

Index

A

- Adaptive coupling, 116, 127, 140–142, 147, 151–153
- Adaptive introgression, 332–333, 486–488, 540–542
- Adaptive landscape, 488–489
- Adaptive peaks, 485–487, 489
- Adaptive radiation
 - avian island, 439–458
 - definition, 470–471
 - determinants of, 470–472
 - ecology role in, 387–401
 - host radiation and symbiont speciation, 421–434
 - hybridization, 333–334, 485–488
 - island systems, 399–400
 - key innovations, 396–397, 413, 470, 472–477, 482, 486–488
 - metabolomic analyses, 488
 - neotropics, 469–490
 - niche theory, 405–417
 - realistic limit to coexisting species during, 413–416
 - whitefish in peri-alpine lakes, 541
- Adaptive radiation events
 - adaptation and increase in genetic diversity, 413
 - initial colonization, 413
 - new arrivals, 414
 - optimization and limits to opportunities, 413–414
- Adaptive radiations, investigations of
 - biotic interactions, 393–395
 - eco-evo-devo, 396–398
 - island systems, 399–400
 - key questions, 391
 - life history strategies, 395–396
 - next steps in research, 398–400
 - niche and ecological speciation, 391–393
 - outstanding challenges, 389–391
 - overview, 388–389
 - separating correlation from causation, 398–399
 - variation through time, assessing, 398
- Adaptive zone, 472, 482, 485–486, 488–489
- Admixture, 325, 327, 332–333
- Admixture gradient, 165–166
- Admixture mapping, 215, 217, 220–221
- Allelic underdominance, 280, 283–284
- Allelic variation, contribution to prezygotic isolation, 231–233
- Allopolyploid hybrid speciation, 324–326, 333
- Anagenesis, 373
- Ancestry heterozygosity, 255–260
- Ancestry proportion, 255–259
- Andes, 474–475
- Antagonistic coevolution, 4, 200, 426
- Anthropogenic change and speciation
 - altered geography, 536–538
 - altered hybridization, 540–542
 - altered selection, 538–540
 - altered species turnover, 542–543
 - examples, 531–534
 - long-term studies, 543–544
 - overview, 529–530, 536
 - schematic, 535
 - whitefish-adaptive radiation in peri-alpine lakes, 541
- Asexual reproduction, in hybrids, 278, 287
- Assortative mating
 - genetic coupling, 199–203, 206–207, 209
 - negative coupling, 182, 184, 195
 - prezygotic isolation, 230–237
- Assortative mating incompatibility, 327
- Avian island radiations
 - bird–parasite interactions, 452–453
 - character displacement, 454
 - ecological release, 453–454
 - evolutionary thinking shaped by, 440–442
 - extinct species, 450–451
 - genomic and ecological data needed, 448–449
 - importance of nonadaptive, 444–447
 - information needed concerning, 455–458
 - molecular techniques for studying diversification in island birds, 447–448
 - on oceanic islands, 442–444
 - questions for future research, 457
 - summary of, 445

B

- Barrier effects, 115, 135–156, 201
- Barrier loci
 - definition, 136–137, 327
 - genomic approaches, 217–221, 235, 249
 - in hybrid zones, 163–167, 173–176
 - linkage disequilibrium, 135–152
 - linking observed phenotypes to underlying, 72
- Barriers to gene exchange. *See specific barriers*

