



Plant Genomes Abstract

Annette Colbert



Plant Genomes Abstract:

Plant Genomes Jean-Nicolas Volff, 2008-01-01 Recent major advances in the field of comparative genomics and cytogenomics of plants particularly associated with the completion of ambitious genome projects have uncovered astonishing facets of the architecture and evolutionary history of plant genomes The aim of this book was to review these recent developments as well as their implications in our understanding of the mechanisms which drive plant diversity New insights into the evolution of gene functions gene families and genome size are presented with particular emphasis on the evolutionary impact of polyploidization and transposable elements Knowledge on the structure and evolution of plant sex chromosomes centromeres and microRNAs is reviewed and updated Taken together the contributions by internationally recognized experts present a panoramic overview of the structural features and evolutionary dynamics of plant genomes This volume of Genome Dynamics will provide researchers teachers and students in the fields of biology and agronomy with a valuable source of current knowledge on plant genomes

Plant Genome Diversity Volume 2 Johann Greilhuber, Jaroslav Dolezel, Jonathan Wendel, 2012-11-13 This second of two volumes on Plant Genome Diversity provides in 20 chapters insights into the structural evolution of plant genomes with all its variations Starting with an outline of plant phylogeny and its reconstruction the second part of the volume describes the architecture and dynamics of the plant cell nucleus the third examines the evolution and diversity of the karyotype in various lineages including angiosperms gymnosperms and monilophytes The fourth part presents the mechanisms of polyploidization and its biological consequences and significance for land plant evolution The fifth part deals with genome size evolution and its biological significance Together with Volume I this comprehensive book on the plant genome is intended for students and professionals in all fields of plant science offering as it does a convenient entry into a burgeoning literature in a fast moving field

Plant Genome Analysis Techniques Annette Colbert, 1995 Abstracts of Funded Research National Research Initiative Competitive Grants Program (United States. Cooperative State Research, Education, and Extension Service), 1997

The Potato Genome Swarup Kumar Chakrabarti, Conghua Xie, Jagesh Kumar Tiwari, 2017-12-26 This book describes the historical importance of potato *Solanum tuberosum* L potato genetic resources and stocks including *S. tuberosum* group Phureja DM1 3 516 R44 a unique doubled monoploid homozygous line used for potato genome sequencing It also discusses strategies and tools for high throughput sequencing sequence assembly annotation analysis repetitive sequences and genotyping by sequencing approaches Potato *Solanum tuberosum* L 2n 4x 48 is the fourth most important food crop of the world after rice wheat and maize and holds great potential to ensure both food and nutritional security It is an autotetraploid crop with complex genetics acute inbreeding depression and a highly heterozygous nature Further the book examines the recent discovery of whole genome sequencing of a few wild potato species genomes genomics in management and genetic enhancement of *Solanum* species new strategies towards durable potato late blight resistance structural analysis of resistance genes genomics resources for

abiotic stress management as well as somatic cell genetics and modern approaches in true potato seed technology The complete genome sequence provides a better understanding of potato biology underpinning evolutionary process genetics breeding and molecular efforts to improve various important traits involved in potato growth and development *Abstracts of Funded Research* National Research Initiative Competitive Grants Program (United States. Cooperative State Research Service),1999

The Maize Genome Jeffrey Bennetzen, Sherry Flint-Garcia, Candice Hirsch, Roberto Tuberosa, 2018-11-24 This book discusses advances in our understanding of the structure and function of the maize genome since publication of the original B73 reference genome in 2009 and the progress in translating this knowledge into basic biology and trait improvement Maize is an extremely important crop providing a large proportion of the world's human caloric intake and animal feed and serving as a model species for basic and applied research The exceptionally high level of genetic diversity within maize presents opportunities and challenges in all aspects of maize genetics from sequencing and genotyping to linking genotypes to phenotypes Topics covered in this timely book range from i genome sequencing and genotyping techniques ii genome features such as centromeres and epigenetic regulation iii tools and resources available for trait genomics to iv applications of allele mining and genomics assisted breeding This book is a valuable resource for researchers and students interested in maize genetics and genomics

The Brassica napus Genome Shengyi Liu, Rod Snowdon, Boulos Chalhouh, 2018-10-22 This book describes how the genome sequence contributes to our understanding of allopolyploidisation and the genome evolution genetic diversity complex trait regulation and knowledge based breeding of this important crop Numerous examples demonstrate how widespread homoeologous genome rearrangements and exchanges have moulded structural genome diversity following a severe polyploidy bottleneck The allopolyploid crop species *Brassica napus* has the most highly duplicated plant genome to be assembled to date with the largest number of annotated genes Examples are provided for use of the genome sequence to identify and capture diversity for important agronomic traits including seed quality and disease resistance The increased potential for detailed gene discovery using high density genetic mapping quantitative genetics and transcriptomic analyses is described in the context of genome availability and illustrated with recent examples Intimate knowledge of the highly duplicated gene space on the one hand and the repeat landscape on the other particularly in comparison to the two diploid progenitor genomes provide a fundamental basis for new insights into the regulatory mechanisms that are coupled with selection for polyploid success and crop evolution

