

# Index

## A

- ABC model gene involvement in rose development, 386–387
- Abiotic stress, strawberry resistance to, 473–475
  - antifreeze protein (AFP), 474
  - cold-induced transcription factor (CBF1), 473–474
  - freezing tolerance, 473
  - glycine betaine, 474
  - heat-shock proteins (HSPs), 475
  - osmotin, 474
  - peptide methionine sulphoxide reductase (PMSR), 475
- Acid composition, in strawberry, 470–471
- ACYL TRANSFERASE 1 (AT1) gene in apples, 135
- Adaptation traits, rose, 365, 371–372
  - See also under* Structural genomics
- Adventitious regeneration, almond, 206–207
- Agrobacterium*-mediated transformation
  - in plums, 281–282
  - roses, 397, 399
  - strawberry, 491–492
- Agronomic characters, almond, 197–208
  - adventitious regeneration, 206–207
  - Almond x Peach crosses, characters studied in, 207–208
    - yield consistency, 207
  - bloom time, 200–203
  - disease resistance, 205–206
  - ESTs, 201–202
  - gametophytic self-incompatibility (GSI), 197
  - genetic basis, 197–208
  - kernel bitterness, 203–204
    - sweet v bitter kernel trait, 203–204
  - pollen-expressed F-box gene, 199
  - self-incompatibility, 197
    - shell hardness, 204–205
    - S-RNase alleles, 197–201
- Agronomically significant traits, genetic basis, 20–26
  - comparative genomics studies, 26
  - functional studies, 26
  - genetics approach, 21
  - genomics approaches, 21
  - mealiness in peach and nectarine, 24–26
  - qualitative traits, 21
  - quantitative traits, 21
  - structural studies, 26
  - See also* Melting Flesh (MF)
- Akame x Juseito (AxJ) maps, 242
- Alcohol acyltransferases (AATs), 459
- Alcohol dehydrogenase (ADH5), 137–138
- Allergenicity, in transformed apple, 156–157
- Allele mining, 41
- Allergens
  - in strawberry, 471
    - lipid transfer proteins (LTPs), 471
    - profilins, 471
  - in transformed apple, 157
- Allotetraploidization, 7
- Almond/Almond genomics, *see Prunus dulcis*
- Alternaria alternata*, 175
- Amelanchier* spp., 12
- American Society of Horticultural Sciences (ASHS), 55–56
- 1-Aminocyclopropane carboxylic acid (ACC) oxidase antisense plums, 282–283
- Amplified fragment length polymorphism (AFLP) markers, 29–30, 581
  - apples, 85
  - apricot, 320
  - taxonomical relationships in *Pyrus* assessed by, 179–180
- Amygdaloideae (prunoideae), 5–7

- Amygdaloideae, 7–10  
 Amylopectin, 107  
 Amylose, 107  
 Angiosperm phylogeny group (APG) system, 2  
 Anthocyanin biosynthesis in rose flower color, 389–390  
 Anthracnose, 476  
   resistance in *Fragaria*, 580–581  
 Antisense technology, for strawberry tissue softening, 495–496  
 Aphids, 102  
   in raspberry, mapping, 513–516  
 Apple genome sequencing, 608–610  
   methodology, 608–610  
   rationale, 608  
   Sanger approach, 609  
 Apple scab (*Venturia inaequalis*), 75  
   resistance genes 1, pyramiding in Rvi6 x Rvi2, 572–574  
   resistance genes 2, pyramiding in Rvi2 x Rvi4, 574–575  
 Apples, *see Malus x domestica*; *Malus pumila*; *Malus* spp.  
 Apricots, *see Prunus armeniaca* L.  
*Arabidopsis*, 388, 551–552, 601–602  
   heterologous expression of apple genes in, 139–140  
 Arbitrary marker systems for strawberry, 440  
 Armenia, 321–322  
*Aronia meloncarpa*, 11  
*Aronia*, *see Aronia meloncarpa*  
 Asia, 317, 347, 526  
   apple production in, 74  
   pears in, 171–172  
 Aspartate aminotransferase (AAT), 87  
 Association mapping  
   almond, 209  
   pear, 181  
   Rosaceae spp., 31, 553–554  
   strawberry, 450  
 Australia, 318
- B**  
 Bacterial artificial chromosome (BAC) libraries  
   apples, 93–94  
   peach, 251–252  
 Bacterial disease resistance, apple, 145–151  
 3-Benzo[b]selenienyl acetic acid (BSAA), 489  
 Benzo-1,2,3-thiadiazole-7-carbothioic acid  
   S-methyl ester (BTH), 404–405  
 6-Benzylaminopurine (BA), 489  
 Bin mapping  
   apples, 110  
   Rosaceae, 30
- Biotechnical approaches to pear improvement, 166–168  
   *See also under* Pear  
 Biotechnology for berry nutritional quality, 497–499  
   *DefH9-iaaM* genes, 498  
   *rolC* genes, 498  
 Biotechnology in Loquat breeding, 535  
   genetic transformation, 535  
 Biotic agents, strawberry resistance to, 466  
   anthracnose, 476  
   *Botrytis cinerea*, 476  
   DNA sequencing technologies, 476–477  
   *Phytophthora cactorum*, 476  
   *Phytophthora fragariae*, 476  
   *Verticillium dahliae*, 476  
 Bitter kernels, almond, 203–204  
 Bitterness, apricot, 328  
 ‘Black Baccara’ (BB), 382  
 Black cherry, 9–10  
 Black spot disease, 175, 361  
 Blackberries, *see Rubus* spp.  
 BLAST analysis, Rosaceae, 28  
 Bloom time  
   almond, 200–203  
   peach, 228  
   alterations in, 228  
*Botrytis cinerea*, 476  
 Brambles, 12  
 Breeding/Breeding programs  
   almond, 189  
   time-tested seedlings selections, 189  
   apples, 75  
   cross breeding, roses, 348–349  
   in peach, 225–230, 235–239  
   *See also under Prunus persica* (Peach)  
   pear, traditional breeding, 165–166  
   fruit tree breeding methods, 165  
 Rosaceae  
   genetic tests in, 41  
   MAS in, 56–58, 564–565  
*Rubus* spp., 507–509  
   strawberry, 426–428  
   *See also under* Strawberry  
   sweet cherries, 294–295  
 Bulk segregant analysis (BSA)  
   in peach, 251  
   strawberry, 448
- C**  
 Caffeic acid O-methyltransferases (COMT)  
   coding, 107–108  
 Candidate gene approach, Rosaceae, 35–37, 262, 548

- altered candidate gene expression, 37
- cauliflower mosaic virus (CaMV) 35S promoter, 37
- co-localization of, 36–37
- expressed sequence tags (ESTs), 36
- gene expression regulation, 38
- gene-specific markers, 35
- inducible promoter for over-expression, 38
- peach, 247–249, 262
- RNA-dependent RNA polymerase (RdRP), 39
- RNA interference (RNAi), 38–39
- suppression subtractive cDNA hybridization (SSH), 36
- transcriptional gene silencing mechanisms, 38
- transient RNAi expression by agroinfiltration, 39
- virus-induced gene silencing (VIGS) system, 39
- Carbohydrate, in strawberry, 496–497
- Cauliflower mosaic virus (CaMV) 35S promoter, 37–38
- cDNA libraries, functional genomics in rose, 381
- cDNA-amplified fragment length polymorphism (cDNA-AFLP), 32–33
- Cell adhesion, in transformed apple, 150
- Chaenomeles* genus, 12
- Cherries
  - botanical descriptions, 292–293
  - history of, 291–293
  - See also *Prunus* spp.; Sweet and sour cherries
- China, 317, 343, 526
  - apple production in, 74
  - peach production, 224
- Chloroplast DNA (cpDNA) fingerprints, 171
  - in strawberry phylogenetic analyses, 439
- Cinnamoyl aldehyde dehydrogenase (CAD), 463–464
- Cisgenics, 77
- Cleaved-amplified polymorphic sequence (CAPS) markers, 63
  - strawberry, 440, 442–443
- Cloning, in almond, 194, 207
- Codon usage assessment, apples, 129–131
  - using cDNA sequences, 129
- Color
  - apricot, 328
  - modification, in transformed apple, 150
  - in roses, 369–370
- Comparative genome mapping
  - among peach or apple, *Arabidopsis* and *Populus*, 551–552
  - in Rosaceae, 549–552
  - in Rosaceae, colinearity between genera belonging to different subfamilies, 551
    - Fragaria*, 551
    - Malus*, 551
    - Prunus*, 551
  - in Rosaceae, colinearity within genera and within subfamilies, 549–551
    - Fragaria* diploid *v* octoploid, 550
    - Fragaria v Rosa*, 550
    - Malus v Pyrus*, 550
    - Prunus v Prunus*, 549
- Comparative genomics in *Prunus*, 239–242
  - between *Prunus* and *Malus*, 239
  - bulk-segregant analysis (BSA), 240
  - DFR (dihydroflavonol 4-reductase), 240
  - EKO (ent-kaurene oxidase), 240
  - SSR markers in, 240
  - synteny analysis, 239
- Comparative genomics, in Rosaceae crop improvement, 28–29
- Comparative mapping, 86
  - strawberry, 440–442
- Conserved Ortholog Set (COS) markers, for Rosaceae species, 547
- Conventional taxonomy, Rosaceae, 5–7
  - intergeneric hybridization, 5
  - Parsimonious tree, 6
  - species definitions, 5
- Coumaroyl CoA reductase (CCR), 463–464
- Crop improvement in Rosaceae, genomics approaches, 26–42
  - comparative genomics, 28–29
  - fields of study, 27–29
  - functional genomics, 28
  - structural genomics, 27
  - techniques, 29–42
    - allele mining, 41
    - candidate gene approach, 35–37
    - centralized web portal and database, 42–43
    - genetic mapping, 29–31
    - Genome Database for Rosaceae (GDR), 42–43
    - genotyping, 40–42
    - marker-assisted breeding (MAB), 40–42
    - marker-assisted selection (MAS), 40
    - marker-trait associations, 40