Index

- Barrier trait, 136–146, 150, 152–156
Bias, study system, 213–223
Biotic interactions, adaptive radiations and, 393–395, 477, 482–485
Bird–parasite interactions, 452–453
Bottom-up approaches, 217–219
Brazilian Shield, 474–475
Breakpoint selection, 371
- C**
- Carrying capacity, 101, 117, 167, 409, 451
Chance, 553–554
Character displacement, 454
Chromosomal rearrangements. *See also* Structural variants
 accumulation of DMIs at non-recombining regions, 285–286
 commonly studied, 370
 detection of, 371–372
 diploidization in plants, 378
 holocentric chromosomes, 377–378
 impact speciation, 369–381
 karyotypic orthoselection, 375–376
 life history and biogeography association, 379
 macroevolution view on speciation, 369–381
 origin and fixation of, 373–376
 in sex chromosomes, 378
 species diversity, correlations to, 377
 underdominance, 284–285
Chromosomal speciation, 348, 369–381
Cladogenesis, 373, 451
Cline
 genomic, 165–170, 172–175, 218
 geographic, 165–169, 172
Cline variance
 measuring, 165–167
 quantitative analyses of coupling in hybrid zones, 163–166, 172–173, 175, 177
 simulations connecting to coupling, 167–170
Coevolution
 antagonistic, 4, 200, 426
 genetic architecture, influence of, 200–201
 sexual and habitat isolation during reinforcement, 115–131
 sexual isolation, 200
Combinatorial speciation, 333
Commensals, 422
Competition, 393–394, 454
Complexity, 553
Congealing, genome-wide, 148, 175, 330
Consumer–resource model, MacArthur’s, 409–411
Contingency, 553–554
Copy number variants, 347–349, 358–359
- Coupling
 adaptive, 116, 127, 140–142, 147, 151–153
 approaches to advance understanding of, 153–156
 causes and consequences, 135–156
 cline variance connected to, 167–170
 as coincidence of barrier effects, 135, 137–139, 150–152
 definitions, 115, 137, 164, 182, 201
 genetic coupling of mate recognition systems, 199–210
 genome-wide linkage disequilibrium, 135, 137–139, 147–150
 linkage disequilibrium build-up among barrier loci, 135, 137–147
 negative, 181–197
 quantitative analyses in hybrid zones, 163–177
 sexual and habitat isolation during reinforcement, 115–131
Coupling coefficient
 cline variance, relationship to, 165
 definition, 136
 linkage disequilibrium, 147–148
 quantitative analyses in hybrid zones, 163–176
Creation, special, 517–518
CRISPR–Cas9, 207–208, 219, 285
- D**
- Darwin, Charles
 on character displacement, 454
 on human ancestry, 519–521
 view of speciation, 497–501
Darwin’s corollary, 308
Desaturase gene (*desat1*), 206–208
Despeciation, 530, 536–538, 540–542
Developmental variation, 396–398
Divergence. *See also* Phenotypic divergence
 anthropogenic impacts, 529–534, 537–539, 541–543
 axis of, 257–258
 genomic view, 286–287
 mode effect on hybrid fitness, 308–313
 niche, 392
 probability of hybridization, 324
Divergence hitchhiking, 148
Divergent selection
 anthropogenic activities, 536–541, 543
 biotic interactions, 393
 ecological hybrid incompatibility under, 257–258
Diversification
 causes of link to molecular evolution, 504–506
 Darwin’s view on speciation, 497–501
 diversity-dependent, 406
 molecular, macroevolutionary, and macroecological perspectives, 487–511

- Diversification rate
 - in birds, 509–510
 - molecular evolution link to, 502–511
 - in plants, 378, 507–508
 - in ray-finned fish, 508–509
- Diversity equilibrium, 452
- DNA repair, 504, 506–507
- Dobzhansky–Muller incompatibilities (DMIs)
 - accumulation at non-recombining regions, 285–286
 - assumptions about, 249, 251
 - ecologically mediated, 247–263
 - intrinsic, 251–252, 255
 - intrinsic postzygotic isolation, 278–281
 - as nonecological, 248–249
 - oligogenic, 249, 255, 259, 262
 - Orr’s model, 313–315
 - parallel natural selection, 255
 - sexual and habitat isolation during reinforcement, 115, 117, 121–126, 129
- Dobzhansky–Muller incompatibility model, 248–252, 262, 314–315, 327
- Duplication
 - of genes and postzygotic isolation, 281–283
 - whole-genome, 285, 378
- Dysgenesis, 287–288, 356–357

- E**
- Ecological differentiation, character displacement and, 454
- Ecological hybrid incompatibility
 - under divergent selection, 257–258
 - under parallel selection, 255–257
- Ecological opportunity
 - context of biotic interactions, 477, 482–485
 - in context of neotropical geology, 472–477
 - definition, 472
 - hybridization, introgression, and admixture, 485–488
- Ecological release, 414, 453–454
- Ecological selection
 - hybrid incompatibility phenotypes under, 253
 - sexual selection, 200
- Ecological speciation
 - adaptive radiations, 391–393
 - falling between niches, 258, 263
 - links between phenotypic divergence and reproductive isolation, 262
 - phenotypic divergence, 262
 - selection against hybrids, 254, 256–258
 - small-effect alleles, selection on, 218
 - through sensory system divergence, 39, 45
- Ecology
 - adaptive radiation, role in, 388–401
 - avian island radiations, 448–449
 - hybrid incompatibilities, 247–263
- Ecomorphs, 407–408, 411, 416
- Environmental DNA (eDNA), 433
- Environmental effects
 - anthropogenic change, 529–544
 - influence of change on sensory communication, 47–51
 - molecular evolution rates, 506–509
 - on relative hybrid fitness, 252–253
- Epidemiological disease modeling, 421, 429–431
- Epigenetic dysregulation, 287–290
- Epistasis
 - definition, 325
 - Fisher’s geometric model, 303, 309–311, 313–314
 - fitness, 141, 251–256, 303
 - negative, 248–249, 252, 257–259, 303, 305, 313–314
 - transgression, 331
- Epistatic selection, 203, 251, 260, 263
- Escape-and-radiate (EAR) hypothesis, 425–426
- Essentialist species concept, 518–519, 523
- Evo-devo studies, on adaptive radiations, 397
- Evolutionary development, as constraint on prezygotic isolation evolution, 237
- Evolutionary history, as constraint on prezygotic isolation evolution, 235–236
- Evolutionary radiation, 440
- Extinction
 - bird–parasite interactions, 452–453
 - human impact, 543
 - island organisms, 449–450, 456
 - link to adaptive radiations, 394–395, 449–450
 - theory of island biogeography, 451–452
- Extrinsic barriers, 248
- Extrinsic reproductive isolation, variation in, 97–111