Papers and Abstracts Presented at the 1994 Second International Symposium on Applications of Biotechnology to Tree Culture, Protection, and Utilization, Bloomington, Minnesota, October 2-6, 1994, 1994

The Tobacco Plant Genome Nikolai V. Ivanov, Nicolas Sierro, Manuel C. Peitsch, 2020-03-16 This book describes the history of tobacco genomics from its discovery by Europeans to next generation omics approaches in plant science The authors primarily focus on the allotetraploid common tobacco plant *N. tabacum* however separate chapters are dedicated to closely related *Nicotiana*

species such as *N. benthamiana* and *N. attenuata* for which substantial progress in omics data analysis has been already achieved. While genetic maps, transcriptomes and physical maps of BAC libraries have significantly enhanced our understanding of the tobacco plant, the genome of tobacco and related *Nicotiana* species has opened a new era in modern tobacco research. This book addresses current and future industrial and research applications as well as central challenges in tobacco science including diseases, low variability of cultivars, the genome's large size, polyploidy and gene duplication.

The Globe Artichoke Genome Ezio Portis, Alberto Acquadro, Sergio Lanteri, 2019-06-08. This book presents the latest information on the genetics and genomics of the globe artichoke. It focuses on the latest findings, tools and strategies employed in genome sequencing, physical map development and QTL analyses as well as genomic resources. The resequencing of four globe artichoke genotypes representative of the core varietal types in cultivation as well as the genotype of cultivated cardoon has recently been completed. Here the five genomes are reconstructed at the chromosome scale and annotated. Moreover, functional SNP analyses highlight numerous genetic variants which represent key tools for dissecting the path from sequence variation to phenotype as well as for designing effective diagnostic markers. The wealth of information provided here offers a valuable asset for scientists, plant breeders and students alike.

The Almond Tree Genome Raquel Sánchez-Pérez, Angel Fernandez i Martí, Pedro Martínez-Gómez, 2023-06-27. This book brings together the latest information on almond genomics and transcriptomics with a particular focus on cutting edge findings, tools and strategies employed in genome sequencing and analysis with regard to the most important agronomic traits. Cultivated almond *Prunus dulcis* Miller D. A. Webb syn. *Prunus amygdalus* Batsch *Amygdalus communis* L. *Amygdalus dulcis* Mill. is a tree crop producing seeds of great economic interest and adapted to hot and dry climates. Domesticated in Southeast Asia, its small diploid genome and phenotypic diversity make it an ideal model to complement genomics studies on peach, generally considered to be the reference *Prunus* species. Both represent consanguineous species that evolved in two distinct environments: warmer and more humid in the case of peach and colder and xerophytic for almond. The advent of affordable whole genome sequencing in combination with existing *Prunus* functional genomics data has now made it possible to leverage the novel diversity found in almond, providing an unmatched resource for the genetic improvement of this species.

The Bitter Gourd Genome Chittaranjan Koley, Hideo Matsumura, Tusar Kanti Behera, 2020-01-29. This book focusing on the bitter melon genome is the first comprehensive compilation of knowledge on the botany, cytogenetic analysis, genetic resources and diversity, traditional breeding, tissue culture and genetic transformation, whole genome sequencing and comparative genomics in the Cucurbitaceae family. It discusses the biochemical profile of the bioactives present in this horticultural crop used both as a vegetable and as a medicine and also addresses sex determination in bitter melon. Written by respected international experts, the book is useful to students, teachers and scientists in academia as well as seed companies and pharmaceutical industries.

