Genetic Improvement of Solanaceous Crops

Volume I : Potato

Editors

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Cover Illustrations

Bottom:
Plant of the dihaploid of potato cv. Kuba, resistant to Potato Virus Y (PVY), leafroll virus (PLRV), mid resistant to late blight and nematodes

Top Inset:
Tubers of dihaploid (left) and tetraploid cv. Kuba (right)
(Courtesy: Dr. Ewa Zimnoch-Guzowska)

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Foreword

Genetic improvement of crops has undergone an unparalleled transition over the past two decades. Practically everything we thought we knew about genes and trait expression has been turned upside down and inside out by technological revolutions at the cellular and molecular level. It's not that previous research led us to the wrong conclusions; it's that so little of the actual process by which cells carry out their functions was revealed. And even though we now have such a grander insight into those processes, we still have to use our new knowledge in real-world, field applications, if they are going to result in benefit to the world. This book provides the context by which our knowledge, from one end of the spectrum of crop improvement to the other, can be drawn together and applied to solve some of the most difficult problems facing improvement of a major global food crop-the potato. Because of its global importance at a time when efforts to eliminate hunger and malnutrition are at the forefront, this book comes at an opportune time to take stock of how well we have integrated the new into the old and formed new approaches that will contribute to increased food security in many parts of the world.

The book includes chapters by an impressive list of authors—those most well known in the potato research community. It covers the breadth and depth of potato improvement from the gene to the field and provides a collective knowledge that will be valued by all potato researchers around the world. The topics discussed are relevant to the most pressing problems facing potato growers, processors, and consumers. The volume highlights, from the beginning chapter, the crucial importance of genetic diversity and the dangers of loss or erosion of that diversity both within and outside genebanks. This is possibly the most complete chapter on genetic diversity of potatoes in existence and provides an excellent foundation for the following chapters which cover the eventual utilization of germplasm in solving the myriad of problems presented by such a genetically complex crop.

And finally, the authors and editors have done an excellent job in demonstrating how new technological approaches are becoming integrated throughout the research spectrum and providing new avenues for improving one of the world's most important crop plants. The book should

quickly become a necessary addition to the reference libraries of scientists and research organizations worldwide.

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Preface

The past few decades have witnessed a marked change in attitudes toward technological applications in crop research and development. Conventional methods of genetic improvement are now supplemented with so called "nonconventional" molecular and biotechnological approaches to gene modifications, particularly to induce higher crop yields, resistance to various types of pathogens, or abiotic environmental stresses, etc. Gene mapping and molecular-assisted selection facilitate improving quantitative traits of interest in plant breeding. Potato is the fourth largest crop after rice, wheat and maize. Agronomists, breeders, and farmers have always had to be concerned with quality and productivity of this important noncereal vegetable and food crop in order to meet the demands of consumers and food processors. It is imperative that potato growers be provided with integrated technical advice enabling them to make the best use of available resources. They also need an understanding of the technological principles for supporting their traditional skills and the art of potato husbandry.

Notwithstanding the fact that areas of genetic manipulation in crops are becoming increasingly specialized, major institutions now recognize that research on potato genetics and improvement be organized as a team activity by maintenance of closer links in R&D (Research and Development), extension programs, and farming through constant flow and exchange of information among them. Considering the fact that rapid advances have been made in improving potatoes using traditional breeding methods as well as genetic engineering technology, the aim of the present volume is to provide a critical appraisal of the state-of-the-art findings on this crop. The book starts with an insight into the origin, history, and conservation of potato germplasm (both *in situ* and *ex situ*) along with data on the existing status of its genetic resources and use of online database for exchange of relevant information (Chapter 1). Application of TPS (True Potato Seed) as a technological alternative to conventional propagation of tubers as a planting source, economic viability and on-farm profitability of TPS-related technology are discussed based on farmer experience at various agroecological sites in Egypt, India, Indonesia, Peru, and Vietnam (Chapter 2). A critical analysis of the shortcomings in traditional potato-breeding strategies due to complexity

