, 798
Ruminococcus hansenii, 804
Ruminococcus obeum, 795
Ruminococcus productus, 804
- S**
- Saccharide metabolism, *Bacillus*, 550
- Saccharolytic representatives
of *Eubacterium*, 823–25, 828
of Haloanaerobiales, 818–20
- Saccharomyces boulardii*, 741
- Saccharomyces cerevisiae*, 977
- Sakacin, *Lactobacillus*, 369
- Salicin metabolism
Bacillus larvae, 573
Brochothrix, 480
Carnobacterium, 380
Pediococcus, 247
- Saline environment,
Desulfotomaculum, 789
- Salinicoccus*, 645
phylogenetic tree of, 11
properties of, 642
- Salinicoccus roseus*, 645
- Saliva
intergeneric coaggregations of, 1032–33
Veillonella in, 1023–24
- Salmonella*, 345
- Salmonella enteritidis*, 1031
- Salmonella typhimurium*, 330, 877, 1031
- Salt concentrations, in
Haloanaerobiales, 817–18
- Salt stress, in Cyanobacteria, 1090
- Sarcina*, 654–55, 795, 798
differentiation of, 803–4
isolation of, 796–97
- Sarcina maxima*, 655, 804
- Sarcina ventriculi*, 655, 665, 795, 798, 804
- SARP proteins, 928
- Scarlet fever, *Streptococcus pyogenes*, 112, 118
- Schwarzia succinivorans*, 965
- Schyttonema*, 1076
- SCPA. *See* C5a peptidase
- Scytonema*, 1070
- Sediment environment
Clostridium, 658–59
Desulfibacterium, 774
Desulfosporosinus, 780
Sedimentibacter hydroxybenzoicus, 658

