

# Index

$\beta$ -Amylase, 125  
 $\beta$ -Carotene, 54  
 $\alpha$ -Cellulose, 39  
4,6-Diamidino-2-phenylindole (DAPI), 129  
454 sequencing, 147, 172

## A

Addition lines, 9, 101, 142–143  
AFLP. *See* Amplified fragment length polymorphism  
*Agrobacterium*, 85  
Allogamous, 7  
Allopolyploid, 111  
Allotetraploid, 82, 110  
Allotriploid, 159  
Amplified fragment length polymorphism (AFLP), 6, 51, 78, 83–85, 111, 117, 135  
Androgenesis, 114  
Aneuploid, 32, 143, 170  
Aneuploidy, 32  
Anisoploid, 8  
Anthracnose, 86  
Apomixis, 9, 147  
*Arabidopsis*, 5  
Asiatic yam, 71–72  
Autosyndetic pairing, 8  
Autotetraploid, 142

## B

BAC. *See* Bacterial artificial chromosome  
Backcrossing, 117  
Bacterial artificial chromosome (BAC), 13, 118, 148, 172  
Bangladesh Jute Research Institute (BJRI), 31  
Beet necrotic yellow vein virus (BNYVV), 12, 16  
*Beta*, 1  
    *B. corolliflora*, 9  
    *B. lomatoona*, 9  
    *B. macrocarpa*, 15  
    *B. nana*, 3  
    *B. patellaris*, 9  
    *B. procumbens*, 9  
    *B. vulgaris* subsp. *maritima*, 1, 12  
    *B. vulgaris* subsp. *vulgaris*, 1  
Betacyanins, 10  
Betalains, 5, 10

BGCI-UK, 162  
Bioactive, 54  
Bioenergy, 104, 160, 172–173  
Bioengineering, 173  
Biofuels, 56, 160  
Biomass, 58, 103, 112, 157, 172–173  
Bitter yam, 71  
BLASTX, 117  
BNYVV. *See* Beet necrotic yellow vein virus  
BSA. *See* Bulked segregant analysis  
Bulked segregant analysis (BSA), 86

## C

Callus culture, 85  
Candidate genes, 89  
Cassava, 133  
Cassava bacterial blight (CBB), 144  
Cassava brown streak disease (CBSD), 144  
Cassava mosaic disease (CMD), 143  
C-banding, 65  
CBB. *See* Cassava bacterial blight  
CBSD. *See* Cassava brown streak disease  
cDNA. *See* Complementary-DNA  
Cellulose biosynthesis, 111  
Cell wall biogenesis, 113  
Central Research Institute for Jute and Allied fibers (CRIJAF), 31  
Central Tuber Crops Research Institute (CTCRI), 140  
Centro Internacional de Agricultura Tropical (CIAT), 139–140  
Centro Nacional de Pesquisas de Recursos Genéticos e Biotecnologia (CENARGEN), 31  
Cercospora leaf spot (CLS), 10  
CGH. *See* Comparative genomic hybridization arrays  
CGIAR. *See* Consultative Group for International Agricultural Research  
Chinese yam, 71  
Chloroplast, 128  
    DNA (cpDNA), 53, 65, 90, 125  
    genome, 90  
Chromosome  
    morphology, 8  
    pairing, 81–82  
CIAT. *See* Centro Internacional de Agricultura Tropical  
CLS. *See* Cercospora leaf spot  
CMap, 118

