

Genome Mapping and Molecular Breeding in Plants
Volume 6

Series Editor: Chittaranjan Kole

Volumes of the Series

Genome Mapping and Molecular Breeding in Plants

Volume 1
Cereals and Millets

Volume 2
Oilseeds

Volume 3
Pulses, Sugar and Tuber Crops

Volume 4
Fruits and Nuts

Volume 5
Vegetables

Volume 6
Technical Crops

Volume 7
Forest Trees

Chittaranjan Kole (Ed.)

Technical Crops

With 35 Illustrations, 2 in Color

 Springer

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Preface to the Series

Genome science has emerged unequivocally as the leading discipline of this new millennium. Progress in molecular biology during the last century has provided critical inputs for building a solid foundation for this discipline. However, it has gained fast momentum particularly in the last two decades with the advent of genetic linkage mapping with RFLP markers in humans in 1980. Since then it has been flourishing at a stupendous pace with the development of newly emerging tools and techniques. All these events are due to the concerted global efforts directed at the delineation of genomes and their improvement.

Genetic linkage maps based on molecular markers are now available for almost all plants of significant academic and economic interest, and the list of plants is growing regularly. A large number of economic genes have been mapped, tagged, cloned, sequenced, or characterized for expression and are being used for genetic tailoring of plants through molecular breeding. An array of markers in the arsenal from RFLP to SNP; tools such as BAC, YAC, ESTs, and microarrays; local physical maps of target genomic regions; and the employment of bioinformatics contributing to all the “-omics” disciplines are making the journey more and more enriching. Most naturally, the plants we commonly grow on our farms, forests, orchards, plantations, and labs have attracted emphatic attention, and deservedly so. The two-way shuttling from phenotype to genotype (or gene) and genotype (gene) to phenotype has made the canvas much vaster. One could have easily compiled the vital information on genome mapping in economic plants within some 50 pages in the 1980s or within 500 pages in the 1990s. In the middle of the first decade of this century, even 5,000 pages would not suffice! Clearly genome mapping is no longer a mere “promising” branch of the life science; it has emerged as a full-fledged subject in its own right with promising branches of its own. Sequencing of the *Arabidopsis* genome was complete in 2000. The early 21st century witnessed the complete genome sequence of rice. Many more plant genomes are waiting in the wings of the national and international genome initiatives on individual plants or families.

The huge volume of information generated on genome analysis and improvement is dispersed mainly throughout the pages of periodicals in the form of review papers or scientific articles. There is a need for a ready reference for students and scientists alike that could provide more than just a glimpse of the present status of genome analysis and its use for genetic improvement. I personally felt the gap sorely when I failed to suggest any reference works to students and colleagues interested in the subject. This is the primary reason I conceived of a series on genome mapping and molecular breeding in plants.

There is not a single organism on earth that has no economic worth or concern for humanity. Information on genomes of lower organisms is abundant and highly useful from academic and applied points of view. Information on higher animals including humans is vast and useful. However, we first thought to concentrate only on the plants relevant to our daily lives, the agronomic, horticultural and technical crops, and forest trees, in the present series. We will come up soon with commentaries on food and fiber animals, wildlife and companion animals, laboratory animals, fishes and aquatic animals, beneficial and harmful insects,

plant- and animal-associated microbes, and primates including humans in our next “genome series” dedicated to animals and microbes. In this series, 82 chapters devoted to plants or their groups have been included. We tried to include most of the plants in which significant progress has been made. We have also included preliminary works on some so-called minor and orphan crops in this series. We would be happy to include reviews on more such crops that deserve immediate national and international attention and support. The extent of coverage in terms of the number of pages, however, has nothing to do with the relative importance of a plant or plant group. Nor does the sequence of the chapters have any correlation to the importance of the plants discussed in the volumes. A simple rule of convenience has been followed.

