

Index

A

AAT. *See* Alcohol acyl transferase (AAT)
Ab initio programs, 163
Abobra, 282
Accessions, 14–15
Acidulus melons, 22, 46
Acorn, 109, 120, 200
ACS7/ACS2 gene, 300
Actinostemma, 2, 6, 7
AFLP. *See* Amplified fragment length polymorphism (AFLP)
After Trinity assembly, 204
AGAMOUS homeotic gene, 302
Agrestis, 19, 161
Alcohol acyl transferase (AAT), 382
Alcohol dehydrogenase (ADH), 382
Allsweet watermelon cultivar, 77, 79
Alsomitra, 2, 281
Ameri melons, 34, 47
 sub-group ananas, 34–35
 sub-group bargi, 35, 36
 sub-group maculati, 35
 sub-group mashhadi, 35, 36
Amino-acids, 382, 384
1-Aminocyclopropane-1-1carboxylic acid (ACC), 336, 348, 349
Ampelocycos, 6
Amplified fragment length polymorphism (AFLP), 148
Androecious gene, 301–302
Andromonoecious lines, 298
Angular leaf spot, of cucumber, 63
Anisosperma, 6
Anthracnose
 of cucumber, 63
 of watermelon, 82

Aphis gossypii, 263
Apocarotenoids, 386
Aquaporins, 319
Arabidopsis, 224, 286, 319, 337, 338, 340, 351
Arabidopsis Reversion To Ethylene Sensitivity 1 (*AtRTE1*), 340
Arabidopsis thaliana, 223, 283, 301, 302, 336
Arabidopsis thaliana Ethylene-resistant 1 (*AtETR1*) receptor, 336
Arkansas Little Leaf cucumber, 60
Arlington White Spine cucumber, 54
Aroma, 16, 17, 381–382
AtHB2 gene, 319, 320
‘Atlantic Giant’ pumpkin, 314, 318
Austrobryonia, 7, 8
A57V transition, 299

B

BAC-end sequences, 162
Bacterial artificial chromosome (BAC), 188
Bacterial wilt, 63, 126, 267
Bactrocera cucurbitae, 145, 156
Banana, 232, 341
Bayabusua, 2
Bayesian evolutionary analysis, 222
Bayesian molecular clock approaches, 8
Begoniaceae, 2, 4
Belly rot, 65
Bemisia tabaci, 125, 263
Benincasa, 152
 B. hispida (*see* Wax gourd)
β-carotene, 351, 375–379
Bicollateral phloem, 280

- Biogeography, 7–8
 Bitter apple. *see* *Colocynthis*
 Bitter gourd, 144–149, 218
 BLAST, 244, 248–249
 Blossom scar, 16
 Boston Pickling cucumber, 54
Botrytis cinerea, 196
 Bottle gourd, 144, 149–151, 218
 BOWTIE2, 207
 Branched-chain amino acids
 aminotransferase (BCAT), 384
Bryonia, 7, 8
 Bulk segregant analysis (BSR-Seq),
 325, 368–369
 Bur gherkin, 218
 Burpee Hybrid cucumber, 61
 Burrows-Wheeler Aligner (BWA), 207
 Byzantine mosaics, 155
- C**
 CABYV. *See* Cucurbit aphid-borne yellow
 virus (CABYV)
 Calabash, 149
 Calcium-dependent protein kinase (CDPK),
 345
 Callicarpa Group, 113
 Calyx, 6, 218
 Cantalupensis melons, 42, 47
 sub-group American Eastern, 44, 45
 sub-group American Western, 44, 45
 sub-group Charentais, 43–44
 sub-group Ogen, 44, 45
 sub-group Prescott, 42, 43
 sub-group saccharinus, 42, 43
 CAP3, 204
Capsicum annuum L., Solanaceae, 121
 Carotenoid cleavage dioxygenase (CCD), 386
 Carotenoids
 accumulation, regulation, 351–353
 melon
 biosynthetic pathway, 375, 376
 determination, 379
 fruit-flesh color, 375
 Genome Wide Association Studies, 379
 mapping approach, 378
 orange flesh, 375
 phenotypes, 375, 377, 378
 pigments, 124
 Carpel primordia, 6
 Casabanana, 218
 Cassaba melons, 36, 47
 hassanbey, 36, 37
 Kirkagac, 36, 37
 kuskular, 37, 38
Castanopsis hystrix, 231
Cayaponia, 6, 8, 282
 cDNA library, 366
 CDPK. *See* Calcium-dependent
 protein kinase (CDPK)
 Cell proliferation, 312
 Centre for Genetic Resources, Netherlands, 54
 Chandalak melons, 32, 46
 sub-group bucharici, 32, 33
 sub-group garma, 32, 33
 sub-group tachmi, 32, 33
 sub-group zami, 32, 33
 Charentais melon, 342
 Charleston Gray watermelon, 79, 81, 84, 90
 Chate melons, 30–31, 46
 Chayote, 218
 Chicago Pickling cucumber, 54
 Chinese Academy of Agricultural Sciences,
 54, 146
 Chinese Long cucumber cultivar, 64, 66
 Chinesis melons, 28, 46
 Chipper, 233
 Chito melons, 20, 21, 46
Chlamydomonas, 236
 Chloroplast, 165, 202
 1-(2-Chloro-4-pyridyl)-3-phenyurea (CPPU),
 322–323
 Chromoplasts, 351
 Chromosomal rearrangement, 220
 Chromosome anchoring, 189
 Chronogram, 8
Cionosicyos macranthus, 6
CitACS4 activity, 195
 Citron watermelon, 78, 80, 82, 83, 85
Citrullus sp., 8, 13, 77, 78
 C. amarus (*see* Citron watermelon)
 C. amarus Schrad., 219
 C. colocynthis, 195, 196
 C. ecirrhosus, 78, 85, 188, 195
 C. lanatus, 100, 188, 195, 398
 C. lanatus subsp. *lanatus*,
 188, 190–192, 194
 C. lanatus subsp. *mucosospermus*, 188,
 190, 191, 194, 195
 C. lanatus subsp. *vulgaris*, 188,
 190–192, 194
 C. lanatus var. *citroides*, 78

