

Index

A

- α -aminoadipic acid (AAA), 239
- ABC. *See* ATP-binding cassette (ABC) transporters
- Acidulants, 264
- Adenylate cyclase, 102, 104
- Aflatoxin, 36, 89, 91, 92, 112
- Agaricomycetes
 - extracellular peroxide generation (*see* Extracellular peroxide generation)
 - Fenton-based brown rot, 324
 - hypothetical and uncharacterized proteins, 322–323
 - laccases, 322
 - metaproteomics, 324
 - peroxidases (*see* Peroxidases)
- Agaricomycotina wood decayers, 193
- Agaricus bisporus*, 2, 16, 192–193, 313, 315
- Agrobacterium tumefaciens*, 276–277, 359–360
- Alaskan boreal forest ecosystem
 - acidic sites, 343
 - black spruce ecosystem, 346
 - Clade I, 346
 - diversity and distribution, 340–343
 - habitat-related environmental variables, 341, 342
 - indicator species analyses, 339, 342, 343, 345
 - ITS and LSU sequences, 337, 338
 - Jackknife analysis, 344
 - lineage-specific analysis, 345
 - mineral soils, 346
 - MRPP, 342
 - NMS, 343, 344
 - OTU13, 345
 - OTUs, 337
 - sequence and statistical analysis, 338–340
 - soil fungal communities, 337
 - soil horizon, 342, 345, 346
 - UP247, 344
- Alternaria alternata*, 178–180
- Amplified-Fragment Length Polymorphism (AFLP), 258
- Appressorium
 - ACE1* expression, 68
 - Δ pmk1 mutants, 61
 - CFEM protein members and PTH11, 54
 - dome-shaped penetration structure, 57
 - Magnaporthe*, 2
 - MAPK, 61
 - penetration peg, 62
- Arbuscular mycorrhizal symbiosis, 74–75
- Archaeorhizomycetes
 - Alaska (*see* Alaskan boreal forest ecosystem)
 - biogeographic patterns, 334
 - free-living saprophytic life strategies, 333
 - global distribution, 334–336
 - ITS and LSU sequences, 334
 - life strategies, 347
 - mycoparasitic, 333
 - soil fungal communities, 336–337
 - Taphrinomycotina, 333
- Aryl-alcohol oxidase (AAO), 321
- Ascomycete, 3, 18, 20, 35, 112, 113, 220, 300
- Aspergillus fumigatus*, 89, 91–94, 98, 99, 101–106, 108–111
- Aspergillus* Genome Database (AspGD), 93, 105
- Assemblers, 12, 13
- ATP-binding cassette (ABC) transporters, 66–69, 175, 241, 245

B

- Bipolar heterothallism, 129
- BLASTn algorithm, 257
- Boreal forests saprotrophic fungi, 192
- Broad Institute, 51, 54, 92, 93, 158, 269, 291

C

- CADRE, 93
- cAMP-PKA, 103
- Carbohydrate active enzymes (CAZymes), 15–16, 36–37, 96, 99, 136, 139, 176, 200, 298–300
- Carbon catabolite repression (CCR), 65, 66
- Catalytic subunits of PKA, 103, 104
- CAZymes. *See* Carbohydrate active enzymes (CAZymes)
- Cellobiose dehydrogenase (CDH), 316, 321
- Cellulose, 35–37, 50, 95–97, 139, 192, 199, 200, 311–312
- Cell wall integrity (CWI), 105, 106, 167
- Cleistothechia, 101, 107, 262
- Cochliobolus heterostrophus*
 - asexual and sexual sporulation, 215–217
 - conidia germination, 217–219
 - Dothideomycete soil biology, 223–225
 - filamentous ascomycete plant pathogen, 215
 - invasion and virulence, 216, 217, 219–220
 - leaf penetration, 219
 - Pleosporales, 213
 - and SCLB, 213–215
 - secondary metabolites (*see* Secondary metabolites)
 - statistics and SNPs, 220–221
 - T-cytoplasm maize, 215
 - Texas male-sterile maize, 214–215
- Conidiation-defective genes, 70
- Conidiophores, 69–70
- Coprinus cinereus* peroxidase (CiP), 315, 317
- Cultivation-independent methods, 196
- Cutinases, 59
- cyclic AMP (cAMP), 102, 103, 161

