

Index

- acorn barnacle, active differentiation for, 117–119
 - gene-frequency shifts for, 117–119
- Acropora*, hybridization among, 182–183
- adaptation, genetic. *See* genetic adaptation
- adaptive differentiation
 - in European white oaks, 101–120
 - ancient examples of, 102–105, 107
 - Bulmer effect in, 112–115
 - components of, 110–111
 - contemporary dynamics of, 109–116
 - dynamics of, 112–115
 - erasure of, migration as influence on, 105–107
 - gene flow and, 115–116
 - historical dynamics of, 102–109
 - LDD in, 105, 107
 - LND in, 107
 - minimal genetic markers for, 104–105
 - pollen flow as influence on, 105–107
 - provenance tests for, 102
 - recent examples of, 107–109
 - for refugial populations, 103–104
 - as transient, during colonization, 105
 - among high-dispersing species, 117–119
 - for acorn barnacle, 117–119
- AFLP. *See* amplified fragment length polymorphism
- agriculture
 - biodiversity and, 35–47
 - development of, 35–36
- allelic recharge, among mammals, 194–196
 - among banner-tailed kangaroo rats, 194–196
 - in bottleneck events, 194–195
 - emigration rates as influence on, 195
- allozymes, 330
- American chestnut trees, 63–64
 - mortality factors for, 63
 - reintroduction efforts for, 63, 307–309
 - disease resistance and, 308–309
 - molecular scatology for, 63–64
- Ammophila breviligulata*, dune restoration and, 213–215
 - molecular and phenotypic data for, 215
- AMOVA analysis, for evolutionary toxicology, 352
- amphibians. *See also* spadefoot toads, hybridization among
 - cryptic species of, phylogenetics for, 21
 - extinction rates for, 5–6
 - sex-determining genes in, 78–79
 - evolution from TSD, 80
 - evolutionary plasticity of, 80
 - GSD and, 80
 - species discovery rates for, 9
- amplified fragment length polymorphism (AFLP), 20
 - evolutionary toxicology and, in detection methods, 331–332
 - in fishes, for sex-determining genes, 88
 - for heritable phenotypes, 56
- anthropogenic hybridization, 174–177
- arthropods, heritable phenotypes for, 54–55
- association genetics, 132–148
 - in animals, 132–141
 - body-color polymorphism and, 138
 - candidate gene approach to, 135, 138
 - genome-wide, 132–138
 - natural selection signature tests in, 141
 - neutrality tests for, 136
 - QTL studies for, 132–138
- methodology for, 125
- natural selection in
 - in animals, 141
 - in candidate genes, 136
 - in plants, 146–148
- in plants, 141–151
 - candidate gene approach to, 145–146
 - in Douglas-firs, 148–151
 - genome wide, 141–145
 - natural selection signature tests in, 146–148
 - neutrality tests for, 147
 - QTL studies in, 141–145
- association mapping, 126
 - for Douglas-firs, 149–151
- Azerbaijan, evolutionary toxicology in, 347–350

- bacteria, species discovery rates for, 9
- banner-tailed kangaroo rats, allelic recharge
 - among, 194–196
- bar coding, 18–20
 - for DNA, 18–19
 - mitochondrial markers in, 20
 - phylogenetic derivation from, 19–20
 - species identification from, 19
- bears. *See* grizzly bears, sex identification and population sampling for; Kermode bears, conservation strategies for
- biodiversity, 2–24
 - advances in medicine as result of, 2
 - for PCR, 2
 - agriculture and, 35–47
 - allelic recharge and, 194–196
 - cryptic species and, 24
 - definition of, 2
 - discovery of, 1–28
 - distribution of, 3–4
 - patterns of, 3
 - enumeration of, 8–13
 - status of species discovery and description, 8–11
 - extinction of species and, 4–8
 - increased rates of, 5
 - IUCN listings for, 5–6
 - mass, 5
 - patterns of, 4–5
 - risks of, 5–6
 - future inventory of, 13–24
 - phylogenetics in, 13
 - taxonomy in, 13
 - gene flow and, 35–47
 - in plants, 36
 - for GM crops, 35–47
 - environmental hazards as result of, 46
 - gene flow in, 36–41
 - non-GM crops v., 35
 - production methods for, 35
 - “hot spots,” 4
 - hybridization and, 169–170
 - importance of, 2–3
 - indirect benefits of, 2–3
 - after landscape fragmentation
 - for endangered species, 212–234
 - immediate consequences on, 190–191
 - “living dead” species and, 208
 - long-term effects of, 192–193
 - polymorphism and, 190–191
 - predictions for, 193, 208
 - short-term effects of, 191–192
 - spatial genetic structure and, 191
 - from weedy rice, 45
 - from gene flow, 47
- Biological Dynamics of Forest Fragments Project, 202
- biomarkers, evolutionary toxicology and, 322
- birds. *See also* black-capped vireo, landscape fragmentation and; golden-cheeked warbler, landscape fragmentation and
 - extinction rates for, 7–8
 - heritable phenotypes for, 55
 - landscape fragmentation as influence on, 217–226
 - for black-capped vireo, 222–226
 - for golden-cheeked warbler, 218–222
 - sex-determining genes in, 77–79
 - molecular assays for, 79
- black-capped vireo, landscape fragmentation and, 222–226
- bottleneck events and, 223
- case study assessment for, 226
- conservation management factors for, 225
- gene flow and, 225
- genetic variations among, 222–224
 - Mantel tests for, 224–225
- golden-cheeked warbler and, biogenetic comparison with, 219
- habitat requirements for, 222, 225–226
- body-color polymorphism, 138
 - among Kermode bears, 260
 - among Soay sheep, 139–141
- bottleneck events, 194–195
 - black-capped vireo and, 223
 - wildlife reintroduction during, 312–313
- Bulmer effect, 112–115
- California tiger salamanders, hybridization of, 180–181
- captive breeding programs, for conservation
 - of species, 267–291
 - coefficient of relatedness for, 270
 - founding populations in, 273
 - gene diversity, 270–271
 - goals of, 267, 272–273
 - inbreeding coefficient in, 269–270
 - incomplete pedigrees in, application of
 - concepts to, 271–272
 - kinship in, 269
 - mean, 269
 - molecular methods for, 267–268, 276–291
 - for allele identification, 288–289
 - with animal models, 291
 - for estimating relatedness, 279–284
 - for gene diversity, 287–288
 - for genetic management, 289–290
 - inbreeding and, 287
 - markers in, 283–284
 - for organisms living in groups, 284–288
 - pedigree issues and, resolution of, 276–279
 - for quantitative genetic analysis, 290–291
 - for relationship categories
 - identification, 282–284
 - studies on, 268
 - for unresolved needs, 289–291
 - for variation in selection, 290
 - population growth in, 273–274
 - population maintenance in, 274–275
 - successes as result of, 267
 - terms for, 269–272

