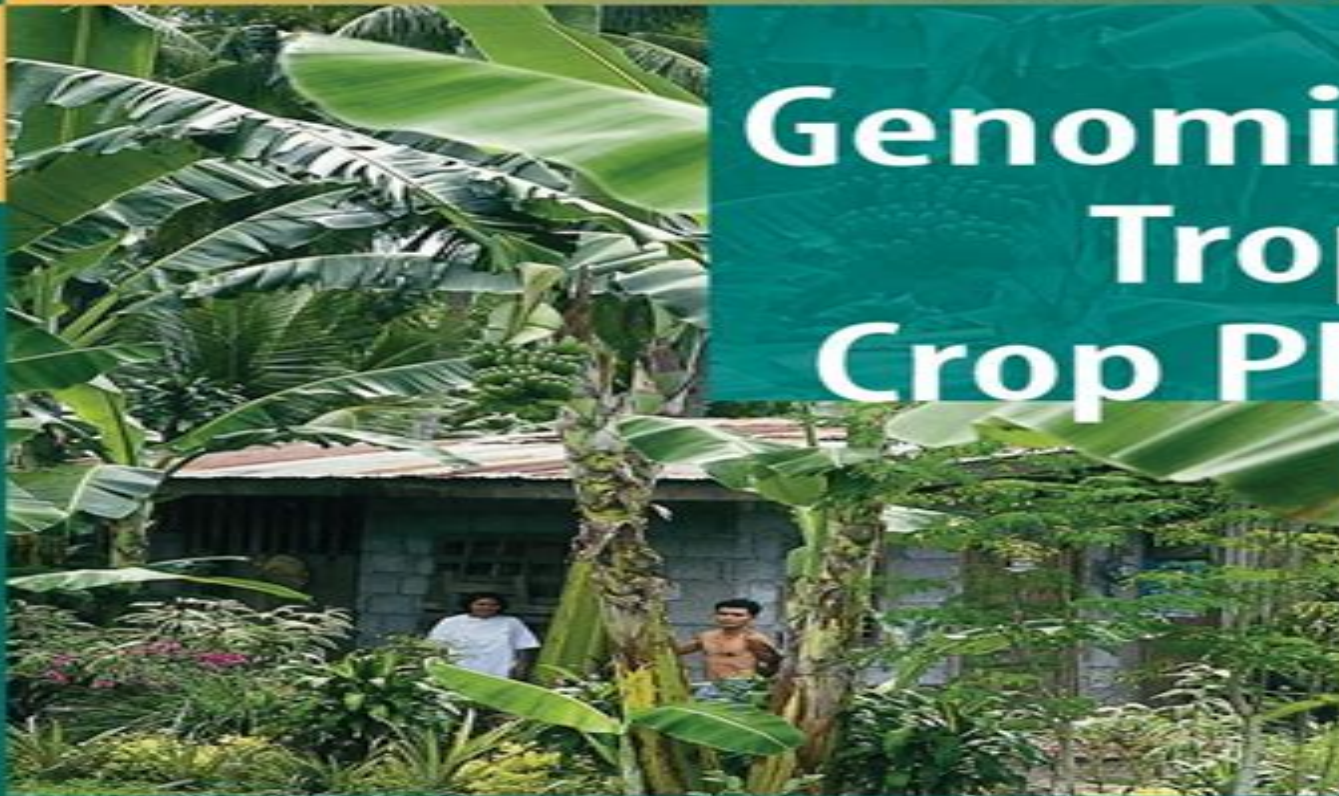


Paul H. Moore  
Ray Ming  
*Editors*

*Plant Genetics / Genomics*      *Volume 1*

# Genomics of Tropical Crop Plants



 Springer

# Genomics Of Tropical Crop Plants Plant Genetics And Genomics Crops And Models

**Andrew H. Paterson**



## **Genomics Of Tropical Crop Plants Plant Genetics And Genomics Crops And Models:**

**Genomics of Tropical Crop Plants** Paul H. Moore, Ray Ming, 2008-01-03 For a long time there has been a critical need for a book to assess the genomics of tropical plant species At last here it is This brilliant book covers recent progress on genome research in tropical crop plants including the development of molecular markers and many more subjects The first section provides information on crops relevant to tropical agriculture The book then moves on to lay out summaries of genomic research for the most important tropical crop plant species *Genetics and Genomics of Pineapple* Ray Ming, 2018-11-27 This book is the first comprehensive volume on the genetics and genomics of pineapple and provides an overview of the current state of pineapple research Pineapple *Ananas comosus* L Merr is the second most important tropical fruit after banana in term of international trade Its features are advantageous for genomic research it has a small genome of 527 Mb which is diploid and vegetatively propagated it is monocot closely related to the grass family that includes major cereal crops wheat rice corn sorghum and millet and it serves as an out group for genetic and genomic research in grasses In addition to exploring the evolution and improvement of pineapple this work examines the pineapple genome with respect to genome structure and organization comparative analyses with other angiosperm genomes transcription factors disease resistance and circadian clock regulation of CAM related genes With chapters covering botanical genetic genomic and applied aspects of pineapple this text also encourages the application of genomic technologies and suggests future prospects

*Genetics and Genomics of Polyploid Plants* Jun Yang, Zhangying Wang, Yiwei Jiang, Shuizhang Fei, 2019-10-15 *Papaya* Parmeshwar Lal Saran, Ishwar Singh Solanki, Ravish Choudhary, 2016-01-05 With coverage that ranges from basic information to advanced research *Papaya Biology Cultivation Production and Uses* pulls together the vast literature scattered over various sources into one practical resource The book provides a solid review of papaya biology production and uses supported by color photographs and illustrations It covers p **Plant Tissue Culture** Zahid Hameed Siddiqui, Khalid Rehman Hakeem, 2025-09-23 Plants are sessile and constantly exposed to changing environmental conditions Seasonal cues govern plant growth development and reproduction In this era of climate change the environment is unstable and takes a toll on the productivity of plants This new book explores this unique area of plant tissue culture in relation to climate change showing how tissue culture techniques can be utilized to create tolerance to disease and stress increase growth and raise yield in plants This book discusses the use of plant tissue culture for producing superior material for planting and creating new elite varieties of different kinds of crops in response to changing climatic conditions It draws attention to the issues and dangers posed by climate change for plants and offers guidance for sustainable development utilizing tissue culture technology In addition it focuses on some fundamental ideas of plant tissue culture presents studies that address climate change and offers sustainable development alternatives The book looks at important topics such as the benefits of synthetic seed technology the impact of phytohormones and growth regulators on plant tissue culture the impact of supplementing