I feel myself fortunate to have received highly positive responses from nearly 300 scientists of some 30-plus countries who contributed the chapters for this series. Scientists actively involved in analyzing and improving particular genomes contributed each and every chapter. I thank them all profoundly. I made a conscientious effort to assemble the best possible team of authors for certain chapters devoted to the important plants. In general, the lead authors of most chapters organized their teams. I extend my gratitude to them all.

The number of plants of economic relevance is enormous. They are classified from various angles. I have presented them using the most conventional approach. The volumes thus include cereals and millets (Volume I), oilseeds (Volume II), pulse, sugar and tuber crops (Volume III), fruits and nuts (Volume IV), vegetables (Volume V), technical crops including fiber and forage crops, ornamentals, plantation crops, and medicinal and aromatic plants (Volume VI), and forest trees (Volume VII).

A significant amount of information might be duplicated across the closely related species or genera, particularly where results of comparative mapping have been discussed. However, some readers would have liked to have had a chapter on a particular plant or plant group complete in itself. I ask all the readers to bear with me for such redundancy.

Obviously the contents and coverage of different chapters will vary depending on the effort expended and progress achieved. Some plants have received more attention for advanced works. We have included only introductory reviews on fundamental aspects on them since reviews in these areas are available elsewhere. On other plants, including the “orphan” crop plants, a substantial amount of information has been included on the basic aspects. This approach will be reflected in the illustrations as well.

It is mainly my research students and professional colleagues who sparked my interest in conceptualizing and pursuing this series. If this series serves its purpose, then the major credit goes to them. I would never have ventured to take up this huge task of editing without their constant support. Working and interacting with many people, particularly at the Laboratory of Molecular Biology and Biotechnology of the Orissa University of Agriculture and Technology, Bhubaneswar, India as its founder principal investigator; the Indo-Russian Center for Biotechnology, Allahabad, India as its first project coordinator; the then-USSR Academy of Sciences in Moscow; the University of Wisconsin at Madison; and The Pennsylvania State University, among institutions, and at EMBO, EUCARPIA, and Plant and Animal Genome meetings among the scientific gatherings have also inspired me and instilled confidence in my ability to accomplish this job.

I feel very fortunate for the inspiration and encouragement I have received from many dignified scientists from around the world, particularly Prof. Arthur

Kornberg, Prof. Franklin W. Stahl, Dr. Norman E. Borlaug, Dr. David V. Goeddel, Prof. Phillip A. Sharp, Prof. Gunter Blobel, and Prof. Lee Hartwell, who kindly opined on the utility of the series for students, academicians, and industry scientists of this and later generations. I express my deep regards and gratitude to them all for providing inspiration and extending generous comments.

I have been especially blessed by God with an affectionate student community and very cordial research students throughout my teaching career. I am thankful to all of them for their regards and feelings for me. I am grateful to all my teachers and colleagues for the blessings, assistance, and affection they showered on me throughout my career at various levels and places. I am equally indebted to the few critics who helped me to become professionally sounder and morally stronger.

My wife Phullara and our two children Sourav and Devleena have been of great help to me, as always, while I was engaged in editing this series. Phullara has taken pains (“pleasure” she would say) all along to assume most of my domestic responsibilities and to allow me to devote maximum possible time to my professional activities, including editing this series. Sourav and Devleena have always shown maturity and patience in allowing me to remain glued to my PC or “printed papers” (“P3” as they would say). For this series, they assisted me with Internet searches, maintenance of all hard and soft copies, and various timely inputs.

Some figures included by the authors in their chapters were published elsewhere previously. The authors have obtained permission from the concerned publishers or authors to use them again for their chapters and expressed due acknowledgement. However, as an editor I record my acknowledgements to all such publishers and authors for their generosity and good will.

I look forward to your valuable criticisms and feedback for further improvement of the series.

Publishing a book series like this requires diligence, patience, and understanding on the part of the publisher, and I am grateful to the people at Springer for having all these qualities in abundance and for their dedication to seeing this series through to completion. Their professionalism and attention to detail throughout the entire process of bringing this series to the reader made them a genuine pleasure to work with. Any enjoyment the reader may derive from this books is due in no small measure to their efforts.

