

Chittaranjan Kole *Editor*

# Genomic Designing for Biotic Stress Resistant Technical Crops

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*Dedicated to*



*Prof. Roger D. Kornberg  
Nobel Laureate in Chemistry 2006  
Professor of structural biology at Stanford  
University School of Medicine*

*With regards and gratitude for his generous  
appreciations of my scientific contributions  
and service to the academic community and  
constant support and encouragement during  
my professional journey!*

# Preface

Crop production is drastically affected due to external or environmental stresses. The biotic stresses cause significant yield losses in the range of 31–42% together with 6–20% loss during the post-harvest stage. The abiotic stresses also aggravate the situation with crop damage in the range of 6–20%. Understanding the mechanisms of interaction of plants with the biotic stresses caused by insects, bacteria, fungi, viruses and oomycetes, etc., and abiotic stresses due to heat, cold, drought, flooding, submergence, salinity, acidity, etc., is critical to develop resilient crop varieties. Global warming and climate change are also causing emergence of new diseases and insects together with newer biotypes and physiological races of the causal agents in one hand and aggravating the abiotic stress problems with additional extremes and unpredictability. Development of crop varieties resistant and/or adaptive to these stresses is highly important. The future mission of crop improvement should, therefore, lay emphasis on the development of crop varieties with optimum genome plasticity by possessing resistance or tolerance to multiple biotic and abiotic stresses simultaneously. A moderate estimation of world population by 2050 is about 9.3 billion that would necessitate an increase of crop production by about 70%. On the other hand, the additional losses due to climate change and global warming somewhere in the range of 10–15% should be minimized. Therefore, increase in the crop yield as well as minimization of its loss should be practiced simultaneously focusing both on ‘adaptation’ and on ‘mitigation.’

Traditional plant breeding practiced in the last century contributed a lot to the science of crop genetic improvement. Classical plant breeding methods including selection, hybridization, polyploidy and mutation effectively catered to the basic F<sup>5</sup> need—food, feed, fiber, fuel and furniture. The advent of molecular breeding and genetic engineering in the latter part of that century complimented classical breeding that addressed the increasing needs of the world. The twenty-first century came with a gift to the geneticists and plant breeders with the strategy of genome sequencing in *Arabidopsis* and rice followed by the tools of genomics-aided breeding. More recently another revolutionary technique, genome or gene editing, became available for genetic correction of crop genomes! The travel from ‘plant breeding’ based on visual or perceivable selection to ‘molecular breeding’ assisted by linked markers to

‘transgenic breeding’ using genetic transformation with alien genes to ‘genomics-aided breeding’ facilitated by known gene sequences has now arrived at the age of ‘genetic rectification’ employing genome or gene editing.

Knowledge on the advanced genetic and genomic crop improvement strategies including molecular breeding, transgenics, genomic-assisted breeding and the recently emerged genome editing for developing resistant, tolerant and/or adaptive crop varieties is useful to students, faculties and scientists in the public and private universities and organizations. Whole genome sequencing of most of the major crop plants followed by genotyping-by-sequencing has facilitated identification of exactly the genes conferring resistance, tolerance or adaptability leading to gene discovery, allele mining and shuttle breeding which in turn opened up the scope for ‘designing’ or ‘tailoring’ crop genomes with resistance/tolerance to biotic and abiotic stresses.

To my mind, the mission of agriculture in this century is FHNEE security meaning food, health, nutrition, energy and environment security. Hence, genome designing of crops should focus on breeding of varieties with higher yields and improved qualities of the five basic F<sup>5</sup> utilities; nutritional and nutraceutical compounds; and other industrially and aesthetically important products and possibility of multiple utilities. For this purpose of ‘precise’ breeding, employment of the genetic and genomic techniques individually or in combination as and when required will play a crucial role.

