Index

1BL.1RS translocation, 264
454 Titanium, 534, 543, 546–548, 550–552

A
Adaptive traits, 68, 69, 71, 76
admixture values, 497
advanced-backcross QTL analysis, 501
_Aegilops biuncialis_, 267
_Aegilops cylindrica_, 267
_Aegilops_ species, 266
AFLP, 486, 534, 535
A-genome, 338, 339
Allelic loss, 71
Allelic richness, 70, 75, 78–81
Allelic shifts, 71
Allopolyploid, 121–123
allozymes, 486
amiprophos-methyl, 331
_Ammona cherimola_, 68
ancestor, 691
ancestral population, 489
Andean gene pool, 487
aneuploid mutants, 328
Annotation, 406, 538, 541, 543, 545, 547
Assembly, 391, 394, 396, 401, 406, 544–548
assembly methods, 325
association genetics, 501
association mapping, 97
_Arabidopsis_, 174, 325, 326
autogamous, 699
autogamy, 698
Autopolyploid, 121

B
BAC end sequences, 412
BAC-by-BAC, 415
backcrossing, 51
Bacterial Artificial Chromosome (BAC), 329, 392, 409
bean germplasm, 495
_beta_ diversity, 79, 81
Best Linear Unbiased Prediction, 96
B-genome, 338, 339
bioenergy, 604
Biogeography, 68
bioinformatic, 406, 525, 538, 599, 600, 602
BLASTX, 538, 545, 547
BLUP, 96
bottleneck, 70, 487, 490
_Brassica_, 121, 123
_Brachypodium_, 394, 411
bread wheat, 326, 328
breeding, 173, 693
bulked segregant analysis, 98
burden of proof, 56

C
(cp)SSR data, 487
_C. cardunculus_, 533, 534, 536, 537, 540–543, 545–553
chromosome approach, 327
candidate gene, 98, 489
cardoon, 560
cDNA libraries, 500
CEL I, 350
Celery Juice Extract, 350
cell cycle synchronization, 327
cell sorter, 323, 329
center of domestication, 491
Centres of domestication, 73
centromeres, 327
Cherimoya, 68, 73, 75–80, 83–86
Cherimoya genetic resources, 78
Chinese Spring, 329
Chloroplast alleles, 72
cromosome, 394–396, 406
chromosome 3B, 410
chromosome approach, 326–329
chromosome banding technique, 256
chromosome discrimination, 327
chromosome genomics, 328, 329
chromosome isolation, 327
chromosome size, 329
Chromosome sorting, 335, 344
Chromosome suspension, 336, 344
Chromosome-mapped markers, 76
Chromosomes, 327
Chromosomes in suspension, 329, 338
CIAT, 501
Circular neighbourhood, 72, 75, 78, 79, 81, 82, 84
Circular neighbourhood approach, 72
cleistogamy, 697
Climate change, 68, 75–77, 79, 83–85
Climate change impact, 75–77, 83, 84
Climate change threats, 75
cclimate data, 73, 78
cclimate models, 79, 85, 86
clustering methods, 497
CNV, 326, 327
coint- retention, 293
collinear, 411
colonization, 687
common bean, 484, 485, 497
Comparative genomic, 308
comparative genomics approach, 497
comparative legume genomics, 497
Conifers, 326
consensus map, 490
conservation genetics, 68, 485
Conservation genomics, 68
Conservation strategies, 69, 72
conservation unit, 72
contig, 394, 396, 397, 399, 400, 415, 534, 538,
  539, 544, 545, 547, 548, 550, 552
contig CL4773Contig1, 539
Copy number variation, 123, 326, 344
corn, 326
cosmetic breeding, 61
cpSSR markers, 495
Creso, 344
crop, 181, 484, 684
Crop diversity, 72, 74
crop varieties, 68
Cross-pollination, 690
cultivated (Glycine max) and wild soybean
  (G. soja), 466
Cy3, 331
Cynara, 560
Cynara cardunculus, 533, 534, 542
Cytogenetic stocks, 303
cytogenetics, 320, 328
cytoplasmic bottleneck, 495
D
β-D-glucan, 261
DAPI, 322, 336, 338
Data integration, 406
data warehouses, 430
Dasypyrum villosum (L.), 331
de novo sequencing, 326, 344
D-genome, 339, 344
deflection, 325
demographic models, 491
denaturation, 329
Denaturation of DNA, 331
Diffusion models, 74
disease resistance, 687
Distinctness, 33
ditelosomic lines, 329
DIVA-GIS, 78
D. villosum, 343
diversification, 74, 484, 486, 686
diversity analyses, 485
Diversity hotspot, 83
Diversity studies, 502
DNA Conservation, 577
DNA content, 326, 329, 336, 340
domesticated gene pools, 491
domesticated populations, 492
Domestication, 68–71, 73, 74, 77, 123, 125,
  126, 465, 483–485, 489, 492, 502, 684
domestication bottleneck, 490
domestication events, 490
domestication syndrome, 489, 490
domestication-related traits (DRTs), 465
dot plot, 325, 336
Double-Haploid, 50
double-strand breaks, 287
duplications, 411