- Crop improvement in Rosaceae (*cont.*)  
 metabolomics, 34–35  
 Pedigree Based Analysis (PBA), 44  
 proteomics, 34–35  
 QTL analysis, 29–31  
 random insertional mutagenesis, 39  
 shared mapping resources, 43  
 standardized phenotyping, 43–44  
 virus-induced gene silencing (VIGS) system, 39  
*See also* Candidate gene approach; Microarray analysis; Transcript profiling
- Crop production techniques, 55  
 transgenic biotechnology, 55  
*See also* Marker assisted selection (MAS)
- Cross breeding, roses, 348–349
- Cryoconservation, apples, 80
- Cultivar identification, in Loquat, 531–532
- Cultivar transformation, plum, 287
- Cultivated octoploid strawberries, 421–422  
 hypothetical genome formulae, 421  
 inheritance patterns, 421–422
- Cut roses, 341  
 adaptation, 341  
 characteristics, 341  
 colors, 341  
 fragrance, 341  
 industry, importance, 341
- Cydonia* genus, 12
- D**
- 2,4-D auxin, 394
- Decamer random oligonucleotide primers, 87–89
- Defense related gene products, roses, 404–405  
 BTH, 404
- DefH9-iaaM* genes, 498  
 for strawberry improvement, 493
- Dihydroflavonol 4-reductase gene, 401–402
- Diploid strawberry species, 414–418  
*See also under* Strawberry
- Direct organogenesis in roses, 398
- 3,5-Dimethoxy toluene (DMT), 385
- Disease resistance, almond, 205–206
- Disease resistance, apple, 145–152  
 apple scab, 145–152  
 bacterial disease resistance, 145–151  
 in transformed apple, 146  
 fire blight, 145–152  
 promoters for, 151  
*NPR1* gene, 151  
*See also* Fungal disease resistance
- Disease resistance, markers for, 60–62  
 in apricot, 61–62  
 powdery mildew resistance genes, 61  
 in strawberry, 61  
*Vf* gene, 60–61
- Disease resistance, peach, 225
- Distribution, Rosaceae, 3–5
- DNA markers, 171–176  
 for roses, 353–356  
 diploid maps, 355  
 PKs (protein kinase), 353  
 RGAs (resistance gene analogues), 353  
 SNPs, 355–356  
 tetraploid maps, 355  
 for *Rubus* spp., 512–513  
 taxonomical relationships in *Pyrus* assessed by, 170–171  
 AFLP, 171–172  
 associated with interest genes, 173–176,  
*See also* Interest genes  
 chloroplast DNA (cpDNA), 171  
 inter-simple sequence repeat (ISSR), 172  
 microsatellites, 171–172  
 RAPD, 171–172  
 SNPs, 171–172  
 SSR marker tool, 169–171
- DNA markers for genetic diversity in apples  
 evaluation, 87–91  
 aspartate aminotransferase (AAT), 87  
 decamer random oligonucleotide primers, 88  
 EST sequence datasets, 86  
 genotyping of apple cultivars, 87–88  
 glutamate oxaloacetate transaminase (GOT), 87  
 18-mer arbitrary primer P-T, 88  
 phosphoglucosyltransferase (PGM), 87  
 RAPDs, 87  
 RFLPs, 87  
 SSR-based maps, 85, 88, 92  
 common set of SSR markers, proposal for, 89–90
- Durable disease resistance apple varieties,  
 strategies for, 75–77  
 cisgenics in fruit trees, 77  
 fire blight resistant apple cultivars, 76  
 marker assisted selection, 76  
 pest resistance, 77  
 QTL, 76
- Dysaphis Devectora*, 103  
*Dysaphis Plantaginea*, 102–103

**E**

- Ecology, Rosaceae, 3–5  
 Economic importance, Rosaceae, 7–13  
   Amygdaloideae, 7–10  
     *See also Prunus* spp.  
   Maloideae, 8, 10–12  
   Rosoideae, 8, 12–13  
   Spiraeoideae, 8  
 Endo-beta-1,4-glucanases (EGases), 495  
 EndoPG studies  
   in mealiness in peach and nectarine, 24–26  
   in peach, 249  
 Endopolygalacturonase (endoPG), 22  
 Endosperm, Rosaceae, 3  
 England, 526  
 Enzyme-linked immuno-sorbent assays  
   (ELISA) test for sharka disease  
   in apricot, 325  
*Eriobotrya japonica* Lindl. (Loquat), 11,  
   525–535  
   biotechnology in Loquat breeding, 535  
   by mutagenesis, 535  
   use of polyploidy in, 535  
 botany, 525–526  
 China, 526–527  
 cultivar identification, 531–532  
 diversity, 526  
 England, 526  
 genetic mapping, 532–534  
 genetic resources, 526  
 India, 526  
 Japan, 526, 527  
 molecular markers for, 528–532  
   *See also* Molecular markers  
 origin, 525–526  
 pedigree analysis, 532  
 pomological characters, studies according  
   to, 526–528  
*Eriosoma Lanigerum*, 103–104  
*Erwinia amylovora*, 101, 145–152  
 Essentially derived varieties (EDV), 356  
 Ethylene, in strawberry ripening, 469  
 Ethylene-induced ripening, apples, 135,  
   137–138  
 Ethylene production in transformed apple, 148,  
   154–156  
 Ethylene signaling in roses  
   genes cloning in, 387–388  
   opening, 387, 388  
   senescence, 388–389  
 Europe, 316–318, 340  
   apple production in, 74

- new world strawberry species brought to,  
     423–424  
   pears, 169–170  
 Expansins, 495  
 Expressed sequence tag (EST) profiling  
   studies, 31–32  
   almonds, 194  
   apples, 86, 121–128  
     clustering of sequences, 128  
     *Malus* cDNA libraries, publicly  
       available, 121–128  
     microRNAs and their targets identified  
       from, 131–133  
     tissues, 128  
   apricot, 321  
   peach, 259–260  
   roses, 381–383  
     *See also under* Functional genomics in  
     rose

**F**

- Ferjalou Jalousia x Fantasia (JxF)  
   maps, 237  
 Field trials, in GM strawberry, 499–501  
 Fingerprinting, 569–570  
 Fire blight disease  
   in apples, 101–102  
     *Erwinia amylovora* causing, 101, 145  
     QTLs in, 101  
     resistance to, creating, 145–152  
 Flavanone 3-hydroxylase (F3H), 442  
 Flesh browning decrease, in transformed apple,  
   147, 149  
 Flower traits, rose, 364, 369  
   recurrent blooming trait, 364  
   *See also under* Structural genomics  
 Flowering control, in strawberry, 472–473  
 Flowering related traits, in apple structural  
   genomics, 106  
 Flowering time, apricot, 328  
 Foreground selection, in MAS, 571  
 Fossil records, Rosaceae, 2  
   Turonian fossils, 2  
*Fragaria* spp. (Strawberry), 413–431,  
   580–581  
   anthocyanins in, 425  
   anthracnose resistance, 580–581  
   aroma, 425  
   biotechnological approaches to genetic  
     improvement, 429–431  
   herbicide-resistant plants, 429  
   methyl bromide (MB) fumigation,  
     429–430