The chapters of the 12 volumes of this twin book series entitled, *Genomic Designing for Biotic Stress Resistant Crops* and *Genomic Designing for Abiotic Stress Resistant Crops* will deliberate on different types of biotic and abiotic stresses and their effects on and interaction with crop plants; will enumerate the available genetic diversity with regard to biotic or abiotic stress resistance among cultivars; illuminate on the potential gene pools for utilization in interspecific gene transfer; will brief on the classical genetics of stress resistance and traditional breeding for transferring them to their cultivated counterparts; will discuss on molecular mapping of genes and QTLs underlying stress resistance and their marker-assisted introgression into elite crop varieties; will enunciate different emerging genomics-aided techniques including genomic selection, allele mining, gene discovery and gene pyramiding for developing smart crop varieties with genetic potential to produce F<sup>5</sup> of higher quantity and quality; and also will elaborate the case studies on genome editing focusing on specific genes. Most of these chapters will discuss on the success stories of genetic engineering in the relevant crops specifically for generating crops with resistance and/or adaptability to diseases, insects and abiotic stresses.

There are obviously a number of reviews and books on the individual aspects of plant molecular breeding, genetic engineering and genomics-aided breeding on crops or on agro-economic traits which includes the 100-plus books edited by me. However, there is no comprehensive reviews or books available that have coverage on crop commodity groups including cereals and millets, oilseeds, pulses, fruits and nuts, vegetables and technical or industrial crops and modern strategies in single volumes with precise focuses on biotic and abiotic stresses. The present volumes will fill this gap with deliberations on about 120 important crops or their groups.

This volume on *Genomic Designing for Biotic Stress Resistant Technical Crops* includes 11 chapters focused on cassava, cocoa tree, Coconut, coffee, cotton, floricultural crops, jute, mulberry, sugarcane, tobacco and yam contributed by 92 scientists from 10 countries including Brazil, China, Costa Rica, D. R. Congo, France, India, Iran, Nigeria, USA, and Venezuela. I remain immensely thankful for their highly useful contributions.

I am indebted to my wife Phullara who as always has assisted me directly in editing these books and indirectly through maintaining an academic ambience to pursue my efforts for science and society pleasantly and peacefully.

New Delhi, India

Chittaranjan Kole



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# Abbreviations

2D gel	Two-dimension gel
Aaa	<i>Acidovorax avenae</i> subsp. <i>avenae</i>
ABA	Abscisic acid
ABS	Access–benefit sharing
ACAC	Agro-Chemical Advisory Committee
ACGC	Arabica Coffee Genome Consortium
ACMV	African cassava mosaic virus
ACT	Artemis comparison tool
AE	Array express
AFLP	Amplified fragment length polymorphism
AGBs	Active Germplasm Banks
AgNPs	Silver nanoparticles
AGO	Argonaute
Ai	Active ingredient
AICEM	All India Coordinated Experiment on Mulberry
AICRP(S)	All India Coordinated Research Project on Sugarcane
AM	Association mapping
AMP1	Antimicrobial protein 1
AMT	<i>Agrobacterium</i> -mediated transformation
AS	Alternative splicing
<i>Avr</i>	Avirulence gene
AVT	Advanced varietal trial
AYT	Advanced yield trial
BAC	Bacterial artificial chromosome
BB	Bacterial blight
BC	Backcross
BG	Bollgard
BHB	Bacterial halo blight
bHLH	Basic helix–loop–helix
BILs	Backcross inbred lines
BLS	Brown leaf spot