culture medium with organic substances various plant tissue culture techniques and more This book will prove beneficial for plant biotechnologists environmentalists ecologists and scientists in enhancing their understanding of the complexities of climate change under in vitro conditions Genetics, Genomics, and Breeding of Bananas Michael Pillay, George Ude, Chittaranjan Kole, 2012-03-07 Musa is one of three genera in the family of Musaceae Over 50 species of Musa exist including bananas and plantains This book assembles the latest information on the genomic research of this genus A group of leading experts in Musa genetics genomics and breeding provide basic as well as advanced information for those interested in learning more about the banana genome The accessible style is easily understood by students and researchers making the book an ideal springboard for those looking to do expanded research into this crop **Plant Genetics and Genomics**, 2008

**Genetics and Genomics of Cotton** Andrew H. Paterson, 2009-03-11 A few members of the Gossypium cotton genus are cultivated for the production of elongated single celled fibers valued worldwide at about 20 billion annually at the farm gate and which sustain one of the world's largest industries textiles with an annual worldwide economic impact of about 500 billion In a number of ways cotton production and the textile industry are closely tied to petrochemical usage At a practical level cotton genomics offers both bio based carbon sequestration alternatives to petrochemical use and improved sustainability of crop production The Gossypium cotton also genus presents novel opportunities to advance our understanding of the natural world and its organic evolution In particular the evolution of cultivated cottons from their wild ancestors has involved a fascinating series of events that offer scientists the opportunity to dissect the evolution of a novel organ the lint fiber and also to unravel the consequences of polyploidy both for the generation of biodiversity and for crop productivity In this book advances of the past decade will be summarized and synthesized to elucidate the current state of knowledge of the structure function and evolution of the Gossypium genome and progress in the application of this knowledge to cotton improvement This book will address five broad topics First as a backdrop for all studies of the genus it is important to understand the naturally occurring diversity in the genus its organization and distribution and its evolutionary history Of special importance is the formation of a single polyploid from two among 8 diploid genome types the radiation of this polyploid and the domestication and improvement of two among 5 extant polyploid species **Quantitative Genetics, Genomics and Plant Breeding, 2nd Edition** Manjit S. Kang, 2020-04-01 This book presents state of the art authoritative chapters on contemporary issues in the broad areas of quantitative genetics genomics and plant breeding Section 1 Chapters 2 to 12 emphasizes the application of genomics and genome and epigenome editing techniques in plant breeding bioinformatics quantitative trait loci mapping and the latest approaches of examining and exploiting genotype environment interactions Section 2 Chapters 13 to 20 represents the intersection of breeding genetics and genomics This section describes the use of cutting edge molecular breeding and quantitative genetics techniques in wheat rice maize root and tuber crops and pearl millet Overall the book focuses on using genomic information to help evaluate traits that can combat biotic