of tetrasomic inheritance, susceptibility to pests and diseases, fertility problems associated with cultivated potato (tetraploid) are assessed with combining ability of desirable attributes in a single clone (Chapter 3). Furthermore, breeding potential of 4x–2x matings in transmission and combining ability of quantitative traits are highlighted (Chapter 4). Of the 200 species in the genus *Solanum*, from Central and South America, an incredible wealth of genetic diversity represented by Ca. 70% diploid species remains vastly underutilized in potato-breeding programs. This wealth of diploid potato germplasm could contribute to allelic diversity, which may be useful for genetic enhancement of important traits in new commercial cultivars. Keeping this objective in mind, breeding strategies have been adopted over the years at North Carolina State University, Raleigh, NC, with a follow-up at USDA/ARS-Beltsville Center, MD, and diploid germplasm base increased for commercial use (Chapter 5), with similar breeding programs executed in Poland, Scotland, and CIP (Peru). Application of molecular markers in gene mapping and fingerprinting of the quantitatively inherited important agronomic traits have contributed to enhancement of germplasm base, recombining ability, and interpretation of taxonomic and phylogenetic interrelationship among various potato taxa (Chapter 6); ploidy manipulation, e.g. application of monoploids, haploids from tetraploid parents, first division restitution (FDR) and second division restitution (SDR) mechanisms of 2n gamete formation, present special unique methods of gene mapping and gene action in potatoes (Chapter 7). Genetic manipulation for economically important traits can be better understood by identification and functional characterization of gene(s) controlling the expression of these traits. Map-based cloning, candidate gene approach, and transposon tagging are some of the novel approaches followed with application to potato (Chapter 8). Cell and tissue culture methods have long been applied in production of monoploid and dihaploid potatoes that are now the subject of intensive genetic analysis in molecular mapping of genes and genetic transformation studies, in particular, introgression of desirable traits through somatic hybridization for release of new improved varieties (Chapter 9). Physiological and biomolecular changes during storage at low temperatures greatly affect the tuber quality of potato. Enzymes regulating starch-sugar interconver-sions in response to changes in temperature play an important role and could be the target of genetic engineering, especially antisensing invertase gene may have long-lasting positive effects in transgenic potato (Chapter 10). Finally, advances made in transgenic technology in production of potato cultivars resistant to insects, nematodes, viruses, bacteria and fungal pathogens are aspects significantly contributing to genetic improvement of potatoes (Chapters 11–15).

This book thus presents the research findings of experts from international institutes and organizations who have coordinated efforts over the past several decades for improvement of the potato crop. It is hoped that this compendium will not only find favor with potato breeders and specialists, but will also have value to teachers and students seeking recent information on potato genetics, physiology and pathology. The Editors sincerely thank the publisher and contributors of the respective chapters for their sincere cooperation and support.

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Abbreviations Used Throughout the Book

acyl-HSL:	N-acyl derivatives of homoserine lacton
ADH:	Alcohol dehydrogenase
ADP:	Adenosinediphosphate
ADPase:	Adenodiphosphatase
AFGC:	*Arabidopsis* Functional Genomics Consortium
AFLP:	Amplified fragment length polymorphism
AGPase:	ADP-glucose pyrophosphorylase
AGPB:	Catalytic subunit of AG Pase
ANOVA:	Variance analysis
APIC:	Association of Potato Intergenebank Collaborators
ATP:	Adenosinetriphosphate
ATPase:	Adenosinetriphosphatase
BA:	Benzyladenine
BAC:	Bacterial artificial chromosome
BC1, BC2, BC3:	Backcross first, second or third
BIBAC:	BAC transformed vectors namely BIBAC vectors
BIO-PCR:	Enrichment PCR
BOX:	Repetitive extragenic palindromic sequence
BSA:	Bulked segregant analysis
BW:	Bacterial wilt
CAPS:	Cleaved amplified polymorphic sequence
cDNA:	Complementary DNA
CEPESER:	Central Peruana de Servicios (Peru)
cfu:	Colony-forming unit
CGIAR:	Consultative Group on International Agricultural Research
CIMMYT:	International de Mejoamiento de Maiz Y Trigo, Mexico
CIP:	International Potato Center, Lima, Peru
CIPC:	Chloroisoprophyl-N-phenylcarbamate
cM:	Centimorgan
CMV:	Cucumber mosaic virus
Ca MV:	Cauliflower mosaic virus
CO:	Crossover