E
Ecotilling, 353
Effective population size, 70
Environmental Envelope Modelling (EEM), 73
Enzymatic mismatch cleavage, 350
epigenetic marker, 521
Epigenomics, 521
Essentially Derived Variety (EDV), 52
EST, 409, 485, 499, 500, 538, 545–547, 550,
  552
EST-SSR, 538, 539, 541
Evolution of P. vulgaris, 492
Evolutionary processes, 69, 70, 71

F
farmer selection, 494
FCY, 327
federated database, 430
fertility, 686
field, 174
FISH, 320, 321, 329, 331
FISH karyotype of the E genome of Elytrigia elongata, 272
FISHIS, 330, 331, 337, 339, 340
FITC, 331
Fitness, 70, 76
flow chamber, 325
Flow cytogenetics, 327, 343
flow cytogenomics, 343
flow cytometer, 321, 329
Flow Cytometry, 321, 330, 335
flow karyotyping, 327
Flow Sorting, 321, 322, 327, 340, 406
Fluorescence in situ hybridization (FISH), 257
fluorescent in situ hybridization (FISH), 257
founder, 493, 687
founder effect, 76, 489
frost hardiness, 687
functional genetic variation, 70
Functional Genomics, 174, 357, 499, 500
future, 70, 75–77, 79, 83–85

G
(GAA)7, 338, 340
GISH, 320
Genlisea, 326
gene banks, 485
gene density, 411
gene flow, 70, 485, 491, 493
Gene Function, 592, 601, 602
gene islands, 412
Gene Ontology, 541, 547
gene pools, 486
Gene silencing, 594, 602
gene-environment interactions, 191
genetic conformity, 56
Genetic distinctiveness, 70
Genetic diversity, 58, 104, 483, 490
Genetic diversity hotspots, 73
genetic drift, 485
genetic engineering, 55
genetic erosion, 68, 71, 75, 77, 83, 690
genetic gain, 28
genetic linkage, 500
genetic map, 498, 515, 533, 537, 542, 543, 553
genetic markers, 97, 515
Genetic responses, 71
Genetic structure, 74, 81, 82
Genome sequence, 406, 591, 597, 599, 604
Genome sequencing, 117, 126, 127, 325
genome structure, 427
Genome wide association (GWAS), 114
Genome-wide association mapping, 485
genome-wide mapping, 76
genome wide selection, 100
genome-wide transcript studies, 500
GenomeZipper, 427
Genomic in situ hybridization (GISH), 257, 320
genomic selection, 114, 127
genomic tools, 484, 497
Genotyping-by-sequencing, 127
Geographic Information Systems, 68
Geographic patterns of diversity, 73
go geographical distribution, 485
go geographical structures, 486
Georeferenced observation points, 73
Georeferenced plant data, 73
Geospatial analyses, 73
Geospatial analysis, 72
Germplasm, 50, 69, 71, 76–78, 485, 564, 591, 592, 595, 606
Germplasm Characterization, 355
Germplasm collection, 68, 484, 497
GIS, 72, 74
Globe artichoke, 533–538, 541–546, 551, 552, 562,
GO categorisation, 538
GO terms, 539
Good Phenotyping Practice (GPP), 185
grape, 326
Grapevine, 683
growth habit, 489
GWS, 101, 103, 106