abiotic stresses genome wide association mapping high throughput genotyping phenotyping biofortification use of big data orphan crops and gene editing techniques The examples featured are taken from across crop science research and cover a wide geographical base Principles and Practices of Plant Genomics, Volume 3 Chittaranjan Kole,Albert G. Abbott,2008 The three volumes in this series containing 41 chapters contributed by over one hundred globally reputed scientists provide lucid deliberations on the concepts strategies tools methodologies and achievements of plant genomics presented in a typical class room approach Back cover

**Molecular Genetics, Genomics and Biotechnology of Crop Plants Breeding** Søren K. Rasmussen,2020-05-27 This Special Issue on molecular genetics genomics and biotechnology in crop plant breeding seeks to encourage the use of the tools currently available It features nine research papers that address quality traits grain yield and mutations by exploring cytoplasmic male sterility the delicate control of flowering in rice the removal of anti nutritional factors the use and development of new technologies for non model species marker technology site directed mutagenesis and GMO regulation genomics selection and genome wide association studies how to cope with abiotic stress and an exploration of fruit trees adapted to harsh environments for breeding purposes A further four papers review the genetics of pre harvest spouting readiness for climate smart crop development genomic selection in the breeding of cereal crops and the large numbers of mutants in straw lignin biosynthesis and deposition

**Wild Crop Relatives: Genomic and Breeding Resources** Chittaranjan Kole,2011-02-24 Wild crop relatives are now playing a significant part in the elucidation and improvement of the genomes of their cultivated counterparts This work includes comprehensive examinations of the status origin distribution morphology cytology genetic diversity and available genetic and genomic resources of numerous wild crop relatives as well as of their evolution and phylogenetic relationship Further topics include their role as model plants genetic erosion and conservation efforts and their domestication for the purposes of bioenergy phytomedicines nutraceuticals and phytoremediation Wild Crop Relatives Genomic and Breeding Resources comprises 10 volumes on Cereals Millets and Grasses Oilseeds Legume Crops and Forages Vegetables Temperate Fruits Tropical and Subtropical Fruits Industrial Crops Plantation and Ornamental Crops and Forest Trees It contains 125 chapters written by nearly 400 well known authors from about 40 countries

Principles and Practices of Plant Genomics, Vol. 1 C Kole,A.G. Abbott,2008-01-03 The three volumes in this series containing 41 chapters contributed by over one hundred globally reputed scientists provide lucid deliberations on the concepts strategies tools methodologies and achievements of plant genomics presented in a typical class room approach Back cover

**Genomics of the Saccharinae** Andrew Paterson,2012-09-13 The Saccharinae clade of the Poaceae grass family of flowering plants includes several important crops with a rich history of contributions to humanity and the promise of still greater contributions as a result of some of the highest biomass productivity levels known resilience to drought and other environmental challenges that are likely to increase amenability to production systems that may mitigate or even reverse losses of ecological capital such as topsoil erosion and the recent blossoming of sorghum as a botanical and