- Fragaria* spp. (Strawberry) (*cont.*)
- RNA interference (RNAi) technology, 430
  - transgenes incorporation, 430
  - botanical history, 413–431
  - chromosomes of, 438
  - cultivation, 413–431
    - classical, 422–423
    - history of, 422–425
    - new world species brought to Europe, 423–424
    - new world, 423
    - old world, 423
  - cytology, 437–438
  - dessert strawberry, 413–414
  - diploid species, 414–418
    - characteristics, 416
    - F. daltoniana*, 415
    - F. gracilis*, 415
    - F. innumae*, 415
    - F. mandshurica*, 415
    - F. nilgerrensis*, 415
    - F. nipponica*, 415
    - F. nubicola*, 415
    - F. pentaphylla*, 415
    - F. vesca*, 415
    - F. viridis*, 415
    - overlapping interfertile groups of, 415
  - Diploid *v* octoploid, 550
  - economic importance, 424
  - evolution, 413–414
  - flavor, 425
  - fragrance content, 425
  - functional genomics, 429
  - genome sequencing, 610–611
  - higher ploidy species, 419–421
    - See also* Cultivated octoploid strawberries
  - interfertility, 437–438
  - intergeneric hybrid, 422
  - new technologies, 413–431
  - nutritional components, 424–425
  - origin, 413–414
  - phylogenetic analyses, 439
    - chloroplast DNA (cpDNA) fingerprints, 439
  - resistance gene analogues, 444
  - speciation, 413–414
  - structural genomics, 428–429, 437–450
    - See also* Molecular markers; Whole genome sequencing
  - titratable acidity (TA), 425
  - traditional breeding, 426–428
    - backcrossing, 426
    - dessert strawberry, 426
    - England, 426–427
    - formal strawberry breeding, 426
    - Germany, 427
    - Holland, 427
    - Scotland, 427
    - selfing, 426
    - world production, 414
    - See also* Functional molecular biology research
  - 'Fragrant Cloud' (FC), roses, 382, 385
  - Freestone* endoPG gene, 23
  - Freestone non-melting flesh (FNMF), 23
  - Fruit, Rosaceae, 3
  - Fruit firmness, strawberry, 466–469
    - DNA microarray technology, 468
    - expansins, 468
  - Fruit flavor, strawberry, 497
  - Fruit quality, apple structural genomics, 106–109
    - amylopectin, 107
    - amylose, 107
    - apple starch, 107
    - caffeic acid *c* O-methyltransferases (COMT) coding, 107–108
    - cDNA-AFLP, 107
    - RT-PCR analysis, 107
    - Sorbitol, 107
  - Fruit quality, peach, 226–227
  - Fruit quality traits, markers for, 62–64
    - acidity in apple fruit, 63
    - apple Md-Exp7<sub>SSR</sub> marker, 63
    - fruit shelf-life and storability, 63
      - Md ACO-1, 63
      - Md-ACS1, 63
    - in pear, 63
      - cleaved-amplified polymorphic sequence (CAPS), 63
    - RAPD markers, 63
  - Fruit-related traits, strawberry, 458
  - Functional genomics
    - apple, 121–141
      - codon usage assessment, 129–131
      - GC content, 129–131
      - heterologous expression, 139–140
      - Malus* EST datasets, 121–129, *See also* under Expressed sequence tag (EST)
      - See also* Gene expression in apple; Transient assays
    - in peach, 259–271
      - BAC fingerprinting, 267

- candidate gene map, 262
  - cDNA arrays, 261
  - ESTs, 259–260
  - integrated genetic/physical/EST functional genomics database, 267–268
  - microarray technologies, 261
  - proteome, peach, 270–271
  - proteomics analysis, 262
  - Prunus* resistance gene map as tool, 268–270
  - transcriptome, 266–267
  - plum, 284–287
    - marker-free transgenic plums, regeneration, 286
    - phytoene desaturase (PDS) sequence, 285
  - in Rosaceae crop improvement, 28
    - BLAST analysis, 28
    - forward approach, 28
    - genome-wide analysis, 28
    - reverse approach, 28
  - strawberry, 429
  - tools for Rosaceae species, 263–265, 548–549
    - candidate gene databases, 265–266
    - candidate gene sequencing, 548
    - EST, 548
    - ESTs, 264
    - gene expression in fruits, 265
    - microarray, 548
    - Prunus persica* ESTs sequences, 266
    - resource development, 263–265
    - transformation, 548–549
  - Functional genomics in rose, 381–390
    - ABC model gene involvement in flower development, 386–387
    - Anthocyanin biosynthesis in flower color, 389–390
    - cDNA libraries, 381
      - ‘Black Baccara’ (BB), 382
      - ‘Fragrant Cloud’ (FC), 382
      - ‘Golden Gate’ (GG), 382
      - Rosa chinensis*, 382
    - 3,5-dimethoxy toluene (DMT), 385
    - EST databases, 383–384
      - GDR, 383
    - opening, ethylene signaling and metabolism in, 387, 388
    - Orcinol O-methyl transferase (OOMTs), 385
    - Rosa chinensis* var *spontanea*, 385
    - senescence, ethylene signaling and metabolism in, 387, 388–389
    - tools available for, 381–387
    - transcriptomic tools (micro-arrays), 384
      - ornamental traits, genes involved in, 384
      - 1,3,5-trimethoxy benzene (TMB), 385–386
      - See also* Scent
  - Functional markers in peach, 247–249
    - candidate gene approach, 247–249
    - candidate gene mapping, 247–249
    - catalase (Cat1) isozyme locus mapping, 248
    - EndoPG studies, 249
    - expressed sequences (ESTs), 247
    - plum pox virus (PPV) resistance, 249
    - in silico single nucleotide polymorphism (isSNP) detection, 248
    - transcripts mapping, 247–249
  - Functional molecular biology research in *Fragaria*, 457–477
    - acid composition, 470–471
    - allergens, 471
    - flowering control, 472–473
    - fruit-related traits, 458
      - See also* Fruit firmness; Hormone metabolism; Polyphenol compounds; Volatile compounds
    - sugar, 470–471
    - vitamins, 470
    - See also* Abiotic stress
  - Fungal disease resistance, apple, 151–152
    - in transformed apple, 146
    - See also* Scab
- ## G
- Gametophytic self-incompatibility (GSI), 64
    - almond, 197
    - sweet and sour cherries, 304
  - Garden roses, 339–340
    - Asia, 339
    - China, 339
    - Diplocarpon rosae* in, causing disease, 340
    - disease resistance, 340
    - Europe, 339
    - Podosphaera pannosa* in, causing disease, 340
  - Gastrodia antifungal protein (GAFP), 283–284
  - Gene expression in apple, global changes in, 133–138
    - AT genes identification, 135
    - ethylene-induced ripening, 135, 137–138
    - gene ontology (GO) examination, 133–134
    - heterologous hybridizations, 135