- CMD. *See* Cassava mosaic disease  
 CMS. *See* Cytoplasmic male sterility  
 Cold, 115  
 Color instability, 39  
 Commonwealth Scientific and Industrial Research Organization (CSIRO), 31  
 Comparative genomic hybridization arrays (CGH), 90  
 Comparative genomics, 89  
 Complementary-DNA (cDNA), 13, 54, 65, 117  
   library, 85–86, 147  
   microarrays, 172  
 Consultative Group for International Agricultural Research (CGIAR), 139–140  
*Corchorus*, 29  
   *C. angolensis*, 46  
   *C. asplenifolius*, 46  
   *C. capsularis*, 29  
   *C. cinerascens*, 46  
   *C. confusus*, 46  
   *C. depressus*, 46  
   *C. junodii*, 46  
   *C. oltorius*, 29  
 Cotton, 109  
 Cottonseed, 115  
   meal, 109  
 C<sub>3</sub> pathway, 104  
 CpDNA. *See* Chloroplast DNA  
 C<sub>4</sub> photosynthesis, 5  
 C<sub>4</sub> photosynthetic pathway, 104  
 CRIJAF. *See* Central Research Institute for Jute and Allied fibers  
 Cross-compatibility, 125–128  
 Cross-incompatibilities, 127–128  
*Crotalaria*, 63  
   *C. juncea*, 63  
   *C. mucronata*, 63  
   *C. paulina*, 63  
   *C. spectabilis*, 63  
 Cryobank, 77–78  
 Cryopreservation, 77, 113, 115, 140  
 Cryoprotectants, 77  
 CSIRO. *See* Commonwealth Scientific and Industrial Research Organization  
 CTCRI. *See* Central Tuber Crops Research Institute  
 Cush-cush yam, 71  
 C-value, 6, 87  
 Cyanide, 134  
 Cytogenetic stocks, 101, 114–115, 170  
 Cytometry, 90  
 Cytoplasmic male sterility (CMS), 7  
 Cytotypes, 7
- D**  
 DAPI. *See* 4,6-Diamidino-2-phenylindole  
 Deforestation, 149  
 Deoxyhypusine synthase (DHS), 65  
 Department of Energy-Joint Genomic Institute (DOE-JGI), 147  
 DHS. *See* Deoxyhypusine synthase  
 Dietary supplements, 54–56  
 Dihaploid, 143  
 Dimethyl sulphoxide (DMSO), 77, 141
- Dioscorea*  
   *D. abyssinica*, 83  
   *D. alata*, 71, 83  
   *D. bulbifera*, 85  
   *D. cayenensis*, 71, 83  
   *D. dumetorum*, 71  
   *D. elephantipes*, 87  
   *D. esculenta*, 71  
   *D. nummularia*, 84  
   *D. opposita*, 85  
   *D. praehensilis*, 83  
   *D. rotundata*, 71, 83  
   *D. transversa*, 84  
   *D. trifida*, 71  
 Dioscorin, 71  
 Diosgenin, 71  
 Diploid, 82, 109  
 DMSO. *See* Dimethyl sulphoxide  
 DNA  
   bank, 140  
   barcode, 90  
   fingerprinting, 117  
   sequencing, 159  
 Domestication, 7, 75, 161  
 Drought, 115  
   tolerance, 47–48, 138
- E**  
 ECP/GR, 4–5  
 Embryo  
   culture, 85  
   rescue, 85, 116  
 Environmental Protection Agency (EPA), 119  
 EPA. *See* Environmental Protection Agency  
*Erianthus*  
   *E. arundinaceus*, 98, 171  
   *E. bengalense*, 99  
   *E. elephantinus*, 99  
   *E. procerus*, 98  
   *E. ravennae*, 99  
 EST. *See* Expressed sequence tag  
 EURSICO, 16  
 Expressed sequence tag (EST), 13, 85, 103, 117, 147  
 Ex situ conservation, 76, 90
- F**  
 FAO. *See* Food and Agricultural Organization  
 FDA. *See* Food and Drug Administration  
 Female sterility, 8–9  
 F<sub>1</sub> hybrids, 11, 131  
 Fiber, 37–39  
   composition, 39–47  
   strength, 49  
 Field genebanks, 140  
 First generation maps, 145–146  
 FISH. *See* Fluorescence in situ hybridization  
 Flow cytometry, 129–131  
 Fluorescence in situ hybridization (FISH), 9, 65, 83, 125  
 Fodder beet, 1  
 Food and Agricultural Organization (FAO), 77, 140  
 Food and Drug Administration (FDA), 119