- C. mucospermus* (see Egusi watermelon)
C. mucospermus Fursa, 219
C. naudinianus, 78, 195
C. rehmi, 78, 85, 195
 germplasm
 molecular characterization of, 87–89
 morphological characterization of, 86
 nomenclatural revisions, 79
Cladosporium cucumerinum, 64
 Climacteric fruit ripening, 335, 342, 343
 Clone-by-clone sequencing, 162
CmACS1 gene, 345
CmACS7 gene, 300
CmBCAT1 gene, 384
CmKFB gene, 380, 381
 CMV. See Cucumber mosaic virus (CMV)
CmWIP1 gene, 303
Coccinia sp., 8
 C. grandis (see Ivy gourd)
 Cocozelle, 118, 200
Coleus blumei, 289
Colletotrichum lagenarium, 63
 Collinear gene-order analysis of cucumber, 223
 Colocynth, 78, 80, 83–85
Colorless-nonripening (Cnr) gene, 339, 340
 Commercial bottle gourd rootstocks, 151
 Comparative genomics, 217–220
 disease resistance genes, 224–225
 gene prediction and annotation, 223–224
 genome duplications, 222–223
 syntenic relationships among cucurbit
 genomes, 220–222
 transposon annotation, 224
 Conomon melons, 23–24, 46
Corallocarpus, 8
 Corolla, 6
 Correlation analysis, of fruit traits, 321
Corynespora cassiicola, 64
 Cottony leak, 65
 Cowcumber. See Cucumber
 Cretaceous–Paleogene (K–Pg)
 extinction event, 222
 Crimson Sweet watermelon cultivar, 77, 79
 Crop germplasm, 128
 Crops, 397–398
 Crop wild relatives, 9
CsERF3 gene, 315
CsGLI gene, 324
 Cucumber, 4, 8, 9, 13, 14, 144, 218, 219, 223,
 230, 231, 243, 283, 288, 296
 ACS7/ACS2 gene in, 300
 centers of diversity for, 52
 chromosomes, 221
 collinear gene-order analysis of, 223
 crosses, 52–53, 55
 cultivar improvement, 54–58
 disease resistance, 63–66
 downy mildew, 64
 draft genome assembly, 174–175
 flower femaleness and
 parthenocarpy, 61–63
 foliage, 60
 fruit rots and seedling
 diseases, 65–66
 further research, 66–67
 genetic resources of, 49–80
 genomes, 164, 171–172
 cucumber draft genome
 assemblies, 174–175
 database, 243
 during *Cucumis* chromosome
 evolution, 179–180
 cytological view of, 172–174
 under domestication, 176–179
 genetic diversity in cucumber natural
 populations, 180–181
 sequence-guided genetic map
 development, 176
 whole genome features of important
 gene families, 176
 locule number variation, 60
 mapping quantitative
 traits, 264–267
 markers associated with phenotypic
 traits, 57–58
 morphological diversity of, 50
 mosaic mutants of, 233
 natural populations,
 genetic diversity in, 180–181
 plant architecture, 59
 populations and genetic maps, 263
 powdery mildew, 64–65
 production of, 51–52
 seedling traits, 59–60
 sexual morphs in, 298
 stem and leaf traits, 60–61
 taxonomy of, 52–54
 top eight producers of, 50
 tree, 4, 8
 vein mosaic virus, 201
 viruses, 66
 yield, 63

- Cucumber mosaic virus (CMV), 152, 263
Cucumeropsis mannii, 218
Cucumis sp., 4, 8, 52, 172, 230
 C. anguria, 14
 C. callosus, 52
 C. carolinus, 14
 C. chate, 14
 C. dipsaceus, 14
 C. dudaim, 14
 C. flexuosus, 14
 C. hirsutus, 4
 chromosome evolution, cucumber genome during, 179–180
 C. humifructus, 14
 C. hystrix, 49, 52–55, 59, 63, 164, 171, 180
 C. hytivus, 53, 59
 C. maderaspatanus L., 14
 C. melo
 ethylene biosynthesis pathway, 336, 337
 ethylene signal transduction, early phase of, 336, 338
 tomato gene, homologues for, 354, 355
 C. melo L. (see Melon)
 C. metuliferus, 14, 53, 54
 C. microcarpus, 14
 C. momordica, 14
 C. picrocarpus, 14
 C. pubescens, 14
 C. pustulatus, 14
 C. sativus, 283, 288
 C. sativus L. (see Cucumber)
 C. sativus L. var. *hardwickii*, 176
 C. sativus L. var. *sativus*, 176
 C. sativus L. var. *xishuangbannanensis*, 177
 C. sativus var. *hardwickii*, 50, 52, 54, 60, 63, 179
 C. sativus var. *sativus*, 49, 51, 53, 60, 220, 221
 C. trigonus, 14, 166
 Cucumis sativus L. (see Cucumber)
 C. utilissimus, 14
 mitochondrial DNAs, 231, 235
 organellar DNAs, 235
 Cucurbitacins, 103
 Cucurbit aphid-borne yellow virus (CABYV), 149
Cucurbita sp., 13, 199–200, 270–271
 biotechnology, 126–127
 C. argyrosperma, 101, 104, 105, 112–116, 119, 201, 210, 219
 C. argyrosperma C. Huber, 201
 C. argyrosperma subsp. *argyrosperma*, 112–113
 C. argyrosperma subsp. *argyrosperma* var. *palmeri*, 112–113
 C. argyrosperma subsp. *sororia*, 112
 C. argyrosperma, 115
 C. californica, 114
 C. cordata, 114
 C. cordata C. *ecuadoriensis*, 210
 C. cylindrata, 114
 C. digitata, 101, 114
 C. ecuadorensis, 101, 106, 116, 126
 C. ficifolia, 101, 104–106, 113–116, 129, 201, 210, 219, 285
 C. foetidissima, 101, 116, 210
 C. galeottii, 101
 C. lundelliana, 101, 116, 201, 210
 C. martinezii, 114
 C. maxima, 101, 104, 105, 111–112, 114, 116, 118, 119, 121, 124, 126, 128, 130, 210, 219, 232, 283, 285, 317
 C. maxima Duchesne, 200, 257
 C. moschata, 7, 101, 104, 105, 108–112, 115–119, 121, 122, 124, 126, 127, 129, 130, 201, 209, 210, 219
 C. moschata Duchesne, 200, 257
 C. okeechobeensis, 101, 114, 116, 117, 126, 130, 201, 210
 C. okeechobeensis subsp. *martinezii*, 114
 collection, maintenance, and characterization of genetic resources, 128–129
 C. palmata, 114
 C. pedatifolia, 101, 116, 210
 C. pepo, 7, 8, 104–109, 112, 114, 116–120, 122, 124–128, 130, 157, 209, 210, 219, 271, 282, 310, 315, 325
 C. Acorn squash cultivar, 205
 genome assembly, 203
 genome sequencing of, 202–203
 genotyping by sequencing in, 205–209
 transcriptome, 203–209
 C. pepo L., 101, 200
 C. pepo subsp. *fraterna*, 107
 C. pepo subsp. *gumala*, 107
 C. pepo subsp. *ovifera*, 200
 C. pepo subsp. *pepo*, 107–109, 118, 120, 122, 126, 129, 157, 200
 C. pepo subsp. *texana*, 106–109, 117–120, 122, 126, 157
 C. radicans, 101
 diseases, 125
 diseases resistance, 126
 distribution and usage of, 118
 diversity and relationships among species, 114–116
 within species, 106
 domestication, 103–106