Pennsylvania,
10 January 2006

Chittaranjan Kole

Preface to the Volume

I believe I owe an explanation to the readers regarding the subtitle of this volume of *Technical Crops* and its contents. There are some crop groups which include a few crop plants, but each of them has immense agricultural importance. These groups comprise fiber crops, forage crops, ornamentals, narcotic crops, plantation crops, and medicinal and aromatic plants. We have included nine chapters on these crop groups devoted to cotton, forage crops, ornamentals, oil palm, coffee, tea, cocoa, rubber, and medicinal and aromatic plants in this volume.

Cotton is the most important fiber crop and progress made on this crop is quite appreciable and up to expectation. The future NSF (USA) Cotton Genome Project will surely facilitate further progress. However, other fiber crops grown in developing countries also require attention and financial support. Jute is an important fiber crop; however, almost no work has been done on this crop on genome mapping and molecular breeding. Sunhemp and sisal are still in the list of “beggar crops.” Flax is another fiber crop that could have been included in this volume; however, considering its primary importance as a source of vegetable oil, we placed it in Vol. 2 dedicated to oilseeds. On the basis of the same logic, we have included cotton in this volume, not in Vol. 2, albeit with full appreciation of its importance as one of the leading oil-yielding crops.

Plantations of oil palm, coffee, tea, cocoa, and rubber provide raw materials for a large number of small-scale industries and provide livelihood for innumerable households in developing countries in Asia and Africa. Currently, improvement of some of these crops, particularly oil palm, coffee, and cocoa, is receiving appreciable international support. We believe all these crops deserve more generous support at national and international levels. We could present comprehensive reviews on traditional genetic and breeding efforts along with preliminary works done on molecular areas in these crops in this volume. We are thankful to all the authors of the chapters on these crops. We omitted, however, the work done on tobacco, an important narcotic crop and wish to include it in future editions.

The three groups on forage crops, ornamentals, and medicinal and aromatic plants include a large number of plants in each of them. Only a few plants in these groups have attracted attention for molecular work. The authors of the chapters on these crop groups have also discussed this. We hope each of these groups will require independent volumes in the near future to present commentary on genome mapping and molecular breeding efforts in their member crop plants. I should mention here that we had a chapter on *Capsicums* in Vol. 5 of the series dedicated to vegetables. A section on them has again been included in the chapter “Medicinal and Aromatic Plants” in this volume. I believe readers will find these two reviews to be completely different in approach and content.

Many crop plants in this volume are being confronted with competition from “synthetic products.” However, growing consciousness for the healthy and ecofriendly attributes of natural plant products is going to reverse the trend of consumer preference. The time has come to realize the threats posed by synthetic products and to welcome again organic and herbal commodities and embrace natural style living, and to live in and with nature.

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Abbreviations

AFIS	Advanced fiber information system
AFLP	Amplified fragment length polymorphism
ASGR	Apospory-specific genomic region
AVROS	Algemene Verneiging Rubber Planters Oostkust, Sumatra
BAC	Bacterial artificial chromosome
BAP	Benzylaminopurine
BC	Backcross
BLAST	Basic Local Alignment Search Tool
BPM	Balai Penelitian Medan
BPRO	Breeding populations of restricted origin
CAP	Coordinated Agricultural Project
CAPS	Cleaved amplified polymorphism sequence
cDNA	Complementary DNA
CIM	Composite interval mapping
CIMAP	Central Institute of Medicinal and Aromatic Plants (Lucknow, India)
CIRAD	Centre de Coopération Internationale en Recherché Agronomique pour le Développement
CLCuV	<i>Cotton leaf curl virus</i>
cM	centimorgan
CMS	Cytoplasmic male sterility
cpDNA	Chloroplast DNA
CSSV	<i>Cocoa swollen shoot virus</i>
CYP80B1	P450 hydroxylase
2,4-D	2,4-Dichlorophenoxyacetic acid
DAF	DNA amplification fingerprinting
DH	Doubled haploid
EST	Expressed sequence tag
F and Fx	Clones from the collections and recombinations of Ford Company in Brazil
FG	Fall growth
FI	Freezing injury
FIS	Family and individual selection
GAM	Generation-wise assortative mating
GA ₃	Gibberellic acid
GCA	General combining ability
GG	Gough Gardens
GISH	Genomic in situ hybridization
Gl	Glenshiel
GLS	Gray leaf spot
GT	Gondang Tapen
HVI	High-volume instrument
IAC	Instituto Agronomico de Campinas, São Paulo, Brazil
IAN	Instituto Agronomico do Norte
IBA	Indolebutyric acid
IPP	Isopentenyl pyrophosphate