BSA	Bulk segregant analysis
Bt	<i>Bacillus thuringiensis</i>
BTH	Benzothiadiazole
Bti B.	<i>Thuringiensis</i> serovar <i>israelensis</i>
bZIP	Basic Leucine Zipper Domain
CAB	Cocoa from the Brazilian Amazon
CABI	Centre for Agriculture and Bioscience International
CAD	Cassava anthracnose disease
CaMXMT1	Chrysanthemum methylxanthinemethyltransferase 1
CAPS	Cleaved amplified polymorphic sequence
Cas	CRISPR-associated protein
Cas 9	CRISPR-associated protein 9
CaXMT1	Chrysanthemum xanthosinemethyltransferase 1
CBB	Cassava bacteria blight
CBB	Coffee berry borer
CBD	Convention on biological diversity
CBSD	Cassava brown streak disease
CCCVd	Coconut cadang–cadang viroid
CcPDS	Phytoene desaturase
CDB	Coffee berry disease
cDNA	Complementary DNA
CE	Carboxylesterase family
CFDV	Coconut foliar decay virus
CGIAR	Consultative Group for International Agricultural Research
CGM	Cassava green mite
CGRD	Coconut Genetic Resources Database
CICF	Centro de investigação das ferrugens do cafeeiro
CIM	Composite interval mapping
CIPO	Canadian Intellectual Property Office
CIRAD	Centre de Coopération Internationale en Recherche Agronomique pour le Développement
CLM	Coffee leaf miner
CLR	Coffee leaf rust
cM	Centimorgan
CMD	Cassava mosaic disease
CMGV	<i>Cassava mosaic geminivirus</i>
CMS	Cytoplasmic male sterility
CMV	<i>Cucumber mosaic virus</i>
CNRA	Center National de Recherche Agronomique
CNTs	Carbon nanotubes
CNV	<i>Cacao necrosis virus</i>
COGENT	International Coconut Genetic Resources Network
CORESTA	Cooperation Centre for Scientific Research Relative to Tobacco
COS	Conserved ortholog sequences
COS-II	Conserved ortholog set II

COSTREL	Combinatorial super transformation of transplastomic recipient lines
CP	Coat protein
CPs	Cuticular proteins
CpYGFp	<i>Chiridius poppei</i> yellow-green fluorescent protein
CRIN	Cocoa Research Institute of Nigeria
CRIP	Coffee gRNA Identification Program
CRISPR	Clustered regularly interspaced short palindromic repeats
cry1Ab	Crystal protein 1 Ab
CSR&TI	Central Sericultural Research and Training Institute
CSSLs	Chromosome Segment Substitution Lines
CSSV	<i>Cacao swollen shoot virus</i>
CTRI	Central Tobacco Research Institute
CVB	<i>Chrysanthemum virus B</i>
CVRC	Central Varietal Release Committee
CWR	Crop wild relatives
CYD	Coconut yellow decline
CYMV	Cacao yellow mosaic virus
dai	Days after inoculation
DArT	Diversity array technology
DAS	Days after sowing
DAVID	Database for annotation, visualization and integrated discovery
dCAPS	Derived CAPS
DDBJ	DNA Databank of Japan
DDVP	Dichlorvos
DGA	Defence gene analog
DH	Doubled haploid
DPMA	German Patent and Trademark Office
DRs	Disclosure requirements
DSBs	Double-strand breaks
dsRNA	Double-stranded RNA
DUS	Distinctness, uniformity and stability
EACMV	East African cassava mosaic virus
EBI	European Bioinformatics Institute
EC	Effective concentration
EC	Emulsified concentrate
EFSA	European Food Safety Authority
eIF4E	Eukaryotic translation initiation factor 4E
EIL	Economic injury level
ELISA	Enzyme-linked immunosorbent assay
EMBL	European Molecular Biology Laboratory
EMS	Ethyl methanesulfonate
EPO	European Patent Office
ERF	Ethylene-responsive factor
ERF	ETS2 repressor factor
<i>ERF1</i>	<i>Ethylene-responsive factor 1</i>

