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Molecular Mechanism of Crucifer's Host-Resistance

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Foreword

Plants are attacked by a wide variety of potential plant pathogens within their environment such as fungi, oomycetes, bacteria, phytoplasmas, viruses, and viroids that cause harmful and economically important diseases across a very broad range of plant species worldwide. The most promising way to manage the losses is to generate disease-resistant varieties, likely involving manipulation of target genes implicated in the induced resistance to pathogens or the signal transduction pathways controlling the expression of the defense-related genes. Plant immune/defense systems rely on their ability to recognize the presence of the pathogen, to carry out signal transduction, and to respond defensively through pathways involving many genes and/or their products. Pathogens actively attempt to evade and interfere with response pathways, selecting for a decentralized, multicomponent immune system. Recent advances in molecular techniques have greatly expanded our understanding of plant resistance and immunity, largely driven by potential application to agricultural systems. The plant immune systems have provided both increased evolutionary opportunity for pathogen resistance and additional mechanisms for pathogen inhibition of such defense responses. The advances in bioinformatics and molecular biology are driving an explosion of information that will advance agricultural production and illustrate the complex molecular interactions involved in disease resistance.

The present book entitled “*Molecular Mechanisms of Crucifer’s Host-Resistance*” authored by Prof. (Dr.) G. S. Saharan, Prof. (Dr.) Naresh K. Mehta, and Dr. P. D. Meena is a comprehensive treatise on molecular aspects of host–pathogen interactions, including induction of signal molecules to express defense genes, against major pathogens of crucifers that have adverse impact at a global level. The book illustrates how the different mechanisms play their roles in imparting disease resistance against the important pathogens of crucifers.

I am confident that this book will serve as a reference for future research work by Brassica scientists, including breeders, molecular biologists, and pathologists. It will also be immensely useful for science teachers and students. In particular, it provides a solid foundation of knowledge and understanding for further investigations concerning the molecular mechanisms of disease resistance. It is highly relevant to all wanting to see profitable cruciferous crops maintained and improved across the world.

My heartiest congratulations to the authors for combining their lifelong professional interests and expertise in diseases of crucifers to make this prestigious book possible for the benefit of all those interested in the research, development, and improvement of cruciferous crops.



A handwritten signature in blue ink, reading "M. J. Barbetti".

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Martin J. Barbetti

Preface

In the galaxy of plant biodiversity at a global level, crucifers share a significant role in feeding human and animal populations with vegetables, edible oil, and fodder crops of rich sources of nutrition and other amenities. Crucifers encompass a very large family Brassicaceae consisting of 325 genera and 3740 species with the genus *Brassica* having 75 accepted species. The gold mine of genomics studies *Arabidopsis thaliana* is also a part of the *Brassica* family which has transformed traditional sciences like Genetics, Plant Breeding, and Plant Pathology into Molecular Genetics, Molecular Breeding, and Molecular Plant Pathology by exploitation of *Arabidopsis* host-pathosystem to reveal molecular mechanisms of host-pathogen interactions. Crucifers are challenged by a large number of biotic and abiotic stresses, but 16 pathogens have received the attention of scientists to reveal molecular mechanisms of host-pathogen interactions and expression of molecular defense mechanisms. During the last three decades, substantial progress has been made on the investigations of molecular mechanisms of host resistance using *Brassica* host pathosystem as a model. After scanning more than 1500 publication, we have compiled the information in the form of a book entitled “*Molecular Mechanisms of Crucifer’s Host-Resistance*” for the benefit of students, teachers, research scientists, and all other who are interested in amelioration of *Brassica* crops production and productivity. The book is a comprehensive treatise on the molecular aspects of host-pathogen interactions and induction of signal molecules to express defense genes against different pathogens of crucifers which have impact at a global level. The information is arranged in nine chapters with proper headings and subheadings, which have been arranged in numbered series to make the subject matter contiguous along with sections of references to consult original publications. It is the eighth book on the diseases of cruciferous crops series after *Sclerotinia*, *Albugo*, *Alternaria*, *Hyaloperonospora*, *Erysiphe*, *Plasmodiophora*, and “*Genomics of Crucifers Host-Resistance*” published by Springer Nature. The chapter-wise sections include information on, viz., molecular mechanisms of disease resistance, molecular mechanisms of host resistance to biotrophs, molecular mechanisms of host resistance to hemi-biotrophs and necrotrophs, biometabolomics of disease resistance to biotrophs, biometabolomics of host resistance to hemi-biotrophs and necrotrophs, and glimpses of host resistance genomics. A chapter on standardized, reproducible techniques has been included for researchers of cruciferous crops for studying the molecular