- environmental effects on production of pumpkins and squash, 119
 - flowering and reproduction, 118–119
 - future of genetic resources, 129–131
 - genetic engineering, 127
 - genomes, 399–401
 - genome sequences, 202
 - germplasm, 126
 - immature vs. mature fruits, production of, 119–125
 - mapping, 127–128
 - mitochondrial DNAs, 230
 - morphology, 102–103
 - NGS in, 202
 - one gene pool, 116–118
 - origin of, 101
 - phloem exudate, 285
 - powdery mildew, 149
 - taxonomy and wild distribution, 101–102
 - transcriptome resequencing in, 209–210
 - unigenes, 205, 206
 - Cucurbit Genetics Cooperative, 55, 258
 - Cucurbit Genomic Database (CuGenDB), 246, 247, 251, 400
 - Cucurbitoidae, 2, 3, 52
 - Cucurbitospermum*, 7
 - CuGenDB. *See* Cucurbit Genomic Database (CuGenDB)
 - Cultigroup, 15
 - Cultivar-groups
 - for *Cucurbita maxima*, 111
 - for *Cucurbita moschata*, 110
 - Cultivated melons, phenotypic diversity, 15–17
 - Cyclanthera pedata*. *See* Slipper gourd
 - Cyclantheropsis*, 7
 - Cyclin, 312, 316
 - Cyclin-dependent kinases (CDKs)
 - genes, 312, 316
 - Cytomegalovirus (CMV), 66
- D**
- Dactyliandra*, 8
 - DAPI-stained pachytene chromosomes, 173
 - Datiaceae, 2, 4
 - de novo* genome assembly, 189, 204
 - Dessert watermelon, 78, 80, 83, 89
 - DH lines. *See* Doubled-haploid (DH) lines
 - Dicaelospermum*, 14
 - Didymella bryoniae*, 59, 64, 125
 - Differentially expressed genes (DEGs), 346, 369, 379
 - Dioecy, 4, 296, 304, 305
 - Disease resistance, 114, 117, 126
 - cucumber, 63–66, 267
 - genes, 191–192, 224–225
 - melon, 262–263
 - watermelon, 79–82, 270
 - Divergence times, 7–8
 - dm-1* gene, 64
 - DNA-sequence polymorphisms, 108
 - Doubled-haploid (DH) lines, 162, 236
 - Downy mildew, cucumber, 64
 - Draft genome assembly, 172, 174, 175, 181
 - Dudaim melons, 31–32, 46
 - Dutch gherkin and greenhouse cucumber, 51, 54
- E**
- Early Cluster cucumber, 54
 - Early Russian cucumber, 54
 - Ecballium*, 7, 8
 - Echinocystis lobata*, 5, 8
 - Eco-TILLING techniques, 342
 - Edible-seed watermelon, 76
 - Egusi watermelon, 78, 80, 83–85
 - Electropotential waves (EPWs), 285
 - Embryo-culture techniques, 126
 - Embryo-rescue techniques, 116–117
 - Epicarp traits, of melons, 16
 - Epigenetic regulation, 304
 - Epigenetics, 299
 - EPWs. *See* Electropotential waves (EPWs)
 - Erwinia tracheiphila*, 63, 125
 - EST. *See* Expressed sequence tag (EST)
 - ESTScan software, 205
 - EST-seq databases, 162
 - Ethylene, 261, 299, 314–315, 322, 335–336
 - biosynthesis pathway, 336, 337
 - fruit ripening, 336–337
 - biosynthesis gene expression, regulation of, 344–346
 - dependent and-independent biochemical processes, 348–349
 - perception and signaling, 347–348
 - signal transduction, early phase of, 336, 338
 - Ethylene Insensitive 3 (EIN3) transcription factor, 336
 - Ethyl methanesulfonate (EMS), 90, 342
 - Evolution, 4–6
 - Exocarp traits, of melons, 16
 - Exogenous L-phenylalanine, 382, 384
 - Expressed sequence tag (EST), 204, 224, 246, 249, 367, 368, 384
 - Extrascicular phloem, 280, 282

