Genome Mapping and Molecular Breeding in Plants
**Volume 3**

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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.)

# Pulses, Sugar and Tuber Crops

With 45 Illustrations, 8 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 genotypte (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, Chittaranjan Kole
10 January 2006

# Preface to the Volume

The number of "groups" of economic plant species is too many! This caused a serious problem in terms of allocating them under the seven planned volumes of the series with consideration of uniformity of size and inclusion of all relevant groups. Certain groups, for example cereals and millets, oilseeds, fruits, vegetables, and forest trees, have enough economic species those attracted the attention of molecular biologists and biotechnologists. In comparison, the number of pulse crops is too few to deserve an entire volume to itself. We had to accommodate pulse crops, sugar crops, and tuber crops together in volume 3 to maintain a more or less uniform coverage across all volumes. Except for the common bean, pea, and cowpea, most pulse crops are grown mainly in developing countries and have attracted relatively little attention of scientists from developed countries. These include the "orphan crops" such as chickpea, pigeonpea, mungbean, lentil, *Lathyrus*, etc. Thanks to certain labs in the USA and Australia, appreciable work has been done on these crops. There are still some more neglected pulse crops, we could easily ascribe the term "beggar crops" to them, such as urdbean, rice bean, adzuki bean, etc. in which almost no molecular work has been done. We must wait for future editions for their inclusion in this series. However, we have included two not-so-well-known pulse crops, quinoa and bambara groundnut, on which considerable work has been done. This volume can boast of introducing these two crops with comprehensive reviews for the first time.

Pulse crops will play a crucial role in global agriculture in the near future. Their shorter duration, docility for adaptation to several cropping schemes, tolerance to abiotic stresses particularly drought, and the preference by people in developing countries for vegetable protein to animal sources will definitely make an impact sooner rather than later. The research on these crops will fill an entire volume in a year or two!

Sugarcane has been included in this volume as well. This cash crop has generated much interest, particularly for its genomic proximity to other members of the "grass family" that comprises extensively studied crop plants like rice and maize. Sugar beet could be included here as well, but we will deal with it under beets in volume 5, which is dedicated to "vegetables".

The tuber crops included in this volume are potato, sweetpotato, cassava, and yam. Granted, potato could have been included under vegetables in volume 5, but that would have forced us to consider another "subvolume" for vegetable crops!

The contents of the chapters in this volume may appear somewhat contrasting. Crops like common bean, pea, cowpea, potato, and sugarcane contain elaborate deliberations on molecular aspects. For others, fundamental information besides preliminary molecular efforts are also discussed in depth. I hope the reader will appreciate the relative importance attached to the formulation of the contents.

In the last few years, my own research interests and research projects of my students and staff in India have mostly related to pulse crops. This gave me access to the literature accumulated on the pulse crops. For sugarcane and the tuber crops included in this volume, I had to be a student again before being an editor. The first two volumes of this series have been well received by readers. We hope this volume will also earn their appreciation.

If this volume finds favor with readers, credit must go to the authors and the publisher. The mistakes are mine alone, and I will rectify them upon the readers' welcome suggestions for improvement.

Pennsylvania, 3 March 2006 Chittaranjan Kole

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# Abbreviations

| | |
|---|---|
| ABA | Abscisic Acid |
| ABR | Ascochyta Blight Resistance |
| AFLP | Amplified Fragment Length Polymorphism |
| ANOVA | Analysis Of Variance |
| AP-PCR | Arbitrarily Primed PCR |
| APR | Adult Plant Resistance |
| ARS | Agriculture Research Service |
| ASAP | Allele Specific Associated Primer |
| AUDPC | Area Under the Disease Progress Curve |
| AYT | Advanced Yield Trial |
| BAC | Bacterial Artificial Chromosome |
| BAMFOOD | Increasing the productivity of Bambara Groundnut (*Vigna subterranea* L. Verdc) for sustainable food production in Semi-Arid Africa |
| BC | Backcross |
| BCMNV | Bean Common Mosaic Necrosis Virus |
| BCMV | Bean Common Mosaic Virus |
| BCTV | Beet Curly Top Virus |
| BGMV | Bean Golden Mosaic Virus |
| BGYMV | Bean Golden Yellow Mosaic Virus |
| BICMV | Blackeye Cowpea Mosaic Virus |
| BLRV | Bean Leaf Roll Virus |
| *Bru*1 | Brassinosteroid-regulated protein |
| BSA | Bulked Segregant Analysis |
| C | Haploid Genome Content |
| CAPS | Cleaved Amplified Polymorphic Sequences |
| CC-NBS-LRR | Coiled-Coiled domain-containing NBS-LRR protein |
| cDNA | Complementary DNA |
| CIAT | Centro Internacional de Agricultura Tropical (Cali, Colombia) |
| CID | Carbon Isotope Discrimination |
| CIM | Composite Interval Mapping |
| cM | centi-Morgan |
| CMD | Cassava Mosaic Disease |
| CMS | Cytoplasmic Male Sterility |
| CPB | Colorado Potato Beetle |
| cpDNA | Chloroplast DNA |
| CRSD | Cowpea Collaborative Research Support Program |
| cSNP | SNP in coding region |
| CTCRI | Central Tuber Crops Research Institute (Trivandrum, India) |
| DAF | DNA Amplification Fingerprinting |
| DH | Doubled Haploid |
| DNA | Deoxyribonucleic Acid |
| DNC | Dry Matter Content |
| DR | Defense-Related |
| DS | Drought-Stressed |
| EBN | Endosperm Balance Number |