mechanisms of resistant cultivars development. The last section deals with the gaps in understanding and knowledge of molecular mechanisms of disease resistance and offers suggestions for future research priorities in order to initiate advanced research programs on disease resistance. The subject matter has been vividly illustrated with photographs, graphs, figures, histogram, tables, and colored plates, which make it stimulating, effective, and easy to comprehend by readers.

We believe that this book will be immensely useful for researchers, especially *Brassica* breeders, molecular biologists, plant pathologists, teachers, extension specialists, students, industrialists, farmers, planners, and all others who are interested in growing healthy and profitable cruciferous crops all over the world. Suggestions by readers are always a source of inspiration for the authors. Any shortcomings, lacunae, and flaws in the book are the responsibility of the authors, and suggestions for its improvement are most welcome.

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List of Abbreviations

AAFC	Agriculture and Agri-Food Canada
AB	Alternaria blight
ABA	Abscisic acid
ABC	ATP-binding cassette
ABP1	Auxin-binding protein 1
AFLP	Amplified fragment length polymorphism
AG	Anastomosis groups
AIP	Aminoindan phosphonic acid
AM	Arbuscular mycorrhizal
ANOVA	Analysis of variance
AOC3	<i>ALLENE OXIDE CYCLASE 3</i>
AOS	<i>ALLENE OXIDE SYNTHASE</i>
ap	Appressorium
APX	Ascorbate peroxidase
ARF-GEF	ADP ribosylation factor-GTP exchange factor
AT	Associative transcriptomics
<i>AtSTP4</i>	<i>Arabidopsis sugar transport protein 4</i>
AUDPC	Area under disease progress curve
Avr	Avirulence
BA	Benzoic acid
BABA	β -amino butyric acid
BC	Backcross
<i>Bgt</i>	<i>Blumeria graminis</i> f. sp. <i>tritici</i>
BiFC	Bimolecular fluorescence complement
BLAST	Basic Local Alignment Search Tool
BLAT	BLAST-like alignment tool
BLUPs	Best linear unbiased predictions
BSA	Bulked segregant analysis
BSMV	Barley stripe mosaic virus
CA	Constitutively activated
CAC	Clathrin adaptor complex
CAD	Cinnamyl alcohol dehydrogenase
CaM	Calmodulin

CaMV	Cauliflower mosaic virus
CAT	Catalase
CBD	Chitin-binding domain
CBIs	Calcineurin-B-like protein
CC	Coiled coil
CDPKs	Calcium-dependent protein kinases
CF	Culture filtrate
ChIP	Chromatin immune precipitation
CK	Cytokinins
cM	centiMorgans
CMLs	Calmodulin-like protein
CNGCs	Cyclic nucleotide-gated ion channels
COIP	Co-immune precipitation
CW	Cell wall
CWAs	Cell wall apposition
CWDE	Cell wall-degrading enzymes
DAI	Days after inoculation
DAMPs	Damage-associated molecular patterns
DAPC	Discriminant analysis of principal components
DAS	Days after sowing
DEGs	Differentially expressed genes
DGE	Differential gene expression
DH	Doubled haploid
DI	Disease indices
DM	Downy mildew
DNA	Deoxyribonucleic acid
dpi	Days post-inoculation
DTT	Dithiothreitol
<i>Ec</i>	<i>Erysiphe cruciferarum</i>
ECD	European clubroot differential
EDS1	ENHANCED DISEASE SUSCEPTIBILITY 1
EHM	Extra-haustorial membrane
ELISAs	Enzyme-linked immunosorbent assays
EMS	Ethyl methane-sulfonate
ENU	Ethyl nitrosourea
<i>Ep</i>	<i>Erysiphe pisi</i>
e-PCR	Electronic PCR
ERK	Extracellular signal-regulated kinase
ESTs	Expressed sequence tags
ET	Ethylene
ETI	Effector-triggered immunity
ETS	Effector-triggered susceptibility
f. sp.	Fungal forma specialis
FCF	Fungal culture filtrate
FDR	False discovery rate