- F**
- Fascism, 522
- Fisher’s geometric model
 - Darwin’s corollary, 308
 - genomics data, 315–316
 - interpretation and applications, 303–316
 - mapping genotype to fitness, 300
 - mode of divergence effect on hybrid fitness, 308–313
 - Orr’s model compared, 313–315
 - parameters n and k , meaning of, 303–307
 - phenotypic model, 301, 305, 308, 314, 317
 - speciation questions addressed with, 302
 - as tool in speciation, 299–317
 - usefulness of, 301–302
- Fitness
 - negative epistasis for, 248–249, 252, 257–259
 - predictability of hybridization outcomes at level of, 335–336

Index

- Fitness advantage, 299, 311, 336, 395
Fitness epistasis, 141, 251–256, 303
Fitness landscapes
 example models, 301
 Fisher's geometric model, 299–317
 overview, 299–300
 phenotypic model, 301, 305, 308, 314, 317
Flexible-stem hypothesis, West-Eberhard's, 397
Flightless birds, 443, 449–450, 455–456
Flowering plants
 prezygotic isolation, 233–234, 237, 239
 sexual isolation, 23–24
fruitless gene, 206–208
Fundamental niche, 391, 414–415
- G**
- Gene conversion, 448
Gene duplication, 281–282
Gene flow
 anthropogenic impacts, 536–537, 539–541
 definition, 325
 genome-wide barrier, 174
 prezygotic barriers, 239–240
 selfing influence on, 1–5, 13
 sexual isolation as barrier, 19–20, 22–23, 25–28, 31
 variation in extrinsic reproductive isolation effect
 on, 97–98, 101–111
Genetic architecture
 adaptive radiation, 486, 488
 clumped, 312
 definition, 230, 325
 Fisher's geometric model,
 312–313
 of incompatibilities, 263
 phenotypic variation in hybrids, 253–254
 of postzygotic isolation, 258
 of prezygotic isolation, 231
 QTL analyses, 215
 of reproductive isolation, 312–313
 transgression, 332
Genetic coupling
 broad-sense, 201–203, 208–209
 of mate recognition systems, 199–210
Genetic distance, 30, 314, 503, 505, 509–510
Genetic diversity loss, of island species, 448
Genetic drift, 3, 8, 200
Genetic studies of speciation
 bottom-up phenotype-naive, 217–219
 classical, 214–215, 223
 contemporary, 215–219, 223
 genomic approaches, 213–223
 at intersection of laboratory and nature,
 219–223
 opportunities for, 219–222
 taxonomic representation in studies, 213–223
 top-down mapping, 215–217
Gene transposition, 282–283
Genomic cline, 165–170, 172–175, 218
Genomic hitchhiking, 148
Genomics
 adaptive radiations and, 488
 avian island radiations, 448–449
 chromosomal rearrangement detection, 371–372
 resolution of study system bias by, 213–223
 taxonomic representation in studies, 213–223
Genomic variation, effect of bird–parasite interactions,
 452–453
Genotypic landscape, hybrid incompatibilities on,
 254–258
Geography, anthropogenic alterations of, 536–538
Geological history of neotropics, 474–475
Guiana Shield, 474–475
Gustatory receptor (Gr) locus, 207, 209
- H**
- Habitat hybridization chance, 325–326
Habitat isolation, sexual isolation interaction with,
 115–131
Habitat loss/fragmentation, 537–538, 542
Habitat matching and choice, sensory system and, 46–47
Haldane's rule, 281–282
Herbivory, in adaptive radiations, 394
Heterochrony, 397
Heterosis, 325, 331, 336
Heterozygosity
 large-effect loci as outliers, 315–316
 level and hybrid fitness, 311
Hill–Robertson effect, 286
Holocentric chromosomes, 377–378
Homopolyploid hybrid speciation, 325–326, 333
Host radiation, 421–434
Human variation, 517–526
Hutchinson's rule, 409
Hybrid breakdown, 252, 255–258, 263, 329, 335–336,
 357
Hybrid fitness
 chromosomal rearrangements, impact of, 372
 coevolutionary sexual and habitat isolation
 interactions, 117
 ecology as mediator of, 249
 environmental effects on relative, 252–253
 extrinsic component of, 308
 Fisher's geometric model, 299, 302, 308–311
 impact of variation in, 97–99, 101, 105–111
 level of heterozygosity, 311
 lowered by structural variants, 350
 mode of divergence, effect on, 308–313
 persistence, 28
Hybrid incompatibility. *See also* Dobzhansky–Muller
 incompatibilities