- Sediments
Sporomusa in, 999
 Syntrophomonadaceae in, 1043
 Selenium oxidation, *Bacillus*, 531
Selenomonas, 965–66, 969, 975–76, 982–99
 applications of, 988
 characteristics of, 968, 986
 cultivation of, 984–85
 habitats of, 982–84
 homology of oral species of, 987
 identification of, 985–88
 isolation of, 984–85
 phenotypic properties of, 985–87
 phylogenetic tree of, 983, 988
 phylogeny of, 987–88
 physiology of, 988
 preservation of, 985
 selective enrichment of, 984
 strains of, 983
Selenomonas acidaminophila, 984–85, 987
Selenomonas artemidis, 987
Selenomonas diana, 985–87
Selenomonas flueggei, 987
Selenomonas infelix, 985–87
Selenomonas lactificifex, 966–67, 969, 974, 988
Selenomonas noxia, 987
Selenomonas palpitans, 983–84
Selenomonas ruminatum, 982, 984–85, 987–88, 1026
Selenomonas ruminatum subspecies *lactilytica*, 982–84, 985
Selenomonas ruminatum subspecies *psychrocataligenes*, 984
Selenomonas sputigena, 982, 985, 987
 Sepsis
 anaerobic cocci, 795
Bacillus, 618–19
Streptococcus, 94–95
Streptococcus agalactiae, 132–33
Streptococcus dysgalactiae, 137
Streptococcus pyogenes, 112, 114
 Septic arthritis, *Bacillus*, 618
 Septicemia
Bacillus anthracis, 612
Bacillus larvae, 574
Carnobacterium, 374
Erysipelothrix, 496–97
Lactococcus, 224
Leuconostoc, 303
Staphylococcus, 60
Streptococcus, 97
 Serine metabolism, *Enterococcus*, 180
 Serology
Brochothrix, 485
Megasphaera, 975–76
 mollicutes, 848, 855–56
Pectinatus, 974
 phytopathogenic spiroplasmas, 916
Serratia marcescens, 915–16
 Sewage environment
Caryophanon, 646
Desulfitobacterium, 774
Erysipelothrix, 495
Eubacterium in, 828–29
Lactobacillus, 336
Selenomonas in, 984
 Syntrophomonadaceae in, 1043
 Sex pheromone, *Enterococcus*, 170
 Sheaths
 Clostridiaceae, 665–66
Clostridium, 665–66
 Sheep. *See* Ovine hosts
 Shellfish hosts
Planococcus, 641
Shigella flexneri, 330, 369, 417–18
 Shrimp. *See* Shellfish hosts
 Shuttle vectors
 in *Butyrivibrio*, 1009–10
 for Cyanobacteria, 1081–83
 Sigma factors, *Bacillus*, 540–41
 Silage. *See* Animal feed
 Sinusitis, anaerobic cocci, 795
 Skin environment
 anaerobic cocci, 795–96
Staphylococcus, 10, 57–58, 61
Streptococcus, 95
Slackia, 795
Slackia exigua, 823, 828, 831
Slackia satelles, 828
 S-layers
Bacillus, 542
Bacillus sphaericus, 594–95
 Clostridiaceae, 666
Clostridium, 666
 Slime
 Clostridiaceae, 665–66
Clostridium, 665–66
Smithella, 1043
 SNAX, Cyanobacteria, 1061–62
 Sodium chloride sensitivity
Brochothrix, 484
Pediococcus, 247
 Sodium transport, *Enterococcus*, 182
 Soil environment
 anaerobic cocci, 795
Bacillus, 531, 563
Bacillus anthracis, 610
Bacillus sphaericus, 592
Bacillus thuringiensis, 577–78, 582
Brochothrix, 477, 486–87
Clostridium, 658–59, 689–90
Clostridium perfringens, 713–14, 759
 Cyanobacteria in, 1057
Desulfitobacterium, 774, 779
Desulfosporosinus, 780
Desulfotomaculum, 787, 792
Erysipelothrix, 503
Eubacterium in, 828
 Heliobacteriaceae in, 956, 961–62
Kurthia, 521, 523
Lactobacillus, 336
Listeria, 405
Sporolactobacillus, 632
Sporomusa in, 991, 999
Sporosarcina, 636–37
Staphylococcus, 59
Streptococcus, 77
 Syntrophomonadaceae in, 1043
Solobacterium moorei, 493, 825
 Sorbitol metabolism
Enterococcus, 176
Gemella, 514–15
 Sorbose metabolism, *Enterococcus*, 176
 Soy, *Leuconostoc*, 284
 Spiralin, 920–21, 928
Spirillum sputigenum, 982
Spiroplasma, 838, 843, 847, 850–51, 855, 861, 863, 871, 905–37, 910–11
 cultivation of, 913–15, 916
 detection of, 914–17
 disease from, 851, 930–35
 epidemiology of, 929–30
 genetics of, 921–26
 groups of, 909–10
 habitat of, 911–13
 homology in, 909–10
 host associations with, 910, 934–36
 identification of, 914–17
 insect interaction with, 926–29, 937
 isolation of, 914–16
 leafhopper interactions with, 912–13, 927–29
 morphology of, 905–8, 914–15
 motility of, 908
 phylogeny of, 909–11
 physiology of, 918–21
 preservation of, 918
 species of, 851, 909–10
 symptoms of, 930–31
 taxonomy of, 909–11
 toxins of, 933
 virulence mechanisms of, 932–35
Spiroplasma apis, 851, 875, 910, 922
Spiroplasma citri, 839, 842, 851, 857, 864, 867, 871, 873, 882, 905–10, 912–25, 927–36
Spiroplasma floricola, 906, 922–23
Spiroplasma kunkelii, 851, 864, 866, 870, 905–25, 927–34, 937
 gene distribution of, 919
Spiroplasma leptinotarsa, 851, 855
Spiroplasma melliferum, 851, 860–61, 870–71, 875, 905–6, 910, 918, 920–22, 924, 926
Spiroplasma mirum, 924
Spiroplasma monobiae, 851, 864, 889
Spiroplasma phoeniceum, 851, 905, 909–10, 916, 921–22, 930
Spiroplasma poulsonii, 851, 855, 924
Spiroplasma taiwanense, 906
 Spiroplasmataceae, *Spiroplasma*, 831–32
Spirulina, 1067–68, 1076, 1091
Spirulina platensis, 1057
 Sporangium, *Bacillus*, 539
 Spores
Bacillus, 530, 539, 552–53
Bacillus anthracis, 609–10
Bacillus larvae, 571–72, 574–75
Bacillus popilliae, 567–68
Bacillus sphaericus, 596
Bacillus thuringiensis, 579–80, 582
 as biological indicators, 553–54
 Clostridiaceae, 659, 662
Clostridium, 659, 662, 669, 689