Agricultural Libraries Information Notes, 1990 *Underutilised Crop*

Genomes Mark A. Chapman, 2022-11-03 This book highlights the uses for underutilized crops presenting the state of the art in terms of genome sequencing for over 30 crops previously understudied and under researched In a changing climate and with significant pressure on the land it is the ideal time to be discussing novel crops with significant biotic and abiotic tolerances and or rich nutrient profiles for consumers Previously the only species with sequenced genomes were high profile internationally recognized crops but in the current era genomes are being sequenced for dozens of crops including those previously classified as underutilized now being investigated This book covers food crops from fruits to tubers and from grasses to legumes as well as crops with non food applications Some of these crops have draft genomes and others have polished genomes with extensive resequencing panels Each chapter tells the story of an individual crop or crop group written by experts focusing on the genome data available revealing more about crop domestication and genetic variation and the current and future prospects given that this data is now becoming available It also highlights how even small sequencing projects can provide draft genome sequences suitable for gene discovery comparative genomics and identification of molecular markers for understanding these crops further

The Barley Genome Nils Stein, Gary J. Muehlbauer, 2018-08-18 This book presents an overview of the state of the art in barley genome analysis covering all aspects of sequencing the genome and translating this important information into new knowledge in basic and applied crop plant biology and new tools for research and crop improvement Unlimited access to a high quality reference sequence is removing one of the major constraints in basic and applied research This book summarizes the advanced knowledge of the composition of the barley genome its genes and the much larger non coding part of the genome and how this information facilitates studying the specific characteristics of barley One of the oldest domesticated crops barley is the small grain cereal species that is best adapted to the highest altitudes and latitudes and it exhibits the greatest tolerance to most abiotic stresses With comprehensive access to the genome sequence barley s importance as a genetic model in comparative studies on crop species like wheat rye oats and even rice is likely to increase

The Sesame Genome Hongmei Miao, Haiyang Zhang, Chittaranjan Kole, 2021-07-14 This book is the first comprehensive compilation of deliberations on whole genome sequencing of sesame including genome assembly annotation structure and synteny analysis and sequencing of its chloroplast genome and also its wild species It presents narratives on classical genetics and breeding tissue culture and genetic transformation molecular mapping and breeding Other chapters describe the beneficial components in sesame protein and oil botanical depictions and cytological features Prospects of designed breeding in the post genomics era including gene discovery have also been enumerated Altogether the book contains 19 chapters authored by globally reputed experts on the relevant field in this crop This book is useful to the students teachers and scientists in the academia and relevant private companies interested in classical and molecular genetics biotechnology breeding biochemistry traditional and molecular breeding and structural and evolutionary genomics The work is also useful to seed and oil industries

The

Foxtail Millet Genome Manoj Prasad, 2017-11-25 This book presents up to date information on foxtail millet genomics with a particular focus on its agronomic importance genome architecture marker development evolutionary and diversity studies comparative genomics and stress biology The topics discussed have the potential to open up a new era of crop improvement in foxtail millet and other related grass species Foxtail millet *Setaria italica* L is the oldest domesticated crop in the world domesticated 8700 years ago and it has been extensively grown in the semi arid regions of Asia Europe and the Americas as a food and fodder crop ever since Further as a C4 crop with close genetic relatedness to several biofuel grasses foxtail millet has been promoted as a model plant In view of its importance the US Department of Energy Joint Genome Institute and Beijing Genomics Institute have independently sequenced the genome of foxtail millet The availability of the draft genome sequence has advanced the genomics and genetics of this important crop resulting in the development of large scale genome wide molecular markers and demonstration of their utility in genomics assisted breeding as well as the identification of the molecular and biological roles of several stress responsive gene families in connection with abiotic stress tolerance In addition several open access databases have been developed to make these resources for crop improvement through structural and functional genomics widely available

The Allium Genomes Masayoshi Shigyo, Anil Khar, Mostafa Abdelrahman, 2018-09-17 This book describes the latest advances in Allium genome research Allium includes plant species known for their huge nuclear genome size which makes them ideal for somatic chromosome observations in high school experiments In order to advance the genome analysis of *A. cepa* and its functional study scientists in international research collaborations have developed several types of artificially manipulated genetic stocks and analyzed them using modern technologies The Allium vegetable crop includes garlic shallot wakegi onion Japanese bunching onion and rakkyo Bulb onion is one of the world's most important Allium commercial crops with an estimated annual production of 85.8 million tons in 2013 and ranking third after tomato and watermelon in terms of global vegetable crops

The Alfalfa Genome Long-Xi Yu, Chittaranjan Koley, 2021-07-17 This book is the first comprehensive compilation of deliberations on whole genome sequencing of the diploid and tetraploid alfalfa genomes including sequence assembly gene annotation and comparative genomics with the model legume genome functional genomics and genomics of important agronomic characters Other chapters describe the genetic diversity and germplasm collections of alfalfa as well as development of genetic markers and genome wide association and genomic selection for economical important traits genome editing genomics and breeding targets to address current and future needs Altogether the book contains about 300 pages over 16 chapters authored by globally reputed experts on the relevant field in this crop This book is useful to the students teachers and scientists in the academia and relevant private companies interested in genetics breeding pathology physiology molecular genetics and breeding biotechnology and structural and functional genomics The work is also useful to seed and forage industries

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