- under divergent selection, 257–258
 - ecology of, 247–263
 - epigenetic dysregulation, 287–290
 - epistasis, 327
 - examples of intrinsic, 279
 - gene duplication as source, 281–282
 - intrinsic postzygotic isolation, 277–291
 - large-effect, 260
 - under parallel selection, 255–257
 - phenotypes under ecological selection, 253
 - on phenotypic and genotypic landscapes, 254–258
 - trait-based pollinator-mediated, 248
 - transgression-based, 249
 - Hybrid index, 165–166, 168, 174, 255, 308, 312
 - Hybrid inviability
 - accumulation of genetic differences, 508–509
 - environmental effects on, 252–253
 - evolution rate of sexual isolation compared, 23
 - inversions, 146
 - postzygotic isolation, 278
 - variation in extrinsic reproductive isolation, 102–103, 110
 - Hybridization
 - adaptive and diversifying outcomes, 331–333
 - adaptive introgression, 332
 - adaptive radiations, 485–488
 - anthropogenic impacts, 529–538, 540–542
 - glossary of terms, 325
 - over space and time, 326, 328
 - predictability of outcomes, 333–336
 - prevalence, 323
 - probability of, 324–327
 - questions for future research, 337
 - role in species formation and persistence, 323–338
 - species boundaries, 328–329
 - transgressive segregation, 331–332
 - Hybrid lethality, 289
 - Hybrid necrosis, 280, 327
 - Hybrids
 - genetic architecture of phenotypic variation in, 253–254
 - holistic view of selection on, 258
 - incidence, consequences, and evolution of phenotypic transgression in, 258–263
 - transgressive phenotypes, 247, 249, 254–256, 258–259, 262, 331
 - Hybrid speciation, 332–333
 - Hybrid species, 325–326
 - Hybrid sterility, 278–279, 281–282, 284–287, 290
 - Hybrid vigor, 325, 336
 - Hybrid zones
 - anthropogenic, 543–544
 - barrier loci in, 163–167, 173–176
 - definition, 324–325
 - linkage disequilibrium, 142, 147, 149, 151
 - negative coupling, 195
 - quantitative analyses of coupling in, 163–177
 - suture zones, 324
- I**
- Immigrant fitness, 109–110
 - Imprinting, 289
 - Incompatibilities. *See also* Hybrid incompatibility
 - assortative mating, 327
 - intrinsic postzygotic isolation, 277–279
 - Orr’s model compared, 313–315
 - snowball effect, 313–315
 - speciation and hybridization, 327–328
 - species boundaries, 328–329
 - substitutions associated with, 505
 - Infectious-disease models, 429–431
 - Insertion/deletions (indels), 348–349, 488
 - Interchromosomal effect, 355–357
 - Intrinsic barriers, 248
 - Intrinsic postzygotic isolation
 - description of, 278
 - Dobzhansky–Muller incompatibilities (DMIs), 278–281
 - extrinsic compared, 278
 - hybrid asexuality, 278
 - mechanisms, 277–291
 - rules of speciation, 282
 - Intrinsic postzygotic isolation mechanisms
 - accumulation of DMIs at non-recombining regions, 285–286
 - allelic underdominance, 283–284
 - chromosomal view, 284
 - duplication/translocation of genes, 281–283
 - epigenetic dysregulation, 287–290
 - genic view, 278–284
 - genomic view, 286–287
 - Introgression
 - adaptive, 332–333, 486–488, 540–542
 - broad-scale, 380
 - coupling, impact of, 152–153
 - definitions, 325
 - ecological opportunity, 485–487
 - environmental factors, 99, 110
 - genetic coupling, 206
 - genomic clines, 218
 - in hybrid zones, 166, 173, 176–177
 - island bird species, 448
 - locus-specific patterns, 176
 - predictability at genomic level, 333–335
 - recombination, influence of, 352
 - sex chromosome contributions, 176
 - sexual isolation, 28–29
 - snowball effect, 314–315
 - Invasiveness, 325–326, 332, 537