F

- FASTA, 244
 Fatty acids, 385
 FCRI. *See* Field Crops Research Institute (FCRI)
 Feral genotypes, 15
 Feral melons, phenotypic diversity, 15–17
Fevillea, 2
 Fevilleaceae, 6
 Fevilleoideae, 2
 Field Crops Research Institute (FCRI), 153–154
 Fig-leaf gourd, 113–114
 Filaments, 6
 FISH-based karyotyping methods, 173
 Flavonoids, 379–381
 Flexuosus melons, 28–29, 46
 adjour, 29
 arya, 29, 30
 tara, 29, 30
 Floral meristem, 297
 Flower femaleness, cucumber, 61–63
 Flowering traits, 269
 Flower morphology, 4–6
 Flower ontogenesis, 297
 Fluorescence in situ hybridization (FISH), 165, 172, 173
 454 GS FLX Titanium technology, 203
 454-pyrosequencing analysis, 367
 Fruit color
 melon, 261
 watermelon, 269
 Fruit development, 401
 Fruit growth, 309–310
 Cucurbitaceae, 310
 fruit development, 310, 326
 ovary development, 310
 carpel number, floral sex expression, and ovule number, 313–315
 distinctive ovary shape, 310, 311
 fruit shape and size establishment, cell division, 310, 311
 post-anthesis
 cell division, regulation of, 316–317
 cell expansion,
 factors affecting, 317–320
 cell number and cell size, 315–316
 QTL identification, fruit size and shape, 320–322
 seed development
 and parthenocarpy, 322–323
 spines, warts, and stripes, 323–325
 Fruit morphology
 cucumber, 265–266
 melon, 259–260
 watermelon, 269
 Fruit quality, 120, 130, 398, 400, 401
 melon
 acidity, sugar, 373–374
 amino-acid derived and sulfur compounds, 382, 384
 aroma, 381–382
 BSR-Seq, 368–369
 carotenoids, 375–379
 cDNA library, 366
 databases, 367
 fatty-acid derived compounds, 385
 flavonoids, 379–381
 454-pyrosequencing, 367
 fruit ripening, 365
 genetic and genomic tools, 387
 genomic research, 387–388
 NGS, 367
 oligo-based microarray, 368
 RNA-Seq, 368–369
 sugar accumulation, 369–373
 terpenoids, 385–386
 transcriptome, 367
 traits
 cucumber, 266
 melon, 261–262
 watermelon, 270
 watermelon, 89
 Fruit ripening, melon, 335, 401
 carotenoid accumulation,
 regulation of, 351–353
 climacteric and non-climacteric fruits, 335
 comprehensive transcriptome analysis,
 353–354
 dissection of, 349–350
 ethylene, 336–337
 biosynthesis gene expression,
 regulation of, 344–346
 dependent and-independent
 biochemical processes, 348–349
 perception and signaling, 347–348
 functional genomics, 342
 genetic regulation, 343–344
 homologues, 354, 355
 physiology, 342–343
 TILLING and genome editing
 technologies, 354
 Fruit rots
 of cucumber, 64–66
 of watermelon, 80
Fusarium sp., 66, 125
 F. oxysporum, 270
 F. oxysporum f. sp. *cucumerinum*, 64
 F. oxysporum f. sp. *niveum*, 151, 196
 Fusarium wilt, 64, 148
 Fuzzy gourd group, 152
Fw2.2, 312

G

Gao Lan Zi Gua watermelon cultivar, 76
 GBS. *See* genotyping by sequencing (GBS)
 G19E amino acid, 300
 Gemsbok cucumber, 85
 Gene annotation of watermelon, 190
 Gene classification tool, 248
 Gene model prediction, 223–224
 Gene Ontology (GO), 190, 205
 Gene promoters, 285
 Genetic diversity, 77–88, 400
 Genetic enhancement, 128
 Genetic maps, 162, 201, 202, 210, 212, 243, 248, 400
 cucumber, 263
 melon, 258–259
 watermelon, 267–268
 Genetic resources, 129–131, 145, 398–399
 collection, maintenance, and
 characterization of, 128–129
 future of, 129–131
 Genome annotation, 163, 223–224
 Genome editing, 354, 388
 Genome evolution, 182
 Genome sequencing, 225, 246, 321
 melon genome, 162–163
 watermelon genome, 189–192
 Genome structure
 melon genome, 163–165
 watermelon genome, 192
 Genomic analysis, 401–402
 Genomic databases, 242–243
 general cucurbit database, 246–249
 species-specific databases
 cucumber genome database, 243
 melon genome databases, 243–244
 squash and pumpkin genome
 databases, 245
 watermelon genome database, 245
 Genomics, 181
 Genotyping by sequencing
 (GBS), 176, 208, 212
 Geranylgeranyl diphosphate
 (GGDP), 351, 352, 354
 German Schalgurken cucumber, 51, 54
 Germplasm, 89–91, 194–195, 398, 399
 Germplasm Resources Information
 Network (GRIN), 90
Gerrardanthus sp., 4
 G. grandiflorus, 5
 GGDP. *See* Geranylgeranyl
 diphosphate (GGDP)
 GoldenGate array, 163
Golovinomyces orontii, 125
 Gomphogyneae, 2, 6, 7
 Gourd, 100. *See also Cucurbita* sp.

Grafting, 151
 Green-leaf volatiles (GLV), 385
 Groups, 14–15
 Gummy stem blight
 of cucumber, 64
 of watermelon, 82
Gurania makoyana, 5
 Gy14 cucumber genome assembly, 173
 Gynoecious lines, 298
 Gynoecium, 218
 Gynoecy, 4
Gyno-hAT transposon, 304

H

H-19, 60
 Hairs, exocarp/epicarp traits, 16
 “Heirlooms,” 128
 Herbarium, publicly available, 9
 Hermaphrodite lines, 298, 304
 Hermaphroditism, 296
 He Tao Wen watermelon, 76
Hexacolpites echinatus, 7
 HFO-TAG markers, 83, 84
 Hidden Markov Models (HMMs), 250
 High-capacity NGS-based genotyping, 387
 High-throughput next-generation DNA
 sequencing, 354
 High-throughput phenotyping methods, 387
 HMMs. *See* Hidden Markov Models (HMMs)
Hodgsonia, 6
 Homozygous lines, RIL, 213
 Honey melon, 296
 Hormones, 299
 androecious gene, 301–302
 monoecious gene, 299–300
 Hubbard squashes, 318
 Hull-less-seed pumpkins, 125
 Hybrid bitter gourd cultivars, 148
 Hydroperoxide lyase (HPL), 385
 Hypanthium, 6, 16