ERIC-PCR	Enterobacterial repetitive intergenic consensus-PCR
EST	Expressed sequence tag
EST-SSR	EST-derived SSR
ET	Ethylene
ETI	Activating effector-triggered immunity
ETR	Electron transport rate
F1	First filial generation
FaNES1	Frankellianerolidol synthase 1
FAO	Food and Agriculture Organization
FAOSTAT	Food and Agriculture Organization Corporate Statistical Database
FCF	Fungus culture filtrate
FCTC	Framework Convention on Tobacco Control
FCV	Flue cured virginia
FDV	<i>Fiji disease virus</i>
FEC	Friable embryogenic calli
FISH	Fluorescence in situ hybridization
FOV	<i>Fusarium oxysporum</i> f. sp. <i>Vasinfestum</i>
FPO	Free Patents Online
FW	Fusarium wilt
FYM	Farm yard manure
GA3	Gibberellic acid
GAB	Genomics-assisted breeding
GAP	Good agricultural practice
GBLUP	Genomic best linear unbiased prediction
GBS	Genotyping-by-sequencing
GE	Genome engineering
GEA	Genomic Expression Archive
GEBVs	Genomic-estimated breeding values
GEO	Gene Expression Omnibus
GhAAT	<i>Gerbera hybrida</i> aspartate aminotransferase
GhFAH	<i>Gerbera hybrida</i> fumarylacetoacetate hydrolase
GhHGD	<i>Gerbera hybrida</i> homogentisate 1,2-dioxygenase
GhHPD	<i>Gerbera hybrida</i> 4-hydroxyphenylpyruvate dioxygenase
GhTAT	<i>Gerbera hybrida</i> tyrosine aminotransferase
GLM	General linear models
GM	Genetically modified
GMD	Golm Metabolome Database
GMO	Genetically modified organism
GO	Gene ontology
GRLs	Guidance residue levels
gRNA	Guide RNA
GRs	Genetic resources
GS	Genomic selection
GSRs	Genome space sequence reads
GSS	Genomic survey sequences

GTE	GATA transcription factor
GUS	<i>β-glucuronidase</i>
GWAS	Genome-wide association study/studies
H <sub>2</sub> O <sub>2</sub>	Hydrogen peroxide
hai	Hours after inoculation
HdT	Timor hybrid
HESP	Haustorial-expressed secreted protein
HG	Homologous groups
hpaGXoo	HarpinXoo
hpRNA	Hairpin RNA
HR	Hypersensitive response
HSF	Heat shock factor
HSP	Heat shock protein
ICAR	Indian Council of Agricultural Research
ICAR-SBI	ICAR—Sugarcane Breeding Institute
ICG	International Coconut Gene Bank
ICGD	International Cocoa Germplasm Database
ICGT	International Cocoa Genbank, Trinidad
ICMV	<i>Indian cassava mosaic virus</i>
ICO	International Coffee Organization
ICS	Imperial College Selection
ICTV	International Committee on Taxonomy of Viruses
IDM	Integrated disease management
IGH	Intergeneric hybrids
IGS	Intergenic spacer
IITA	International Institute of Tropical Agriculture
IM	Interval mapping
Indels	Insertion or deletion mutations
INM	Integrated nutrient management
INSDC	The International Nucleotide Sequence Database Collaboration
IPM	Integrated pest management
IPM/IDM	Integrated management of pests and disease
IPR	Intellectual Property Rights
IRAD	Institute of Agricultural Research for Development
IRD	Institut de Recherche pour le Développement
ISAAA	International Service for the Acquisition of Agri-biotech Applications
ISH	Interspecific hybrids
ISSCT	International Society of Sugarcane Technologists
ISSR	Inter-simple sequence repeat
ISTR	Inverse sequence tagged repeat
ITPGRFA	International Treaty for Plant Genetic Resources for Food and Agriculture
ITS	Internal transcribed spacer
JA	Jasmonic acid