Index

- Inversions, 146, 195. *See also* Structural variants
 capturing, 352–353
 gaining, 352–353
 genetic coupling, 200, 203, 205, 209
 speciation and, 347–361
- Island biogeography, theory of, 451–452
- Island syndrome, 453, 455–456
- Island systems, in adaptive radiations, 399–400, 439–458
- K**
- Karyotypic orthoselection, 375–376
- Key innovations
 adaptive radiations, 396–397, 413, 470, 472–477, 482, 486–488
 context of biotic interactions, 477, 482–485
 in context of neotropical geology, 472–477
 one-allele mechanisms, 233
- L**
- Large-effect alleles
 evolutionary rescue by fixation of, 312
 in floral isolation, 231
 as outliers in heterozygosity, 315–316
 phenotypic divergence, 253
 reproductive isolation, contribution to, 315
- Large X (or Z) effect, 282
- Life history
 molecular evolution rates, 507
 strategies, variation in, 395–396
 of symbionts, 430–431
- Linkage disequilibrium
 assortative mating, 209
 build-up among barrier loci, 135, 137–147
 chromosomal rearrangements, 372
 coevolution, 200
 definition, 136, 230, 325
 genome-wide, 135, 137–139, 147–150
 increase by structural variants, 350–351
 negative coupling, 181–197
 prematuring barriers, 181–197
 prezygotic isolation, 234, 236
 recombination effect on, 144–147, 231
- Local adaptation
 selfing influence on, 3, 5
 to sensory conditions, 39–46
- M**
- MacArthur's consumer–resource model, 409–411
- Macroecological perspective on speciation, 498, 500–501, 506
- Macroevolution, 499–501, 505–506
- Macroevolutionary view of chromosomal speciation
 chromosomal rearrangements, 369–381
- life history and biography associations, 379
 overview, 369–371
 pitfalls in interpretation, 379–380
 reconciling microevolutionary theory with
 macroevolutionary inferences, 372–373
 unanswered questions, 380–381
 understanding already observed macroevolutionary
 patterns, 377–379
 understanding origin and fixation of chromosomal
 rearrangements, 373–376
- Magic trait models, 230, 233–236
- Magic traits
 coupling of barriers to gene exchange, 144, 146, 151
 definition, 136, 202
 genetic coupling, 199, 201
 negative coupling, 182–184, 187
 prezygotic isolation, 233–236
 sexual isolation, 24, 31
- Major histocompatibility complex (MHC), 432, 448
- Matching trait assortment, 202–203
- Mate recognition systems, genetic coupling of, 199–210
- Mating preference
 linkage disequilibrium, 144, 146
 negative coupling, 182–183, 185
 QTL, 235
 sensory signals, 37, 39, 41, 46, 51, 237, 239
 sexual isolation, 28, 120–121
 sexual selection, 440, 452
- Mating preference penetrance, 120
- Mating success
 linkage disequilibrium, 146, 193
 negative coupling, 181, 185, 187, 189, 193–196
 sensory signals, 46
- Mating systems
 diversity in flowering plants, 11–13
 negative coupling, 196
 process of speciation, impact on, 1–5, 10–13
- Mating trait loci, 181–196
- Mayr, Ernst, 497–498, 523–524
- Meiosis, disruption by structural variants, 350–351
- Meiotic drive, 283, 285, 360, 375–376
- Metabolomics, 488
- Microspecies, 2
- Mimicry, 45, 202, 235, 484, 486
- Mimulus* (monkeyflowers)
 ecologically mediated hybrid incompatibility, 248, 251–252
 extrinsic PMPZ isolation, 64
 pollinator-mediated reproductive isolation, 23, 220
 QTL mapping, 145, 215, 352
 structural variants, 352
- Minimization principle, 405, 407, 410
- Modeling
 epidemiological disease, 421, 429–431
 Fisher's geometric model as tool in speciation, 299–317