Index

365

- chromosomes, sex-determining genes and, 77
 - in fishes, 85, 86
 - in reptiles, 79
- climate change
 - community genetics and, 66–68
 - in deserts, 66
 - in mountain forests, 66
 - prediction models for, 67–68
 - conservation and, 66
 - hybridization of species as result of, 180
 - Pacific salmon recovery planning and, 262
- community genetics, 50
 - case studies for, 51
 - climate change and, 66–68
 - in deserts, 66
 - in mountain forests, 66
 - prediction models for, 67–68
 - conservation and management in, 52–53
 - population analysis for, 52–53
 - three-way interactions in, 52
 - for foundation species, 50
 - as community drivers, 50
 - definition of, 55–56
 - dependent communities influenced by, 51–52
 - heritable phenotypes in, 56–57
 - for GEOs, 61–66
 - ecological consequences of, 62, 65–66
 - ecosystem phenotypes in, 62
 - fitness of, 62
 - as foundation species, 61–62
 - native species hybridization by, 62
 - nontarget phenotypes in, 62
 - heritable phenotypes, 53–59
 - AFLP molecular markers for, 56
 - for arthropods, 54–55
 - for birds, 55
 - conservation consequences for, 56–59
 - in foundation species, 56–57
 - for insects, 55
 - Mantel tests for, 56
 - for microbes, 55
 - with species-area relationships, 58–59
 - species differentiation from, 57–58
 - support for similar genotypes, 56
 - management applications for, 68–69
 - donor tagging as part of, 69
 - for MVPs, 60–61
 - for MVPs, 59–61
 - for generalist species, 60
 - population size as factor in, 60
 - transfer experiments for, 60
 - terms for, 51
 - variation in, 50
- conservation, of species
 - for black-capped vireo, management factors for, 225
 - with captive breeding programs, 267–291
 - coefficient of relatedness in, 270
 - founding populations in, 273
 - gene diversity, 270–271
 - goals of, 267, 272–273
 - inbreeding coefficient in, 269–270
 - incomplete pedigrees in, application of concepts to, 271–272
 - kinship in, 269
 - molecular methods for, 267–268, 276–291
 - population growth in, 273–274
 - population maintenance in, 274–275
 - successes as result of, 267
 - terms for, 269–272
 - climate change and, 66
 - community genetics and, 52–53
 - population analysis for, 52–53
 - three-way interactions in, 52
 - in dune restoration, 214–215
 - for *Ammophila breviligulata*, 214–215
 - EDGE scores for, 15
 - genetic adaptation for, 123–153
 - association genetics and, 132–148
 - detection methods for, 125–132
 - natural populations in, 125
 - population genetics and, 123–124, 129–132
 - genetic markers in, 74–77
 - DNA fingerprinting, 74, 75
 - individual identification in, 74
 - sexing assays, with DNA, 74–77
 - for golden-cheeked warbler, landscape fragmentation and, 220
 - hybridization and, 169–185
 - among *Acropora*, 182–183
 - anthropogenic, 174–177
 - with applied studies, 184–185
 - biodiversity and, 169–170
 - case studies for, 173–174, 175
 - categorization of, 170
 - correlates for, 176
 - disease resilience as result of, 183
 - ecological correlates of, 177
 - extinction and, 169
 - habitat specialization as correlate for, 180–181
 - mating issues, for original species, 171–172
 - natural, 174–177
 - predictors of, 178–181
 - selective removal of nonendangered species and, 179
 - among spadefoot toads, 183
 - species fitness as result of, 169
 - zone dynamics for, 177, 181–182
 - hybridization and applied studies for, 184–185
 - for Kermode bear, 259–261
 - landscape fragmentation as influence on, literature survey of, 229–230
 - for Pacific salmon, 244–262
 - abundance and productivity assessments in, 248–250
 - climate change as influence on, 262