- Clostridium difficile*, 732, 736
Clostridium perfringens, 701–2, 759
Desulfotomaculum, 788, 792–93
 resistance of, 552–53
Sporolactobacillus, 634
Sporosarcina, 638–39
Sporobacter, 654
Sporohalobacter, 997
Sporohalobacter lortetii, 658, 809–12, 815–16
Sporolactobacillus, 530, 631–30–31
 cultivation of, 633
 genetics and phylogenetic relationships of, 634
 habitats of, 632
 identification of, 635
 isolation of, 632–33
 morphology of, 633–34
 phylogenetic tree of, 478
 preservation of, 633
 properties of, 634–35
Sporolactobacillus inulinus, 632–35
Sporolactobacillus laevis, 632, 634
Sporolactobacillus laevis var. *intermedius*, 632
Sporolactobacillus racemicus, 632, 634
Sporomusa, 664, 809, 966, 991–99, 1022
 cultivation of, 993–96
 ecology of, 998–99
 habitat of, 991–92
 identification of, 996–97
 isolation of, 993–96
 morphology of, 994, 996
 phenotypic properties of, 992
 phylogeny of, 991
 physiology of, 997–98
 preservation of, 997
 taxonomy of, 991
Sporomusa acidovorans, 993, 998
Sporomusa malonica, 993, 996, 998
Sporomusa ovata, 991, 993, 995–98
Sporomusa paucivorans, 965, 982, 987, 993, 996–99
Sporomusa silvacetica, 993, 997–99
Sporomusa sphaeroides, 991, 993, 995–98
Sporomusa subbranch, 965–66
Sporomusa termitida, 993–94, 996–98
Sporosarcina, 520, 530, 536, 631–32, 635–41, 643, 665
 cultivation of, 637–38
 genetic and phylogenetic relationship, 640
 habitats of, 636
 identification of, 640
 isolation of, 636–37
 morphology of, 635–36, 638
 preservation of, 638
 properties of, 639–41, 642
Sporosarcina halophila, 636–41
Sporosarcina pulmonum, 636
Sporosarcina urea, 536, 631, 636–41, 646, 648
Sporovibrio desulfuricans, 787
 Sporulation
Bacillus, 538–42
Bacillus anthracis, 610
Bacillus larvae, 571, 574–76
Bacillus lentimorbus, 567
Bacillus popilliae, 567
Bacillus thuringiensis, 577, 579, 581, 588
 Clostridiaceae, 666–70
Clostridium, 666–70
Clostridium perfringens, 701–2
 SpV1 phages, 924–25
 SpV2 phages, 924
 SpV3 phages, 924–25
 SpV4 phages, 925
Staphylococcus, 5–61, 404, 536, 643, 669
 ecology of, 57–59
 genomics of, 46–50
 identification of, 11–17
 pathogenicity, 52–53, 59–61
 phylogenetic tree of, 11–12
 phylogeny of, 11
 physiology of, 17–46
 catabolite regulation, 22–24
 cell wall, 30–43
 metabolism, 17–22, 24
 protein secretion, 45–46
 respiration, 24–30
 slime and biofilm formation, 43–45
 quorum sensing, 51–52
 regulatory network in, 50–57
 accessory gene regulation, 50–53
 exoprotein gene regulator, 54–55
 staphylococcal accessory regulator, 53–54
 species and subspecies of, 6, 13–17
Staphylococcus albus, 5
Staphylococcus arlettae, 58
Staphylococcus aureus, 5–8, 11, 17–27, 30–59, 190, 224, 369, 406, 433, 482, 548, 730, 934, 1010, 1030
Staphylococcus aureus subsp. *anaerobius*, 11, 58, 799
Staphylococcus auricularis, 58
Staphylococcus capitis, 11, 17, 57–58, 60
Staphylococcus capitis subsp. *ureolyticus*, 58
Staphylococcus caprae, 11, 58, 60
Staphylococcus carnosus, 11, 18, 21–22, 27–30, 33, 46–50, 59, 61, 177
Staphylococcus carnosus subsp. *utilis*, 59
Staphylococcus chromogenes, 59–60
Staphylococcus cohnii, 58, 60
Staphylococcus condimentii, 59
Staphylococcus delphini, 11, 58–59
Staphylococcus dermidis, 5
Staphylococcus epidermidis, 11, 17, 20, 23–24, 26, 30, 33, 43, 46–47, 50, 52, 57, 60
Staphylococcus equorum, 58
Staphylococcus felis, 58, 60
Staphylococcus fleuretti, 13, 59
Staphylococcus gallinarum, 58
Staphylococcus haemolyticus, 11, 17, 57, 60
Staphylococcus hominis, 11, 20, 57–58, 60
Staphylococcus hominis subsp. *novobiosepticus*, 58
Staphylococcus hyicus, 22, 45–46, 59–60
Staphylococcus intermedius, 11, 17, 20, 23, 58–59
Staphylococcus lentus, 5, 11, 13, 26, 59
Staphylococcus lugdunensis, 58, 60
Staphylococcus lutrae, 58
Staphylococcus pasteurii, 58
Staphylococcus piscifermentans, 59
Staphylococcus saccharolyticus, 11, 795, 799
Staphylococcus saprophyticus, 5, 11, 17, 20, 58, 60
Staphylococcus schleiferi, 58–60
Staphylococcus schleiferi subsp. *coagulans*, 58–59
Staphylococcus sciuri, 5, 11, 13, 26, 38, 58–60
Staphylococcus sciuri subsp. *carnaticus*, 58
Staphylococcus sciuri subsp. *rodentium*, 58
Staphylococcus simulans, 11, 17, 33, 52, 60
Staphylococcus vitulus, 5, 11, 13, 59
Staphylococcus warneri, 11, 52, 57, 60
Staphylococcus xylosus, 11, 17–22, 24, 41, 58–59
 Starch fermentation
Butyrivibrio, 1011
Veillonella, 1031
 Starch metabolism
Bacillus, 531, 550
Pediococcus, 247
 Steroids, biotransformation of, 831
Stigonema, 1070
 Stigonematales, 1054
 genera of, 1068–70
 key to, 1070
 Strep throat. *See* Pharyngitis
 Streptococcal impetigo,
Streptococcus pyogenes,
 112–13
Streptococcus, 229, 249, 404, 493, 669, 741, 795, 843, 872, 1030
 anginosus group, 79–80, 82–86, 94
 characteristics of, 83–84, 86, 88–89
 disease from, 92–97
 genomics of, 92
 habitat of, 77, 95
 α-hemolytic, 108, 149–71
 β-hemolytic, 108–38
 identification of, 91–92
 isolation of, 77–80
 mitis group, 80, 85–91
 molecular studies of, 98
 mutans group, 80–83
 oral, 76–98
 pathogenicity of, 95–96
 phylogenetic tree of, 109, 321