D

- Dothideomycete genomes, 213, 214
- Dothideomycetes, 17. *See also Cochliobolus heterostrophus*
- Dye-decolorizing peroxidases (DyPs), 318–319

E

- Ectomycorrhizae (EM), 3, 16, 194–195
- Ectomycorrhizal fungi (ECM)
 - carbon and nitrogen, 201–203
 - development of novel biomarkers, 206–207
 - extrametrical mycelium (*see* Extrametrical mycelium)
 - fungal hyphae-SOM-mineral assemblies, 192
 - iron-reducing compounds, 197
 - litter decomposition, 193
 - novel spectroscopic methods, 204–205
 - organic N compounds, 191
 - organic nitrogen theory, 192
 - protein degradation pathways, 203–204
 - SOM degradation reaction, 192
 - spectroscopic techniques, 196–198
 - transcriptome profiling, 198–200
 - trimmed saprophytic activity, 200–201
- Effector proteins, *Fusarium oxysporum*
 - bioinformatic analysis, 172
 - Fo5176-SIX4* gene, 172
 - Fov-SIX6* and *Fol-SIX6* protein, 171–172
 - non-host cells, 171
 - PEP1 and PEP2 encodes, 172–173
 - SIX3/Avr2 proteins, 171
 - SIX proteins, 170–171
 - VCGs, 171
- Effector-triggered immunity (ETI), 67
- Electroporation, 359
- Encyclopedia of DNA elements (ENCODE), 11–12, 20
- Enzyme cocktail, 99, 358
- 12,13-epoxytrichothec-9-ene (EPT), 143
- Exportin-5/Msn5p (EXP5), 72
- Expressed sequence tags (ESTs), 37
- Extracellular matrix (ECM), 58–59
- Extracellular peroxide generation
 - copper radical oxidases, 319–320
 - GMC oxidoreductases, 320–321
 - lignocellulose biotransformation, 319
- Extracellular proteome, 97
- Extrametrical mycelium
 - enzyme activity profiling, 196
 - humic soil layer, 196
 - hydrolytic and oxidative enzymes, 195
 - isotope analyses, 195
 - nutrient-mobilizing enzymes, 195–196
 - Pinus contorta*, 195
 - plant root system, 194
 - saprotrophic fungi, 196
 - soil microcosms, 195

F

- Fenton-based biodegradation system, 198
 Fluffy autolytic dominant phenotype, 101
fos-1, 110
 Fowl1, 75
fphA, 109, 111
 Fumaric and malic acid (FMA), 258, 264
 Fumonisin, 113, 169
 Functional genomics, 17, 19–20.
 See also Neurospora
 Fungal blast, 51
 Fungal genetics
 agrobacterium, 359–360
 Aspergillus, 362–364
 auxotrophic complementation, 360
 biolistic, 359
 chemical transformation, 359
 chlorate resistance, 364
 drug resistance, 361
 electroporation, 359
 emphasis, 353
 FGSC collection, 365
 fluorescent protein (*see* Green fluorescent protein (GFP))
 gene manipulations, 351
 GMO organisms, 352
 impact of, 369–370
 interspecific transfer, 364
 mendelian genetics, 353–354
 mutagenesis (*see* Mutagenesis)
 Neurospora, 362
 non-mendelian genetics, 354–355
 novel methods, 361–362
 polyethylene glycol, 358
 protoplast fusion, 358
 purification, 369
 recyclable markers, 361
 research *vs.* commercial, 351–352
 visualization, 369
 1000 fungal genomes project, 18
Fusarium oxysporum
 A. nidulans, 166
 AreA transcription, 164
 cAMP level, 161
 chitin synthase, 166
 CWDE genes, 165, 166
 deletion mutant, 167
 effector proteins (*see* Effector proteins, *Fusarium oxysporum*)
 environmental condition, 160–161
 FGA1/FGA2 mutants, 161–162
 Fnr1/AreA, 164
 forma specialis, 158
 G-proteins, 161