I

Ibericus melons
 sub-group rochet, 38, 40
 sub-group tendral, 38, 39
 ICuGI. *See* International Cucurbit Genomics
 Initiative (ICuGI)
 ICuGI database, 163
 Illumina paired-end sequencing, 166
 Illumina sequencing technology, 192–193
 Illumina Solexa technology, 204
 Inbred backcross lines (IBL), 63
 Inbreeding depression, 119
 Indian bitter gourd market, 148

- Indicus melons, 34
Indomelothria, 8
Inodorus melons, 18, 41, 47
 sub-group Earl's, 41, 42
 sub-group honeydew, 41
 Intermediary cells, 288
 International Code of Nomenclature for
 Cultivated Plants (ICNCP), 15
 International Cucurbit Genomics Initiative
 (ICuGI), 244, 258–259
 Interspecific hybridization, 117
 iTAK, 250
 Ivy gourd, 218
- K**
- Kachri melons, 18–20, 46
Kedrostis, 8
 Keto acids, 384
 “Key” sexual genes, 297
Khmeriosicyos, 2
- L**
- Lagenaria siceraria*, 7, 54. *See also* Bottle
 gourd
 Laigua/Laiputao, 148
 La Ma Gua watermelon, 76
 Landrace-derived cultivars, 157
 Landraces, 15, 152
 Lanzhou Da Bang Hong Zi Gua watermelon
 cultivar, 76
 LD mapping. *See* Linkage disequilibrium
 (LD) mapping
 Leaf traits, 60–61
 Linkage disequilibrium (LD) mapping, 259
Linnaeosicyos, 6
 Lipoxygenase (LOX) genes, 191, 385
 LJ 90430, 63
Ll Ll gene, in cucumber, 60
 L-methionine, 384
 Locule number (*LC*), 312–313
 Long-fruited edible bottle gourds, 149
 Long terminal repeat (LTR) retrotransposons,
 190, 224
 LOX genes. *See* Lipoxygenase (LOX) genes
 L-phenylalanine, 384
Luffa sp., 7, 8, 156, 218
 L. acutangula, 156, 157
 L. aegyptiaca, 145
 L. astorii, 155
 L. cylindrica, 156
 L. echinata, 154
 L. graveolens, 154
 L. hermaphrodita, 156
 L. quinquefida, 155
 L. saccata, 155
 L. siceraria, 150, 151, 157
 L. tuberosa, 154–155
 L. umbellata, 155
- M**
- Makuwa* melons, 24, 46
 sub-group ginmakuwa, 25, 27
 sub-group kanro, 25, 26
 sub-group nashi-uri, 24, 25
 sub-group ogon, 24, 25
 sub-group seikan, 27
 sub-group yuki, 24, 26
 Ma Ling Gua watermelon, 76
 Mapping quantitative traits
 cucumber, 264–267
 melon, 259–263
 watermelon, 268–271
 Marker-based clustering, 180
 Markers, 243
 Mate-pair chimeric, 202
 Mature fruits, 145
 Mel2, 366
 MeloGene, 244
Meloidogyne, 14
 Melon, 8, 50, 52–54, 64, 144, 218, 219, 223,
 230–231, 243, 258
 accessions and groups, 15
 acidulus, 22
 ACS7/ACS2 gene in, 300
 agrestis, 19
 ameri, 34–36
 Cantalupensis, 42–43
 cassaba, 36–38
 chandalak, 32–33
 chate, 30–31
 chinesis, 28
 chito, 20, 21
 chloroplast, 165
 Cm*ACS7* gene in, 300
 conomon, 23–24
 and cucumber genomes, comparison
 between, 164
 dudaim, 31–32
 exocarp/epicarp traits, 16
 flexuosus, 28–30
 flowers, 16
 fruit development and conservation, 17–18
 fruit quality
 acidity, sugar, 373–374
 amino-acid derived and sulfur
 compounds, 382, 384
 aroma, 381–382