- phylogeny of, 80
 salivarius group, 80, 82, 84
 species of, 80, 83–84, 86, 88–89, 110
 taxonomy of, 80–91, 109–110
 tufted mitior strains, 91
Streptococcus acidilactici, 234
Streptococcus agalactiae, 108–110, 116, 124, 130–36, 167
 disease and epidemiology of, 131–35
 genetics of, 135–36
 identification of, 130–31
 pathogenicity of, 133
Streptococcus anginosus, 79–80, 84–85, 94–95, 795, 799
Streptococcus australis, 80, 85, 90
Streptococcus bovis, 96, 167, 328
Streptococcus constellatus, 80, 83–85, 95–97, 795, 799
Streptococcus constellatus subsp. *constellatus*, 85
Streptococcus constellatus subsp. *pharyngis*, 85
Streptococcus criceti, 76
Streptococcus cricetus, 80–82
Streptococcus crista, 80, 85, 89–90
Streptococcus damnosus, 234
Streptococcus damnosus subsp. *diastaticus*, 234
Streptococcus downei, 80–82
Streptococcus dysgalactiae, 110, 136–38
 pathogenicity of, 137–38
 taxonomy of, 136–37
Streptococcus dysgalactiae subsp. *dysgalactiae*, 136–37
Streptococcus dysgalactiae subsp. *equisimilis*, 136–37
Streptococcus faecalis, 546, 589–91.
See also Enterococcus faecalis
Streptococcus ferus, 80–82
Streptococcus gordonii, 77, 79–80, 85–86, 89–91, 96, 126, 129
Streptococcus infantis, 80, 85, 90
Streptococcus intermedius, 80, 83–85, 95–97, 795, 799
Streptococcus lactis, 367
Streptococcus lindneri, 234
Streptococcus macacae, 80–82
Streptococcus MG, 83
Streptococcus milleri, 81, 83–84, 94–95
Streptococcus mitior, 81, 87, 90, 96
Streptococcus mitis, 79–80, 82, 85–87, 89, 91, 93, 96–98, 153, 1034
Streptococcus morbillorum, 511
Streptococcus mutans, 77–78, 81–82, 91–94, 96, 98, 181, 324–25, 1028–30, 1034
Streptococcus oralis, 79–80, 85, 87, 90, 93, 96–98, 1033
Streptococcus orisratti, 80–82
Streptococcus parasanguinis, 76, 79–80, 85, 89–90, 96
Streptococcus peroris, 80, 85, 90
Streptococcus pleomorphus, 799
Streptococcus pneumoniae, 80–81, 85, 90, 96, 98, 108, 136, 149–60, 189
 disease of, 155–60
 epidemiology of, 155–60
 genetics of, 151–53
 identification of, 149–51
 phylogeny of, 149
Streptococcus porcinus, 167
Streptococcus pyogenes, 108–29, 133–34, 137, 187, 493
 disease and epidemiology of, 112–24
 genetics of, 124–29
 genome sequence, 124–25
 global regulators, 125–26
 reporter genes, 128
 variability of, 124
 Vir regulon, 125
 identification of, 110–12
 M protein of, 110–13
 pathogenicity of, 114
Streptococcus rattii, 76
Streptococcus rattus, 80–82
Streptococcus salivarius, 77, 79–82, 85, 93, 96–97, 1027–28, 1031–33
Streptococcus salivarius subsp. *salivarius*, 82
Streptococcus salivarius subsp. *thermophilus*, 82, 338
Streptococcus sanguis, 76–77, 79–81, 85–91, 93, 97, 324, 1028, 1032, 1034
Streptococcus sobrinus, 79–82, 93–94
Streptococcus suis, 81
Streptococcus thermophilus, 80, 82, 210–11, 214, 255, 299, 332, 339, 345, 367, 485
Streptococcus uberis, 167
Streptococcus vestibularis, 77, 79–80, 82
 Streptokinase, *Streptococcus pyogenes*, 121–22
 Streptolysin O, *Streptococcus pyogenes*, 120–21
 Streptolysin S, *Streptococcus pyogenes*, 120–21
 Streptomycin resistance
Enterococcus, 186, 190, 192
Gemella, 515
 Stress response, *Oenococcus*, 302
 Subgingival plaque
 intergeneric coaggregations of, 1032
Veillonella, 1023–24, 1028
 Succinate decarboxylation
Sporomusa, 998
Veillonella, 1026–27
Succinivibrio dextrinosolvens, 985
 Sucrose metabolism
Carnobacterium, 380
Gemella, 514
Pediococcus, 247, 249
Sporolactobacillus, 635
Staphylococcus, 21–22
 Sugar metabolism
 Cyanobacteria, 1089–90
 phytopathogenic spiroplasmas, 919–20, 933–34
 Sugar transport
Lactobacillus, 366–67
Leuconostoc, 294
Oenococcus, 294
Staphylococcus, 17–22
 glycolytic pathway, 20
 PTS, 17–19
 PTS-independent, 18–20
Weissella, 294
 Sulfamethoxazole resistance,
Enterococcus, 189
 Sulfate reduction
 Cyanobacteria, 1075
Desulfosporosinus, 772, 780–81
Desulfotomaculum, 787, 789, 792
 Sulfide oxidation, 69
 Cyanobacteria, 1075
 Sulfide production, Cyanobacteria, 1075
 Sulfidic environments
 Cyanobacteria, 1076–78
 Sulfidogens, *Sporomusa*, 998–99
 Sulfonamide resistance
Erysipelothrix, 497
Gemella, 515
 Sulfur compounds,
 Haloanaerobiales use of, 818
 Sulfur limitation, Cyanobacteria, 1090
 Sulfur reduction, Cyanobacteria, 1078
 Superantigens, *Streptococcus pyogenes*, 118–20
 Superoxide production
Enterococcus, 170
Mycoplasma, 879, 881, 887
 Supragingival plaque, *Veillonella* in, 1023–24
 Surface proteins
Streptococcus agalactiae, 133–34
Streptococcus pneumoniae, 156–58
 Swine hosts
Clostridium perfringens, 721, 725
Erysipelothrix, 492, 494–95
Gemella, 512
Lactobacillus, 325, 328
Staphylococcus, 59
Synechococcus, 1061, 1065, 1076, 1078, 1101–2, 1104–7
Synechococcus lividus, 1076
Synechococcus PCC 6301, 1082, 1089–90
Synechococcus PCC 7002, 1080, 1082, 1084
Synechococcus PCC 7942, 1079–82, 1089–91
Synechococcus sp. PCC 6301, 1079–80, 1083, 1085
Synechococcus sp. PCC 7002, 1083
Synechococcus sp. PCC 7942, 1084, 1087
Synechococcus sp. PCC 73109, 1079
Synechococcus WH8102, 1106–7
Synechocystis, 858, 1065, 1076, 1086
Synechocystis PCC 6701, 1086
Synechocystis PCC 6714, 1083