- HapX, 174–175
 histidine kinase, 163
 LS regions (*see* Lineage-specific (LS) regions, *Fusarium oxysporum*)
 MAPK pathway, 162–163
 MeaB protein, 164
M. oryzae, 165
 pathogenicity, 163
 plant defence compounds, 168–169
 plant infection, 159–160
 role of GAS1, 167
 SCF complex, 166
SGE1 gene encodes, 173–174
SNF1 gene, 165–166
 Ste12 functions, 163
 supernumerary chromosomes, 179
 TOR, 164–165
 toxin production, 169–170
U. maydis, 165
 VCGs, 158–159
 xylanase encoding, 165
 Zn2Cys6 transcription factor, 173

G

- Gaeumannomyces graminis*, 48–50
 G α -G β -G γ , 101
 Gene prediction, 13, 14, 53
 Genetic models, 2, 215, 291
 Genetics and molecular biology,
 Rhizopus oryzae
 Agrobacterium tumefaciens, 276–277
 filamentous mold, 272
 gene disruption, 277–278
 homologous integration, 273
 human fungal pathogens, 272
 markers, reporters, and inducible promoters, 275–276
 mutagenesis, 274–275
 transformation, 273–274
 Genome annotation, 94, 270
 Genome finishing, 12
 Genome sequence, *Rhizopus oryzae*
 duplicated protein complexes, 270–271
 fungal phylogenetic tree, 269
 gene families, 272
 genome annotation, 270
 Genomic Encyclopedia of Fungi, 16
 Genoscope, 291–292
 Global distribution, 91, 334–336
 Glyoxal oxidase (GLX), 319–320
 G-protein coupled receptors (GPCR), 101–104, 107
 Green fluorescent protein (GFP)

Green fluorescent protein (GFP) (*cont.*)

- Aspergillus*, 366
- gGFP plasmid, 366
- Neurospora*, 366
- visualization tags, 366–368

H

- Heme-thiolate peroxidases (HtPs), 317–318
- Hemicellulose, 37, 95, 96, 139, 312
- Heterokaryon incompatibility (HET), 133–134, 286
- Histidine-containing phosphotransfer (HPT) protein, 108–110
- Histidine kinase, 105, 107–111
- Human Genome Project, 11, 15
- Human mucormycosis, 255
- Hydrophilic polystyrene (PHIL-PS), 72
- Hyphal fusion, 162, 163, 180
- Hyphal Interference, 288, 298, 301

I

- Induced systemic resistance (ISR), 130, 142, 234
- Industrial applications, 89, 236
- Internal transcribed sequences (ITS), 18–19
- Intracellular proteome, 99
- Isocitrate lyase enzyme (*ICL1*), 62, 166
- Isopenicillin N-acyltransferase (IAT), 239

J

- Jackknife analysis, 340, 344
- Joint Genome Institute (JGI), 3, 14, 92–94, 213, 220

K

- Krebs cycle, 264

L

- Laccaria bicolor*, 3, 15
- Leaf infection process
 - ABC transporters, 69
 - ACE1 gene, 67–68
 - appressorium differentiation, 57, 59–60
 - AVR effector function, 67
 - biotrophy-associated secreted, 68
 - conidiation and light regulation, 60, 69–71
 - ECM, 58–59
 - ETI, 67

- fungal effectors, 67
 - fungal metabolism and plant infection, 64–66
 - fungal plant penetration, 62–63
 - invasive hyphae (IH), 63–64
 - Mag-toxin, 69
 - orchestrated cellular processes, 60–62
 - plants secrete toxic compounds, 69
 - PTI, 67
 - PWL gene, 68
 - pyrichalasin H, 68
 - secreted proteins, 67
 - Slp1, 67
 - wind-dispersed/water-splashed conidium lands, 57
- Leucine auxotrophy, 291
- Light-dependent disease suppression, 70
- Lignin, 2, 5, 16, 17, 95–96, 169, 192, 198, 312, 321
- Lignin decay mechanisms, 192
- Lignin peroxidase (LiP), 314–316
- Lignocellulose degradation, 15, 16, 33, 34, 311, 316, 320
- Lignocellulose metabolism
 - Aspergillus*, 36
 - biofuel feedstock, 33
 - brown rot fungi, 37
 - CAZy family, 36–37
 - cbhl* cluster, 35
 - cDNA and rRNA tags, 37
 - C. subvermispota*, 36
 - decomposition, 34, 38
 - enzyme expressions, 36
 - FTIR-ATR, 34
 - fungal–fungal interactions, 38
 - industrial fermentation, 33
 - natural ecosystems, 35
 - Neurospora*, 33–34
 - P. chrysosporium*, 36
 - saprotrophic species, 35
 - soil component, 35
 - soil processes, 37
 - Trichoderma*, 37
 - VOC production, 38
- Lineage-specific (LS) regions,
 - Fusarium oxysporum*
 - ABC transporters, 175
 - Alternaria alternata*, 180
 - ascomycetes, 175
 - CAZyS, 176–177
 - C. lindemuthianum*, 180–181
 - conidial and hyphal fusions, 180
 - F. graminearum*, 176