- Gene expression (*cont.*)  
 LOX genes identification, 135, 137  
 microarray analysis, 134  
 PD genes identification, 135  
 transcription regulation in, 138  
 using pathway maps, 135
- Gene function validation, apple, 144–157
- Gene ontology (GO) examination, in apples, 133–134
- Gene pyramiding, 571–572  
 apple scab resistance genes 1  
 Rvi6 x Rvi2, 572–574  
 apple scab resistance genes 2  
 Rvi2 x Rvi4, 574–575  
 woolly apple aphid resistance genes  
 Er1 x Er3, 575–576
- Genes for strawberry improvement, 491–497  
*Agrobacterium*-mediated approach, 494  
 carbohydrate, 496–497  
*DeffH9-iaaM* gene, 493  
 disease resistance, 491–493  
 flower, 493–494  
 fruit flavor, 497  
 fruiting, 493–494  
 MADS-box genes, 497  
 pest resistance, 491–493  
 quality – maturation, 494–495  
*rol* genes, 493  
 SAAT gene, 497  
 wild strawberry, 494  
*See also* Biotechnology; Tissue softening
- Gene-specific markers, for strawberry, 441–442
- Genetic diversity in Loquat wild species, 529–531  
 ISSR, 530  
 RAPDs/AFLPs, 530  
 rDNA ITS sequences, 530
- Genetic diversity in *Malus* spp., evaluating, 88–89  
*See also under* DNA markers
- Genetic engineering of Plum (*Prunus domestica*), 277–288  
 acclimatization, 278  
*Agrobacterium tumefaciens* mediated transformation, 277, 284  
 cultivar transformation, 287  
 functional genomics, 284–286  
 marker-free transgenic plums, regeneration, 286  
 phytoene desaturase (PDS) sequence, 285  
 methodology description, 278–281  
 new traits introduction, 281–284  
 1-Aminocyclopropane carboxylic acid (ACC) oxidase antisense plums, 282–283  
 gastrodia antifungal protein (GAFP), 283–284  
 honeysweet, 281–282  
 intron hairpin PPV-CP, 282  
 small interfering RNA (siRNA) production, 283  
 transgenic plums, regeneration, 280
- Genetic engineering of roses, 393–405  
 defense related gene products, 404–405  
 expression in model organisms, studies, 401–405  
 genes related to flower color, 401–402  
 genes related to flower structure, 402  
 genetic transformation, 397–401  
*Agrobacterium*-mediated transformation, 397–399  
 neomycin phosphotransferase gene (nptII), 399  
*in vitro* plant regeneration, 393–394  
 2.5 Na<sup>+</sup>/H<sup>+</sup> antiporter genes, 404  
 proteomic studies, 404  
 scent related gene products, 405  
 senescence related genes, 403–404  
*See also* Regeneration
- Genetic linkage maps in pear, 173
- Genetic mapping, Rosaceae, 29–31  
 association mapping, 31  
 Bin-mapping, 30  
 in Loquat, 532  
*Prunus* reference map, 30  
 reference maps, 30  
 sweet and sour cherries, construction, 295–299  
*See also under* Sweet and sour cherries  
*See also* Marker technology
- Genetically-modified (GM) strawberry plants, *see* GMO strawberry
- Genetic traits in peach, 228–229
- Genome content, cherries, 293–294
- Genome Database for Rosaceae (GDR), 42–43
- Genome sequencing, Rosaceae, 601–611  
 BAC approach, 603  
 next generation technologies, 605  
 perspectives, 601–611  
 progress, 601–611  
 strategies, 603–604  
 whole genome shotgun (WGS) sequencing strategy, 604



- See also* Apple genome sequencing; *Fragaria* spp.; Peach genome sequencing; Sequencing technologies
- Genome structure  
 between species based on *Pyrus* linkage maps, 179–180  
 of Rosaceae, 541–544  
 chromosome numbers, 541–543  
 genome size, 541–543  
 ploidy levels, 543–544
- Genomic research in Rosaceae crops, 19–46  
 genetic basis of agronomically significant traits, 20–26  
 impacting established plantings  
 production, 20  
*See also* Crop improvement; Functional genomics; Structural genomics
- Genomic resources in peach, 228–229
- Genomics, Rosaceae, 13–14  
 genetic improvement, 14  
 physiological development, 14  
 systematic challenges, 13–14
- Genomics opportunities, 55–66  
*See also* Crop production techniques; Marker assisted selection (MAS)
- Genomics tools across Rosaceae species, 539–554  
 comparative genome mapping, 539–540  
 Genomics Database for the Rosaceae (GDR), 544  
 QTLs, 539  
*See also* Structural genomic tools
- Genotypic versus phenotypic selection, cost of, 565–566
- Genotyping, in Rosaceae, 40–42
- Genus names within Rosaceae, ICBN accepted names, 4
- Glutamate oxaloacetate transaminase (GOT), 87
- Glycine betaine, 474
- GMO strawberry  
*Agrobacterium* Transformation, 488–491  
 benefits, 487–502  
 field trials, 499–501  
 methods, 487–502  
 risk, 487–502  
 assessment, 499–501  
 strawberry regeneration, 488–491  
 ‘Golden Gate’ (GG), roses, 382, 385  
 Grey mold, 492  
 Guardian x Nemaguard (GxN) maps, 238
- H**  
 Haploidization, 348  
 Harrow Blood (HB) x Okinawa (Oki) (PMP2) maps, 238  
 Hawthorn, 11  
 Health issues, apples, 80–81  
 Heat-shock proteins (HSPs), in strawberry, 475  
 Heterologous expression, apple genes, 139–140  
 in *Arabidopsis*, 139–140  
 LHP1, 139  
 High-density genetic linkage maps, pear, 179  
 High information content fingerprinting (HICF) technique, peach, 251–252  
 Honeysweet, 281–282  
 Hormone metabolism, strawberry, 469  
 auxin levels, 469  
 ethylene, 469  
 Horticultural traits, apples, 104–106  
 Hunza apricot, 318  
 4-Hydroxy-2,5-dimethyl-3(2H)-furanone (HDMF) in strawberry, 460  
 4-Hydroxy-5-methyl-2-methylene-3(2H)-furanone (HMMF), 461  
 Hygromycin phosphotransferase (*hpt*), 196
- I**  
 Illumina’s Solexa sequencing technology, 605  
 Immediately Quick Frozen fruit market (IQF), 57  
 India, 526  
 Indole-3-butyric acid (IBA), 489  
 Integrated genetic/physical/EST functional genomics database, peach, 267–268  
 Integrated high-density genetic linkage maps, 177  
 Intergeneric strawberry hybrid, 422  
 International Society of Horticultural Science (ISHS), 55–56  
 Inter-simple sequence repeat (ISSR), taxonomical relationships in *Pyrus* assessed by, 172  
 Intra-specific sweet cherry genetic linkage map, 296  
 Intron hairpin PPV-CP, 282  
 Isoenzymes/Isozyme markers  
 almond, 191–194  
 electrophoresis method, 198  
 for *Eriobotrya japonica* Lindl. (Loquat), 528–529  
 for strawberry, 443

- Isoenzymes/Isozyme markers (*cont.*)  
 Leucine aminopeptidase (LAP), 443  
 peroxidase (PX) isozyme system, 443  
 phosphoglucoisomerase (PGI) isozyme system, 443  
 Phosphoglucomutase (PGM), 443
- J**  
 Japan, 526  
 Juvenile period, reducing, 583–584
- K**  
 Kanamycin selection, in almond genetic transformation, 196  
 ‘Kecskemeter’ cotyledonary tissues, 329–330  
 Kernel bitterness, almond, 203–204
- L**  
 ‘Lapins’, 296  
 Leaves, Rosaceae, 2  
 LeExp1, 495  
 Leucine aminopeptidase (LAP), 99, 443  
 LIKE HETEROCHROMATIN PROTEIN1 (LHP1), 139  
 Linkage disequilibrium (LD), 553  
 almond, 209  
 apples, 85–86  
 Linkage mapping  
 almond, 191  
 main characteristics, 192  
 for apple genomics, 89–92  
 apricot, 319–320  
 for *Rubus* spp., 513–516  
 aphids, 514–515  
 RAPD-based linkage map, 514  
 raspberry bushy dwarf virus (RBDV), 515  
 RGAP markers, 514  
 in Rosaceae crop improvement, 27  
 pear, 177–180  
 European pears, 177–179  
 Japanese pears, 177–179  
 sweet and sour cherries, 291–308  
 Linkage maps, roses, 357–364  
 90–69 F<sub>2</sub>, 359  
 94/1, 358  
 94/1R, 358  
 97/7, 359  
 AFLPs, 363  
 current situation for, 357–364  
 diploid populations, 357  
 ‘Fragrant Cloud’, 357  
 ‘Golden Gate’, 357  
 tetraploid populations, 357  
 diploid maps, 363  
 Hw, 360  
 pseudo test cross approach, 363  
 RAPDs, 363  
 rose mapping families, 361–362  
 Spain, 360  
 tetraploid mapping, 363  
 Linkage maps-diploid, strawberry, 444–450  
 association mapping, 450  
 bulked segregant analysis (BSA), 448  
 codominant markers, 449  
 comparative mapping, 446–448  
 construction, 445–446  
 molecular markers, 446  
 morphological markers, 444–445  
 octoploid mapping, 448–449  
 pedigree genotyping concept, 450  
 selective mapping, 446  
 single dose restriction fragments (SDRFs), 449  
 Lipid transfer proteins (LTPs), 471  
 LIPOXYGENASE (LOX) genes in apples, 135  
 Long sylleptic axillary shoots (LSAS), 106  
 Loquat, *see Eriobotrya japonica* Lindl.  
 Lovell x Nemared (LxN) maps, 242
- M**  
 Maloideae, 5, 8, 10–12  
*Malus pumila* (apples), 11  
*See also* Apple genome sequencing  
*Malus* spp.  
 MAS in, 572  
 microarrays, 34  
*Malus x domestica* (Apples), 73–81  
 breeding, 75–78  
*See also* Recurrent breeding strategies  
 ‘Delicious’ cultivars, 73–74  
 disease resistance varieties, strategies for, 75–77  
*See also* Durable disease resistance apple varieties  
 genetics of, 77–78  
 ‘Golden Delicious’ cultivars, 73–74  
 health issues, 80–81  
 nutritional value, 80–81  
 in Switzerland, quality and production criteria, 75  
 worldwide production, 74  
 America, 74  
 Asia, 74  
 China, 74  
 Europe, 74  
 Russia, 74