- Synechocystis* PCC 6803, 1079–80, 1082–85, 1088–90, 1103
 Synthetic oligonucleotides, for isolation of Cyanobacterial DNA, 1084–85
Syntrophobacter, 1043
Syntrophobotulus, 772–73
 properties of, 773
 Syntrophomonadaceae, 1041–48
 biochemistry of, 1047–48
 cultivation of, 1044–45
 habitat of, 1043
 identification of, 1045–47
 isolation of, 1043–45
 maintenance of, 1045
 phenotypic characteristics of, 1046
 phylogenetic tree of, 1042
 phylogeny of, 1041–43
 physiology of, 1047–48
 taxonomy of, 1041–43
Syntrophomonas, 1041–43, 1045–46
Syntrophomonas sapovorans, 1041–43
Syntrophomonas wolfei, 1041–44, 1046–48
Syntrophospora, 1046–47
Syntrophospora bryantii, 658, 1041–42, 1047
Syntrophothermus, 1041, 1046–47
Syntrophothermus lipocalidus, 1042–43, 1044, 1047

T

- Tagatose pathway
Carnobacterium, 380
Lactococcus, 221
 Tartaric acid metabolism,
Lactobacillus, 340–41
 Taxonomy
Bacillus, 530–37
Clostridium, 654–55
Clostridium difficile, 731
Desulfotomaculum, 792–93
Erysipelothrix, 493–94
Eubacterium, 823–25
 Haloanaerobiales, 809–10
 Heliobacteriaceae, 953
Lactococcus, 205
Leuconostoc, 271–73
Megasphaera, 968–69
 mollicutes, 843–47
Oenococcus, 271–73
Pectinatus, 966–68
Pediococcus, 233–34
 phytopathogenic spiroplasmas, 909–11
Sporomusa, 991
Streptococcus, 80–91, 109–10
Streptococcus dysgalactiae, 136–37
 Syntrophomonadaceae, 1041–43
Tetragenococcus, 233–34
Veillonella, 1022–23
Weissella, 271–73
Zymophilus, 969
 TCA. *See* Tricarboxylic acid cycle