- conservation, of species (*cont.*)
 ESU viability and, 240, 254–257, 258
 future applications of, 257–262
 integration strategies for, 241
 methodologies for, 247–248
 molecular approaches to, 262
 population identification in, 246–248
 population viability and, 248–254
 Recovery Domains in, 244–245
 risk factor integration in, 252–254
 spatial structure and diversity
 assessments in, 251–252
 terms for, 240
 TRTs in, 244
 VSP and, 246, 254, 257, 258
 with pedigree reconstruction, 285–286
 phylogenetics and, 13–17
 delimiting species and, 14–15
 PSC and, 14
 pollen and seed movement and, with
 landscape fragmentation, 206–207
 management strategies for, 207
 promotion of, from hybridization,
 182–184
 with wildlife reintroduction, 296–314
 development of, 296
 founding event phase of, 303–305
 genetic consequences of, 299–303
 population establishment phase of,
 305–310
 population growth phase of, 310–313
 population theory and, 297–298, 299
 variation predictions for, 298
 conspecific sperm precedence (CSP),
 181–182
 crustaceans. *See* rusty crayfish, hybridization
 among, zone dynamics as factor in
 CSP. *See* conspecific sperm precedence
- Darwin, Charles, 1
 geological study by, 1
 DDT. *See* dichlorodiphenyltrichloroethane
 deoxyribonucleic acid (DNA)
 bar coding for, 18–19
 evolutionary toxicology as influence on,
 evidence of, 321
 adduct studies in, 324–325
 in anonymous markers, 331–332
 detection methods for, 331–337
 marker selection criteria for, 336–337
 in MHC, 333
 with microarrays, 334
 in organelles, 332–333
 with sequencing, 333–334
 in SNPs, 333–334
 fingerprinting from, in conservation
 management, 74, 75
 RAPD and, 90
 sexing assays with, 74–77
 deserts, climate change in, community
 genetics and, 66
 drought-adaptive genotypes in, 66
 dichlorodiphenyltrichloroethane (DDT), 327
 Dinizia excelsa, pollen movement for,
 202–203
 discovery of species. *See* species discovery,
 rates of
 disease resistance
 in American chestnut trees, 308–309
 in GM crops, 36
 “distinct population segments” (DPS),
 243–244
 DNA. *See* deoxyribonucleic acid
 DNA adduct studies, 324–325
 measurement methods in, 325
 phases of, 324–325
 Douglas-firs, association genetics in, 148–151
 mapping studies for, 149–151
 population genomics in, 149
 QTL mapping for, 149
 DPS. *See* “distinct population segments”
 dune restoration, 214–215
 Ammophila breviligulata and, 214–215
 molecular and phenotypic data for,
 215
 E. cyclocarpum, pollen movement for,
 204–206
 mean parameters for, 205
 study sites for, 204–205
 ecosystem genetics, 50
 case studies for, 51
 climate change and, 66–68
 in deserts, 66
 in mountain forests, 66
 prediction models for, 67–68
 conservation and management in, 52–53
 population analysis for, 52–53
 three-way interactions in, 52
 for foundation species, 50
 as community drivers, 50
 definition of, 55–56
 dependent communities influenced by,
 51–52
 heritable phenotypes in, 56–57
 for GEOs, 61–62, 66
 ecological consequences of, 62, 65–66
 ecosystem phenotypes in, 62
 fitness of, 62
 as foundation species, 61–62
 native species hybridization by, 62
 nontarget phenotypes in, 62
 heritable phenotypes, 53–59
 AFLP molecular markers for, 56
 for arthropods, 54–55
 for birds, 55
 conservation consequences for, 56–59
 in foundation species, 56–57
 for insects, 55
 Mantel tests for, 56
 for microbes, 55
 with species-area relationships, 58–59
 species differentiation from, 57–58
 support for similar genotypes, 56

Index

367

- management applications for, 68–69
 - donor tagging as part of, 69
- for MVPs, 60–61
- for MVPs, 59–61
 - for generalist species, 60
 - population size as factor in, 60
 - transfer experiments for, 60
- variation in, 50
- ED. *See* evolutionary distinctiveness
- EDGE score. *See* evolutionary distinct and globally endangered score
- EE. *See* environmental effects (EE), on sex-determining genes in fishes
- EMBL. *See* European Molecular Biology Laboratory
- emigration rates, allelic recharge among mammals and, 195
- Endangered Species Act (ESA)
 - Pacific salmon under, 239, 244–246
 - delisting of, 255
 - population identification for, 246–248
 - Recovery Domains in, 244–245
 - strategy mandates for, 245–246
 - protection criteria for, 243–244
 - DPS in, 243–244
- endangered species, landscape
 - fragmentation as influence on, 212–234. *See also* black-capped vireo, landscape fragmentation and; golden-cheeked warbler, landscape fragmentation and; Pacific salmon among birds, 217–226
 - for black-capped vireo, 222–226
 - for golden-cheeked warbler, 218–222
 - genetic consequences of, 212–213
 - literature survey of, 226–233
 - for conservation status, 229–230
 - for genetic responses to fragmentation, 228–229
 - for habitat structure, 232–233
 - for species vagility, 230–232
 - population fragmentation among, 213–216
 - in structurally complex habitats, 217
 - vagility of, 217
- environmental effects (EE), on sex-determining genes in fishes, 81
- environmental sex determination (ESD), 79–80
 - behavior as influence on, in fishes, 81–82
 - social structure as factor in, 82
 - in fishes, 81–83
 - behavior as influence on, 81–82
 - in protogynous species, 82
 - temperature as influence on, 82–83
 - TSD and, 83
- ESA. *See* Endangered Species Act
- ESD. *See* environmental sex determination
- ESU. *See* evolutionarily significant unit
- eukaryotes, phylogenetics of, 18–20
 - with bar coding, 18–20
 - with mitochondrial markers, 20
 - species identification from, 19
- European Molecular Biology Laboratory (EMBL), 19
- European white oaks
 - adaptive differentiation in, 101–120
 - ancient examples of, 102–105, 107
 - Bulmer effect in, 112–115
 - components of, 110–111
 - contemporary dynamics of, 109–116
 - dynamics of, 112–115
 - erasure of, migration as influence on, 105–107
 - gene flow and, 115–116
 - historical dynamics of, 102–109
 - LDD in, 105, 107
 - LND in, 107
 - minimal genetic markers for, 104–105
 - pollen flow as influence on, 105–107
 - provenance tests for, 102
 - recent examples of, 107–109
 - for refugial populations, 103–104
 - as transient, during colonization, 105
 - genetic differentiation among, 106, 109
- evolutionarily significant unit (ESU), 15
 - categorization of, 15–16
 - criteria for, 15
 - NOAA guidelines for, 244
 - Pacific salmon as, in recovery planning, 240, 254–257, 258
 - risk integration for, 256–257
 - phylogeographic concordance for, 15
- evolutionary distinct and globally endangered (EDGE) score, 16
 - for conservation of species, 15
- ED criteria for, 16
- evolutionary distinctiveness (ED), 16
- evolutionary toxicology, 320–355
 - case studies for, 347–352
 - in Azerbaijan, 347–350
 - in Pigeon River region, 351–352
 - causality assessment for, 337–347
 - by biological gradient, 344
 - by consistency of association, 339–340
 - with experimental evidence, 344–346
 - plausibility as factor in, 346–347
 - by specificity of association, 340–342
 - by strength of association, 338–339
 - by time order, 342–344
 - from DDT, 327
 - definition of, 320
 - with microsatellites, 330–331
 - detection methods, 329–347
 - with AFLP, 331–332
 - with allozymes, 330
 - through DNA, 331–337
 - for genotoxics, 329–330
 - genetic ecotoxicology, 322–325
 - DNA adduct studies in, 324–325
 - future applications for, 325
 - historical background of, 322–324