Fig.	Figure
FPKM	Fragments per kilobase of transcript per million mapped
FTIR	Fourier-transform infrared spectroscopy
GA	Gibberellins
GBS	Genotyping by sequencing
<i>GC</i>	<i>Golovinomyces cichoracearum</i>
GC-MS	Gas chromatography-mass spectrometry
GCRMA	Guanine Cytosine Robust Multi-Array Analysis
GDI _s	Guanine nucleotide dissociation inhibitors
GDP	Guaiacol-dependent peroxidase
GFP	Green fluorescent protein
GISH	Genomic in situ hybridization
GLM	Generalized linear models
GM	Genetically modified
GO	Gene ontology
<i>Go</i>	<i>Golovinomyces orontii</i>
GSS	Genomic survey sequences
GWAS	Genome-wide association analysis
HGP	Human Genome Project
HIGS	Host-induced gene silencing
HMM	Hidden Markov Model
HNRT	Homeologous non-reciprocal transposition
<i>Hp</i>	<i>Hyaloperonospora parasitica</i>
<i>Hpa</i>	<i>Hyaloperonospora arabidopsidis</i>
hpi	Hours post-inoculation
HR	Hypersensitive response
HRMS	High-resolution mass spectrometry
HS	Highly susceptible
HSPs	Heat shock proteins
HTGs	High-throughput genome sequences
HTS	Host targeting signal
IAA	Indole-3-acetic acid
IAN	Indole-3-acetonitrile
IAOx	Indole-3-acetaldoxime
IC	Isochorismate
ICAR	Indian Council of Agricultural Research
ICIM	Inclusive composite interval mapping
ICM	Composite interval mapping
ICS	Isochorismate synthases
iGS	Indole glucosinolates
ILs	Introgression lines
IM	Interval mapping
INA	Isonicotinic acid
IP	Intron polymorphic
IPG	Immobilized pH gradient strips

ISSRs	Inter-simple sequence repeats
ITCs	Isothiocyanates
ITS	Internal transcribed spacer
JA	Jasmonic acid
KASP	Kompetitive Allele-Specific PCR
LD	Linkage disequilibrium
LGs	Linkage groups
LIF	Lignification inducing factor
<i>Lm</i>	<i>Leptosphaeria maculans</i>
LOD	Logarithm of odds difference
LRR	Leucine-rich repeat
LRR-RLKs	Leucine-rich repeat receptor-like kinase
LRR-RLPs	Leucine-rich repeat receptors-like protein
LRRs	Leucine-rich repeats
LysM	Lysine motif
LZ	Leucine zipper
MAB	Marker-assisted backcross breeding
MAMPs	Microbe-associated molecular patterns
MAP	Mitogen-activated protein
MAPK	Mitogen-activated protein kinase
MAPKKK	MAP kinase kinase kinase
MAS	Marker-assisted selection
MeSA	Methyl salicylate
MET	Multi-Environment Trials
MKK	MAP kinase kinase
ML	Maximum likelihood
MLM	Mixed linear model
MLO	Mildew resistance locus O
MPK	MAP kinase
MPTO	Methylthiopentanaloxime
MQM	Multiple QTL mapping
MR	Moderately resistant
MS	Mass spectrometry
MSA	Multiple sequence alignment
MT	Microtubule
MTAs	Marker trait associations
MYA	Million years ago
MYB	Myeloblastosis
NBS	Nucleotide-binding site
NBS-LRR	Nucleotide-binding site leucine-rich repeat
NBT	Nitro blue tetrazolium
NC	Nucleotidyl cyclase
NCBI	National Centre for Biotechnology Information
NGS	Next generation sequencing
NHR	Non-host resistance