- Teichoic acid
Bacillus, 542–43
Listeria, 412, 438, 440
Staphylococcus, 5, 12–13, 30, 38–42
Streptococcus, 87
Streptococcus pneumoniae, 149, 155–56, 159
 Teichuronic acid, *Bacillus*, 542
 Teicoplanin resistance,
Enterococcus, 192
 Temperature tolerance
Bacillus lentimorbus, 566
Bacillus popilliae, 566
Brochothrix, 484
Clostridium, 670–71, 680
Clostridium perfringens, 759
 Cyanobacteria incubation, 1062
Desulfotomaculum, 787
Erysipelothrix, 492
Gemella, 514
Listeria, 408
 TeNT. *See* Tetanus neurotoxin
 Termite gut environment
Lactococcus, 208
Sporomusa in, 991–93, 999
 Terrestrial environment,
Prochlorococcus, 1100
 Tetanus
Clostridium perfringens, 753
 description of, 691–92
 epidemiology of, 692
 Tetanus neurotoxin (TeNT). *See*
also Neurotoxins
 action of, 686–89
Clostridium tetani, 679
 structure of, 682–86
 Tetracycline resistance
Clostridium perfringens, 755–56
Enterococcus, 183, 186–87, 192–93
Gemella, 515
Pediococcus, 254
Streptococcus, 97
Streptococcus pyogenes, 126
Veillonella, 1030
 Tetracycline sensitivity
Bacillus, 618
Brochothrix, 480
Gemella, 515
Listeria, 408
 mollicutes, 873, 878
 phytopathogenic spiroplasmas,
 936
Planococcus, 644
Tetragenococcus, 163–64, 229–56
 applications of, 254–56
 characteristics of, 230, 235, 245–46
 epidemiology and disease of,
 253–54
 genetics of, 248–53
 habitats of, 234–41
 identification of, 244–46
 isolation of, 241–44
 morphology of, 233–34
 phylogenetic tree of, 321
 phylogeny of, 231–33
 physiology of, 247–49
 preservation of, 246–47
 species of, 234, 245–46
 taxonomy of, 233–34
Tetragenococcus halophilus, 230, 233–34, 240–41, 243, 248–49, 253–54
Tetragenococcus halotolerans, 249
Tetragenococcus muriaticus, 230, 233–34, 240–41, 243, 248–49, 253–54
Thermoactinomyces, 530, 536
Thermoactinomyces vulgaris, 536
Thermoanaerobacter, 665–66, 671, 1041
Thermoanaerobacter brockii, 666, 1042
Thermoanaerobacter kivui, 1042
Thermoanaerobacter thermocopriae, 658, 1042
Thermoanaerobacter thermohydrosulfuricus, 658
Thermoanaerobacter thermosaccharolyticum, 658
Thermoanaerobacter thermosulfurigenes, 658
 Thermoanaerobacteriaceae
Thermoanaerobacter, 671
Thermoanaerobacterium, 671
Thermoanaerobacterium, 666, 671
Thermoanaerobacterium thermosaccharolyticum, 669
Thermobrachium, 654, 658, 665
Thermobrachium celere, 659, 671
Thermodesulfobacterium, 787, 789
Thermohalobacter, 654
Thermohalobacter berrensensis, 671
Thermosyntropha, 1041, 1046–47
Thermosyntropha lipolytica, 1042, 1044, 1047
Thicapsa pfennigii, 1076
Thioploca, 1076
 Throat environment, *Enterococcus*, 165
 Thrombophlebitis, anaerobic cocci, 795
Tindallia, 654
Tissierella praeacuta, 669
 Tobramycin sensitivity, *Brochothrix*, 480
 Tongue dorsum, 1034
 intergeneric coaggregations of, 1032
Veillonella in, 1023–24
 Tonsils
Enterococcus, 165
Gemella, 516
Streptococcus pyogenes, 112
 Toxic shock syndrome
Staphylococcus, 59
Streptococcus pyogenes, 114, 129
 Toxin(s)
Bacillus anthracis, 611, 613
Clostridium difficile, 731–36
Clostridium perfringens, 754–58, 759
 phytopathogenic spiroplasmas, 933
Staphylococcus, 48, 55