- BSR-Seq, 368–369
- carotenoids, 375–379
- cDNA library, 366
- databases, 367
- fatty-acid derived compounds, 385
- flavonoids, 379–381
 - 454-pyrosequencing, 367
- fruit ripening, 365
 - genetic and genomic tools, 387
 - genomic research, 387–388
 - NGS, 367
 - oligo-based microarray, 368
 - RNA-Seq, 368–369
 - sugar accumulation, 369–373
 - terpenoids, 385–386
 - transcriptome, 367
- fruit ripening, 335
 - carotenoid accumulation, regulation of, 351–353
 - climacteric and non-climacteric fruits, 335
 - comprehensive transcriptome analysis, 353–354
 - dissection of, 349–350
 - ethylene, 336–337
 - ethylene biosynthesis gene expression, regulation of, 344–346
 - ethylene-dependent and-independent biochemical processes, 348–349
 - ethylene perception and signaling, 347–348
 - genetic regulation, 343–344
 - homologues, 354, 355
 - physiology, 342–343
 - TILLING and genome editing technologies, 354
- genetic resources, 13–14
- genome, 161–162
 - databases, 243–244
 - improvements of published genome version, 165–166
 - resequencing of melon germplasm, 166–167
 - sequence, 162–163
 - structure, 163–165
- germplasm, 166–167, 261
- horticultural taxonomy, 18–19
- ibericus, 37–39
- indicus, 34
- inodorus, 41–42
- kachri, 19–20
- makuwa, 24–26
- mapping quantitative traits, 259–263
- mesocarp traits, 16
- momordica, 22–23
 - phenotypic diversity in wild, feral and cultivated melons, 15–17
 - placenta and seeds, 17
 - plastid DNA, 230
 - populations and genetic maps, 258–259
 - resequencing of, germplasm, 166–167
 - sexual morphs in, 298
 - size and shape, 16
 - tibish, 20–22
- Melon fruit fly, 156
- Melon linkage group 1 (LG1), 164
- Melon marker–cucumber genome sequence alignment, 179
- Melon mitochondrial genome, 165
- MELONOMICS, 161, 243–244
- Melon phylome, 164
- Melon pseudochromosome, 165
- Melon vein-banding mosaic virus*, 152
- Melon yellow spot virus (MYSV), 267
- Melothria*, 8
- Mesocarp traits, of melons, 16
- Mickylee watermelon, 80
- Microtubules, 312
- Middle eastern Beit Alpha cucumber, 51, 55, 63
- Miniature inverted transposable elements (MITEs), 250
- Minor vein companion cells, 288
- Minor vein structure, 287–289
- Minus lines, 298
- miRNA, 210, 247–248
- MITEs. *See* Miniature inverted transposable elements (MITEs)
- Mitochondria, 202, 230–231
 - “knock-downs,” 236
 - mitochondrial DNA, 231, 232
 - transformation, 236–237
- Mitochondrial genomes, 165
- Mitotic kinesins, 312
- Modern genome mapping strategies, 225
- Molecular clock, 2, 8
- Molecular-genetic techniques, 114, 116
- Molecular marker, 258, 264
- Molecular phylogenetics, 2
- Momordica*, 4, 8
 - M. balsamina*, 145
 - M. charantia*, 157
 - M. charantia* L. (*see* Bitter gourd)
 - M. leiocarpa*, 5
- Momordica melons, 22–23, 46
- Monoecious cucumber, 61, 171
- Monoecious* gene, 299–300
- Monoecious melon lines, 298
- Monoecy, 4, 296, 304, 305
- Monoterpenes, 385, 386

- Moroccan watermelon mosaic virus (MWMV), of cucumber, 66
- Mosaic (MSC) lines, 234
- MSU 713-5 cucumber, 61
- MU-CU-16, 202
- Mukia*, 14
- Multi-allelic mapping, 387
- Multiparent Advanced Generation Inter-Cross (MAGIC), 387
- Musa acuminata*. *See* Banana
- Mutations, 231, 232
- Myrmecosicyos*, 14
- MYSV. *See* Melon yellow spot virus (MYSV)
- N**
- Naringenin chalcone (NarCh), 380
- National Botanical Research Institute (NBRI), 90
- National Bureau of Plant Genetic Resources (NBPGR), 150
- National Plant Genetic Resources Centre (Namibia), 90
- National Plant Germplasm System (NPGS), 90
- NBPGR. *See* National Bureau of Plant Genetic Resources (NBPGR)
- NBS-LRR genes. *See* Nucleotide-binding site and leucine-rich repeat (NBS-LRR) genes
- NCBI BLASTP, 190
- ncRNAs. *See* Noncoding RNAs (ncRNAs)
- Neolalsomitra*, 2
- Nested-association mapping (NAM), 387
- Never-ripe 2 mutant, 314–315
- Next generation sequencing technologies (NGS), 80, 162, 163, 167, 202, 367, 399
- NGS. *See* Next generation sequencing technologies (NGS)
- Nhandiroboideae, 2
- Nicotiana benthamiana*, 196
- N.I. Vavilov Research Institute of Plant Industry, 90
- Non-climacteric fruits, 335
- Noncoding RNAs (ncRNAs), 163, 191
- Nonripening* (*(NOR)*) gene, 339, 340
- Norisoprenes, 385
- Normalized cDNA libraries, 203–204
- Nothoalsomitra*, 8
- Nucleotide-binding site and leucine-rich repeat (NBS-LRR) genes, 191
- O**
- Oligo-based microarray, 368
- Oligonucleotide chromosome-painting technique, 180
- Open growth habit, 121
- Oreosyce*, 14
- Organellar DNAs encode, 229
- Organellar genomes, 229–230, 400
- sequence of, 165
- sizes and structures of
- mitochondria, 230–231
- plastids, 230
- Organellar phenotypes, 232–235
- Organellar transmission, 231, 235–236
- Organic acids, melon fruit quality
- acidity, 373–374
- sugar accumulation and, 369–373
- Oriental trellis cucumber, 51, 55
- Oryza sativa*, 302
- Ovary development, cucurbit
- fruit growth, 310
- carpel number, floral sex expression, and ovule number, 313–315
- distinctive ovary shape, 310, 311
- fruit shape and size establishment, cell division, 310, 311
- Ovary hairs, of melons, 16
- OVATE* gene, 312
- Ovules, 6
- P**
- Papaya ringspot virus (PRSV), 201, 267
- Papaya ringspot virus (PRSV-W), 66
- Parthenocarpy, 4, 61–63, 322–323
- Paternal transmission of mitochondrial DNA, 231
- Pathway tool, 248
- Pc* gene, 62
- Pentamerous (*p*) gene, 313
- Persian cucumber, 51
- PGDD. *See* Plant Genome Duplication Database (PGDD)
- PGIT toolkit, 166
- Phaseolus vulgaris*, 283
- Phenotypic diversity, 257, 258
- in watermelons, 81–82
- in wild, feral and cultivated melons, 15–17
- Phenotypic markers, 57–59
- Philippines bitter gourd market, 149
- Phloem, 401
- exudate, 283–284
- loading, 287–289