- evolutionary toxicology (*cont.*)
 genetic systems influenced by, 321–329
 allele frequency in, 328–329
 AMOVA analysis for, 352
 assignment tests for, 354
 Bayesian analysis for, 353–354
 in biomarkers, 322
 coalescent-based analysis for, 352–353
 within DNA, 321
 history of, 321–322
 MLE analysis for, 353
 multivariate analysis for, 352
 population-level consequences in, 325–329
 reproduction effects, 321
 response categories for, 327–328
 statistical assessment methods for, 352–354
 transgenerational inheritance in, 327
 mutations from, 320–321, 329
 toxicogenomics, 335–336
 workshops and symposia for, 323
 Ewens-Watterson neutrality test, 130
 extinction, of species, 1
 biodiversity and, 4–8
 hybridization and, 169
 increased rates of, 5
 for amphibians, 5–6
 for birds, 7–8
 for fishes, 8
 for mammals, 6–7
 for reptiles, 8
 IUCN listings for, 5–6
 mass, 5
 patterns of, 4–5
Rhogeessa tumida, 22–23
 risks of, 5–6
 Tree of Life and, 1

 female-heterogametic systems, in fishes, 81
 fishes. *See also* lake sturgeon, sex-determining genes in; Pacific salmon
 ESD in, 81–83
 behavior as influence on, 81–82
 in protogynous species, 82
 temperature as influence on, 82–83
 TSD and, 83
 extinction rates for, 8
 genetically engineered, 38, 47
 case study for, 37–39
 QTLs for, 37–38
 GSD in, 83–86
 sex-determining genes in, 81–94
 with AFLPs, 88
 as autosomal, 86
 chromosomal influences on, 85, 86
 EE as influence on, 81
 ESD and, 81–83
 female-heterogametic systems and, 81
 GSD and, 83–86
 hermaphroditism and, 81
 isolation of markers for, 86–88
 in lake sturgeon, 88–94
 loci for, 84
 male-heterogametic systems and, 81
 in monosex cultures, 86–87
 for population structure studies, 87
 transcriptome analysis for, 88
 unisexuality and, 81
 TSD and, 83
 forests. *See* American chestnut trees; pollen and seed movement, with landscape fragmentation
 foundation species
 community genetics for, 50
 as community drivers, 50
 definition of, 55–56
 dependent communities influenced by, 51–52
 heritable phenotypes in, 56–57
 GEOs as, 61–62
 heritable phenotypes in, 56–57

 gene(s), sex-determining, in vertebrates, 74
 genetic markers, in conservation, 74–77
 gene flow
 adaptive differentiation and, 115–116
 biodiversity and, 35–47
 in plants, 36
 among black-capped vireo, 225
 definition of, 36
 in GM crops, 36–41
 aggressive weed formation from, 41
 community-wide changes from, 40–41
 plant fitness as factor for, 40
 population genetics as factor for, 39–40
 selective advantages from, 40
 studies on, 39
 from pollen and seed movement, with landscape fragmentation, 203
 for weedy rice, 43, 46
 genetic evidence of, 44
 genetic adaptation, 123–153. *See also* association genetics
 association genetics, 132–148
 in animals, 132–141
 methodology for, 125
 in plants, 141–151
 detection methods for, 125–132
 association mapping, 126
 candidate gene approaches in, 126–127
 genome-wide association approaches in, 127–129
 with LD, 126, 127–128
 population genetic approaches in, 129–132
 quantitative approaches in, 126
 natural populations in, 125
 definitions of, 125
 QTL methodologies for, 125, 128–129
 population genetics and, 123–124, 129–132
 hitchhiking mapping in, 129–131
 LD in, 124, 126

