INDEX

A
Adaptor ligation and preamplification
AFLP .................................................................180–181
microsatellite library ......................................178, 180–182
Allopolyploid ......................................................142–144, 325
Amplified fragment length polymorphism
(AFLP) ..................................................23, 42–44, 48, 72, 76, 77, 82,
192–194, 211–231, 235, 388, 390
Arbitrary primed polymerase chain reaction
(AP-PCR) ........................................194, 197, 203, 206

B
Barcode of Life Data Systems ..................................100
BARE1 element .....................................................235–237, 244

C
CAPS. See Cleaved amplified polymorphic sequences
(CAPS)
Cereba (LTR primer design) .......................243
Character matrix ...................................................258–260
Chloroplast DNA (cpDNA) ..................42, 43, 45, 54, 85–116,
122, 126–128, 375
Chromosome ......................................................2, 44, 50, 86, 120, 125, 143,
161–163, 212, 233, 282–284, 294, 305, 309, 310,
312, 313, 316, 321, 325–328, 330–332, 334, 335
Chromosome banding
DAPI banding ....................................................288
fluorochrome banding ..................................309, 310
Giemsa C-banding ...........................................309–311
Hoechst banding .............................................317
Cleaved amplified polymorphic sequences
(CAPS) ..................................................194, 195, 199, 205–206
Cloning
of PCR fragment
from retrotransposon ..................................239, 244
from SCAR ........................................193, 194, 196–197
in pGEM-T
microsatellite library ..................................179–188
Clusia multiflora (genome size analysis) ..............298
Coping DNA ....................................................44
Codominant ...........................................48, 49, 177, 191, 193, 195, 213
Complete chloroplast sequences ...........95, 105, 112, 115
Complete mitochondrial sequences ..............48
Conserved primers (= universal primers) ..42, 90, 105,
112, 122, 126, 128, 130–131, 135, 142, 238
Consortium for the Barcode of Life
(CBOL) ..................................................14, 87, 145
Convergence ...............................................25, 45, 380
Copia element ..................................................236, 238
Crepis sp. (chromosome banding) ..................310, 311, 319
Cryptic ..................................................22, 24, 27
Cypripedium sp. (genome size analysis) .................282–283
Cytogenetics .................................................26, 144, 309–322, 326, 330

D
Dactylorhiza sp. (genome size analysis) ..............299, 301
DAMD. See Directed amplification
of minisatellite-region DNA (DAMD)
DArT. See Diversity array technology (DArT)
Databases
for chloroplast plant DNA primers
(http://bfw.ac.at/rz/bfwcms.web?dok=4977) ...87, 91, 130
for plant DNA barcoding
Barcode of Life Data Systems
(http://www.boldsystems.org/views/login.php) ......100
for plant DNA sequences
DNA Database of Japan, DDBJ .........................263
EMBL Nucleotide Sequence Database, EMBL-
Bank ..........................................................263
GenBank (www.ncbi.nlm.nih.gov/genbank/)
(http://www.ncbi.nlm.nih.gov/genbank/) ............91
for plant genome sizes
FLOWer database ........................................281
Plant DNA C-values database ..........................281
Denaturing high-performance liquid chromatography
(dHPLC) ........................................86, 88–90, 93–94, 101–104,
108, 109, 114, 116
Destaining slides
after FISH ...............................................321
after fluorochrome bandings ..........................318
Digestion (= restriction enzymes) ...55, 58, 74, 80, 85,
86, 92, 97, 98, 105, 110, 128, 131, 194, 195, 199,
212, 218–219, 225, 235, 236, 241, 242, 247–249,
253, 321, 329, 330, 334
Directed amplification of minisatellite-region DNA
(DAMD) ..................................................212
Diversity array technology (DArT) .....................43
Index