IRAP	Interretrotransposon amplified polymorphism
IRCA	Institut de Recherches sur le Caoutchouc en Afrique
IRD	Institute of Research for sustainable Development (Paris, France)
IRRDB	International Rubber Research and Development Board
ISSR	Intersimple sequence repeat
ITS	Internal transcribed spacer
kb	kilobase
LD	Linkage disequilibrium
LOD	Logarithm of odds
LR	Likelihood ratio
LSCT	Large-scale clone trial
LTR-RTN	Long-terminal-repeat retrotransposon
MAB	Marker-assisted breeding
MAS	Marker-assisted selection
Mb	Million bases
Mbp	Million base pairs
MPM	Maximum parsimony method
MPOB	Malaysian Palm Oil Board
mtDNA	Mitochondrial DNA
NAA	Naphthaleneacetic acid
NDF	Neutral detergent fiber
NIBGE	National Institute for Biotechnology & Genetic Engineering
NJM	Neighbor-joining method
NMT	<i>N</i> -Methyltransferase
PAUP	Phylogenetic Analysis Using Parsimony
PB	Prang Besar Rubber Estate
PBIG	Prang Besar Isolated Gardens
PCA	Principal component analysis
PCR	Polymerase chain reaction
PHB	Polyhydroxybutyrate
Pil	Pilmoor Proefstation, Indonesia
PK	Protein kinase
PR	Proefstation, Indonesia
QTL	Quantitative trait locus
RAPD	Randomly amplified polymorphic DNA
rDNA	Ribosomal DNA
REF	Rubber elongation factor
REMAP	Retrotransposon microsatellite amplified polymorphism
<i>Rf</i>	Fertility restoration
RFLP	Restriction fragment length polymorphism
RGA	Resistance gene analog
RHM	Radiation hybrid mapping
RIL	Recombinant inbred line
RRIC	Rubber Research Institute of Ceylon
RRII	Rubber Research Institute of India
RRIM	Rubber Research Institute of Malaysia
RRIT	Rubber Research Institute of Thailand
RRIV	Rubber Research Institute of Vietnam
rRNA	Ribosomal RNA
RRS	Reciprocal recurrent selection
SALB	South American leaf blight

SCA	Specific combining ability
SCAR	Sequence-characterized amplified region
SCATC	South China Academy of Tropical Crops
SDRF	Single-dose restriction fragment
SET	Seedling evaluation trial
SNP	Single nucleotide polymorphism
SRF	Seedling root florescence
SRPP	Small rubber particle protein
SSCT	Small-scale clonal trial
SSR	Simple sequence repeat
STMS	Sequence-tagged microsatellite site
STS	Sequence-tagged site
TIA	Terpenoid indole alkaloid
TILLING	Targeted induced local lesions in genomes
Tjir	Tjirandji, Indonesia
UPGMA	Unweighted pair group method with arithmetic mean
WI	Winter injury
WSC	Water-soluble carbohydrate content
WWRH	Radiation hybrid wide-cross whole genome