JPO	Japan Patent Office
KASP	Kompetitive allele-specific PCR
KEGG	Kyoto Encyclopedia of Genes and Genomes
LD	Linkage disequilibrium
LD50	Lethal dose 50
LG	Linkage group
LIWRKY	Lilium W-box binding transcription factor
LIWRKY10	Lilium W-box binding transcription factor 10
LIWRKY12	Lilium W-box binding transcription factor 12
LIWRKY3	Lilium W-box binding transcription factor 3
LIWRKY4	Lilium W-box binding transcription factor 4
LIWRKY5	Lilium W-box binding transcription factor 5
LMOs	Living modified organisms
LMoV	Lily mottle virus
LOD	Logarithm of odds
LrPR10-2	Lilium regale pathogenesis-related gene—2
LrPR10-4	Lilium regale pathogenesis-related gene—4
LrPR10-5	Lilium regale pathogenesis-related gene—5
LrPR10-6	Lilium regale pathogenesis-related gene—6
LrPR10-7	Lilium regale pathogenesis-related gene—7
LrPR10-9	Lilium regale pathogenesis-related gene—9
LRR	Lucien-rich repeat
LRR-RLK	Llr-like kinase
LSA	Locus-specific amplification
LSD	Leaf scald disease
Lxx	<i>Leifsonia xyli</i> subsp. <i>xyli</i>
LY	Lethal yellowing
MAB	Marker-assisted breeding
MABC	Marker-assisted backcrossing
MACC	Marker-assisted complex or convergent crossing
MAGIC	Multiparent advanced generation intercross
MAPK	Mitogen-activated protein kinase
MARB	Marker-assisted resistance breeding
MAS	Marker-assisted selection
<i>mcbt</i>	Modified <i>cryIAb</i> gene of <i>Bacillus thuringiensis</i>
MegaN	Meganuclease
MeJA	Methyl jasmonate
miRNA	Micro-RNA
<i>MLO</i>	<i>Mildew resistance locus O</i>
MLT	Multi-location trial
MMS	Methyl methane sulfonate
MNPs	Magnetic nanoparticles
MNs	Meganucleases
MoNA	Massbank of North America
MRL	Maximum residue level

MSNs	Mesoporous silica NPs
MTD	Mannitol dehydrogenase
MTI	Mite tolerability index
MYB	Myeloblastosis
MYC	Master regulator of cell
NACN	Acetylcysteine
<i>NaDH</i>	<i>Nicotiana attenuata</i> data hub
NattCyc	<i>N. attenuata</i>
NBS	National Bureau of Standards
NBS	Nucleotide-binding site
NCBI	National Center for Biotechnology Information
nCBP	Novel cap-binding protein
NDR1	Non-race-specific disease resistance
NFYC	Nuclear transcription factor Y
NGS	Next-generation sequencing
NHEJ	Non-homologous end-joining
NIH	National Human Genome Research Institute
NILs	Near-isogenic lines
NIX	<i>Nicotiana</i> multiple (X) genome
NMR	Nuclear magnetic resonance
NPBTs	New plant breeding technologies
NPL	Non-patent literature
NPR	Non-expressor or pathogenicity related
NPs	Nanoparticles
NPV	Nuclear polyhedrosis virus
NSKS	Neem seed kernel suspension
<i>OPR3</i>	<i>Oxoplytodienotae reductase 1-like</i>
ORF	Open reading frame
OXO	Oxalate oxidase
PAM	Proto spacer adjacent motif
PAMPs	Pathogen-associated molecular patterns
PB	Pokkahboeng
PBR	Plant Breeders' Rights
PCA	Principal coordinate analysis
PCT	Patent Cooperation Treaty
PCV	<i>Peanut clump virus</i>
PDB	Protein Data Bank
PDR	Pathogen-derived resistance
PGDBs	Pathway–genome databases
PI	Proteinase inhibitor
PIB	Population of improved <i>S. barberi</i>
PIO	Population of improved <i>S. officinarum</i>
PIR	Population of improved <i>S. robustum</i>
PIR	Protein Information Resource
PIS	Population of improved <i>S. spontaneum</i>