MOLECULAR PLANT TAXONOMY: METHODS AND PROTOCOLS

DNA amplification fingerprinting (DAF) ..................149–195, 197–198, 203–204, 206
DNA barcoding ..............................................14, 20–21, 87, 100, 144
DNA extraction
   algae (DNA extraction from herbarium specimen) ..........71, 74, 79
   cetyl trimethylammonium bromide (CTAB) extraction ..........70, 73, 74, 77–79, 81, 83
   DNA concentration (= DNA quantification) ............58, 64, 107, 110, 131–132, 200, 207, 214, 249, 252
   DNA purity (contaminants, impurities) ........55, 57, 58, 64, 251
DNA barcoding ..............................................1 4, 20–21, 87, 100, 144
DNA sequencing
DNA purity (contaminants, impurities) ..........55, 57, 58, 64, 251
DNA extraction from herbarium specimen) ..........70, 71, 73–74, 77–79
   leaf (leaves) sampling for DNA extraction ..........53–65
   lichens (DNA extraction from herbarium specimen) ..........70, 71, 73–74, 77–79
   mosses (DNA extraction from herbarium specimen) ..........71
   mucilaginous tissues (DNA extraction from herbarium specimen rich in) ..........72, 73, 77–79
   mushrooms (DNA extraction from herbarium specimen) ..........71, 74, 80
   Nucleo Spin Plant II kit (Macherey-Nagel) ..........70, 73, 74, 81
   phenolic compounds (DNA extraction from herbarium specimen rich in) ..........58, 72
   plant bulking or DNA pooling for DNA extraction ..........55
   polysaccharides compounds (DNA extraction from herbarium specimen rich in) ..........57, 71–73, 77, 107, 246
   seeds (DNA extraction from herbarium specimen) ..........72, 73, 76–77
   vascular plants/conifers (DNA extraction from herbarium specimen) ..........70, 71, 76
DNA sequencing
   Illumina GoldenGate sequencing ..........155–158, 163–170
   Illumina Infinium HD sequencing ..........158–159, 170–173
   next-generation sequencing (NGS) ..........24, 25, 90, 94, 105–107, 116, 360
   Sanger dideoxy nucleotide sequencing ..........92
   Dominant ..............................................48, 49, 193–195, 204, 213, 302
   SNP discovery ...........................................95–154, 156, 157
   Flow cytometry (FCM) ....................................279–305
   Fluorescent in situ hybridization (FISH) ..........144, 309–322, 325
   Gap extension penalty (GEP) ..........267, 268
   Gap open penalty (GOP) ..........267, 268
   Gel electrophoresis
      ethidium bromide (EB) staining ..........63, 101, 146, 147, 205
      GelRed™ staining ..........146–148
      silver staining ..........93, 113, 114, 204, 206, 217–218, 224–225
   SYBR Gold staining ..........113, 114
   SYBR green staining ..........113, 114, 241, 242, 251
   Genetic distance ..........259, 390
   Genome size
      2C-value ..........282
      1Cx-value ..........282
      holoploid 1C-value ..........282
      monoploid 1C-value ..........282
   standard references for 1C-DNA content ..........285
   Genomic in situ hybridization (GISH) ..........325–326
   Gentianella (alignment of chloroplast DNA sequences) ..........115, 116
   Glass-fibre filtration (GF) ..........74, 80
   Guzmania monostachia (genome size analysis) ..........293
   Gypsy element ..........238
   Herbarium ..........5, 7, 8, 20, 21, 25, 27, 69–83, 284, 303
   Heteroduplex DNA ..........86, 89–90, 94, 102
   Hordeum spontaneum (IRAP analysis) ..........237
   Hybrid ..........48, 49, 143, 144, 192–193, 206, 327–328, 390
   Inheritance ..........48, 126, 191–192, 194, 213
   In situ SNP discovery ..........153–154, 156, 157
   Integrative taxonomy ..........25–28
E

Enzymatic digestion and glass-fiber filtration (EDGF) ..........74, 80
Erianthus sp. (GISH analysis) ..........144, 326, 328
Evolutionary rate ..........44, 45, 47, 125, 126, 144
Extraction of PCR product from gel (SCAR) ..........193, 194, 196–197, 202, 203, 208

F

FASTA format ..........95, 161, 266–270
Flow cytometry (FCM) ..........279–305
Fluorescent in situ hybridization (FISH) ..........144, 309–322, 325

G

Gap extension penalty (GEP) ..........267, 268
Gap open penalty (GOP) ..........267, 268

H

Herbarium ..........5, 7, 8, 20, 21, 25, 27, 69–83, 284, 303
Heteroduplex DNA ..........86, 89–90, 94, 102
Hordeum spontaneum (IRAP analysis) ..........237
Hybrid ..........48, 49, 143, 144, 192–193, 206, 327–328, 390