genomic model for the clade In Genomics of the Saccharinae advances of the past decade and earlier are summarized and synthesized to elucidate the current state of knowledge of the structure function and evolution of the Sorghum Saccharum and Miscanthus genera and progress in the application of this knowledge to crop improvement As a backdrop it is important to understand the naturally occurring diversity in each genus its organization and distribution and its evolutionary history Genomic tools and methods for Saccharinae biology and improvement have improved dramatically in the past few years a detailed summary of these tools and their applications is a central element of this book Application of genomic tools to priorities in crop improvement including understanding and manipulating plant growth and development composition and defense as well as increasing the quality and productivity of seed grain sugar biomass and other value added products under a range of conditions and inputs are addressed In particular as the first native African crop to emerge as a genomic model sorghum offers an excellent case study of challenges and opportunities in linking new advances in biosciences to solving some of Africa s major agricultural problems Several members of the clade exemplified by Sorghum halepense Johnsongrass offer insights into weediness and invasion biology The first sequence for a member of the clade sorghum as well as progress and challenges toward sequencing of additional members and the new opportunities that this will create are also explored Indeed the very complexities that have hindered study of some clade members also offer intriguing opportunities to gain insight into fundamental questions such as roles of polyploidy in agricultural productivity and post polyploidy evolution

Genetics and Genomics of the Triticeae Catherine Feuillet, Gary J. Muehlbauer, 2009-06-10 Sequencing of the model plant genomes such as those of *A. thaliana* and rice has revolutionized our understanding of plant biology but it has yet to translate into the improvement of major crop species such as maize wheat or barley Moreover the comparative genomic studies in cereals that have been performed in the past decade have revealed the limits of conservation between rice and the other cereal genomes This has necessitated the development of genomic resources and programs for maize sorghum wheat and barley to serve as the foundation for future genome sequencing and the acceleration of genomic based improvement of these critically important crops Cereals constitute over 50% of total crop production worldwide [http www fao org](http://www.fao.org) and cereal seeds are one of the most important renewable resources for food feed and industrial raw materials Crop species of the Triticeae tribe that comprise wheat barley and rye are essential components of human and domestic animal nutrition With 17% of all crop area wheat is the staple food for 40% of the world s population while barley ranks fifth in the world production Their domestication in the Fertile Crescent 10 000 years ago ushered in the beginning of agriculture and signified an important breakthrough in the advancement of civilization Rye is second after wheat among grains most commonly used in the production of bread and is also very important for mixed animal feeds It can be cultivated in poor soils and climates that are generally not suitable for other cereals Extensive genetics and cytogenetics studies performed in the Triticeae species over the last 50 years have led to the characterization of their chromosomal composition and origins and have supported intensive

work to create new genetic resources Cytogenetic studies in wheat have allowed the identification and characterization of the different homoeologous genomes and have demonstrated the utility of studying wheat genome evolution as a model for the analysis of polyploidization a major force in the evolution of the eukaryotic genomes Barley with its diploid genome shows high collinearity with the other Triticeae genomes and therefore serves as a good template for supporting genomic analyses in the wheat and rye genomes The knowledge gained from genetic studies in the Triticeae has also been used to produce Triticale the first human made hybrid crop that results from a cross between wheat and rye and combines the nutrition quality and productivity of wheat with the ruggedness of rye Despite the economic importance of the Triticeae species and the need for accelerated crop improvement based on genomics studies the size 1.7 Gb for the bread wheat genome i.e. 5x the human genome and 40 times the rice genome high repeat content 80% and complexity polyploidy in wheat of their genomes often have been considered too challenging for efficient molecular analysis and genetic improvement in these species Consequently Triticeae genomics has lagged behind the genomic advances of other cereal crops for many years Recently however the situation has changed dramatically and robust genomic programs can be established in the Triticeae as a result of the convergence of several technology developments that have led to new more efficient scientific capabilities and resources such as whole genome and chromosome specific BAC libraries extensive EST collections transformation systems wild germplasm and mutant collections as well as DNA chips Currently the Triticeae genomics toolbox is comprised of 9 publicly available BAC libraries from diploid 5 tetraploid 1 and hexaploid 3 wheat 3 publicly available BAC libraries from barley and one BAC library from rye 3 wheat chromosome specific BAC libraries DNA chips including commercially available first generation chips from AFFYMETRIX containing 55 000 wheat and 22 000 barley genes A large number of wheat and barley genetic maps that are saturated by a significant number of markers The largest plant EST collection with 870 000 wheat ESTs 440 000 barley ESTs and about 10 000 rye ESTs Established protocols for stable transformation by biolistic and agrobacterium as well as a transient expression system using VIGS in wheat and barley and Large collections of well characterized cultivated and wild genetic resources International consortia such as the International Triticeae Mapping Initiative ITMI have advanced synergies in the Triticeae genetics community in the development of additional mapping populations and markers that have led to a dramatic improvement in the resolution of the genetic maps and the amount of molecular markers in the three species resulting in the accelerated utilization of molecular markers in selection programs Together with the development of the genomic resources the isolation of the first genes of agronomic interest by map based cloning has been enabled and has proven the feasibility of forging the link between genotype and phenotype in the Triticeae species Moreover the first analyses of BAC sequences from wheat and barley have allowed preliminary characterizations of their genome organization and composition as well as the first inter and intra specific comparative genomic studies These later have revealed important evolutionary mechanisms e.g. unequal crossing over illegitimate recombination that have