POGs	Peroxidase genes
PPB	Participatory plant breeding
PPVFRA	Protection of Plant Varieties and Farmers' Rights Authority
PR	Pathogenesis related
<i>PR10</i>	<i>Pathogenesis-related 10</i>
PRR	Pachymetra root rot
PRRs	Pattern recognition receptors
PRT	Progeny row trial
PTGS	Post-transcriptional gene silencing
PTIPAMP	Triggered immunity
PVP	Plant variety protection
PVY	<i>Potato virus Y</i>
PYT	Preliminary/primary yield trial
QTA	Quantitative trait allele
QTL	Quantitative trait locus
QTLs	Quantitative trait loci
R	Resistance
RAD sqe	Restriction site-associated DNA sequencing
RAMP	Random amplified microsatellite polymorphism
RAPD	Random amplified polymorphic DNA
REP-PCR	Repetitive element sequence-based PCR
RFLP	Restricted fragment length polymorphism
RFS	Rainfed selection
RGA	Resistance gene analog
RGAP	Resistance gene analog polymorphism
R-gene	Resistance gene
RhMLO	Rhodopsin mildew resistance locus O
RhMLO1	Rhodopsin mildew resistance locus O 1
RhMLO2	Rhodopsin mildew resistance locus O 2
RhMLO3	Rhodopsin mildew resistance locus O 3
RILs	Recombinant inbred lines
RISC	RNA-induced silencing complex
RKHS	Reproducing Kernel Hilbert space
RKN	Root-knot nematode
RLK	Receptor-like kinase
RLKs-LRRs	Receptor-like kinases LRR
RNAi	RNA interference
RNA-seq	RNA sequencing
ROS	Reactive oxygen species
RP	Recurrent parent
<i>Rpp1</i>	Recognition of <i>Peronospora Parasitica</i>
RR	Roundup Ready
RSD	Ratoon stunting disease
RTP1	Rust transferred protein 1
RT-qPCR	Quantitative reverse transcription PCR



RWD	Root (wilt) disease
SA	Salicylic acid
SACMV	South African cassava mosaic virus
SAGE	Serial analysis of gene expression
SAH	Semi-autotrophic hydroponic
SAR	Systemic acquired resistance
SCAR	Sequence-characterized amplified region
SCBV	Sugarcane bacilliform virus
SCGS	Sugarcane grassy shoot disease
SCMMV	Sugarcane mild mosaic virus
SCMV	Sugarcane mosaic virus
SCSMaV	Sugarcane striate mosaic associated virus
SCSMV	Sugarcane steak mosaic virus
SCW	Silicon carbide whiskers
SCWL	Sugarcane white leaf disease
ScYLV	Sugarcane yellow leaf virus
SD	Single dose
SES	Standard evaluation system
SFP	Single feature polymorphism
SGN	Sol Genomics Networks
sgRNA	Single guide RNA
shRNA	Short hairpin RNA
SIB	Swiss Institute of Bioinformatics
siRNA	Small interfering RNA
SLCMV	Sri Lankan cassava mosaic virus
SNP	Single nucleotide polymorphism
Solana Cyc	Solanaceae database
SRA	Sequence Read Archive
SRAP	Sequence-related amplified polymorphism
SrMV	Sorghum mosaic virus
SSA	Sub-Saharan Africa
SSAP	Sequence-specific amplification polymorphism
SSH	Suppression subtractive hybridization
SSLP	Simple sequence length polymorphism
SSNs	Sequence-specific nucleases
SSR	Simple sequence repeat
ssRNA	Single-stranded RNA
STR	Short tandem repeat
STRs	Short repetitions in tandem
STS	Sequence tagged site
SUCEST	Sugarcane expressed sequence tags
SVI	Somaclonal variant-1
TAC	Transformation-competent artificial chromosome
TAL	Transcription activator-like
TALENs	Transcription activator-like effector nucleases