COS:	Conserved orthologue set (i.e., conserved regions of functional genes)
cp:	Chloroplast
CP:	Coat protein
CPMR:	Coat-protein-mediated resistance
cpDNA:	Chloroplast DNA
CPRI:	Central Potato Research Institute (Shimla, HP, India)
cpSSR:	Chloroplast single sequence repeat
CRN:	Columbia root-knot nematode
CRS:	Corky ringspot disease
CV. (or cv.):	Cultivar
2,4-D:	2, 4-dichlorophenoxyacetic acid
DD:	Degree days
DEFRA:	Department of Environment, Food and Rural Affairs
DET:	Double exchange tetrad
DFID:	Department of International Development
DNA:	Deoxyribonucleic acid
DR:	Double reduction
DTS:	Distribution of tuber size
EAPR:	European Association for Potato Research
EB:	Early blight
EBN:	Endosperm balance number
ELISA:	Enzyme-linked immunosorbent-assay
EPG:	Electrical penetration graph
EPPO:	European and Mediterranean Plant Protection Organization
ER:	Extreme resistance
ERIC:	Enterobacterial repetitive intergenic consensus sequence
ESTs:	Expressed sequence tags
FAMEs:	Fatty acid methyl esters
FAO:	Food and Agriculture Organization
FAP:	Fatty acid profiles
FCM:	Flow Cytometry
FDR:	First division restitution
FISH:	Fluorescence *in situ* hybridization
GA:	Gibberellic acid
GCA:	General combining ability
gDNA:	Genomic DNA
GFG:	Gene for gene resistance
GISH:	Genomic insitu hybridization
GM:	Genetically modified
GPT:	Glucose phosphate translocator
GS:	Genetic similarity

ha:	Hectare
HR:	Hypersensitive response
IAA:	Indole acetic acid
ICTVdB:	International Committee on Taxonomy of Viruses Database
IFAS:	Indirect immunofluorescent assay/Immunofluorescence antibody staining
IHAR:	Institut Hodowli i Aklimatyzacji Roslin
IHN:	Internal heat necrosis
IITA:	International Institute for Tropical Agriculture
INCAGRO:	Innovacion y Competitividad para el Agro-Peruano
INCRISAT:	International Crop Research Institute for the Semi-arid Tropics
INRA:	Institut Nationale des Research Agronomiques
IPC:	Isopropyl-N-phenylcarbamate
ISSR:	Intersimple sequence repeat
ITS:	Intergenic transcribed spacer
JRN:	Javanese root-knot nematode
Kin:	Kinetin
LAR:	Local acquired resistance
LB:	Late blight
LI:	Lesion index
LRR:	Class/motif of a plant resistance gene (Leucine rich repeats)
MAPK:	Mitogen activated protein kinase
MAS:	Marker-assisted selection
MT:	Methyltryptophan
MS:	Murashige and Skoog Medium
mtDNA:	Mitochondrial DNA
NAA:	Naphthalene acetic acid
NASBA:	Nucleic acid sequence based amplification
NBS-LRR:	Nucleotide budding site-leucine rich repeat
NCM-ELISA:	Nitrocellulose membrane-ELISA
NCO:	Non crossover
NET:	No exchange tetrad
Non-DR:	Nondouble reduction
NPS:	National Park Service (USA)
NPT II:	Neomycin phosphotransferase II
NRA:	Newly reclaimed areas
NRC:	National Research Council (USA)
NRN:	Northern root-knot nematode
PAL:	Phenylalanine ammonia lyase
PARC:	Pakistan Agricultural Research Council