Index

369

- neutrality tests for, 131–132
 - in nonmodel organisms, 130–131
 - outlier analysis in, 129–131
- for species conservation and management, 151–153
- genetic ecotoxicology, 322–325
 - DNA adduct studies in, 324–325
 - future applications for, 325
 - historical background of, 322–324
- genetic sex determination (GSD)
 - in amphibians, 80
 - evolution from TSD, 80
- in fishes, 83–86
 - chromosomal influence on, 85
 - in lake sturgeon, 89
- genetically engineered organisms (GEOs),
 - community genetics for, 61–66
 - ecological consequences of, 62, 65–66
 - ecosystem phenotypes in, 62
 - fitness of, 62
 - as foundation species, 61–62
 - native species hybridization by, 62
 - nontarget phenotypes in, 62
- genetically modified (GM) crops, 35–36
 - biodiversity and, 35–47
 - environmental hazards as result of, 36
 - disease resistance as, 36
 - to nontarget organisms, 36
 - transgene movements as, 36
- gene flow in, 36–41
 - aggressive weed formation from, 41
 - community-wide changes from, 40–41
 - plant fitness as factor for, 40
 - population genetics as factor for, 39–40
 - selective advantages from, 40
 - studies on, 39
- non-GM crops v., 35
- production methods for, 35
- genetics. *See also* association genetics;
 - community genetics; ecosystem
 - genetics; genetic adaptation; genetic
 - sex determination; population
 - genetics
- association, 132–148
 - in animals, 132–141
 - methodology for, 125
 - in plants, 141–151
- community and ecosystem, 50
 - case studies for, 51
 - climate change and, 66–68
 - conservation and management in, 52–53
 - for foundation species, 50
 - for GEOs, 61–66
 - heritable phenotypes, 53–59
 - management applications for, 68–69
 - for MVPs, 60–61
 - for MVPs, 59–61
 - terms for, 51
 - variation in, 50
- phylogenetics
 - bar coding and, 19–20
 - biodiversity and, 13
 - conservation of species and, 13–17
 - for cryptic species, 20–24
 - databases for, 27–28
 - ESU and, 15
 - of eukaryotes, 18–20
 - lineage divergence and, 16
 - MU and, 15
 - PD and, 16–17
 - of prokaryotes, 17–18
 - species discovery rates with, 26
- population, 123–124, 129–132
 - hitchhiking mapping in, 129–131
 - LD in, 124, 126
 - neutrality tests for, 131–132
 - in nonmodel organisms, 130–131
 - outlier analysis in, 129–131
 - quantitative, 123
- GEOs. *See* genetically engineered organisms
- GM crops. *See* genetically modified crops
- golden-cheeked warbler, landscape
 - fragmentation and, 218–222
- black-capped vireo and, biogenetic
 - comparison with, 219
- case study assessment for, 226
- conservation and recovery efforts for, 220
- genetic variation among, 220–222
 - Mantel tests for, 221–222
- habitat specificity for, 219–220
- vagility of, 232
- Gorman, George, 299
- grizzly bears, sex identification and
 - population sampling for, 76–77
- GSD. *See* genetic sex determination
- Guaiacum sanctum*, pollen movement for, 206
- habitat restoration. *See* dune restoration
- Hacienda Solimar, pollen movement in, 204–205
- heritable phenotypes
 - AFLP molecular markers for, 56
 - for arthropods, 54–55
 - for birds, 55
- community genetics and, 53–59
 - conservation consequences for, 56–59
 - in foundation species, 56–57
 - Mantel tests for, 56
 - with species-area relationships, 58–59
 - species differentiation from, 57–58
 - support for similar genotypes, 56
- for insects, 55
- for microbes, 55
- hermaphroditism, in fishes, 81
- high-yielding varieties (HYVs), of weedy rice, 41–42
 - first observation of, 42
- hitchhiking mapping, 129–131
- “hot spots,” of biodiversity, 4
- establishment of, 4
- PD and, 16–17
- plant diversity and, 4