- hybrid incompatibilities on phenotypic and genotypic landscapes, 254–258
- negative coupling, 181–197
- quantitative analyses of coupling in hybrid zones, 163–177
- sexual and habitat isolation during reinforcement, 115–131
- standard model of speciation, 557–562
- symbiosis and parasite diversification, 429–431
- variation in extrinsic reproductive isolation effect on gene flow, 101, 104–109
- Molecular evolution, 487–511
- Molecular phylogenies
 - branch lengths, 501, 503–504, 510
 - rate of molecular evolution and rate of diversification compared, 500–505, 509–511
 - sister pairs analyses, 503
 - speciation rate estimates, 502, 509–511
- Muller’s ratchet, 286
- Multiple-effect traits
 - definition, 136, 202
 - genetic coupling, 201–202, 204
 - linkage disequilibrium, 143–144, 150–152
- Multiregionalism, 524–525
- Museomics, 457
- Mutation-order speciation, 151, 254–258, 262, 302, 440, 442, 446, 452, 455, 540
- Mutation rate, 497, 501–502, 504–509, 511
- Mutualism, 394, 422, 425, 484

- N**
- Natural selection
 - extrinsic postmating prezygotic (PMPZ) isolation, 63–64
 - parallel, 255
- Nearly neutral theory, 452
- Negative coupling, 181–197
- Negative epistasis, 248–249, 252, 257–259, 303, 305, 313–314
- Neotropics
 - adaptive radiations, 469–490
 - animal adaptive radiations, 477, 480–481
 - geology, 472–477
 - plant adaptive radiations, 476–479
 - plant–herbivore interactions, 477, 482–484
- Neural divergence during ecological divergence, 41–45
- Neutral divergence, 183, 446
- Neutral theory of molecular evolution, 452, 523
- Next-generation sequencing (NGS), 215, 217–218, 447
- Niche conservation, 446, 456
- Niche differentiation, 391–394
- Niche theory
 - adaptive radiations, 391–393, 405–417
 - evolution of niche concepts, 407–408
- MacArthur’s consumer–resource model, 409–411
- open questions for future research, 417
- realistic limit to coexisting species during adaptive radiations, 413–416
- theoretical limit to coexisting species, 408–412
- Nonadaptive radiation
 - avian island, 439–458
 - definition, 440
 - determinants of, 472
 - geographical barriers, 472
 - island birds, 439–447, 450–454
 - oceanic island ecosystems, 444–447

- O**
- Oligogenic DMIs, 249, 255, 259, 262
- One-allele mechanism, 126, 136, 143, 151, 201, 230–232, 235–236
- Opportunity costs, 64–65
- Opposite-ancestry alleles, 248–249, 251–253, 255, 257–259, 262
- Ornstein–Uhlenbeck models, 489
- Orrery, 551–553
- Orr’s model of genetic incompatibilities, 313–315
- Out of Africa replacement model, 525

- P**
- Parallel selection, ecological hybrid incompatibility under, 255–257
- Parasites
 - bird–parasite interactions, 452–453
 - epidemiology disease modeling, 429–431
 - host physiological traits, 431–432
 - host radiation and symbiont speciation, 421–434
- Parasite speciation
 - case studies from animal parasitology, 426–427
 - case studies from plant parasitology, 427, 429
 - studies on, 428–429
- Parasitism, in adaptive radiations, 394
- Pebas lacustrine system, 474
- P-element, 287–288
- Pericopulatory barriers, 61, 70–71
- period* gene, 202–203, 208
- Persistence, long-term, 27–29
- Phenotype matching, 206, 230, 235–236
- Phenotypic divergence
 - of barrier trait, 138
 - biotic interactions, 393
 - character displacement, 454
 - disruptive selection, 444
 - genetic architecture of, 253
 - gradual, 218
 - hybrid incompatibilities, 247, 249, 259–262
 - transgression change to function of, 259–262