**G**

GABIPD, 16  
 Garden beet, 1  
 GBIF. *See* Global Biodiversity Information Facility  
 GenBank, 159–160  
 Gene  
   discovery, 17, 86–89  
   flow, 10, 15, 148–149  
   pool, 31, 136  
 Genebank, 77  
 GENE-DB, 118  
 Genetic  
   diversity, 5, 51, 76, 116, 160  
   engineering, 51  
   erosion, 64, 80, 138–139, 160  
   fingerprinting, 144  
   map, 6, 83–84, 145–146, 170  
   modification, 171  
   reserve, 5  
   transformation, 112, 147, 171  
 Genetically modified (GM), 119, 173  
 Genome size, 83, 87, 111, 137–138, 167  
 Genomic DNA, 65  
 Genomic in situ hybridization (GISH), 83, 101, 169  
 Germplasm, 31, 113  
   banks, 159, 168  
   conservation, 159  
   pool, 7  
 Germplasm Resources Information Network (GRIN),  
   3, 11, 87  
 GISH. *See* Genomic in situ hybridization  
 Global Biodiversity Information Facility (GBIF), 16  
 Global warming, 3  
 GM. *See* Genetically modified  
 GOBASE, 89  
*Gossypium*, 109  
   *G. anomalum*, 112  
   *G. arboreum*, 110  
   *G. ardidum*, 112  
   *G. barbadense*, 110  
   *G. bickii*, 111, 112  
   *G. darwinii*, 111  
   *G. davidsonii*, 112  
   *G. harkensii*, 112  
   *G. herbaceum*, 110  
   *G. herbaceum* var. *africanum*, 111  
   *G. hirsutum*, 110  
   *G. longicalyx*, 111  
   *G. mustelinum*, 111  
   *G. raimondii*, 110  
   *G. rainmondii*, 112  
   *G. somalense*, 112  
   *G. stocksii*, 112  
   *G. sturtianum*, 112, 115  
   *G. thurberi*, 112  
   *G. tomentosum*, 111, 112  
 Gossypol, 115  
 Greater yam, 71  
 GRIN. *See* Germplasm Resources Information Network

**H**

Haploid, 114, 170  
 HCN. *See* Hydrocyanic acid  
 Heat, 115  
 Hemicelluloses, 39  
 Hexaploid, 32, 82  
 Hybridization, 124  
 Hydrocyanic acid (HCN), 137  
 Hyperploid, 32  
 Hypoploid, 32

**I**

IBPGR. *See* International Board for Plant Genetic Resources  
 ICAR. *See* Indian Council of Agricultural Research  
 ICSB. *See* International Sugarcane Biotechnology Consortium  
 IDBB. *See* International Data Base for *Beta*  
 IITA. *See* International Institute of Tropical Agriculture  
 IJO. *See* International Jute Organization  
 Indian Council of Agricultural Research (ICAR), 31  
 In situ conservation, 5, 76  
 In situ hybridization, 101  
 Instituto Nacional de Investigaciony Extension Agraria  
   (INIEA), 140  
 Intergeneric crosses, 171  
 Internal transcribed spacer (ITS), 65  
 International Board for Plant Genetic Resources (IBPGR), 31  
 International Data Base for *Beta* (IDBB), 3, 11  
 International Institute of Tropical Agriculture (IITA), 76,  
   139–140  
 International Jute Organization (IJO), 31  
 International Plant Name Index (IPNI), 159  
 International Society of Sugarcane Technologists (ISSCT), 100  
 International Sugarcane Biotechnology Consortium  
   (ICSB), 171  
 International Treaty on Plant Genetic Resources for Food  
   and Agriculture (ITPGRFA), 78  
 Inter-simple sequence repeat (ISSR), 51  
 Interspecific  
   cross, 171  
   hybridization, 49, 84, 116  
   hybrid, 9, 49, 127, 143  
 Introgression, 103, 142  
 IPNI. *See* International Plant Name Index  
*Ipomoea*, 123  
   *I. batatas*, 124, 128  
   *I. gracilis*, 128  
   *I. grandifolia*, 131  
   *I. leucantha*, 125, 128  
   *I. littoralis*, 124, 125  
   *I. purpurea*, 131  
   *I. tabascana*, 128  
   *I. tiliacea*, 128  
   *I. trichocarpa*, 128  
   *I. trifida*, 124, 128  
   *I. triloba*, 124, 128  
 Isoenzyme, 145  
 Isozyme, 75–76, 137  
 ISSCT. *See* International Society of Sugarcane Technologists  
 ISSR. *See* Inter-simple sequence repeat