- F. verticillioides*, 176
 mobile chromosome, 181
 non-orthologous chromosomes, 177–178
 pathogenicity chromosome, 177
 SIX proteins, 176
 supernumerary chromosomes, 178
 transcription factors, 175
 VCGs, 178
- Lovastatin, 91, 113
- M**
- Macroconidia, 69
- Magnaporthaceae
 fungal databases, 76
Gaeumannomyces graminis, 48–50
 genome sequences, 53–55
 pathogens (*see* Root-infecting pathogens)
 rice blast disease, 51–53
 root-infecting fungus, turfgrasses, 49, 51
 taxonomy, 45–48
- Magnaporthe oryzae*. *See also*
 Magnaporthaceae
 leaf infection process (*see* Leaf infection process)
 reproduction, 55–56
- Magnaporthe poae*, 51
- Manganese peroxidase (MnP), 314–316
- Markov cluster algorithm (MCL), 133
- MC69, 67
- Melampsora laricis-populina*, 15
- Melanin-deficient mutants, 49–50
- Mesosyteny, 17
- Metagenomics, 18, 20
- Metatranscriptomics, 19, 323
- MgFowl, 75
- Microplate enzymatic tests, 195–196
- Mitochondrial respiratory activity, 75
- Mitogen-activated protein kinase (MAPK),
 2, 61, 104–107, 162–163, 217
- mpkA*, *mpkB*, *sakA/HogA*, 105
- mpkC*, 105, 106
- Mucor circinelloides*, 261
- Mucormycosis, 255
- Mutagenesis
 classic mutant strains, 356
 genome lineage, 356
 mating type, 355
N. crassa, 355–356
 penicillin-producing strains, 357
 polymorphisms, 357
 transcriptome analysis, 357
- Mycocosm, 14, 92, 94, 132, 133
- Mycoparasitism. *See Trichoderma*
- Mycorrhizal fungi, 3, 17, 131, 192, 203,
 206, 337
- Mycotoxins, 91, 107, 111, 113, 128, 169
- N**
- Neurospora*
 functional genomics, 29–30
 lignocellulosic biomass (*see* Lignocellulose metabolism)
N. crassa, 12–13, 20
 sensing light, 30–32
- Next-generation sequencing (NGS), 11–13, 19,
 30, 289, 296
- nika*, *tcsA*, *tcsB*, 109
- Nitrogen metabolite repression (NMR), 65, 66
- Nonribosomal peptide synthases, 221–222
- Non-ribosomal peptide synthetase (NRPS),
 113, 114, 140–142, 222, 239, 300
- Novel methods, 361–362
- O**
- Ochratoxin, 89, 91, 92, 112–113
- Oidiodendron maius*, 3
- Opportunistic pathogens, 5, 89, 91, 109,
 128, 131
- Organic matter, ectomycorrhizal fungi (ECM)
 iron-reducing compounds, 197
 spectroscopic techniques, 196–198
 transcriptome profiling, 198–200
 trimmed saprophytic activity, 200–201
- Organic nitrogen theory, 192
- Osmotic stress, 105, 110, 111
- Oxidative stress, 104, 106, 111, 168, 177,
 219, 220
- P**
- PACC gene, 160–161
- PAMP-triggered immunity (PTI), 67
- Pathogens, 11, 12, 15–17, 19, 20
- Paxillus involutus*, 3, 195–198, 313
- Penicillin biosynthesis
 α -amino adipic acid (AAA), 239
 β -lactam molecule, 239
 compartmentalization, 238–240
 genome insights, 243–244
 IAT, 239
 penicillin gene cluster, 241–243
- Penicillium chrysogenum*
 antimicrobial compounds, 234–236