Index

- Phenotypic landscape, hybrid incompatibilities on, 254–258
- Phenotypic model, 301, 305, 308, 314, 317
- Phenotypic transgression, 247, 249, 254–256, 258–259, 262, 331
- Phenotypic variation in hybrids, genetic architecture of, 253–254
- Pheromones, genetic coupling in, 206–209
- Phoenix hypothesis of speciation, 312
- Phyletic evolution, 558–559
- Piwi-interacting RNAs (piRNAs), 287–288
- Plant defenses, 482–484
- Plant–herbivore interactions, 477, 482–484
- Pleiotropy
- coupling, 143–146, 150–152
 - definition, 136, 230
 - genetic coupling of mate recognition systems, 199–210
 - prezygotic isolation, 231–241
- Pollinator-mediated reproductive isolation, 23, 220
- Polygenism, 517–519, 521
- Population size, anthropogenic effects on, 538
- Postmating prezygotic (PMPZ) isolation
- barriers and underlying mechanisms, 61–62
 - diversity of measures, 68–69
 - extrinsic, 63–64
 - molecular mechanisms and targets of, 65–66
 - opportunity costs and reinforcement as drives of, 64–65
 - research, future, 71–72
 - role in speciation, 57–73
 - role of sexual selection and sexual conflict in evolution of, 60–63
 - survey of, 66–71
- Postzygotic barriers, 8–10
- Postzygotic isolation
- chromosomal rearrangements, 284–285
 - Dobzhansky–Muller model as mechanism of, 249–252
 - extrinsic, overview of mechanisms of, 256
 - falling between niches, 258, 263
 - mechanisms of intrinsic, 277–291
- Prdm9* gene, 284, 286–287, 290
- Predator–prey relationships, 484–485
- Predictability in speciation, 553, 558, 563–565
- Prediction
- causal, 556–557, 564
 - correlational, 556–557
 - definition, 552
 - evolution versus speciation, 558
 - function and value, 555–557
 - retrodiction versus, 558–559
 - role in science, 556
- Preference loci, 181–196
- Premating isolating barriers, 181–197
- Prezygotic barriers
- gene flow, effect on, 239–240
 - selfing and evolution, 4–8
- Prezygotic isolation
- allelic variation, 231–233
 - definition, 230
 - evolutionary history and development as constraints, 235–239
 - gene flow, impact on, 239–240
 - genetic associations between components of, 233–235
 - genetics and evolution of, 229–241
 - glossary of terms, 230
 - loci contributing to, 231
 - one-allele and two-allele mechanisms, 230–232
 - postmating (PMPZ), 57–73
 - recombination as constraint on evolution of, 230–231
- ## Q
- Quantitative trait locus (QTL) mapping
- contemporary research use of, 215, 220
 - genetic architecture of phenotypic variation in hybrids, 253–254
 - genetic coupling, evidence for, 203–206
 - prezygotic isolation, loci contribution to, 231
- ## R
- Races, 517–526
- Racism, 525–526
- Reciprocal diversification, 426
- Recombination
- chromosomal rearrangements, 285
 - as constraint on evolution of prezygotic isolation, 230–231
 - in hybrid zones, 163–164, 167, 172–173, 177
 - linkage disequilibrium, effect on, 144–147, 200, 231
 - negative coupling, 181–183, 185–192, 194–196
 - ratio of selection to, 147, 163, 177
 - reduction by structural variants, 350–355
 - reduction with chromosomal rearrangements, 372–373
- Redundancy, 554
- Regulatory divergence, 199, 208
- Reinforcement
- definition, 136
 - as driver of postmating prezygotic (PMPZ) isolation, 64–65
 - habitat isolation, 115–131
 - selfing, 4
 - sexual isolation, 24–25, 115–131
 - variation in reproductive isolation, influence of, 97–98, 101
- Reproductive barriers. *See also specific barriers*