| | |
|---|---|
| EM | Expectation Maximization (algorithm) |
| EMBRAPA | Empresa Brasileira de Pesquisa Agropecuária (Goiana, Brazil) |
| EST | Expressed Sequence Tag |
| EU | European Union |
| FAO | Food and Agricultural Organization |
| FGS | Fast-Growing Salmon |
| FISH | Fluorescence In Situ Hybridization |
| Foc | Fusarium Wilt Resistance |
| GAT | Zentralinstitut für Genetik und Kulturpflanzenforschung (Gatersleben, Germany) |
| gDNA | Genomic DNA |
| GISH | Genomic In Situ hybridisation |
| GM | Genetically Modified |
| GMO | Genetically Modified Organism |
| GMS | Genetic Male Sterility |
| GP | Gene Pool |
| GP1 | Primary Gene Pool |
| GP1A | Primary Gene Pool – Domesticated |
| GP2 | Secondary Gene Pool |
| GP3 | Tertiary Gene Pool |
| GPIB | Primary Gene Pool – Wild |
| GRIN | Germplasm Resources Information Network |
| GSIRI | Guangzhou Sugarcane Industry Research Institute (China) |
| Hs | Average Hardy-Weinberg expected heterozygosity per subpopulation |
| Ht | Hardy-Weinberg heterozygosity of the total population |
| ICARDA | International Center for Agriculture Research in the Dryland Areas (Aleppo, Syria) |
| ICRISAT | International Center of Research For Semi-Arid Tropics (Hyderabad, India) |
| IDS | Initial Disease Score |
| IITA | International Institute of Tropical Agriculture (Ibadan, Nigeria) |
| ILDIS | International Legume Database & Information Service |
| IM | Interval Mapping |
| indel | insertion/deletion |
| IPGRI | The International Plant Genetic Resources Institute (Harare, Zimbabwe) |
| ISSR | Inter Simple Sequence Repeat |
| ITS | Internal Transcribed Spacer |
| JIC | John Innes Center |
| LD | Linkage Disequilibrium |
| LG | Linkage Group |
| LOD | Logarithm Of Odds |
| LRR | Leucine Rich Repeat |
| LRS | Likelihood Ratio Statistic |
| LTR | Long Terminal Repeat |
| MAS | Marker-Assisted Selection |
| MDSS | Mean Disease Severity Scores |
| MIM | Multiple Interval Mapping |
| mRNA | Messenger Ribonucleic Acid |
| mtDNA | Mitochondrial DNA |

| | |
|---|---|
| MtGI | *Medicago truncatula* Gene Index |
| MYMV | Mungbean Yellow Mosaic Virus |
| NARS | National Agricultural Research System |
| NBPGR | National Bureau of Plant Genetic Resources (New Delhi, India) |
| NBS | Nucleotide Binding Site |
| NIL | Near Isogenic Lines |
| NOR | Nucleolar Organizer Region |
| NPGS | National Plant Germplasm System |
| NRCRI | National Root Crop Research Institute (Umuahia, Nigeria) |
| NS | Non-Stressed |
| ODAP | $\beta$-N-Oxalyl-L-$\alpha$,$\beta$-DiaminoPropanoic acid |
| ORSTOM | Institut Français de la Recherché Scientifique pour le Développement en Coopération (now IRD; Montpellier, France) |
| PCN | Potato Cyst Nematode |
| PCR | Polymerase Chain Reaction |
| PEMV | Pea Enation Mosaic Virus |
| PI | Plant Introduction |
| PIs | Proteinaceous Inhibitors |
| PPB | Participatory Plant Breeding |
| PPD | Post harvest Physiological Deterioration |
| PPO | PolyPhenol Oxidase |
| PRINS | Primed In Situ (DNA Labeling) |
| PSbMV | Pea Seed-borne Mosaic Virus |
| PVX | Potato Virus X |
| PYT | Preliminary Yield Trial |
| QTA | Quantitative Trait Allele |
| QTL | Quantitative Trait Loci |
| RAF | Randomly Amplified Fragment |
| RAPD | Random Amplified Polymorphic DNA |
| rDNA | Ribosomal DNA |
| RFLP | Restriction Fragment Length Polymorphism |
| RGA | Resistant Gene Analog |
| RI | Recombinant Inbred |
| RIL | Recombinant Inbred Line |
| RSD | Ratoon Stunting Disease |
| SAM | Shoot Apical Meristem |
| SAT | Semi Arid Tropics |
| SCAR | Sequence Characterized Amplified Region |
| SDM | Single Dose Marker |
| SG | Striga Race |
| SGG | Slow-Growing Gray |
| SI | Self Incompatibility |
| SLA | Specific Leaf Area |
| SNP | Single Nucleotide Polymorphism |
| SPLAT | Specific Polymorphic Locus Amplification Test |
| SR | Specific Resistance |
| SSD | Single Seed Descent |
| SSLP | Simple Sequence Length Polymorphism |
| SSR | Simple Sequence Repeat |
| STMS | Sequence Tagged Microsatellite Site |
| STS | Sequence Tagged Sites |

| | |
|---|---|
| SUCEST | Sugarcane EST project |
| TCA | TriCarboxylic Acid |
| TIGR | The Institute for Genomic Research |
| TIR | Toll and Interleukin Receptor |
| UHD | Ultra-High Density |
| USAID | United States Agency of International Development |
| USDA | United States Department of Agriculture |
| UYT | Uniform Yield Trial |
| VIGS | Virus Induced Gene Silencing |
| WASDU | West African Seed Development Union |
| WHO | World Health Organization |
| WUE | Water Use Efficiency |
| YAD | Yam Anthracnose Disease |
| YMV | *Yam Mosaic Virus* |