- minor vein structure and
 - phloem loading, 287–289
 - organization, 280–282
 - phloem-specific proteins, 284–286
 - PP1 and PP2, 286–287
 - P-protein, 284–286
 - proteins 1, 286–287
 - proteins 2, 287
 - sieve tube, 283
 - “Phloem” exudate, 283–284
 - Phytoene synthase (PSY), 351
 - Phytohormone, 335, 351
 - Phytohormone jasmonic acid, 351
 - Phytophthora* sp.
 - P. capsici*, 64, 65, 80, 125, 126, 151, 201
 - P. dreschleri*, 65
 - Pickling cucumber, 51, 52
 - Pigmentation system, 380, 381
 - Pistillate flowers, 102
 - Pixie cucumber cultivar, 64
 - Placenta, of melons, 17
 - Plant
 - architecture, 59
 - breeding, 130, 162, 167
 - cytoplasm, 229
 - Plant Genome Duplication Database (PGDD), 249
 - Plant MITE (P-MITE) database, 250
 - Plant transcription factor database (PlantTFDB), 250
 - Plasma membrane intrinsic proteins (PIPs), 319
 - Plastid DNAs, 230, 233
 - Plastids, 230
 - Plastid-sequence variation, 230
 - PLAZA, 249–250
 - Pleiotropic effects, 260
 - PMCs. *See* pollen mother cells (PMCs)
 - P-MITE database. *See* Plant MITE (P-MITE) database
 - Podosphaera fusca*, 64–65
 - Podosphaera xanthii*, 64, 125, 151, 201
 - Poinsett cucumber cultivar, 64
 - Pollenizer, 62, 77
 - Pollen mother cells (PMCs), 172
 - Polymer trapping, 288, 289
 - Polymorphisms of chloroplast DNA, 116
 - Potyviruses
 - of cucumber, 66
 - of watermelon, 83
 - Powdery mildew (PM)
 - cucumber, 64–65
 - watermelon, 80, 83
 - Praecitrullus fistulosus*. *See* Tinda
 - Pre-publication zucchini genome sequences, 245
 - Preserving melon. *See* Citron watermelon
 - PRSV. *See* Papaya ringspot virus (PRSV)
 - PS 547 cucumber cultivar, 65
 - Pseudomonas lachrymans*, 63–64
 - Pseudoperonospora cubensis*, 63, 64, 125
 - Pumpkins, 99–100, 219, 243, 280
 - genome database, 245
 - sRNAs, 247
 - Pythium* sp., 64
 - P. aphanidermatum*, 65
- Q**
- qRT-PCR, 385
 - Quantitative trait loci (QTLs), 64–66, 89, 213, 259–260, 264–266, 268, 270, 271
 - cucurbit fruit growth, 310, 315, 320–322
 - fruit ripening, 342
 - melon fruit quality, 371–373
- R**
- Random amplified polymorphic DNA (RAPD), 148
 - RAPD. *See* Random amplified polymorphic DNA (RAPD)
 - Rapid amplification of cDNA ends (RACE), 386
 - Recombinant inbred line (RIL), 210, 212, 213
 - Restriction-enzyme analyses, 230
 - Restriction Fragment Length Polymorphisms (RFLP), 258
 - Rhizoctonia solani*, 64–66
 - Ridged winter-melon group, 152
 - Ridge gourds, 145, 154–157
 - RIL. *See* Recombinant inbred line (RIL)
 - Ripening behavior, 261
 - Ripening-inhibitor (Rin)* gene, 339, 340
 - RNA-Seq, 209, 211, 368–369
 - databases, 162
 - melon fruit quality, 380
 - Root-knot nematodes, 82
 - Ruthalicia eglanulosa*, 5

S

- S*-AdoMet hydrolase (*SAMase*) gene, 349
- San Bai Gua watermelon, 76
- Sanger sequencing, 162
- Scallop morphotype, 204
- Schizopepon bryoniifolius*, 4
- Sechium edule*. *See* Chayote
- Seeds, 77
 - cucumber, 59–60, 65–66
 - cucurbit fruit growth, 322–323
 - of melons, 17
 - watermelon, 270
- SEOR. *See* sieve element occlusion-related (SEOR)
- Sepals, of melons, 16
- Sequence-related amplified polymorphism (SRAP) markers, 151, 156
- Sesquiterpenes, 386
- Sex determination, 296, 401
 - A*, *M*, *G* gene molecular interaction and evolution of, 304–305
 - epigenetic regulation, 304
 - flower ontogenesis, 297
 - hormones, 299
 - androecious* (*a*) gene, 301–302
 - monoecious* (*M*) gene, 299–300
 - mechanism of, 297–299
 - transcriptional regulation, 302–303
- Sex expression, of melons, 16
- Sex-specific organs, development of, 302
- Sexual morphs
 - in cucumber, 298
 - in melon, 298
- Sexual systems
 - of Cucurbitaceae, 4
- Shamrock cucumber, 64
- Sheath, in melons, 17
- Sicana* Naudin, 101
- Sicana odorifera*. *See* Casabanana
- Sicydium*, 2
- Sicyos* sp., 7
 - S. angulatus*, 8
 - S. edulis*, 5
- Sieve element occlusion-related (SEOR), 285
- Sieve tube, 283
- Silene conica*, 232
- Silverseed gourd, 112–113
- Simple sequence repeat (SSR), 106
 - genetic analysis, 151
 - molecular markers, 53, 148
- Single nucleotide polymorphism (SNP), 79, 165, 207, 209, 212
 - map, 163, 259
 - markers, 53, 196, 244
- Single-nucleotide polymorphism (SNP) based map, 128
- Siolmatra*, 7
- Siraitia*, 8
- Sister groups, 8
- Slf1* gene, 312
- Slime plugs, 284
- Slipper gourd, 218
- Small RNAs (sRNAs), 243, 247–248
- Snake gourd, 145, 154
- Snow's Pickling cucumber, 54, 55
- Southern African Development Community (SADC)
 - National Plant Resources Centre Regional Network, 90
 - Plant Genetic Resources Centre, 90
- Spartan Dawn cucumber, 62
- Specific length amplified fragment sequencing (SLAF-seq), 319
- Spines, 323–325
- Sponge gourd, 145, 154–157
- Squash, 99–100, 219, 242–243, 257. *See also* *Cucurbita* sp.
 - genome database, 245
 - leaf curl virus, 201
- Squash leaf curl virus, 125
- Squash phloem exudate contains
 - an aspartic acid proteinase inhibitor (SQAPI), 285
- Squash vein yellowing virus (SqVYV), 80
- SRAP markers. *See* Sequence-related amplified polymorphism (SRAP) markers
- SSR. *See* Simple sequence repeat (SSR)
- SSR-sequence polymorphisms, 124–125
- Stachyose, 282, 288, 289
- Stamen primordia, 6
- Staminate flowers, 102
- Stem traits, cucumber, 60–61
- Stenosperma Group, 113
- Striping patterns, 323–325
- Stylodia, 6
- Sub-group, 15
- Sublobata*, 154
- Sugar
 - melon fruit quality
 - acidity, 373–374
 - sugar accumulation, 369–373
 - in melons, 17
- Sugar Baby watermelon, 80
- Sulfur compounds, 382
- SUN* gene, 312
- Symplastic phloem, 288
- Syntenic blocks, 225
- Synteny, 218, 220, 221