- α -Toxin, 735
Clostridium perfringens, 699–700, 702, 759–64
 structure-function relationship, 762–64
- β -Toxin
Clostridium perfringens, 699–700, 702, 707–8, 713
 diseases from, 708, 717
 genetics of, 707–8
 mechanism of action, 708
 structure and function of, 708
- β 2-Toxin
Clostridium perfringens, 699–700, 702, 708
 diseases from, 708, 725
 genetics of, 708
 mechanism of action, 708
 structure and function of, 708
- ϵ -Toxin
Clostridium perfringens, 708–9
 diseases from, 709
 genetics of, 708–9
 mechanism of action, 709
 structure and function of, 709
- κ -Toxin
Clostridium perfringens, 702
- θ -Toxin. *See* Perfringolysin O
- τ -Toxin, 735–36
Clostridium perfringens, 699–700, 702, 709–11
 disease from, 711
 genetics of, 710
 mechanism of action, 710
 structure and function of, 710–11
- Toxin A, 731, 733–36
 in disease, 737–38
 genetics of, 733–34
 mechanism of action of, 735
 structure of, 734–35
 tests for detection of, 739–40
 treatment of, 741
- Toxin B, 731, 733–36
 in disease, 737
 genetics of, 733–34
 mechanism of action of, 735
 structure of, 734–35
 tests for detection of, 739–40
- Toxin LT, 735, 737
- Toxinotypes, 737
- Trace metals metabolism,
Prochlorococcus, 1105
- Transcription
Bacillus, 549–51
 mollicutes, 846, 867, 871, 888
- Transposons
Bacillus thuringiensis, 589
Clostridium, 673
Clostridium perfringens, 702
Enterococcus, 185–87, 189
Listeria, 412–14
 mollicutes, 874
- Trehalose metabolism
Bacillus larvae, 574
Bacillus lentimorbus, 567, 570
Bacillus popilliae, 567, 570
Brochothrix, 480
Carnobacterium, 380
Enterococcus, 176
Pediococcus, 247
 phytopathogenic spiroplasmas, 919, 934
Sporolactobacillus, 635
 Triazine resistance, Cyanobacteria, 1091
 Tricarboxylic acid cycle (TCA),
Staphylococcus, 24–26
Trichococcus, phylogenetic tree of, 321
Trichodesmium, 1060–62, 1077–78
Trichodesmium erythraeum, 1061
Trichodesmium thiebautii, 1060–61
 Trichomes, Cyanobacteria, 1054, 1067–70, 1069–70
 Trimethoprim resistance
Enterococcus, 189
Gemella, 515
Streptococcus pneumoniae, 155
 Trovafloxacin sensitivity, anaerobic cocci, 805
 Tryptamine production
Leuconostoc, 295
Weissella, 295
 Type IV pili, 907
 Tyramine production
Leuconostoc, 295
Oenococcus, 295
Pediococcus, 239
Weissella, 295
 Tyrothricin sensitivity, *Gemella*, 515
- U**
- Ultrastructure
Caryophanon, 648
Planococcus, 643
Sporolactobacillus, 634
Sporosarcina, 639
 Urea metabolism, *Selenomonas*, 988
Ureaplasma, 836–37, 842–43, 847, 855
Ureaplasma parvum, 924
Ureaplasma urealyticum, 853, 876, 879
 Urethritis
Mycoplasma, 879
Staphylococcus, 60
Ureaplasma, 879
 Urinary tract infection
Bacillus, 618
Enterococcus, 169
Lactococcus, 205
Leuconostoc, 303
 Urine environment, *Staphylococcus*, 10
 Urogenital tract
Gemella, 516
 mollicutes, 849–50, 861–63, 879, 882
Staphylococcus, 60
Streptococcus, 94–95
Streptococcus agalactiae, 131–32
 UV radiation
 Cyanobacteria protection from, 1090–91
 phytopathogenic spiroplasmas, 923
- V**
- Vaccine
Bacillus anthracis, 609, 612–13
Clostridium perfringens, 725, 729–30
 for dental caries, 94
 mollicutes, 876–77, 888–89
Streptococcus agalactiae, 136
Streptococcus pneumoniae, 155
Streptococcus pyogenes, 129
 Vaginal environment
 anaerobic cocci, 795
Enterococcus, 165
Lactobacillus, 333–34, 346, 371
Streptococcus agalactiae, 132
Vagococcus, 163, 229, 231
 phylogenetic tree of, 321
 Vancomycin resistance
Enterococcus, 186, 192
Erysipelothrix, 497
Leuconostoc, 302–3
Pediococcus, 254
 Vancomycin sensitivity
 anaerobic cocci, 805
Bacillus, 618–20
Clostridium difficile, 741
Enterococcus, 170–71
Gemella, 515
 Vegetables
Bacillus cereus, 615
Erysipelothrix, 492, 504
Kurthia, 523
Lactobacillus, 336–37, 347
Leuconostoc, 280–84, 304–5
Listeria, 409
Oenococcus, 280–84
Pediococcus, 255
Weissella, 280–84
 Vegetative cell
Bacillus, 530, 537–40, 552
Bacillus anthracis, 610–11
Bacillus larvae, 572–75
Bacillus lentimorbus, 564–66
Bacillus popilliae, 564–68
Bacillus sphaericus, 596
Bacillus thuringiensis, 583
 Clostridiaceae, 662
Clostridium, 662
Sporosarcina, 638–39
Veillonella, 966, 968–69, 982, 987, 1022–35
 adherence by, 1031–35
 gnotobiotic animal model, 1032–34
 intergeneric aggregation, 1032–34
 nichrome steel wire model, 1031–32
 applications of, 1030–31
 characteristics of, 1023
 disease from, 1030
 ecology of, 1027–29
 from healthy gingiva to
 periodontal disease, 1028
 metabolic communication, 1028–29
 before and after tooth eruption, 1027–28