PCN: Potato cyst nematode
PCR: Polymerase chain reaction
PEBV: Pea early browing virus
PEG: Polyethylene glycol
PEP: Phosphoenyl pyruvate
PGA: Phosphoglyceric acid
PGIP: Polygalacturonase-inhibiting proteins
PGM: Phosphoglucomutase
PGRFA: Plant Genetic Resources for Food and Agriculture (FAO)
PL: Pectate Lyase
PLRV: Potato leafroll virus
PNW: Pacific North West of USA
PPG: Price per grade
PPO: Polyphenol oxidase
PRN: Peanut root-knot nematode
PRC: Potato Research Center (New Brunswick, Canada)
PRSV: Pepper ringspot virus
PS: Price seasonality
PTGS: Post-transcriptional gene silencing
PTM: Potato tuber moth
PVA: Potato virus A
PVM: Potato virus M
PVS: Potato virus S
PVV: Potato virus V
PVX: Potato virus X
PVY: Potato virus Y
QRTs: Quantitative resistance traits
QTA: Quantitative trait allele
QTL: Quantitative trait loci
RAPD: Randomly amplified polymorphic DNA
rDNA: Ribosomal DNA
recA PCR-RFLP: Restriction analysis of amplified *recA* gene fragment
rep-PCR: Repetitive element sequence PCR
rt-PCR: Reverse transcriptase PCR
RELP: Restriction fragment length polymorphism
REP: Repetitive extragenic palindromic sequence
RGL: Resistance gene like
RH: Relative humidity
RKN: Root-knot nematode
RNA: Ribonucleic acid
RT-PCR: Reverse transcriptase-polymerase chain reaction
SAI: Surface area infected
SAR: Systemic acquired resistance

SCA:	Specific combining ability
SCAR:	Sequence characterized amplified region
SCRI:	Scottish Crop Research Institute
SDR:	Second division restitution
SEERAD:	Scottish Executive Environment and Rural Affairs Department
SET:	Single exchange tetrad
SG:	Specific gravity
SH:	Schenk and Hildebrandt medium
SGT:	Solanidine glucosyltransferase
SI:	Scab index/Self-incompatible
SNPs:	Single nucleotide polymorphisms
SPS:	Sucrose phosphate synthase
SRN:	Southern root-knot nematode
SSR:	Single sequence repeat
ST:	Seedling tuber
STEM:	Symbiosis of Technology Environment and Management
STS:	Silver thiosulfate
SuSy:	Sucrose synthase
t:	Ton
TaqMan PCR:	fluorogenic PCR, real-time PCR
T-DNA:	Ti plasmid DNA segment
TDZ:	Thidiazuron
TEV	Tobacco etch polyvirus
TMV:	Tomato mosaic virus
TP:	Transplants/TPS transplants
TPNI:	Tachyplesin I protein
TPS:	True potato seed
TRN:	Thames' root-knot nematode
TRV:	Tobacco rattle virus
TZC:	Tetrazolium chloride
UDP:	Uridine diphosphate
UDPase:	Uridine diphosphatase
UGPase:	UDP-Glucose pyrophosphorylase
UHD:	Ultrahigh density
USDA:	United States Department of Agriculture
UTP:	α-D-glucose phosphate uridyl transferase
VIR:	Vavilov Research Institute (St. Petersburg, Russia)
WIEWS (FAO):	World Information and Early Warning System on Plant Genetic Resources of FAO
WRKY:	Consensus sequence involved in elicitor induction of pathogenesis-related genes

Contents