ITPGRFA. *See* International Treaty on Plant Genetic Resources for Food and Agriculture  
 ITS. *See* Internal transcribed spacer

**K**

Karyotype, 32, 63, 137, 166  
 Karyotyping, 32

**L**

Landraces, 139–140  
 LD. *See* Linkage disequilibrium  
 Leaf beet, 1  
 Lignin, 39  
 Linkage  
   disequilibrium (LD), 52  
   map, 83–84  
   mapping, 86  
*Lotononis*, 64

**M**

Male fertility, 8  
*Manihot*, 133  
   *M. aesculifolia*, 141–142  
   *M. attenuata*, 134  
   *M. augustiloba*, 134  
   *M. brachyloba*, 141–142  
   *M. carthaginensis*, 134, 141–142  
   *M. chlorostica*, 134  
   *M. dichotoma*, 134  
   *M. esculenta*, 133  
   *M. esculenta* ssp. *esculenta*, 134  
   *M. esculenta* ssp. *flabellifolia*, 135  
   *M. esculenta* ssp. *peruviana*, 135  
   *M. glaziovii*, 134  
   *M. glaziovii*, 134  
   *M. grahami*, 134  
   *M. irwinii*, 134  
   *M. neusana*, 134, 138  
   *M. orbicularis*, 134  
   *M. pohlii*, 134  
   *M. pringlei*, 134  
   *M. pseudoglaziovii*, 134  
   *M. reptans*, 134  
   *M. rubricaulis*, 134  
   *M. tripartita*, 134  
   *M. tristis*, 134  
 Maritime beet, 1  
 Marker-assisted breeding, 51–52  
 Marker-assisted selection (MAS), 52, 116  
 Marker density, 145–146  
 MAS. *See* Marker-assisted selection  
*Medicago*, 66  
*Meloidogyne* ssp., 13  
 Metabolites, 172  
 Microarray, 89, 118  
 Micropropagation, 112  
 Microsatellite, 51, 117, 125  
 Microspore culture, 143  
*Miscanthus*, 98, 157  
   *M. × giganteus*, 158  
   *M. sacchariflorus*, 158

*M. sinensis*, 158  
 Mitochondrial DNA (mtDNA), 65  
 mtDNA. *See* Mitochondrial DNA

**N**

National Agricultural Technology Project (NATP), 31  
 National Bureau of Plant Generic Resources (NBPGR), 31  
 National Center for Biotechnology Information (NCBI), 13, 65  
 National plant germplasm system (NPGS), 3, 11  
 NATP. *See* National Agricultural Technology Project  
 Natural fiber, 109  
 NBPGR. *See* National Bureau of Plant Generic Resources  
 NCBI. *See* National Center for Biotechnology Information  
 NOR. *See* Nucleolus organizer region  
 NPGS. *See* National plant germplasm system  
 Nucleolus organizer region (NOR), 63

**O**

Octaploid, 82  
 Oligo-fingerprinting, 13  
 Overgrazing, 2–3

**P**

PA. *See* Pyrrolizidine alkaloids  
 PAL. *See* Phenylalanine ammonia lyase  
 Paper industry, 56  
 Participatory plant breeding (PPB), 144  
 PCA. *See* Principal component analysis  
 Pharmaceuticals, 54  
 Phenylalanine ammonia lyase (PAL), 39–47  
 Phylogenetic relationships, 124–125  
 Plant regeneration, 85  
 Plastid genome, 87–89  
 Ploidy, 82  
   level, 8, 128, 159  
 Polyploid, 110–111  
 Polyploidization, 110, 143, 147, 159  
 Polyploidy, 111  
 PPB. *See* Participatory plant breeding  
 Primary gene pool (GP-1), 136  
 Principal component analysis (PCA), 125  
 Progesterone, 73–74  
 Pro-phloem, 38  
 Proto-phloic fibers, 38  
 Protoplast  
   culture, 85  
   isolation, 85  
 Pulp, 56  
 Pyrrolizidine alkaloids (PA), 64–66