epidemiology of, 1029–30
 experimental animal models for, 1024
 genetics of, 1027
 habitat of, 1022–24, 1034
 identification of, 1025–26
 isolation of, 1024–25
 pathogen inhibition by, 1031
 phylogeny of, 1022
 physiology of, 1026–27
 preservation of, 1026
 serology of, 1023
 taxonomy of, 1022–23
Veillonella alcalescens, 1023
Veillonella atypica, 1023–28, 1032, 1033
Veillonella caviae, 1023, 1026
Veillonella criceti, 1023, 1035
Veillonella dispar, 987, 1023–25, 1028–30, 1032
Veillonella parvula, 965, 968, 987, 1022–32, 1034
Veillonella ratti, 1023, 1031
Veillonella rodentium, 1023
Veillonellaceae, 966
 Veterinary enterotoxemia
Clostridium perfringens, 713–15, 717–30
 diagnosis of, 725–29
 prevention of, 729–30
Vibrio anguillarum, 375
Vibrio salmonicida, 375
Vibrio subtilis, 530
Virgibacillus, 520
 Virulence factors
Bacillus anthracis, 613–14
Listeria, 419–46
Streptococcus pyogenes, 118
 Virulence mechanisms,
 phytopathogenic
 spiroplasmas, 932–35
 Viruses. *See also* Bacteriophage
 phytopathogenic spiroplasmas,
 924–25
 spiroplasma, 907
Vitreoscilla, 645–46
 properties of, 646
Vitreoscilla stercoraria, 646

W

Wall teichoic acid (WTA)
 properties of, 40
 structure and biosynthesis of,
 38–39
 Wastewater environment
Enterococcus, 165
Kurthia, 521
Sporomusa in, 991
 Water stress, Cyanobacteria, 1091
Weissella, 234, 240–41, 243, 249,
 267–305, 320, 336, 349, 355
 applications of, 304–5
 characteristics of, 268, 274–75
 cultivation and preservation of,
 293–94
 ecology of, 302
 genetics of, 296–302
 habitats of, 273–84
 identification of, 289–93
 isolation of, 284–89
 morphology of, 272, 289
 phylogenetic tree of, 269, 321, 350
 phylogeny of, 267–71
 physiology of, 267, 294–96
 species of, 271–72, 289
 taxonomy of, 271–73
Weissella cibaria, 269–72, 281, 291
Weissella confusa, 236, 269, 272,
 280–81, 283, 289, 295–96, 303,
 324, 336
Weissella halotolerans, 269, 272, 276,
 278, 289
Weissella hellenica, 267, 269, 272,
 278, 289, 291
Weissella kandleri, 269–72, 289
Weissella minor, 269, 272, 278, 289,
 324
Weissella paramesenteroides, 267,
 269, 272, 275, 277–83, 289–91,
 293, 297, 302–3, 305
Weissella thailandensis, 267, 269, 272,
 280
Weissella viridescens, 269, 272–73,
 276, 278, 280, 289, 291, 296
 Wine
Lactobacillus, 340–41, 347

Leuconostoc, 282, 287
Oenococcus, 282, 287, 292, 295,
 301, 305

Wood-Ljungdahl pathway,
Sporomusa, 997–98

Wound infection

Lactococcus, 205

Leuconostoc, 303

WTA. *See* Wall teichoic acid

X

Xenococcus, 1066–67
 Xylan metabolism
Butyrivibrio, 1008–9
Butyrivibrio fibrisolvens, 1006
Eubacterium, 828
 Xylanase, in *Butyrivibrio*, 1010
 Xylitol metabolism, *Enterococcus*,
 176
 Xylose metabolism
Carnobacterium, 380
Staphylococcus, 21–22

Z

Zeaxanthin, *Prochlorococcus*, 1103
Zopfius, 519
Zymophilus, 965–78
 characteristics of, 968–78
 cultivation of, 972–73
 detection of, 972–73
 differentiation of, 969
 habitat of, 969–70
 identification of, 976
 isolation of, 972–73
 morphology of, 976
 phylogeny of, 966
 physiology of, 978
 preservation of, 976
 taxonomy of, 969
Zymophilus paucivorans, 965–67,
 969–70, 973–74, 976, 978
Zymophilus raffinovorans, 965,
 967, 969–70, 973–74, 976,
 978