- Hudson-Kreitman-Aguade test, 131
- hybridization, in endangered taxa, 169–185
 among *Acropora*, 182–183
 anthropogenic, 174–177
 applied studies for, 184–185
 biodiversity and, 169–170
 case studies for, 173–174, 175
 missing data for, 178
 categorization of, 170
 correlates for, 176
 habitat specialization as, 180–181
 disease resilience as result of, 183
 ecological correlates of, 177
 extinction and, 169
 habitat specialization as correlate for,
 180–181
 for California tiger salamanders,
 180–181
 climate change as influence on, 180
 mating issues
 for original species, 171–172
 for rusty crayfish, 171–172
 natural, 174–177
 predictors of, 178–181
 demography as, 178–179
 habitat modification as, 178
 population size as, 179
 promotion of conservation as result of,
 182–184
 with applied studies, 184–185
 selective removal of nonendangered
 species and, 179
 among spadefoot toads, 183
 species fitness as result of, 169
 zone dynamics for, 177, 181–182
 CSP and, 181–182
 for rusty crayfish, 171–172
- HYVs. *See* high-yielding varieties
- insects
 heritable phenotypes for, 55
 species evaluation of, shortcomings for, 9
- International Union for Conservation of
 Nature (IUCN)
 species life span listings, 5–6
 threatened species compilation, 7
- IUCN. *See* International Union for
 Conservation of Nature
- Kermode bears, conservation strategies for,
 259–261
 color polymorphism among, 260
 logging as factor in, 260–261
 genetic consequences from, 261
- lake sturgeon, sex-determining genes in,
 88–94
 candidates genes, 89
 GSD and, 89
 random markers in, 90
 alternatives to, 90
 with RAPD, 90
- RDA for, 90
 sexual maturity for, 89
 subtractive hybridization for, 90
 transcriptome pyrosequencing for, 90–93
- landscape fragmentation
 allelic recharge and, among mammals,
 194–196
 for banner-tailed kangaroo rats,
 194–196
 in bottleneck events, 194–195
 emigration rates as influence on, 195
- biodiversity and
 for endangered species, 212–234
 immediate consequences on, 190–191
 long-term effects of, 192–193
 polymorphism and, 190–191
 predictions for, 193
 short-term effects of, 191–192
 spatial genetic structure and, 191
- endangered species and, 212–234
 among birds, 217–226
 genetic consequences of, 212–213
 literature survey of, 226–233
 population fragmentation among,
 213–216
 in structurally complex habitats, 217
 vagility of, 217
- pollen and seed movement and, 190–208
 biodiversity after, 190–191
 case studies for, 201–206
 conservation and, 206–207
 estimates of, 193–200
 gene flow with, 203
 genetic relatedness and, 201
 seed dispersal, 200–201
 among tropical plant species, 197
- LD. *See* linkage disequilibrium
- LDD. *See* long-distance dispersal
- linkage disequilibrium (LD)
 in genetic adaptation, 124, 126, 127–128
 QTL mapping v., 127–128
- “living dead” species, 208
- LND. *See* Local Neighborhood Diffusion
- Local Neighborhood Diffusion (LND), 107
- long-distance dispersal (LDD), 105, 107
- major histocompatibility complex (MHC),
 333
- male-heterogametic systems, in fishes, 81
- mammals. *See also* banner-tailed kangaroo
 rats, allelic recharge among; grizzly
 bears, sex identification and
 population sampling for; Kermode
 bears, conservation strategies for;
 Soay sheep, body-color
 polymorphism among
 allelic recharge among, 194–196
 among banner-tailed kangaroo rats,
 194–196
 in bottleneck events, 194–195
 emigration rates as influence on, 195
- association genetics in, 132–141

Index

371

- body-color polymorphism and, 138
- candidate gene approach to, 135, 138
- genome-wide, 132–138
- natural selection signature tests in, 141
- neutrality tests for, 136
- QTL studies for, 132–138
- cryptic species of, phylogenetics for, 24
- extinction rates for, 6–7
 - Rhogeessa tumida*, 22–23
- sex-determining genes in, 77–79
 - exceptions for, 77–78
 - molecular assays for, 78
 - primary products in, 78
- sex identification and population
 - sampling for, 76–77
 - among grizzly bears, 76–77
- species discovery rates for, 9
- management unit (MU), 15
- Mantel tests, 56
 - for black-capped vireo, for genetic variation, 224–225
 - for golden-cheeked warbler, for genetic variation, 221–222
- McDonald-Kreitman test, 131
- MHC. *See* major histocompatibility complex
- microbes
 - heritable phenotypes for, 55
 - species discovery rates for, 9, 25
- microsatellites, 330–331
- minimum viable interacting populations (MVIPs), community genetics for, 60–61
- minimum viable populations (MVPs), community genetics for, 59–61
 - for generalist species, 60
 - population size as factor in, 60
 - transfer experiments for, 60
- mitochondrial markers, 20
- MLSA. *See* multilocus sequence analysis
- molecular taxonomy, 17–18
 - of eukaryotes, 18–20
 - with bar coding, 18–20
 - with mitochondrial markers, 20
 - species identification from, 19
- of prokaryotes, 17–18
 - distance-based approaches to, 17
 - MLSA for, 18
 - sequencing for, 18
 - species recognition in, 18
- mountain forests, climate change in, community genetics and, 66
- MU. *See* management unit
- multilocus sequence analysis (MLSA), 18
- mutations, from evolutionary toxicology, 320–321, 329
- MVIPs. *See* minimum viable interacting populations
- MVPs. *See* minimum viable populations
- National Oceanic and Atmospheric Administration (NOAA), 244
 - ESU criteria under, 244
- National Science Foundation, 1
- natural hybridization, 174–177
- natural selection, in association genetics
 - in animals, 141
 - among candidate genes, 145–146
 - in plants, 146–148
- naturalists. *See* Darwin, Charles; Wallace, Alfred Russel
- neutrality tests, for population genetics, 131–132
 - in animals, 136
 - Ewens-Watterson test, 130
 - Hudson-Kreitman-Aguade test, 131
 - limitations of, 131
 - McDonald-Kreitman test, 131
 - in plants, 147
- NOAA. *See* National Oceanic and Atmospheric Administration
- outlier analysis, in population genetics, 129–131
 - Ewens-Watterson neutrality test and, 130
 - testing parameters in, 130
- Pacific salmon, 239–262
 - ecological role of, 239
 - under ESA, 239, 244–246
 - delisting of, 255
 - Recovery Domains in, 244–245
 - strategy mandates for, 245–246
 - evolution history as factor in, 241–243
 - diversity patterns in, 242
 - dynamic adaptations in, 243
 - replaceable populations within, 243
 - transplant limitations in, 242–243
 - federal protection for, 243–244
 - under ESA, 244–246
 - recovery planning for, 244–262
 - abundance and productivity assessments in, 248–250
 - climate change as influence on, 262
 - ESU viability and, 240, 254–257, 258
 - future applications of, 257–262
 - integration strategies for, 241
 - methodologies for, 247–248
 - molecular approaches to, 262
 - population identification in, 246–248
 - population viability and, 248–254
 - Recovery Domains in, 244–245
 - risk factor integration in, 252–254
 - spatial structure and diversity assessments in, 251–252
 - terms for, 240
 - TRTs in, 244
 - VSP and, 246, 254, 257, 258
- Palo Verde National Park, pollen movement in, 204–205
- PCR. *See* polymerase chain reaction
- PD. *See* phylogenetic diversity
- pedigree reconstruction, 285–286
 - for western larch, 285–286