- Penicillium chrysogenum* (cont.)
 biochemical arsenal, 236
 β -lactam molecules, 246–247
 classical strain improvement, 244–245
 evolutionary path, 229, 237–238
 genomics-based strain improvement, 245–246
 gram-positive bacteria, 229
 metabolites, 229–231
 natural habitats, 230, 234
 penicillin biosynthesis (see Penicillin biosynthesis)
 peptidoglycan polymers, 229
 taxonomy, 237
- Peroxidases
 dye-decolorizing peroxidases (DyPs), 318–319
 heme-thiolate peroxidases (HtPs), 317–318
 high oxidation potential class II peroxidases, 314–316
 low oxidation potential class II peroxidases, 315, 317
 manganese peroxidase (MnP), 314–316
 NC-IUBMB system of nomenclature, 313
- Pezizomycotina, 132, 133, 135, 139, 283, 292, 293
- Phanerochaete chrysosporium*, 16, 36, 312, 315–322
- Phycomyces blakesleeana*, 261
- Phylogeny, *Rhizopus oryzae*
 actin (act-1), 257
 BLASTn algorithm, 257
 medical mycology, 256, 257
 molecular methods, 257
 vs. *Rhizopus delemar*, 258–259
 taxonomy, 257
 translation elongation factor 1 alpha (EF1 α) genes, 257
- Pinus contorta*, 195
- Piriformospora indica*, 4
- PKA regulatory subunit, 103, 104
- PKA regulatory subunit (pkaR), 104
- Plant biomass, 33, 92, 95, 97, 99, 127, 236, 263, 283, 284, 300
- Podospora anserina*
 agilent microarray, 296
 ascospore ejection, 298
 ascospore formation, 284
 barrage phenomenon, 285
 basidiomycetes, 300
 biomass degradation, 299
 BLAST analyses, 293
 CAZy repertoire, 298
 chromatograms, 293
 coprophilous species, 284
 cytosolic translation, 297
 DNA banks, 294
 ecology and life cycle, 287–288
 gene-by-gene analysis, 292
 genetic analysis, 288–290
 genetic transformation, 290–291
 green fluorescent protein (GFP), 296
 Het-s protein, 297
 hyphal fusion, 284
 life cycle, 284, 286
 microarray analysis, 292
 mus51 coding sequence, 294, 296
 popular fungal models, 284
 pseudohomothallism, 284, 287
 repeat-induced point mutations (RIP), 293
Saccharomyces cerevisiae genome sequence, 291–292
 SAMtools package, 296
 secondary metabolites, 300–301
 split marker method, 294, 295
- Polyethylene glycol (PEG), 358
- Polyketide synthase, 112–114, 142, 221–223, 300
- Polysaccharide hydrolyzing enzymes, 138–139
- Postia placenta*, 199
- 12,827 protein-coding genes, 53
- Protein release, 98
- Proteomics, 19, 20, 37, 94, 97–98
- Pyranose 2-oxidase (P2O), 320
- Pyrosequencing, 12, 19, 35, 37
- Q**
 Quantitative trait loci (QTL), 2, 54
 Quorum sensing mechanism, 129
- R**
 Repeat-induced point mutation (RIP), 56, 132, 293, 355
 Re-sequencing, 13
 Response regulator, 107–108
 Restriction-site-associated DNA (RAD), 30
Rhizopus delemar, 258–259
Rhizopus oryzae
 clinical manifestations and infection sites, 266, 267
 enzymes, 263
 filamentous fungus, 255
 genome sequence (see Genome sequence, *Rhizopus oryzae*)