T

- Tailby's Hybrid cucumber, 54
 Targeting Induced Local Lesions in Genomes (TILLING), 90–91, 205, 301, 303, 354, 402
 Target leaf spot, of cucumber, 64
 TE. *See* Transposable element (TE)
Telfairia, 6, 218
T. occidentalis, 5
 TEs. *See* Transposable elements (TEs)
 Tetramelaceae, 2, 4
 Texture, of melons, 16, 17
 Thai bitter gourd market, 148
 Thermal desorption gas chromatography
 mass spectrometry
 (TD-GC-MS), 350
Thladiantha
T. dubia, 8
T. hookeri, 5
 Tibish melons, 20–22, 46
 TILLING. *See* Targeting Induced
 Local Lesions in Genomes
 (TILLING)
 Time tree, 8
 Tinda, 218
 Tissue-culture protocols, 127
Tomato leaf curl New Delhi virus
 (ToLCNDV), 156
 Tonoplast intrinsic proteins (TIPs), 319
 Tonoplast Sugar Transport gene, 89
 Traditional plant breeding, 130
 Transcriptional regulation, 302–303
 Transcriptome
 Cucurbita pepo, 203–209
 resequencing in *Cucurbita*
 genus, 209–210
 Transcriptome v3, 207
 Transcriptomics analysis,
 312, 322, 348
 Transcripts, 204
 Transformation, mitochondria, 236–237
 Transposable element (TE), 190
 amplification, 164
 fraction, 163
 Transposon annotation, 189–190, 224
 Tribe Cucurbiteae, 281
 Triceratieae, 2, 7
 Trichomes, 323–325
Trichosanthes sp., 6, 8, 218
T. cucumerina, 5, 154, 157
T. cucumerina L. (*see* Snake gourd)
T. lobata, 154
 Triploid cultivars, 323
 Trypsin inhibitor, 285
 Tsamma melon. *See* Citron watermelon

U

- Ultrahigh-density SNP map, 193
 Unassembled reads, watermelon, 189–190
 Uniparental effects, 235
 Unisexuality, 296
 Unridged winter melon group, 152
 USDA/ARS Plant Genetic Resources Unit
 (PGRU), 76, 90
 U.S. National Plant Germplasm
 System, 53, 54
 U.S. Vegetable Laboratory (USVL), 79

V

- Vegetable Marrow, 200
 Vegetative traits
 cucumber, 266–267
 melon, 262
 Vein tracts, of melons, 16
 Vietnamese bitter gourd market, 149
 Vine length, of cucumber, 60
 Viruses
 cucumber, 66
 of watermelon, 80
 Volatile organic compounds
 (VOCs), 381–382

W

- Warts, 323–325
 Water column, 286
 Watermelon, 8, 9, 13, 144, 218, 219, 243, 296
 breeding programs, 85
 center of origin and genetic diversity of,
 77–88
 fresh market value of, 76–77
 fruit quality and morphology, 89
 genetic maps, 267–268
 genetic resources of, 75–77
 genome, 187–188
 database, 245
 germplasm, resequencing of, 194–195
 published genome version,
 improvements of, 192–193
 sequence, 189–192
 structure, 192
 utility of, 195–196
 germplasm resources useful for enhancing
 cultivars, 89–91
 global production of, 76
 mapping quantitative traits, 268–271
 phenotypic diversity in, 81–82
 populations, 267–268
 United States plant introductions with
 resistance to diseases or pests of, 82

- Watermelon mosaic virus (WMV),
66, 201, 263
- Wax gourd, 145, 151–154, 218
- West Indian gherkin, 50
- WGDs. *See* Whole-genome
duplications (WGDs)
- White-flowered gourd, 149
- Whole-genome duplications (WGDs), 163,
174, 222–223
- Whole-genome resequencing, 387
- Whole genome sequencing, 204, 205, 351
- Whole-genome shotgun strategy, 202
- Wild genotypes, 15
- Wild gourd fruits, 103
- Wild melons, 14–17
- Wild relatives, 9, 50, 55, 157
- WIP transcription factors, molecular
characterization of, 305
- Wisconsin SMR 18 cucumber, 61
- World Vegetable Center (WorldVeg), 146, 150,
154, 157
- Wound inducible protein 1 (WIP1), 314
- X**
- Xerosicyos*, 4, 7
- Xiao Hua Li Hu watermelon, 76
- Xishuangbanna cucumber (XIS), 179
- Xishuangbanna group, 181
- Y**
- Yield related traits
cucumber, 265
melon, 259
- Yuanfeng cucumber cultivar, 64
- Z**
- Zambia Agriculture Research Institute (ZARI),
90
- Zanonia*, 7
- Zanoniaceae, 2, 6, 7
- Zanonioidae, 2, 3
- Zapallitos*, 111
- Zehneria hermaphrodita*, 4
- Zhenzhu, 148
- Zucchini, 200, 207, 212
genotype, 204
morphotype, 202
TILLING population, 205
- Zucchini-Scallop transcriptome, 208
- Zucchini yellow mosaic virus (ZYMV), 66,
125, 201