- See also* Functional genomics, apple;  
Structural genomics, apple
- MapQTL, Rosaceae, 31
- Maps  
derived from peach intraspecific crosses,  
237–239  
derived from peach x almond crosses,  
236–237  
*See also* Linkage maps; Physical maps
- Marker-assisted backcross approach (MABC),  
565
- Marker assisted breeding (MAB), application  
in Rosaceous crops, 40–42,  
563–565
- Marker assisted seedling selection (MASS), 41
- Marker assisted selection (MAS), 40, 567–568  
in apple structural genomics, 109  
application in Rosaceous crops, 563–565  
breeding strategies and, 568–569  
cost/benefit of, 565–569  
genotypic *versus* phenotypic selection,  
565–566  
labor costs reduction, 566  
minimal MDP, 566  
single core system use, 567  
foreground selection, 571  
*Malus*, 572  
PCR-based markers, 567  
in peach, 249–251  
F/f (flesh adhesion) character, 249–250  
*Ma/ma* resistance gene, 250  
root-knot nematode resistance (RKN),  
250–251  
resistance gene pyramiding, 571–572  
SSR markers, 557  
sweet and sour cherries, 291–308
- Marker assisted selection (MAS), in Rosaceae  
breeding programs, 56–58  
important categories, 57  
private breeding programs, 56–58  
questions, 56  
response duration, 56  
traits for developing new crops, 59–65  
disease resistance traits, apple, 59  
powdery mildew resistance genes, 61  
QTL markers in, 59  
resistance to diseases, markers for,  
60–62, *See also* Diseases  
resistance  
resistance to nematode pathogens,  
markers for, 59–60  
scab resistance genes, 60–61  
self-incompatibility, markers for, 64–65
- See also* Fruit quality traits; Pests  
resistance; Tree architecture  
traits listing, 57–58
- Marker-free transgenic plums, regenera-  
tion, 286
- Marker maps, almond  
main characteristics, 192  
major gene mapping, 191–194  
QTL mapping, 191–194
- Marker technology in Rosaceae, 563–585  
advances in, 568  
diversity array technology (DArT), 568  
linkage disequilibrium (LD)  
mapping, 569  
PCR-free large parallel assays, 568  
background selection, 582–584  
reducing the juvenile period, 583–584  
whole-genome selection (WGS),  
582–583  
breeding parent selection, 569–571  
fingerprinting, 569–570  
genetic diversity, 569–571  
*See also* Marker assisted selection (MAS)
- Marker-trait associations, 40
- Mealiness in peach and nectarine, 24–26  
endoPG enzyme in, 25  
heritability in, 25  
QTL analysis, 25  
quantitative traits, 25–26
- Medicinal fruits, roses, 343
- Medlar, *see Mespilus germanica*
- Melting Flesh (MF)  
*Freestone* endoPG gene, 23  
*Melting flesh* endoPG gene, 22  
in nectarine, 21–24  
in peach, 21–24
- 18-mer arbitrary primer P-T, 88
- Mespilus germanica*, 11
- Metabolism modification, in transformed  
apple, 147, 154–156  
alergenicity, 156–157  
flavor composition, 154–156  
*Mal d 1* allergen, 156–157  
*See also* Ethylene production; Sugar:  
accumulation
- Metabolomics, Rosaceae, 34–35
- Methyl bromide (MB) fumigation,  
429–430
- Mexico, 318
- Microarray analysis  
of gene expression in apple, 133–134  
in peach, 261  
for Rosaceae species, 548

- Microarray analysis, Rosaceae, 33  
 advantages, 34  
 limitations, 33–34  
*Malus* microarrays, 34  
 one-channel arrays, 33  
 two-channel arrays, 33
- MicroRNAs (miRNAs), apples,  
 identification  
 from EST databases, 131–133  
 miR156, 132  
 miR167, 132
- Microsatellites, *see* simple sequence repeats (SSRs)
- Mildew Immune Seedling (MIS), PI-m Gene from, 100
- 'Modern Roses', 346
- Molecular maps, for apple genomics, 92
- Molecular markers  
 in apricot, 319–321  
*See also under Prunus armeniaca* L.  
 development in almond, 189–190  
 for *Eriobotrya japonica* Lindl. (Loquat), 528–531  
 genetic diversity, 529–530  
 genetic diversity in wild species, 529–531  
 isoenzymes, 528  
 RAPDs, 529  
 in peach, 235–239  
 for Rosaceae species, 545–548  
 COS (Conserved Ortholog Set) markers, 547  
 EST-based markers, 546–547  
 gDNA SSRs, 545–546  
 gene pair markers, 547–548  
*See also* Functional genomics tools  
 for strawberry, 439–444  
 arbitrary marker systems, 440  
 cleaved-amplified polymorphic sequence (CAPS) markers, 440, 442–443  
 gene-specific markers, 441–442  
 isoenzymes, 443  
 microsatellites, 440–441  
 RAPD, 439–440  
 RFLPs, 443–444  
 SCARs, 440  
 STS markers, 442
- Monogenic apple traits, genomic location, 94–109
- Mountain ash, 11
- Multi-autonomous-transformation (MAT)-vector system, 286
- Mutagenesis, Loquat breeding by, 535
- Mutation induction, pear, 166
- N**
- 2.5 Na<sup>+</sup>/H<sup>+</sup> antiporter genes, roses, 404
- Near-isogenic line (NIL) collections, almond, 209
- Nectarine, *see Prunus persica*
- Nematode pathogens  
 markers for resistance to, 59–60  
*Ma* resistance alleles, 59–60  
 root knot nematode (RKN), 60
- Nematode resistance, 365
- Neomycin phosphotransferase gene (*nptII*), 196, 399
- New crops/products, 55–66  
*See also* Crop production techniques;  
 Marker assisted selection (MAS)
- New Jersey Pillar x KV 77119 (NJxKV)* maps, 238
- Nomenclature, Rosaceae, 1–7
- Non-melting flesh (NMF) peach, 22
- Nucleotide binding site-leucine-rich-repeat (NBS-LRR) proteins, 324
- Nutritional value, apples, 80–81
- O**
- Octoploid mapping, strawberry, 448–449
- 'Old Garden Roses' (OGR), 346
- Oligonucleotide probes, 33
- O-methyltransferases (OMT), 403
- One-channel arrays, 33
- Opening of rose flower, ethylene signaling and metabolism in, 387, 388
- Orcinol O-methyl transferase (OOMTs), 385
- Organogenesis, of roses, 397  
 direct organogenesis, 398  
*in vitro* shoot organogenesis, 397
- Origins, Rosaceae, 1–2  
 fossil records, 2  
 Turonian fossils, 2
- Ornamental cherries, 10
- Ornamental fruits, roses, 342–343
- Osmotin, 474
- Ovary, Rosaceae, 3
- P**
- Pakistan, 318
- Papaya ringspot virus (PRV) coat protein (CP) gene, 281
- Peach, *see individual entries below; Prunus persica*
- Peach genome sequencing, 606–608  
 annotation, 608