H
Haplotype, 118, 121, 122, 124–126, 686
Heterochromatin, 124
heterosis, 698
High-resolution physical map, 287
high-throughput genomic technologies, 485
high-throughput genotyping, 498
high-throughput selection, 502
homeologous genomes, 328, 344
homeologus chromosomes, 326
Homologous recombination, 287
Hotspots of genetic diversity, 84
hybridization, 338, 487, 496, 690
Hybrids, 496, 565

I
γ-irradiation, 270
In situ conservation, 68, 70
In situ fluorescent hybridization, 321, 329
in situ hybridization, 330
Illumina, 533, 534, 542–544, 546–548, 550, 552
Illumina GoldenGate assay, 501
imaging spectroscopy, 184
in vitro storage, 564
inbreeding, 698
Inbreeding depression, 69
Indel, 350
intellectual property protection (IPP), 28, 50
intercrossable, 486
intergenomic translocations, 270
International Wheat Genome Sequencing Consortium (IWGSC), 328, 407
Interspecific Hybridization, 256
introgression, 491, 501, 684

K
k-mers, 419
karyotype, 422
KASPar technology, 501
kinship, 70, 697

L
Locally common alleles, 70
landraces, 68, 70, 71, 494
lignocellulosic biomass, 562
Linkage disequilibrium, 114, 118, 123, 124, 126
linkage disequilibrium analysis, 498
linkage drag, 99
linkage mapping, 97
local adaptation, 485
loss of diversity, 487
LTR retroelements, 545
lysis buffer, 331

M
map-based cloning, 597–599
mapping populations, 429, 498
marker assisted backcrossing (MABC), 98
Marker Assisted Recurrent Selection (MARS), 104
marker loss, 295
marker-assisted selection, 502
MARS, 106
MAS, 104, 106
maximum likelihood approach, 496
MDA, 343, 344
metabolomics, 527, 528
metaphase, 327, 331
metaphase chromosomes, 321
Microsatellite, 329, 340, 344
microsatellite DNA probe, 343
Microsatellite markers, 68, 78
minimal tiling path, 414
miRNAs, 548
mitotic index, 327
model plant, 603
model species, 587, 588, 591, 594–596, 599, 602, 604, 605
Molecular Assessment, 569
molecular marker, 28, 55, 344, 407, 500, 586, 591, 595–598, 603
Morphological Characterization, 71, 490, 567
multilocus molecular markers, 498
multilocus sequence data, 491
multiple domestications, 491
mutagen, 286
mutagenesis, 290
mutation breeding, 50

N
N. sylvestris, 512, 513, 515, 519, 524
N. tomentosiformis, 512, 513, 515, 519, 524
N. tabacum, 512, 513, 515, 518, 520–522, 524, 527
Neighbourhood-by-distance, 79
nick-translation, 331
non collinear genes, 412
non-homologus end joining, 287
nozzle tip, 325
nucleic acids probes, 321
nucleotide diversity, 487, 498

O
Oryza, 325
oligonucleotides, 335
On farm conservation, 69
Optical mapping, 429
ornamental plants, 191
orthologous, 700
P

P. acutifolius, 484
P. coccineus, 484
P. lunatus, 484
P. vulgaris, 484, 486, 497
Paris japonica, 326
P. dumosus, 484
panel, 299
pangenome, 326
pedigree, 51, 691
Perennial tree crops, 73
perennials, 687
petunia, 178
phaseolins, 492
Phaseolus, 484
Phaseolus vulgaris, 483
Phaseomics, 498
phenylpropanoids, 536
photoperiod sensitivity, 489
phylogenetic, 589, 600
physical map, 286, 397, 400, 406
plagiarism, 52
plant architecture, 600, 605
Plant Breeders’ Rights (PBR), 32
Plant breeding, 114, 123, 126, 496
plant evolution, 326
Plant Variety Protection (PVP), 28
Plastic responses, 76
pollination, 77, 83
polymorphism, 422
Polyploid, 406, 594
polyploidization, 596
polyploidy, 325, 326, 344
poplar, 178
population structure, 487
positional cloning, 304
Post-glacial migration routes, 73
potato, 326
Predominant derivation, 55
principal coordinate analysis, 497
Proteomics, 528
pseudogenes, 427
pseudomolecule, 429
pTa71, 331, 340
purity, 342, 344
purity checking, 340

Q

QTL analysis, 498, 500
QTL Pyramiding, 98
quantitative trait loci (QTL), 97
quantitative trait locus (QTL), 489
R