I

Inheritance ..........48, 126, 191–192, 194, 213
In situ SNP discovery ..........153–154, 156, 157
Integrative taxonomy ..........25–28
Internal transcribed spacer (ITS) ........................................ 39, 45, 141–148, 310, 357, 374–375, 378, 387–388
Inter-primer binding site polymorphism (IPBS) ........................................... 233–253
Inter-retrotransposons amplified polymorphism (IRAP) .................................. 41, 233–253
Inter-simple sequence repeats (ISSR) ......................................................... 40, 44, 48, 211–231, 237, 243–244
Introgression ................................... 22, 50, 193, 325, 389–390, 392
Intron ........................................ 44, 86, 87, 111, 112, 115, 122, 128, 357, 375
K
Kalanchoe marnieriana (genome size analysis) ........................................... 298–299, 304
L
Long interspersed nuclear element (LINE) .............................................. 234, 238
Long terminal repeats (LTR) ......................................................... 40–41, 43, 234–239, 242–244, 248, 249, 252
Low-copy nuclear genes (LCNG) .............................................................. 42
M
Malvaceae (taxonomic revision) .............................................................. 337–360
Maximum likelihood (ML) ......................................................... 49, 259–262, 269, 271, 273, 275, 390
Maximum parsimony (MP) .......................................................... 49, 241, 260, 378
Microsatellite enriched library .............................................................. 177–188
Minisatellite .................. 39–40, 44, 90, 94, 96, 105, 115, 128
Mitochondrial DNA (mtDNA) .................................................. 43, 45, 106, 111, 121–123, 125–128, 135
ML. See Maximum likelihood (ML)
Morphological ................. 2, 258, 281, 335, 338, 366
MP. See Maximum parsimony (MP)
mtDNA. See Mitochondrial DNA (mtDNA)
N
Neighbor joining (NJ) .......................................................... 49, 202, 259
Newick format .................................................. 271
Non-coding DNA ..................................................... 39–40, 44, 112
Nuclear DNA .................................................. 39–42, 106, 107, 211, 289–294, 299, 305, 388
Nuclear ribosomal ITS .......................................................... 39, 141–148
Nucleolar organizer regions (NORs) .................................................. 142, 310
O
Organelle (organellar) DNA .................................................. 24, 25, 43, 45, 54, 106
Outlier sequence .......................................................... 261, 266, 267
P
PCR-RFLP (Restriction Fragment Length Polymorphism) (of chloroplast DNA) ........................................... 89, 92, 94, 96–98, 116, 128, 195
PDR1 retrotransposon ........................................... 235
Phylogeography ........................................... 90, 125–126
Physaria sp. (genome size analysis) ........................................... 283–284
Pinus nigra (chromosome banding and FISH analysis) ........................................... 312–313
Piper nigrum (RAPD amplification and dendrogram) ........................................... 201, 202
Plant DNA barcode ........................................... 144–145
Ploidy .......................................................... 28, 279–305
Plum (AFLP and ISSR amplification) ........................................... 225
Poaceae (ribosomal ITS alignment) ........................................... 142, 143
Polymere chain reaction (PCR) ........................................... 14, 40, 53, 71, 86, 128, 141, 155, 174, 191, 212, 233, 263, 373
Polyploidy ........................................... 50, 282, 283
Positive clone screening using PCR (microsatellite library) ........................................... 180, 185–186
Preparation of protoplasts ........................................... 316
Pretreatment and fixation of root-tips ........................................... 314, 316, 330
Primers arbitrary primers (RAPD) ........................................... 193–195, 206, 207
PBS 18–mers primers ........................................... 244–246
primers for chloroplast DNA ........................................... 87, 94–96
primers for microsatellite (for REMAP) ........................................... 44, 237, 243–244
retrotransposon LTR primers ........................................... 40–43, 234–236, 238, 239, 242–244, 248, 252
universal plant ITS primers ........................................... 145, 146
Proteaceae (taxonomic revision) ........................................... 365
Pseudogene ........................................... 135, 136, 144
Purification of PCR product before sequencing (mitochondrial DNA) ........................................... 131, 186
Purification of the preamplification product (microsatellite library) ........................................... 179, 182–183
R
Random amplified hybridization microsatellites (RAHM) ........................................... 194, 195, 199, 205
Random amplified microsatellite polymorphism (RAMPO) ........................................... 194, 195, 198, 205, 208