- assembly, 608
- methodology, 606–607
- rationale, 606
- transferable markers, 606
- whole genome shotgun (WGS), 603
- Peach tree short life (PTSL), 220
- Pear/Pear genomics, 11–12, 163–181
  - biotechnical approaches to improvement, 166–168
    - gene transfer, 168
    - genetic linkage maps in pear, 172
    - haploidization, 166–167
    - in vitro* methods, 167
    - protoplast technology, 167
    - transgenes introduction, 167
  - botanic characteristics, 163–164
  - fruit tree breeding methods, 165
  - marketing, 167
  - mutation induction, 166
  - origin, 163–164
  - production, 164–165
  - rootstock breeding programs, 166
  - self-sterility, 166
  - speciation, 163–164
  - traditional breeding, 165–166
  - utilization, 164–165
  - worldwide production, 164–165
  - See also* Structural genomics
- Pedigree analysis
  - in Loquat, 532
  - Pedigree Based Analysis (PBA), 44
  - for QTLs mining and detection, 110
- Pedigree genotyping concept, strawberry, 450
- Peptide methionine sulphoxide reductase (PMSR), in strawberry, 475
- Peroxidase (PX) isozyme systems, 443
- Pest resistance
  - apple varieties, strategies for, 77
  - peach, 225–226
- Pests resistance, markers for, 62
  - Er1* apple gene, 62
  - Er2* apple gene, 62
  - Er3* apple gene, 62
  - Sd1* gene, 62
  - Sd2* gene, 62
- Phenolic methyl esters, 385–386
- Phenylpropanoid pathway in raspberry, 518
- 6-Phosphogluconatedehydrogenase (6-PGD), 87
- Phosphoglucoisomerase (PGI) isozyme systems, 443
- Phosphoglucomutase (PGM), 87, 443
- Phosphomanose isomerase gene (*pmi*), 196
- Physical mapping
  - for apple genomics, 91–93
  - diploid, strawberry, 444–450
  - molecular markers, 445
  - morphological markers, 444–445
  - peach, 252–253
    - AFLP-based genetic linkage maps, 252
    - BAC libraries, 251
    - HICF technique, 251
    - use of, 251–252
  - pear, 177–180
    - European pears, 177–179
    - Japanese pears, 177–179
  - in Rosaceae crop improvement, 27
  - for Rosaceae species, 544–545
  - for *Rubus* spp., 516–517
    - BAC library, 517
    - DNA isolations, 516–517
    - MADS-box gene, 517
- Phytochemicals, *Rubus* spp., 510
- Phytophthora cactorum*, 476
- Phytophthora fragariae*, 476
- Phytophthora* root rot resistance in Raspberry, 581–582
- Pl-1* mildew resistance gene from *M. robusta*, 97
- Pl-2* mildew resistance gene, 99
  - from *M. zumi*, 101
- Pl-d* mildew resistance gene, 100
  - from D12, 100
- Pl-m* mildew resistance gene, 100
  - from Mildew Immune Seedling (MIS), 100
- Ploidy levels, Rosaceae, 543–544
- Ploidy strawberry species
  - higher ploidy species, 419–421
  - hexaploid, 419
  - octoploid, 419
  - pentaploid, 420
  - tetraploids, 419
- Plum, *see Prunus domestica*
- Plum pox virus (PPV) disease (Sharka), 59, 225, 249, 268–270, 281, 325
  - in apricot, 324–325
  - See also under Prunus armeniaca* L.
- Pl-w* mildew resistance gene, 98
  - from White Angel, 99–100
- Polygenic apple traits, genomic location, 94–109
- Polygenic traits mapping in peach, 242–247
  - anchored markers distribution on LGs of, 243
  - QTLs for, 242–247

- Polymerase chain reaction (PCR)-based markers application in Rosaceae crops, 564
- Polyphenol compounds, in strawberry, 462–466
- cinnamoyl aldehyde dehydrogenase (CAD), 463
  - coumaroyl CoA reductase (CCR), 463
  - flavonoid biosynthesis, 464–465
  - A dual *O*-methyltransferase (FaOMT), 463
- Polyphenol oxidase (PPO), 156
- Polyploidy in Loquat breeding, 535
- Populus*, 551–552
- Positional cloning, roses, 372–373
- physical maps for, 372–373
  - BAC libraries, 372–373
  - current situation for, 372–373
- Pot roses, 341–342
- dwarf roses, 342
- Powdery mildew (*Podosphaera leucotricha*), 76
- resistance genes, 61, 362
  - structural genomics, 96–97
- Precosity, in transformed apple, 147
- Profilins, 471
- Proteome, peach, 270–271
- two dimensional gels (2D-gels) in, 270
- Proteomics analysis
- in peach, 262
  - quantitative comparative proteomics, 262
- Rosaceae, 34–35
- roses, 404
- Prunus armeniaca* L. (Apricot), 9, 315–330
- bitterness, 328
  - botanical attributes, 316
  - classification, 315
  - color, 328
  - cultivation, history, 316–318
  - dried apricots, 317
  - flowering time, 328
  - genetic linkage maps, 321–322
  - genomic architecture, 316
  - genomics-based opportunities in, 315–330
  - genomics resources, 329
  - Hunza apricot, 318
  - molecular markers, 320–321
    - AFLP markers, 316–318
    - development, 319
    - EST libraries, 321
    - heterologous SSR markers, 320
    - RAPD markers, 319
    - RFLP analyses, 319–321
    - SSR markers, 320–321
    - origin, 316–318
    - pathogen resistance, 324
      - AFLP-resistance gene analogue (RGA), 324    - regeneration, 329–330
    - ripening, genes associated, 328–329
    - self-incompatibility, 323–324
      - S-RNase in, 323    - Sharka disease, 324–327
      - causative agent, 325
      - PPV detection, 325–326
      - PPV resistance, sources of, 326
      - resistance mechanisms, genetic analysis, 326–327
      - symptoms, 325
      - transgenic mitigation of, 327    - significant traits, 323–329
    - traits of economic importance, 318
    - transformation, 329–330
    - wild trees, 316
- Prunus avium* L. (sweet cherry), 291–308
- See also* Sweet and sour cherries
- Prunus cerasus* L. (sour cherry), 291–308
- See also* Sweet and sour cherries
- Prunus domestica*
- adventitious shoot regeneration in, 278
  - transformation, 279
  - See also* Genetic engineering
- Prunus dulcis*, 9, 187–211
- agronomic characters, and their genetic basis, 197–208
  - See also* Agronomic characters
  - association mapping, 209
  - breeding for improved cultivars, 188–189
  - cDNA-AFLP technique, 194
  - EST collections, 194–208
  - evolution, 187–188
  - gene cloning, 194–208
  - genetic transformation, 194–197
  - See also* Transformation
  - history, 187–188
  - linkage disequilibrium conservation (LD), 209
  - molecular markers development, 189–190
    - isozyme genes for, 189–190  - near-isogenic line (NIL) collections, 209
  - self-incompatibility systems in, 190
  - variability analysis, 189–190
- Prunus fruticosa* Pall. (ground cherry tree), 292
- Prunus persica* (Peach), 223–230
- breeding programs, traditional, 225–230
  - bloom time, 227