- definition, 325
 - relative rates of evolution of different, 22–25
 - relative strength of, 25–27
 - selfing and evolution, 4–10
 - sexual isolation, 19–31
 - Reproductive interference, sexual isolation
 - and, 24–25
 - Reproductive isolation. *See also specific types of isolation*
 - anthropogenic impacts, 530, 536–544
 - avian island radiation, 456
 - context-dependent, 97–111
 - Darwin on, 499
 - definition, 136, 325
 - genomics data, 315–316
 - island birds, 440–441, 444, 447–448, 453–454, 456–458
 - large-effect alleles, contribution of, 315–316
 - negative coupling, 181–197
 - selfing, 2–13
 - sensory adaptation, role of, 39–46
 - sensory ecology, 37–52
 - substitution rate association with, 505
 - variation in extrinsic, 97–111
 - Reproductive isolation barriers. *See specific barriers*
 - Retrodiction, 558–559
 - Robertsonian fusions, 350, 360, 370, 375–376
- S**
- Satellite repeats, 287–288
 - Selection, anthropogenic alterations in, 538–540
 - Selfing, 1–14, 283
 - Sensory drive, 37–41, 51, 327
 - Sensory ecology of speciation, 37–52
 - Sensory environment
 - local adaptation to sensory conditions, 39–46
 - neural divergence during ecological divergence, 41–45
 - rapid change influence on reproductive isolation, 47–51
 - sensory signals, habitat matching, and habitat choice, 46–47
 - Sequential diversification, 391
 - Sex chromosomes
 - chromosomal rearrangements, 378
 - coupling, 176
 - gene transposition, 282–283
 - Sexual conflict, 4, 60, 63, 66, 452, 539
 - Sexual isolation
 - coevolution, 200
 - as gene flow barrier, 19–20, 22–23, 25–28, 31
 - habitat isolation interaction with, 115–131
 - importance to speciation, 19–31
 - long-term persistence, role in, 27–29
 - in sympatric species, 25–27
 - variation in reproductive isolation, effect of, 110
 - Sexual selection
 - assortative mating incompatibility, 327
 - by females, 120–121
 - homogenizing effect, 184, 186–187, 189, 192, 194–196
 - hybrid incompatibilities, 253
 - link between molecular evolution and diversification rates, 509
 - mate recognition systems, 200
 - mating preference, 440, 452
 - negative coupling, 181–196
 - nonadaptive radiation, 440–442
 - parallel natural selection, 452
 - rate of evolution, 22–25
 - role in postmating prezygotic (PMPZ) isolation, 60–63
 - selfing influence on, 4
 - sexual isolation, 20–21, 23, 25, 27, 31
 - Single-nucleotide polymorphisms (SNPs), 348–349, 352, 359–361
 - Sister pairs analyses, 503
 - Small-effect loci
 - assortative mating, 206
 - ecological speciation by selection on, 218
 - in floral isolation, 231
 - negative epistasis for fitness, 259
 - Snowball model/effect, 25, 313–315, 323–325, 329–330, 505
 - Specialization, 405, 411–416
 - Speciation
 - allopatric, 523
 - predicting evolution versus, 558
 - race conceptions and, 517–526
 - Speciation clock, 260, 262, 505, 510
 - Speciation continuum, 325, 329–331
 - Speciation machine, 551, 553–554, 557, 562–564
 - Speciation pluralism, 551, 562–565
 - Speciation potential, chromosomal number and, 378–379
 - Speciation rate
 - estimates from molecular phylogenies, 502
 - molecular phylogeny estimates of, 502, 509–511
 - selfing influence on, 1–14
 - Speciation rules, 281–282
 - Species boundaries, 328–329
 - Species diversity, limits to, 405–407, 409–410
 - Species flocks, 421–426, 429–433
 - Species packing, evolutionary origins of, 405–417
 - Species richness, 405–408, 412, 422–429, 431
 - Species turnover rates, anthropogenic alterations in, 542–543
 - Standard model of speciation, 557–562
 - State-dependent speciation and extinction (SSE) models, 373
 - Sterility, hybrid, 278–279, 281–282, 284–287, 290

Index

- Structural variants
distribution of fitness effects, 348, 359
diversity in type and length, 349
genome-wide impact, 355–357
hybrid fitness reduction, 350
outstanding questions, 360
overview, 347–350
recombination reduction, 350–355
relevance of length of, 357–359
- Study system bias, 213–223
- Substitution rate, 501–502, 504–505, 507–511
- Substitutions
molecular evolution and, 501–505, 507–509, 511
nonsynonymous, 501–502, 507, 509
synonymous, 501–502, 504, 507, 509
- Susceptible–infected–recovered (SIR) model, 430–431
- Suture zones, 324
- Symbiont radiation, 422–425
- Symbionts
diversification mechanisms, 422–423
diversity relative to hosts, 424
life history, 430–431
molecular approaches to study of, 433
questions for future research, 433
research gaps in monitoring, 432
species richness, 422–429, 431
- Symbiont speciation, 421–434
- Sympatric species, and sexual isolation, 25–27
- System drift, 255, 302
- T**
- Temporal isolation, 110–111
- Top-down mapping, 215–217
- Topologically associated domains (TADs), 355
- Trait-based pollinator-mediated hybrid
incompatibility, 248
- Trait-preference rules, 230, 234
- Transgression-based hybrid
incompatibilities, 249
- Transgressive phenotypes, 247, 249, 254–256,
258–259, 262, 331
- Transgressive segregation, 325, 331–332
- Translocation, gene, 282–283
- Transposable elements, 348, 357, 359–360
- Triploid block, 285
- Two-allele mechanism, 116–117, 128, 136, 230–232,
235–236
- U**
- Ultraviolet light exposure, 506
- Unbalanced gametes, 285, 348, 350–351, 375
- Unbalanced mutations, 199, 210
- Underdominance
allelic, 280, 283–284
chromosomal rearrangements, 284–285,
372–373, 375
model of chromosomal speciation, 350
structural variants, 350–351
- V**
- Variation in extrinsic reproductive isolation
cases, 102–103
current research, 99–101
modeling effect on gene flow, 101, 104–109
overview, 97–98
prevalence, 109–111
- Vector-borne disease systems, 431
- W**
- Whitefish, adaptive radiation in, 541
- Wolbachia*, 289–290
- Y**
- YUP* locus, 235, 248, 251–252