- phylogenetic diversity (PD), 16–17
 - biodiversity “hot spots” and, 16–17
- phylogenetic species concept (PSC), 14
 - delimiting species and, 14–15
- phylogenetics
 - bar coding and, 19–20
 - biodiversity and, 13
 - conservation of species and, 13–17
 - delimiting species and, 14–15
 - EDGE scores for, 16
 - PSC, 14
 - for cryptic species, 20–24
 - from AFLP, 20
 - amphibians, 21
 - mammals, 24
 - sorting of, 21–24
 - databases for, 27–28
 - systematic development of, 27
- ESU and, 15
 - categorization of, 15–16
 - criteria for, 15
 - phylogeographic concordance for, 15
- of eukaryotes, 18–20
 - with bar coding, 18–20
 - with mitochondrial markers, 20
 - species identification from, 19
- lineage divergence and, 16
- MU and, 15
- PD and, 16–17
- of prokaryotes, 17–18
 - distance-based approaches to, 17
 - MLSA for, 18
 - sequencing for, 18
 - species recognition for, 18
- species discovery rates with, 26
- phylogeographic concordance, 15
- Pigeon River region, evolutionary toxicology in, 351–352
- plants, biodiversity of. *See also* American chestnut trees; Douglas-firs, association genetics in; European white oaks; pollen and seed movement, with landscape fragmentation; weedy rice
 - association genetics and, 141–151
 - candidate gene approach to, 145–146
 - in Douglas-firs, 148–151
 - genome wide, 141–145
 - natural selection signature tests in, 146–148
 - neutrality tests for, 147
 - QTL studies in, 141–145
 - gene flow and, 36
 - in GM crops, 36–41
 - for weedy rice, 43, 46
 - in GM crops, 35–41
 - environmental hazards as result of, 36
 - gene flow in, 36–41
 - non-GM crops v., 35
 - production methods for, 35
 - as “hot spots,” 4
 - pedigree reconstruction for, 285–286
 - for western larch, 285–286
 - weeds, 41
 - for weedy rice, 41–45
 - biodiversity effects of, 45
 - first observations of, 42
 - fitness of, 43–44, 45–46
 - gene flow for, 43, 46
 - HYVs for, 41–42
 - molecular markers for, 47
 - morphology of, 42
 - origin of, 41
 - population spread of, 44–45
 - wild, 42
 - wildlife reintroduction of, 307–309
 - for American chestnut tree, 307–309
- pollen and seed movement, with landscape fragmentation, 190–208
 - biodiversity after
 - immediate consequences on, 190–191
 - “living dead” species and, 208
 - long-term effects of, 192–193
 - polymorphism and, 190–191
 - predictions for, 193, 208
 - short-term effects of, 191–192
 - spatial genetic structure and, 191
 - case studies for, 201–206
 - Dinizia excelsa*, 202–203
 - E. cyclocarpum*, 204–206
 - flow rates in, 198
 - Guaiacum sanctum*, 206
 - S. globulifera*, 203–204
 - S. humilis*, 202
 - conservation and, 206–207
 - management strategies for, 207
 - estimates of, 193–200
 - factors as influence on, 193–196
 - for mean/maximum distances, 201
 - studies for, 197–200
 - gene flow with, 203
 - genetic relatedness and, 201
 - seed dispersal, 200–201
 - new populations as result of, 200–201
 - among tropical plant species, 197
- pollen flow, 105–107
- pollutants. *See* evolutionary toxicology
- polymerase chain reaction (PCR), 2
- polymorphism. *See also* body-color polymorphism
 - landscape fragmentation and, as influence on, 190–191
- population genetics, 123–124, 129–132
 - hitchhiking mapping in, 129–131
 - LD in, 124, 126
 - neutrality tests for, 131–132, 136
 - Ewens-Watterson test, 130
 - Hudson-Kreitman-Aguade test, 131
 - limitations of, 131
 - McDonald-Kreitman test, 131
 - in nonmodel organisms, 130–131
 - outlier analysis in, 129–131
 - testing parameters in, 130