TBIA	Tissue-blot immunoassay
TDFs	Transcript-derived fragments
T-DNA	Transfer DNA
TEV	Tobacco etch virus
TF	Transcription factor
TGATGACG	Binding (TGA) transcription factors
TGI	Tobacco Genome Initiative
TIGR	The Institute of Genome Research
TK	Traditional knowledge
TLCV	Tobacco leaf curl virus
TMV	Tobacco mosaic virus
TobEA	Tobacco Expression Atlas
TOBFAC	Tobacco transcription factors
TPA	Third-party annotation
TPS1	Trehalose-6-phosphate synthase
TRAP	Target region amplification polymorphism
TRIPs	Trade-Related Aspects of Intellectual Property Rights
TSH	Trinidad selected hybrids
TSWV	Tomato spotted wilt virus
TVMV	Tobacco vein mottling virus
UC	Davis University of California, Davis
UNICAMP	Universidade estadual de Campinas
UniParc	UniProt Archive
UPOV	Union for the Protection of New Varieties of Plants
USDA	United States Department of Agriculture
USDA-ARS	USDA—Agricultural Research Service
UV	Ultraviolet
UYT	Uniform yield trial
VIGS	Virus-induced gene silencing
VPg	Viral genome-linked protein
VW	Verticillium wilt
WCSRG	World Collection of Sugarcane and Related Grasses
WFT	Western flower thrips
WGP	Whole genome profile
WHO	World Health Organization
WIPO	World Intellectual Property Organization
WLS	White leaf spot
WNTD	World No Tobacco Day
WRKY	W-box binding transcription factor
WTO	World Trade Organization
WUE	Water use efficiency
<i>Xam</i>	<i>Xanthomonas axonopodis</i> pv. <i>manihotis</i>
<i>Xcm</i>	<i>Xanthomonas citri</i> pv. <i>malvacearum</i>
YAC	Yeast artificial chromosome
YAD	Yam anthracnose disease

YLD	Yellow leaf disease
YLS	Yellow leaf syndrome
YMV	Yam mosaic virus
ZFN	Zinc finger nuclease
ZnONP	Zinc oxide nanoparticle

# Chapter 1

## Genomic Designing for Biotic Stress Resistant Cassava



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**Abstract** Cassava is essential food security, mostly in Africa, South America, and other major regions of the world where cassava is cultivated. It is very high in caloric value and resilient to climate change, drought, and low fertility. Biotic stress limits cassava cultivation and utilization with an impact that could range from 20 to 90% loss in yield and food quality. Diseases including viral, fungal, bacterial, and nematodes as well as diverse kinds of pests such as cassava whitefly and cassava green mites (CGM) are considered important biotic factors that impact cassava production. Diverse measures and techniques have been implored in cassava towards genomic designing for biotic stress resistance. These techniques range from traditional breeding to genomic selections and other new breeding technologies such as genetic engineering and genome editing. This chapter outlines the most significant biotic stresses in cassava, their prevalence, and impact on yield as well as different technologies being utilized towards the development of biotic stress-resistant cassava.

**Keywords** Cassava · Biotic stresses · Genomic selection · Genetic engineering · Genome editing

### 1.1 Biotic Stress in Cassava

Cassava, *Manihot esculenta* Crantz, (Family Euphorbiaceae) is an essential staple crop cultivated across the tropics and subtropics primarily for its starchy roots, which for over a billion serves as a source of calories and for industrial purposes (Lyons et al.