- disease resistance, 225
  - fruit quality, 226
  - pest resistance, 225
  - plum pox (PPV) disease, 226
  - replant problems, 226
  - ripening times, 227
  - tree borer problems, 226
  - China, 223
    - genetic traits in, 228–229
    - genomic resources in, 224–225
      - public molecular resources, 229
    - genomics to breeding programs,
      - translating, 229
    - mealiness in, 24
    - Melting Flesh (MF) in, 21–24
    - Prunus persica* x (*P. persica* x *P. ferganensis*) (PxF) maps, 237
    - worldwide production, 224
    - See also* Functional genomics; Structural genomics
  - Prunus* resistance gene map as functional genomics tool, 268–270
    - candidate resistance gene database, 269
    - plum pox (Sharka) disease, 268–270
    - resistance gene analogues (RGAs), 269
    - SNP markers, 268
  - Pseudo test cross approach, in roses linkage maps, 363
  - Pyramiding, *see* Gene pyramiding
  - Pyrosequencing, 604–605
  - Pyrus* genus, 11–12
    - primary species in, 164
      - Circum-Mediterranean, 164
      - East Asian, 164
      - European, 164
      - Mid-Asian, 164
    - See also* Pear
  - Pyruvate decarboxylase (PDC), in strawberry, 459
  - PYRUVATE DECARBOXYLASE 1 (PD1) gene in apples, 135
- Q**
- Quality–maturation, genes for strawberry improvement, 494–495
  - Quantitative trait loci (QTLs)
    - almond, 191–194
    - apples, 85
    - application in Rosaceous crops, 29–31, 564–565
      - association mapping, 31
      - Bin-mapping, 30
      - JoinMap software, 31
      - MapQTL use, 31
    - Prunus* reference map, 30
    - reference maps, 30
      - traditional, 30
    - for durable disease resistance apple varieties, 75–77
    - in new crops development, 59
    - for peach, 227, 244–246
      - for resistance, 246–247
    - sweet and sour cherries, 299–303
      - bloom time QTL, identification, 300
  - Quince, 12
- R**
- Random Amplified Polymorphic DNA (RAPD) markers, 29, 292
    - apples, 85, 87
    - apricot, 319
    - for *Eriobotrya japonica* Lindl. (Loquat), 525
    - taxonomical relationships in *Pyrus* assessed by, 170–171
  - Random insertional mutagenesis, 39
  - Rapid amplification of cDNA ends (RACE), 202
  - Raspberries, *see* *Rubus* spp.
  - Raspberry bushy dwarf virus (RBDV), 515
  - Ready screening, 40
  - Recurrent blooming trait, roses, 364
  - Recurrent breeding strategies, apples, 77
    - genetic diversity increase, sources for, 78
    - genetic resources, 79–80
      - Convention on Biological Diversity (CBD), 79
      - cryoconservation, 80
      - European Cooperative Program for Plant Genetic Resources (ECPGR), 79
      - International Network for the Improvement of Banana and Plantain (INIBAP), 79
      - plant genetic resources (PGR), 79–80
      - sources for increased genetic diversity, 78
  - Reference maps, 30
  - Regeneration, roses, 394–401
    - organogenesis, 397
    - Somatic Embryogenesis (SE), 394–397
      - 2,4-D auxin, 394
      - in vitro* multiplication via, 394–397
  - Regeneration, strawberry, 488–491
    - MS medium, 489
  - Resistance gene analogues (RGAs)
    - Prunus*, 269
    - strawberry, 444

- Resistance gene pyramiding, 571–572
- Restriction fragment length polymorphism (RFLP) analyses, 29, 296
- apples, 85, 87
  - apricot, 319
  - in Rosaceous crops, 564
  - strawberry, 443–444
- Reverse genetics, apple, 145–157
- Ripening times, peach, 227
- Ripening, apricot, genes associated, 328–329
- Risk assessment, in GM Strawberry, 499–501
- RNA interference (RNAi) technology, 430
- Robustness, 40
- RolC* genes, 493, 494, 498
- Root-knot nematode resistance (RKN), 60
- in peach, 250–251
  - resistance in *Prunus* rootstocks, 577–580
- Rootstock breeding programs
- pear, 166
  - roses, 343–344
- Rosa chinensis* var *spontanea* (RcOMT), 385
- Rosaceae Consortium of Mapping Populations (RosPOP), 43
- Roses, 13, 339–349
- classification, 344–347
    - RAPD based phenetic analysis, 344
    - Rehder's classification system, 344
  - cross breeding, 348–349
    - among diploids, 348
    - between different ploidy levels, 348
    - raise diploids to tetraploid level, 348
  - culinary fruits, 337
  - cultivars
    - classification, 345–347
    - identification, 345–347
    - 'Modern Roses', 346
    - 'Old Garden Roses' (OGR), 346
    - '*Rosa*' cluster, 346
    - '*Synstylae*' cluster, 346
  - economic value, 339
  - genetic resources, 347
  - genetics, major features of, 347–348
  - medicinal fruits, 343
  - ornamental fruits, 342–343
  - production limitations, 339
  - rootstocks, 343–344
  - rose oil production, 342
    - plants propagated with cuttings for, 342
  - taxonomy, 344–347
    - DNA-based approaches, 344–345
    - of wild species, 344–345
- See also* Cut roses; Garden roses; Genetic engineering; Pot roses; Structural genomics; Tissue culture
- Rosoideae, 5, 8, 12–13
- Brambles, 12
  - Rosa* spp., 13
  - strawberry, 13
- Rubus* spp., 12, 507–519, 581–582
- breeding, 509–511
  - diversity, 507–508
  - DNA markers, 512–513
  - domestication, 508
  - fruit characters, 509
  - fruit quality characteristics in raspberry, 518
    - genes encoding 4-coumarate, 518
    - limitations, 511–512
    - phenylpropanoid pathway in raspberry, 518
  - phytochemicals, 510
  - phytophthora* root rot resistance in, 581–582
  - plant characters, 509
  - production, 510–511
    - machine harvesting of processing raspberries, 511
  - structural genomics, 512
  - taxonomy, 507
  - See also* Linkage mapping; Physical mapping
- Russia, apple production in, 74
- Rvi2 x Rvi4, pyramiding in, 574–575
- Rvi6 x Rvi2, pyramiding in, 572–574
- ## S
- Sakura*, 10
- S-allele typing
- sweet and sour cherries, 304–306
- Sanger chemistry, 604
- Scab disease, apple, 145–151, 173–174
- control, 151
  - hcrVf2* gene resisting, 152
  - progression, *in vitro* test evaluating, 152
  - Venturia inaequalis*, 151–152
- Scab resistance, 60–61, 94–96
- EST-derived STSs (E-STSS), 95
  - QTLs for, 96
  - RAPD markers in, 94
  - SCAR markers in, 95
- Scent, roses
- 'Fragrant Cloud' (FC), 382
  - 'Golden Gate' (GG), 382
  - micro-array tools, 384–385
  - production and emission, 384–385



- related genes, 402–403
  - alcohol acetyltransferase, 403
  - geraniol, 403
  - octanol, 403
  - O-methyltransferases (OMT), 403
  - roses, 401–402
- See also* Volatile acetate esters
- Selective mapping, strawberry, 446
- Self-fertility, in transformed apple, 147
- Self-incompatibility (SI), 175–176
  - in almond, 197, 199
  - apricot, 323–324
  - markers for, 64–65
    - PCR-based S-allele typing, 64
    - S-allele typing, 64–65
    - S-RNase-based S typing, 65
  - sweet and sour cherries, 303–304
    - breeding for self-compatibility, 306–307
  - gametophytic self-incompatibility (GSI), 304
  - MAS, 307–308
  - S-allele typing, 304–306
  - SFB sequence polymorphism, 305
  - S-RNase-based self-incompatibility, 304
- Senescence in rose flower, ethylene signaling and metabolism in, 383, 384–385
- Senescence related genes, roses, 403–404
  - Lipoxygenase activity, 403
- Sequence-characterized amplified regions (SCARs), strawberry, 440
- Sequence-tagged site (STS) marker in *Fragaria*, 442
- Sequencing technologies, 604–605
  - Illumina's Solexa sequencing technology, 605
  - pyrosequencing, 604–605
  - SOLiD technology, 605
  - See also* Apple genome sequencing; *Fragaria* spp.; Genome sequencing, Rosaceae; Peach genome sequencing
- Serviceberry, 12
- Sharka disease, *see* Plum pox virus (PPV) disease
- Shell hardness, almond, 204–205
- Simple sequence repeat (SSR) markers, 29, 88–91
  - in apples, 85, 88, 89–91
    - common set of SSR markers, proposal for, 89–90
  - apricot, 319–321
    - heterologous SSR markers, 320
    - nucleotide repeats detection, 91
    - in pear, 91
    - in quince, 91
    - for roses, 353
    - for strawberry, 440–441
    - taxonomical relationships in *Pyrus* assessed by, 170–171
- Single-dose restriction fragments (SDRF), 299
  - strawberry, 449
- Single nucleotide polymorphism (SNP) markers, 268
  - roses, 353
    - taxonomical relationships in *Pyrus* assessed by, 170–171
- S locus F-box brothers (SFBB), 176
- Small interfering RNA (siRNA) production, in plum leaves, 283
- Solexa sequencing technology, 605
- SOLiD technology, 605
- Somatic Embryogenesis (SE), of roses, 394–397
  - 2,4-D auxin, 394
  - in vitro* multiplication via, 394–397
- Sorbitol, 107
- Sorbitol-6-phosphate dehydrogenase gene (S6PDH), 155
- Sorbus* spp., 11
- Spiraeoideae, 5, 7, 8
- S-RNase alleles of almond, 201–203
- Standardized phenotyping, Rosaceae, 43–44
- Strawberry, *see* *Fragaria* spp.
- Structural genomics, apple, 85–111
  - BAC libraries, 93–94
  - bin mapping, 110
  - linkage maps, 91–93
  - marker-assisted selection, 109
  - molecular maps, 92
  - monogenic traits, 94–109
  - pedigree-based approaches for mining and detection of QTLs, 110
  - physical maps, 91–93
  - polygenic traits, 94–109
  - QTLs, 85
  - RFLPs, 85
  - SSR-based maps, 85, 88, 92
  - whole genome physical map, 110–111
  - whole genome sequencing, 111
  - See also* DNA markers
- Structural genomic tools for Rosaceae species, 544–548
  - association mapping, 553–554
  - physical maps, 544–545