shaped the wheat and barley genomes during their evolution. These breakthroughs have demonstrated the feasibility of developing efficient genomic studies in the Triticeae and have led to the recent establishment of the International Wheat Genome Sequencing Consortium IWGSC (<http://www.wheatgenome.org>) and the International Barley Sequencing Consortium ([www.isbc.org](http://www.isbc.org)) that aim to sequence respectively the hexaploid wheat and barley genomes to accelerate gene discovery and crop improvement in the next decade. Large projects aiming at the establishment of the physical maps as well as a better characterization of their composition and organization through large scale random sequencing projects have been initiated already. Concurrently a number of projects have been launched to develop high throughput functional genomics in wheat and barley. Transcriptomics, proteomics and metabolomics analyses of traits of agronomic importance such as quality, disease resistance, drought and salt tolerance are underway in both species. Combined with the development of physical maps, efficient gene isolation will be enabled and improved sequencing technologies and reduced sequencing costs will permit ultimately genome sequencing and access to the entire wheat and barley gene regulatory elements repertoire. Because rye is closely related to wheat and barley in Triticeae evolution, the latest developments in wheat and barley genomics will be of great use for developing rye genomics and for providing tools for rye improvement. Finally, a new model for temperate grasses has emerged in the past year with the development of the genetics and genomics including a 8x whole genome shotgun sequencing project of *Brachypodium*, a member of the Poaceae family that is more closely related to the Triticeae than rice and can provide valuable information for supporting Triticeae genomics in the near future. These recent breakthroughs have yet to be reviewed in a single source of literature and current handbooks on wheat, barley or rye are dedicated mainly to progress in genetics. In *Genetics and Genomics of the Triticeae*, we will aim to comprehensively review the recent progress in the development of structural and functional genomics tools in the Triticeae species and review the understanding of wheat, barley and rye biology that has resulted from these new resources as well as to illuminate how this new found knowledge can be applied for the improvement of these essential species. The book will be the seventh volume in the ambitious series of books *Plant Genetics and Genomics*, Richard A. Jorgensen series editor, that will attempt to bring the field up to date on the genetics and genomics of important crop plants and genetic models. It is our hope that the publication will be a useful and timely tool for researchers and students alike working with the Triticeae.

*Genetics and Genomics of Papaya* Ray Ming, Paul H. Moore, 2013-08-13. This book reviews various aspects of papaya genomics including existing genetic and genomic resources, recent progress on structural and functional genomics and their applications in papaya improvement. Organized into four sections, the volume explores the origin and domestication of papaya, classic genetics and breeding, recent progress on molecular genetics and current and future applications of genomic resources for papaya improvement. Bolstered by contributions from authorities in the field, *Genetics and Genomics of Papaya* is a valuable resource that provides the most up to date information for papaya researchers and plant biologists.