Random amplified polymorphic DNA (RAPD) ........................................... 23–24, 42–44, 48, 71, 191–208, 212, 213
Repeated DNA sequences ........................................ 39–42, 115, 116, 122, 154, 212
Reproducibility .................................................. 152, 177, 191–194, 207, 212
Restriction enzymes (digestion) ....................... 97, 105, 110, 194, 195, 199, 212, 236, 241, 242, 248
Retrotransposon .................................................. 40, 234, 235
Retrotransposon–microsatellite amplification
polymorphism (REMAP) ................................ 43, 44, 233–253
Ribosomal DNA heterogeneity ......................... 42
Ribosomal RNA (rDNA) .................. 39, 48, 49, 89, 256
Ribosomal DNA heterogeneity ......................... 42
Ribosomal RNA (rDNA) .................................... 39, 141–148, 310, 392
Rooted phylogenetic tree ................................... 257–258, 266
Selective amplification of microsatellite
polymorphic loci (SAMPL) .................. 42, 44, 211–231
Sequence characterized amplified regions
(SCAR) ..................................................... 193, 194, 196–197, 202–203, 208
Sequence-related amplified polymorphism
(SRAP) .................................................. 194, 195, 198, 204, 206
Sequence-specific amplified polymorphism
(SSAP) .................................................. 43, 234–236, 239, 253
Short interspersed nuclear element
(SINE) .................................................. 40–42, 234, 238, 253
Simple sequence repeats (SSR)
(microsatellites) ............................................ 39, 40, 90, 105, 152, 177, 192, 199, 205, 212, 215–216, 220–221
Single primer amplification reaction (SPAR) ........... 212
Softwares
for analysing and aligning sequence data ................ 49, 256
BIOEDIT ...................................................... 99–111
MEGA5 (ClustalW, Muscle) ......................... 267, 268
for analysing gel images
Gene Profiler .................................................. 93
for Bayesian phylogenetic inference
BEAST .................................................... 275, 376, 380, 381, 383
MrBayes3 .................................................. 275
for designing primers
Amplicon .................................................... 96, 102, 103, 194, 195
Greene SCPrimer ............................................. 96
iCODEHOP .................................................. 96
Primer 3 .................................................. 187, 214, 220
for determining melting temperature
of a double strand DNA
Melt .................................................. 103, 130, 247
for determining the best-fit nucleotide
substitution model
jModelTest2 .................................................. 269–271
for DNA homology search
BLAST .................................................. 194, 258–264, 267, 268, 326
for Illumina GoldenGate Genotyping Assay
GenomeStudio ........................................ 157–158, 163–170
for phylogenetic tree construction
with maximum likelihood
PhyML3 .................................................. 261–262, 390
for phylogenetic tree construction with UPGMA/NJ
MEGA5 .................................................. 262, 267, 268
NTSYS-PC 2.01 ........................................... 201, 202
for SNP analysis
autoSNP ........................................... 154, 155, 157, 160, 163
AutoSNPdb ........................................... 154, 155, 157, 160, 163
SNPserver .............................................. 154
for SNP analysis in wheat
wheatgenome.info ........................................... 157, 161–163
for Tms calculation and corresponding instructions
(http://primerdigital.com/tools/) ...................... 252
for visualization and editing of phylogenetic trees
FigTree .................................................. 262, 273–274
Sorbus sp. (genome size analysis) ..................... 22, 294, 295
Spacer .................................................. 39, 86, 87, 90, 92, 100, 101, 111, 112, 141, 142, 172, 217, 222, 224, 229, 230, 239, 310, 374, 375
Species concept ........................................ 2, 15, 23, 28–30
Strueptophyta sp. (mt DNA cladogram) .............. 126, 127
Sugar cane (Saccharum sp.) (GISH analysis) .......... 326–328, 331
Sukkula (IRAP analysis) ................................... 244, 249
Tandem repeats ........................................... 39–41, 44, 105, 115, 128, 141, 142
Taxonomy .............................................. 1, 39, 85, 141, 152, 201, 265, 326, 342, 375
Transposable element (TEs) ................... 40, 41, 45, 233, 234, 253
Transposon ............................................ 40, 233–253
Type I transposable element ..................... 40–41
Type II transposable element .................... 40
Unrooted phylogenetic tree ......................... 257–258, 266
Unweighted pair grouping with arithmetic
mean (UPGMA) .................................. 49, 202, 259, 390
V
Vanilla sp. (rbcL phylogenetic analysis) ................. 262–265, 267, 273, 274
Wheat (searching for SNPs in) ................. 154, 157, 160–163