Index

373

- population theory, wildlife reintroduction and, 297–298
- prokaryotes, phylogenetics of, 17–18
distance-based approaches to, 17
MLSA for, 18
sequencing for, 18
species recognition in, 18
- provenance tests, 102
- PSC. *See* phylogenetic species concept
- QTLs. *See* quantitative trait locis
- quantitative genetics, 123
- quantitative trait locis (QTLs)
in association genetics
in animals, 132–138
for Douglas-firs, 149
in plants, 141–145
for genetic adaptations, 125, 128–129
for genetically engineered salmon, 37–38
LD mapping v., 127–128
- randomly applied polymorphic DNA (RAPD), in lake sturgeon, 90
alternatives to, 90
- RAPD. *See* randomly applied polymorphic DNA
- RDA. *See* representational difference analysis
- Recovery Domains, 244–245
- representational difference analysis (RDA), 90
- reptiles. *See also* California tiger salamanders, hybridization of
extinction rates for, 8
sex-determining genes in, 79–80
chromosomal influence on, 79
ESD and, 79–80
TSD and, 80
- resistance to disease. *See* disease resistance
- restriction fragment length polymorphisms (RFLP), 331–332
- RFLP. *See* restriction fragment length polymorphisms
- Rhogeessa tumida*, 22–23
DNA sequencing for, 22
genetic variation within, 22–23
- rice. *See* weedy rice
- rusty crayfish, hybridization among, zone dynamics as factor in, 171–172
- S. globulifera*, pollen movement for, 203–204
- S. humilis*, pollen movement for, 202
flow rates, 198
- SARST. *See* serial analysis of ribosomal sequence tags
- SBH. *See* sequencing by hybridization
- seed movement. *See* pollen and seed movement, with landscape fragmentation
- sequencing by hybridization (SBH), 26
- serial analysis of ribosomal sequence tags (SARST), 26
- sex-determining genes, 77–94
in amphibians, 79–80
evolution from TSD, 80
evolutionary plasticity of, 80
GSD and, 80
in birds, 77–79
molecular assays for, 79
chromosomes and, 77
in fishes, 81–94
with AFLPs, 88
as autosomal, 86
chromosomal influences on, 85, 86
EE as influence on, 81
ESD and, 81–83
female-heterogametic systems and, 81
hermaphroditism and, 81
isolation of markers for, 86–88
in lake sturgeon, 88–94
loci for, 84
male-heterogametic systems and, 81
in monosex cultures, 86–87
for population structure studies, 87
transcriptome analysis for, 88
TSD and, 83
unisexuality and, 81
- genetic markers in
assays as, with DNA, 74–77
DNA fingerprinting, 74
individual identification in, 74
- in mammals, 77–79
exceptions for, 77–78
molecular assays for, 78
primary products in, 78
- in reptiles, 79–80
ESD and, 79–80
TSD and, 80
- in vertebrates, 74
in amphibians, 79–80
in birds, 77–79
diversity of, 78
in fishes, 81–94
in mammals, 77–79
in reptiles, 79–80
- single nucleotide polymorphisms (SNPs), 333–334
- SNPs. *See* single nucleotide polymorphisms
- Soay sheep, body-color polymorphism among, 139–141
with animal model approach, 140
genotypic fitness and, 140
- spadefoot toads, hybridization among, 183
- species discovery, rates of, 8–11
for amphibians, 9
for bacteria and microbes, 9, 25
for cryptic species, 20–24
from AFLP, 20
amphibians, 21
mammals, 24
sorting of, 21–24

- species discovery, rates of (*cont.*)
 - enhancement of, 24–27
 - for microbes, 25
 - with phylogenetics, 26
 - with SARST, 26
 - with SBH, 26
 - from T-RFLP, 25
 - from taxonomic databases, 25
 - limitation factors for, 11–13
 - inventory assessment, rates of, 12–13
 - regional inventories, lack of, 12
 - taxonomic experts, shortage of, 12
 - for mammals, 9
 - T-RFLP. *See* terminal restriction fragment length polymorphism
 - taxonomy
 - biodiversity and, 13
 - molecular, 17–18
 - of eukaryotes, 18–20
 - of prokaryotes, 17–18
 - Technical Recovery Teams (TRTs), 244
 - temperature-dependent sex determination (TSD), 80
 - in fishes, 83
 - terminal restriction fragment length polymorphism (T-RFLP), 25
 - toxicogenomics, 335–336
 - transgenerational inheritance, 327
 - Tree of Life, 1
 - tropical landscapes. *See also* pollen and seed movement, with landscape fragmentation
 - pollen and seed movement in, 197
 - TRTs. *See* Technical Recovery Teams
 - TSD. *See* temperature-dependent sex determination
 - unisexuality, in fishes, 81
 - vertebrates. *See also* amphibians; birds; fishes; mammals; reptiles
 - sex-determining genes in, 74
 - in amphibians, 79–80
 - in birds, 77–79
 - diversity of, 78
 - in fishes, 81–94
 - in mammals, 77–79
 - in reptiles, 79–80
 - viable salmonid population (VSP), 246, 254, 257, 258
 - VSP. *See* viable salmonid population
 - Wallace, Alfred Russel, 1
 - geological study by, 1
 - weeds
 - from GM crops, aggressive formation of, 41
 - rice as, 41–45
 - weedy rice, 41–45
 - biodiversity effects of, 45
 - from gene flow, 47
 - cross-fertilization of, 43
 - first observations of, 42
 - fitness of, 43–44, 45–46
 - gene flow for, 43, 46
 - biodiversity influenced by, 47
 - genetic evidence of, 44
 - HYVs for, 41–42
 - molecular markers for, 47
 - morphology of, 42
 - origin of, 41
 - population spread of, 44–45
 - wild, 42
- western larch, pedigree reconstruction for, 285–286
- wild rice, 42
- wildlife reintroduction, 296–314
 - development of, 296
 - early limitations in, 297
 - for forest species, 307–309
 - American chestnut tree, 63, 307–309
 - disease resistance and, 308–309
 - founding event phase of, 303–305
 - age structures in, 305
 - capture techniques during, 303–304
 - population size in, 304
 - sex composition during, 304–305
 - genetic consequences of, 299–303
 - to gene flow, 301
 - genetic drift as, 299
 - from interdependent sampling events, 301–302
 - lack of genetic diversity as, 299–301
 - from sampling period, 303–313
 - population establishment phase of, 305–310
 - environmental factors in, 306–309
 - mating tactic as factor during, 309–310
 - social structure as factor during, 310
 - population growth phase of, 310–313
 - behavioral constraints in, 312
 - biological constraints in, 311
 - during bottleneck event, 312–313
 - environmental constraints in, 311
 - spatial constraints in, 312
 - temporal components in, 313
- population theory and, 297–298, 299
- variation predictions for, 298