*Genetics and Genomics of the Brassicaceae* Renate



Schmidt, Ian Bancroft, 2010-12-03 The Genetics and Genomics of the Brassicaceae provides a review of this important family commonly termed the mustard family or Cruciferae. The family contains several cultivated species including radish, rocket, watercress, wasabi and horseradish in addition to the vegetable and oil crops of the Brassica genus. There are numerous further species with great potential for exploitation in 21st century agriculture particularly as sources of bioactive chemicals. These opportunities are reviewed in the context of the Brassicaceae in agriculture. More detailed descriptions are provided of the genetics of the cultivated Brassica crops including both the species producing most of the brassica vegetable crops *B. rapa* and *B. oleracea* and the principal species producing oilseed crops *B. napus* and *B. juncea*. The Brassicaceae also include important model plant species. Most prominent is *Arabidopsis thaliana*, the first plant species to have its genome sequenced. Natural genetic variation is reviewed for *A. thaliana* as are the genetics of the closely related *A. lyrata* and of the genus *Capsella*. Self-incompatibility is widespread in the Brassicaceae and this subject is reviewed. Interest arising from both the commercial value of crop species of the Brassicaceae and the importance of *Arabidopsis thaliana* as a model species has led to the development of numerous resources to support research. These are reviewed including germplasm and genomic library resources and resources for reverse genetics, metabolomics, bioinformatics and transformation. Molecular studies of the genomes of species of the Brassicaceae revealed extensive genome duplication indicative of multiple polyploidy events during evolution. In some species such as *Brassica napus* there is evidence of multiple rounds of polyploidy during its relatively recent evolution, thus the Brassicaceae represent an excellent model system for the study of the impacts of polyploidy and the subsequent process of diploidisation whereby the genome stabilises. Sequence level characterization of the genomes of *Arabidopsis thaliana* and *Brassica rapa* are presented along with summaries of comparative studies conducted at both linkage map and sequence level and analysis of the structural and functional evolution of resynthesised polyploids along with a description of the phylogeny and karyotype evolution of the Brassicaceae. Finally some perspectives of the editors are presented. These focus upon the Brassicaceae species as models for studying genome evolution following polyploidy, the impact of advances in genome sequencing technology, prospects for future transcriptome analysis and upcoming model systems.

*Wild Crop Relatives: Genomic and Breeding Resources* Chittaranjan Kole, 2011-09-01 Wild crop relatives are now playing a significant part in the elucidation and improvement of the genomes of their cultivated counterparts. This work includes comprehensive examinations of the status, origin, distribution, morphology, cytology, genetic diversity and available genetic and genomic resources of numerous wild crop relatives as well as of their evolution and phylogenetic relationship. Further topics include their role as model plants, genetic erosion and conservation efforts and their domestication for the purposes of bioenergy, phytomedicines, nutraceuticals and phytoremediation. *Wild Crop Relatives: Genomic and Breeding Resources* comprises 10 volumes on Cereals, Millets and Grasses, Oilseeds, Legume Crops and Forages, Vegetables, Temperate Fruits, Tropical and Subtropical Fruits, Industrial Crops, Plantation and Ornamental Crops and Forest Trees. It contains 125

chapters written by nearly 400 well known authors from about 40 countries      *Wild Crop Relatives: Genomic and Breeding Resources* Chittaranjan Kole, 2011-02-21 Wild crop relatives are now playing a significant part in the elucidation and improvement of the genomes of their cultivated counterparts This work includes comprehensive examinations of the status origin distribution morphology cytology genetic diversity and available genetic and genomic resources of numerous wild crop relatives as well as of their evolution and phylogenetic relationship Further topics include their role as model plants genetic erosion and conservation efforts and their domestication for the purposes of bioenergy phytomedicines nutraceuticals and phytoremediation Wild Crop Relatives Genomic and Breeding Resources comprises 10 volumes on Cereals Millets and Grasses Oilseeds Legume Crops and Forages Vegetables Temperate Fruits Tropical and Subtropical Fruits Industrial Crops Plantation and Ornamental Crops and Forest Trees It contains 125 chapters written by nearly 400 well known authors from about 40 countries      Global Report International Assessment of Agricultural Knowledge, Science, and Technology for Development (Project), 2009 In addition to assessing existing conditions and knowledge the IAASTD uses a simple set of model projections to look at the future based on knowledge from past events and existing trends such as population growth rural urban food and poverty dynamics loss of agricultural land water availability and climate change effects This set of volumes comprises the findings of the IAASTD It consists of a Global Report a brief Synthesis Report and 5 subglobal reports Taken as a whole the IAASTD reports are an indispensable reference for anyone working in the field of agriculture and rural development whether at the level of basic research policy or practice BOOK JACKET

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