- growth and identification, 259–260
- host status, 265–266
- human mucormycosis, 255
- Mucorales/Entomophthorales, 255
- organic acids, 264–265
- pathogenic zygomycetes, 256
- phylogeny (*see* Phylogeny, *Rhizopus oryzae*)
- sexual cycle, 261–262
- tempe production, 262–263
- treatment, 269
- virulence factors, 267–269
- zygomycotic infections, 255
- Rice blast disease symptoms, 51–53
- Root-infecting fungus of turfgrasses, 49, 51
- Root-infecting pathogens
 - arbuscular mycorrhizal symbiosis, 74–75
 - Exp5, 72
 - G. graminis*–*Phialophora* complex, 59, 71
 - hydrophilic polystyrene (PHIL-PS), 72
 - hyphopodia-mediated root penetration, 71
 - melanin-independent mechanism, 71
 - pre-invasive hyphae (pre-IH), 72
 - root specific infection-deficient phenotype, 72–74
- S**
- Sanger sequencing, 12, 13, 19
- Saprotrophic fungi, 192
- Schizophyllum commune*, 20, 325
- Secondary metabolites
 - Aspergillus* spp., 5, 111–114
 - chemical structures, 197
 - Fusarium* species, 169–170
 - melanins, 49
 - M. oryzae*, 68
 - non-penicillin-producing conditions, 235
 - NRPS, 221–222
 - penicillin production strains, 234
 - PKSs, 222–223
 - SSCPs, 223
 - Trichoderma* spp (*see* *Trichoderma*)
 - wine yeasts, 38
- Secreted in the xylem (SIX), 170–171
- Secreted LysM Protein1 (Slp1), 67
- Secretome, 97, 99. *See also* *Trichoderma*
- Signal transduction
 - Aspergilli*, 100
 - cAMP/PKA-signaling cascade and G-protein-coupled receptors, *Aspergillus*, 101–104
 - environmental signals, 100
 - filamentous fungi, 100
 - fungal cells, 100
 - histidine kinase (HK) phosphorelay system, 107–111
 - MAPK, 104–107
- Single molecule sequencing, 12
- Single-nucleotide polymorphisms (SNPs), 220–221
- Skp1–Cullin–F-box protein (SCF) complex, 166
- Small secreted cysteine-rich proteins (SSCPs), 136–137, 146, 147, 221, 223
- Small secreted proteins, 1–4, 15
- Soilborne fungi, 4, 158
- Soil microcosms, 195
- Southern Corn Leaf Blight (SCLB), 213
- Sporangiophores, 259
- sskA*, 108, 110, 111
- ssrA*, 111
- ssrB*, 111
- ssrC*, 111
- Sucrose non-fermenting (*SNF1*) gene, 165–166
- Sustainable energy, 95
- Symbionts, 3, 4, 11, 12, 15, 16, 20, 74, 192, 225
- T**
- Taphrinomycotina, 333
- Target of rapamycin (TOR), 64–65, 164–165
- tcsC*, 110–111
- Teleomorph, 47–48, 127, 129, 132–133, 354
- Transcriptome, 20, 33, 37, 70, 74, 99, 147, 197–199, 204, 221, 240, 302, 357
- Transcriptomics, 3, 13, 19, 20, 36, 37, 54, 94, 99, 141, 147, 206
- Trichoderma*
 - cellulase and hemicellulase production, 146
 - developmental biology, 129
 - genomic features, 131–133
 - habitats, 130–131
 - high-frequency homologous transformation, 146
 - high-throughput techniques, 145
 - isoprenoid derivatives, 142–143
 - mycoparasitism, 133–134
 - NRPS, 140–142
 - opportunistic pathogens, 128
 - pezizomycotina, 135
 - polyketide synthases, 142
 - polysaccharide hydrolyzing enzymes, 138–139
 - proteolytic enzymes, 140
 - SSCPs, 136–137
 - T. atroviride*, 147

Trichoderma (cont.)

taxonomy and phylogeny, 128–129

T. reesei wild-type, 144–145*T. virens*, 147

volatile metabolites, 144

Trichoderma reesei, 20, 129, 131–134,
138–144, 147–145**U**

Ubiquitin–proteasome pathway, 271

Uracil auxotrophy, 290

US DOE Joint Genome Institute (JGI), 14

Ustilago maydis, 2, 5, 20, 165, 223, 358**V**

V-ATPase complex, 271

Vegetative compatibility group (VCG),
158–159, 171, 366

Versatile peroxidase (VP), 313

Verticillium, 3, 366

Volatile organic compounds (VOCs), 38, 129

Volatile secondary metabolites, 144

W

Wood decay, 15, 16, 312, 320, 321

Y*ypdA*, 111**Z**

Zygomycete fungi, 5