NILs	Near isogenic lines
NIRS	Near-infrared reflectance spectroscopy
NLRs	Nucleotide-binding site leucine-rich repeats
NMR	Nuclear magnetic resonance
NO	Nitric oxide
NPR1	Non-expressor of Pathogenesis-Related Genes 1
NWCVT	National Winter Canola Variety Trials
OA	Oxalic acid
OD	Optical density
OGs	Oligogalaturonides
<i>On</i>	<i>Oidium neolycopersici</i>
OST1	Open stomata 1
PA	Phosphatidic acid
PAD4	Phytoalexin-deficient 4
PAL	Phenylalanine ammonia lyase
PAMP	Pathogen-associated molecular pattern
PCA	Principal component analysis
PCD	Programmed cell death
PCR	Polymerase chain reaction
PDA	Potato dextrose agar
PDI	Per cent Disease Index
PDR	Pleiotropic drug resistance
<i>PEIs</i>	Pectinesterase inhibitors
PEN2	Peroxisome-associated myrosinase penetration 2
PFK	Phosphofructokinase
PGA	Polygalacturonase
PGIPs	Polygalacturonase inhibitor proteins
PIC	Polymorphic information content
PIPs	Phosphatidylinositol phosphates
PM	Plasma membrane
PM	Powdery mildew
<i>PMEI</i>	Pectin methylesterase inhibitors
PMSF	Phenylmethylsulfonyl fluoride
PO	Peroxidase
pp	Penetration peg formation
PPO	Polyphenol oxidase
PPT	Phosphinothricin
PR	Pathogenesis related
PRRs	Pattern recognition receptors
PTI	Pathogen-associated molecular patterns (PAMPs)-triggered immunity or pattern-triggered immunity
pv.	Pathovar
QDR	Quantitative disease resistance
qRT-PCR	Real-time quantitative-PCR
QTL	Quantitative trait locus

R	Resistance
RAPD	Random amplification of polymorphic DNA reaction
RFLP	Restriction fragment length polymorphism
RGL	Resistant genes like
RIN	RNA integrity numbers
RLCK	Receptor-like cytoplasmic kinase
RLKs	Receptor-like kinases
RLPs	Receptor-like proteins
RNA	Ribonucleic acid
RNAi	RNA interference
ROI	Reactive oxygen intermediates
ROP	Rho of plants
ROS	Reactive oxygen species
RT-PCR	Reverse transcription and quantitative reverse transcription-polymerase chain
SA	Salicylic acid
SAG	Salicylic acid glycoside
SAG101	Senescence-associated gene 101
SAM	<i>S</i> -adenosine- <i>L</i> -methionine
SAR	Systemic acquired resistance
SARF	Sum of adjacent recombination fractions
SCAR	Sequence characterized amplified region
SD	Standard deviation
Si	Silicon
SMA	Single marker analysis
SMRT	Single-molecule real-time
SNAP	Soluble <i>N</i> -ethylmaleimide-sensitive factor adaptor protein
SNP	Single nucleotide polymorphism
SOD	Superoxide dismutase
SR	Sclerotinia rot
SRAP	Sequence-related amplified polymorphism
SSR	Simple sequence repeat
STK	Serine-threonine kinase
STS	Sequence tagged sites
TAIR	The <i>Arabidopsis</i> Information Resource
TBIAs	Tissue blot immunoassays
TBS	Tris-buffered saline
TDFs	Transcript-derived fragments
TFs	Transcription factors
TGS	TRIS-glycine-SDS
TIGS	Transient-induced gene silencing
TIR	Toll/interleukin-1 receptor
TM	Trans-membrane
TMM	Trimmed mean of means
TNL	TIR-NBS-LRR