- Structural genomic tools (*cont.*)  
 whole genome sequencing, 552–553  
*See also* under Comparative genome mapping; Molecular markers
- Structural genomics, in Rosaceae crop improvement, 27  
 genome maps, 27  
 bin-mapping approach, 27  
 linkage maps, 27  
 physical maps, 27
- Structural genomics, peach (*Prunus persica*), 235–253  
 breeding in, 235–239  
 maps derived from intraspecific crosses, 237–239  
 Akame x Juseito (AxJ), 238  
 Ferjalou Jalousia x Fantasia (JxF), 237  
 Guardian x Nemaguard (GxN), 238  
 Harrow Blood (HB) x Okinawa (Oki) (PMP2), 238  
 Lovell x Nemared (LxN), 238–239  
 New Jersey Pillar x KV 77119 (NJxKV), 238–239  
*Prunus persica* x (*P. persica* x *P. ferganensis*) (PxF), 237  
 Suncrest x Bailey (ScxB), 238–239  
 maps, markers available on, 240  
 molecular markers in, 235–239  
 peach x almond crosses, maps derived from, 236–237  
*See also* Comparative genomics; Functional markers; Marker assisted selection (MAS); Physical mapping; Polygenic traits mapping
- Structural genomics, pear, 168–181  
 association mapping, 181  
 genetic diversity, 168–171  
 Asian pears, 168–170  
 European pears, 168–170  
 linkage maps, 177–180  
 European pears, 177–179  
 genome structure between species based on, 179–180  
 integrated high-density genetic linkage maps, 177  
 Japanese pears, 177  
 partial genetic linkage maps, 177  
 physical maps, 177–180  
 European pears, 177–179  
 high-density genetic linkage maps, 177  
 Japanese pears, 177  
 RAPD-based genetic maps, 177  
 taxonomical relationships assessed by DNA markers, 171–172  
*See also* DNA markers
- Structural genomics, roses, 353–374  
 adaptation traits, 365, 371–372  
 black spot resistance, 365, 371  
 cold hardiness, 365  
 nematode resistance, 365, 372  
 powdery mildew resistance, 365, 372  
 color, 367, 369  
 white stripes, 370  
 yellow/orange range, 370  
 flower form, inheritance of, 369  
 flower production, 369  
 flower traits, 364, 366  
 color, 367, 369  
 flowering time, 366  
 fragrance, 367, 370  
 male sterility, 367  
 moss character, 367  
 number of petals, 366  
 recurrent blooming, 366  
 repeat flowering ability, 366  
 size, 367, 368  
 flowering time, 366  
 inheritance of known characters, 364  
 markers for identification and studies, 356–357  
 diversity studies, 356–357  
 domestication, 356–357  
 population structure, 356–357  
 taxonomy, 356–357  
 varietal identification, 356  
 phenotypic characters, genetic control of, 365  
 plant traits, 368, 370–371  
 growth type, 370  
 leaf size, 371  
 vigor, 371  
 SSRs developed for, 354  
*See also* DNA markers; Linkage maps; Positional cloning
- Structural genomics, strawberry, 428–429, 437–450
- Sugar  
 accumulation in transformed apple, 148, 154–155  
 in strawberry, 470–471
- Suncrest x Bailey (ScxB) maps, 239
- Supported Oligonucleotide Ligation and Detection Platform (SOLiD), *see* SOLiD technology

- Suppression subtractive hybridization (SSH), 32  
 disadvantage, 32
- Sweet and sour cherries  
 breeding objectives, 294–295  
 economic importance, 294  
 gene mapping and QTLs detected, 299–303  
   bloom time QTL, identification, 300  
 genetic maps construction, 295–299  
   intra-specific sweet cherry genetic linkage map, 296  
   random amplified polymorphic DNA (RAPD), 296  
 genome content, 293–294  
 linkage maps, 291–303  
 marker assisted selection, 291–303  
 QTL detection, 291–303  
 self incompatibility (SI), 299–303  
   *See also individual entry*
- Switzerland, apple production, quality and production criteria, 76
- T**
- Tart cherry, 9
- Taxonomy, Rosaceae, 1–7  
   *See also Conventional taxonomy*
- Terpenoids, in strawberry, 459
- Tetraploid mapping, roses, 357, 363
- Tissue culture of roses, 393–405
- Tissue softening, in strawberry, 495–496  
 antisense technology, 496  
 endo-beta-1,4-glucanases (EGases), 495  
 expansins, 495  
 FaExp2, 495  
 LeExp1, 495
- Tobacco, transient assays of apple genes in, 140
- Transcript profiling, Rosaceae, 31–34  
 cDNA-amplified fragment length polymorphism (cDNA-AFLP), 32, 36  
 expressed sequence tag (EST) profiling studies, 31–32  
   disadvantage, 32  
   microarray analysis, 33  
   oligonucleotide probes, 33  
   suppression subtractive hybridization (SSH), 32
- Transcriptome, *Prunus persica*, 266–267
- Transcriptomic tools (micro-arrays), roses, 384
- Transcripts mapping in peach, 247–249
- Transformation, apple, 143–157  
 of Greensleeves, 144  
 leaf disk transformation method, 144  
 traits expressed in transformed apple, 146  
   allergens, 150  
   apple allergen, 150  
   bacterial resistance, 146  
   cell adhesion, 150  
   colors, 150, 152–154  
   decreased flesh browning, 147, 149  
   down regulation of ethylene production, 148  
   fungal resistance, 146  
   modified metabolism, 147, 154–155  
   precocity, 147, 153–154  
   self-fertility, 147, 153  
   size, 152–153  
   sugar accumulation, 148  
   tree characteristics, 147, *See also individual entry*  
   tree height, 147, 152–154
- Transgenic analysis, Rosaceae, 37–40  
*Agrobacterium*-mediated plant transformation technology, 37  
 strawberry, 429  
 transgenic biotechnology, 55  
 transgenic mitigation of sharka in apricot, 327
- Transient assays of apple genes in tobacco, 140  
 MYB transcription factors, 140  
 promoter activity, 140
- Tree architecture, apple, 104–106  
 QTLs for, 105
- Tree architecture, markers for, 64  
 1,3,5-Trimethoxy benzene (TMB), 385–386
- Two-channel arrays, 33
- V**
- Variability analysis in almond, 189–190
- Venturia inaequalis*, 151–152
- Venturia nashicola*, 173–174
- Venturia pirina*, 173
- Verticillium dahliae*, 476
- Virus-induced gene silencing (VIGS) system, 39
- Vitamins, in strawberry, 470
- Volatile acetate esters, roses  
 production, 386  
   geranyl acetate, 386  
   2-phenylethyl acetate, 386
- Volatile compounds, strawberry, 458–462  
 chalcone isomerase (CHI), 464  
 chalcone synthase (CHS), 464

- HDMF (4-hydroxy-2,5-dimethyl-3(2H)-furanone), 460–461  
4-hydroxy-5-methyl-2-methylene-3(2H)-furanone (HMMF), 461  
pyruvate decarboxylase (PDC), 459  
terpenoids, 459
- W**  
Web portal and database, Rosaceae, 42–43  
White Angel, Pl-w Gene from, 99–100  
Whole genome physical map, apples, 110–111  
Whole genome sequencing  
    Rosaceae species, 552–553  
    strawberry, 450  
Whole genome shotgun (WGS) sequencing  
    strategy, 582–583, 603–604, 610  
Wild species of rose, taxonomy of, 344–345  
Wild strawberry, 494  
Woolly apple aphid (WAA), 103–104  
    pyramiding in  
        Er1 x Er3, 575–576  
Worldwide apple production, 74–75