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2021; Rabbi et al. 2014a). Cassava leaves also have considerable nutritional qualities and serve as food for humans and animals alike (El-Sharkawy 2004; Wasonga et al. 2020). Cassava is an ideal food security crop with the ability to produce optimal yields and can be stored in the ground for long periods allowing harvest flexibility while adapting to the effects of drought and marginal soils (Ceballos et al. 2020). Despite its many strengths, cassava production is hindered by a myriad of abiotic and biotic stresses. Across cassava growing regions, diverse pathogens (including viruses, phytoplasma, bacteria, or fungi) have been implicated in several cassava diseases, and approximately 200 pests (insects and mites) are known to feed off the crop inadvertently causing severe damages and enabling the spread of diseases (Herren and Neuenschwander 1991; Lozano and Booth 1974). Over the years, pests and disease management strategies have seen some successes in mitigating the spread of cassava pests in regions where they are alien, however, mitigation or elimination efforts for diseases caused by viruses or pests native to a region had been challenging (Herren and Neuenschwander 1991; Legg et al. 2015). Current efforts to combat cassava diseases include the development of early phenotyping and detection tools (Okereke et al. 2017; Ramcharan et al. 2017; Sambasivam and Opiyo 2021), cleaning infected planting materials (Maruthi et al. 2019), and genetic improvement for disease resistance through conventional and molecular breeding techniques (Ezenwaka et al. 2018; Rabbi et al. 2014b; Tembo et al. 2017; Wolfe et al. 2015), genetic engineering (Vanderschuren et al. 2012), and genome editing (Gomez et al. 2019; Mehta et al. 2019). This book chapter will focus on the most economically important biotic factors that impede cassava production and we will be reviewing the current biotechnological strategies to develop disease-resistant cassava varieties. In so doing, we identify challenges from these approaches, highlight avenues for further research and conclude with an outlook for pest and disease management in cassava.

## ***1.1.1 Prevalent Cassava Biotic Factors***

### **1.1.1.1 Cassava Diseases**

Like most root and tuber crops, cassava is propagated vegetatively to ensure crop uniformity from one planting season to the next. This, unfortunately, contributes to the proliferation and spread of diseases throughout cassava-producing regions. With increasing globalization and urbanization in cassava growing regions, as well as the variability and pervasiveness of climate change, native and emerging cassava disease outbreaks are on the rise in Africa, the Asia–Pacific, and Latin America. Both foreign or alien and native pests and disease pathogens that negatively impact cassava production are not so easy to mitigate (Legg et al. 2015). In sub-Saharan Africa (SSA), viral diseases including cassava mosaic disease (CMD) and cassava brown streak diseases (CBSD) cause devastating losses, affecting the food and income of, especially limited-resource farmers. Many economically important diseases significantly

contribute to yield losses of the host crop, attacking the roots, stems, or leaves. The pathogen, *Xanthomonas axonopodis* pv. *manihotis* which causes cassava bacterial blight (CBB) disease ranks as the 6th most relevant bacterial pathogen in the world (Mansfield et al. 2012). For some of these diseases, their transmission to a cassava host plant is carried out by destructive pests, which feed off the crop, including its succulent green leaves and stems.

### 1.1.1.2 Cassava Pests

By damaging the leaves, cassava pests affect the photosynthetic capacity of the crop. Several pests damage cassava while feeding, but only a few are considered to be economically important (Table 1.1). There is a significant variation among pests that attack cassava by continent, and foreign pests that are inadvertently introduced in a region where they are not common, cause devastating losses. For example, arthropods such as the cassava mealybug (*Phenacoccus manihoti* Mat.-Ferr.) and CGM (*Mononychellus tanajoa* Bondar), introduced into Africa and South-East Asia in the 1970s and early 2000s, respectively, potentially cause up to 50% yield losses in local cassava crops (Graziosi et al. 2016). Also, prevailing seasons impact the activities of pests. Arthropod pest complexes for instance, mostly occur in the dry season and not so much in humid regions of heavier rains (Lebot 2008).

**Table 1.1** Some economically important biotic stresses across cassava growing regions

Type of pathogen	Disease	Regions		
		Africa	Asia-Pacific	Latin-America
Virus	Cassava mosaic disease	x	x	
	Cassava brown streak disease	x		
	Cassava frogskin disease		x	x
Bacteria	Cassava bacterial blight	x	x	x
Fungi	Cassava brown leaf spot	x	x	x
	Cassava white leaf spot	x	x	x
	Cassava root rot disease	x	x	x
	Cassava anthracnose disease	x	x	x
Pests	Cassava mealybug disease	x	x	x
	Cassava green mite disease	x	x	x

Source Lebot (2008)