**Q**

QTL. *See* Quantitative trait loci  
 Quantitative trait loci (QTL), 8, 51–52, 84, 86, 101, 117, 144, 170

**R**

Random amplified polymorphic DNA (RAPD), 6, 51, 85, 100, 116, 125, 138  
 RAPD. *See* Random amplified polymorphic DNA  
 Resistance gene analog (RGA), 89, 148

- Restriction fragment length polymorphism (RFLP), 6, 76, 98, 116, 125, 138
- Reverse genetics, 90
- RFLP. *See* Restriction fragment length polymorphism
- RGA. *See* Resistance gene analog
- Ribosomal-DNA (rDNA), 5, 125
- RKN. *See* Root-knot nematode
- RNA editing, 8
- RNA polymerase, 54
- Root-knot nematode (RKN), 13
- S**
- Saccharum*, 165
- S. alopecuroideum*, 100
- S. balwinnii*, 100
- S. barberi*, 166
- S. coarctatum*, 100
- S. edule*, 166
- S. giganteum*, 100
- S. officinarum*, 99, 165
- S. robustum*, 165
- S. sinense*, 166
- S. spontaneum*, 98, 165
- Sapogenin, 71
- SBCN. *See* Sugarbeet cyst nematode
- SCAR. *See* Sequence characterized amplified region
- SDS-PAGE. *See* Sodium dodecyl sulfate-polyacrylamide gel electrophoresis
- Second-generation map, 146
- Seed hull, 109
- Segmental allopolyploid, 32
- Self-incompatibility (SI), 7
- Sequence characterized amplified region (SCAR), 117
- Sequence tagged microsatellite (STMS), 51
- Sequence-tagged site (STS), 117, 146
- Simple sequence repeat (SSR), 6, 84, 125, 138, 171
- Single nucleotide polymorphism (SNP), 6, 85, 170
- SMTA. *See* Standard Material Transfer Agreement
- SNP. *See* Single nucleotide polymorphism
- Sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE), 51
- Somatic
- embryogenesis, 113
  - hybrid, 85
- South American yam, 71–72
- Soybean, 66
- Spinach, 5–6
- Spontaneous polyploid, 138
- SPV. *See* Sweetpotato virus
- SSR. *See* Simple sequence repeat
- Standard Material Transfer Agreement (SMTA), 140
- STMS. *See* Sequence tagged microsatellite
- STSS. *See* Sequence-tagged site
- Substitution
- lines, 101, 142–143
- SUCEST, 172
- Sucrose content, 170
- Sugar, 172
- Sugarbeet, 1, 5
- Sugarbeet cyst nematode (SBCN), 9, 13
- Sugarcane, 165
- Sunn hemp, 63
- Super weed, 57
- Sweetpotato virus (SPV), 131
- Synonymy, 34
- T**
- TCL. *See* Total complement length
- Tetraploid, 8, 82, 109, 125
- Therapeutic, 54
- Tilling, 90
- Total complement length (TCL), 32
- Totipotency, 53
- Transgene, 146–147
- Transgenic, 146
- beets, 15
- Triploidy, 142
- Tuber, 79
- U**
- United States Department of Agriculture (USDA), 31, 98, 119
- United States Department of Agriculture-Agriculture Research Service (USDA-ARS), 3, 11, 112
- United States Agency for International Development (USAID), 86
- UNO, 57
- Unreduced microspore, 142
- Unweighted pair group method with arithmetic mean (UPGMA), 125
- UPGMA. *See* Unweighted pair group method with arithmetic mean
- USAID. *See* United States Agency for International Development
- USDA. *See* United States Department of Agriculture
- USDA-ARS. *See* United States Department of Agriculture-Agriculture Research Service
- W**
- Water stagnation, 47–48
- Weediness, 173
- White guinea yam, 71
- Wild
- gene pool, 136
  - sea beet, 1
  - yams, 76
- Y**
- YAC. *See* Yeast artificial chromosome
- Yam mosaic virus (YMV), 84, 86, 90
- Yams, 71
- Yeast artificial chromosome (YAC), 13–14
- Yellow guinea yam, 71
- Yellowing, 39
- Yellow yam, 71
- YMV. *See* Yam mosaic virus