γ-rays, 290
races, 491
RAD, 533, 542–545, 551–553
Radiation, 286
radiation hybrid, 285, 286
RADseq, 543
RADSequencing, 543
random amplified polymorphic DNA, 486
rDNA, 344
Re-sampling without replacement, 73, 78, 79, 81
rearrangements, 411
Recalcitrant seed, 68
recombinant inbred population, 489
recombination, 293, 487, 700
Reduced complexity, 116, 126
Reference genome, 122, 125, 126
refugia, 70, 73
relict population, 489
remote sensing, 179
renewable energy, 537
repetitive DNA, 328, 392, 393, 400, 401
repetitive DNA probe, 344
repetitive sequences, 331
Resistance Gene Analogs, 548
resource-use efficiency, 173
restriction fragment length polymorphism, 486
retention/loss frequency, 297
retrotransposon, 412, 587, 591
reverse genetics, 307
RFLP, 586
RGAs, 548
Rice, 326, 394, 411
root tip, 327, 331
roots, 174
rRNA, 327

S

Sanger sequencing, 325, 391, 392
satellites, 327
scaffold, 396–398, 400, 415
Seed banks, 68
seed dormancy, 489
seed oil, 562
seed propagated, 564
seed protein phaseolin, 486
seed proteins, 486
seed system, 71
selection, 407, 490, 493, 502, 693
Selective sweeps, 693
Self-compatibility, 697
Sequence capture, 116
sequence data, 487
sequencing, 485
sesquiterpene lactones, 536
SHATTERPROOF 1, 489
sheath fluid, 323
short repeats, 327
short tandem repeats, 327
shotgun sequencing, 394, 397, 400
signature of domestication, 490
Simple sequence repeat, 68
single nucleotide polymorphism (SNP), 28, 100
SNP Calling, 119, 545, 546, 548, 550
SNP discovery, 501
SNPs, 533, 534, 538, 542, 543, 545, 546, 550–553
somatic mutations, 692
sorghum, 411
sorting chromosomes, 323
sorting gate, 325, 341
sorting windows, 336
soybean, 497
soybean genome, 497
Spatial genetics, 68
spatial isolation, 492
Spatial principle component analysis, 83
speciation, 484
species distribution, 69
SSR, 78, 329, 533, 535, 538–541
standard operation protocols (SOP), 185
structural variation, 700
Structure analysis, 497
Survey Sequencing, 394, 426
Suspensions of Plant Chromosomes, 331
synteny, 498, 586–590, 593, 596, 597, 599, 600, 603, 685
T
T. aestivum, 329, 344
T. durum, 325, 338, 344
tblastx, 539
Telomeric sequences, 327
Telosomic, 422
test, 538
tetraploid, 326
the Convention on Biological Diversity, 565
Threat information, 75
Threats, 75, 83, 84
TILLING, 350, 588, 591–594
Tobacco, 512
Transcription, 595, 600–602, 604, 605
Transcriptome sequencing, 115–117, 123, 126
transcriptomics, 527
Transformation, 52, 588, 593, 594, 602, 604
transgenic, 51
transposable DNA element, 545
transposable elements (TE), 326, 329, 393, 406
tree genetic resources, 68, 72, 73
Tris-HCl, 331
type I phaseolin, 486
U
uniform, 296
Uniformity, and Stability, 34
unigene, 534, 538, 542, 548
uniparental inheritance, 495
upcoming, 534, 552
USDA-ARS, 501
Utility patents, 33
V
V. faba, 327
varieties, 684
variety identification, 33
vegetative propagation, 692
VIGS, 594
viticulture, 687
VV genome, 340
W
Wheat, 115, 117, 121–123, 325, 326, 406, 586–590, 594–600, 603, 605, 606
Wheat Thinopyrum (syn. Agropyron) Hybrids, 270
Wheat Rye Crossability, 263
wheat-Ae. biuncialis amphiploids, 269
wheat-Th. ponticum partial amphiploid, 272
Wheat-barley chromosome pairing, 259
wheat-rye addition lines, 264
Wheat/Barley Translocations, 261
Wheat/Rye Translocations, 264
Whole Chromosome Shotgun, 411
Wild P. vulgaris, 486
wild and the domesticated forms, 484
Wild P. vulgaris, 486
wild relatives, 483
Y
yield, 587, 588, 598, 601, 603, 605