

Polyploidy And Genome Evolution

Sujay Rakshit, Yi-Hong Wang



Polyploidy And Genome Evolution:

Polyploidy and Genome Evolution Pamela Soltis, Douglas E. Soltis, 2012-10-03 Polyploidy whole genome duplication WGD is a fundamental driver of biodiversity with significant consequences for genome structure organization and evolution Once considered a speciation process common only in plants polyploidy is now recognized to have played a major role in the structure gene content and evolution of most eukaryotic genomes In fact the diversity of eukaryotes seems closely tied to multiple WGDs Polyploidy generates new genomic interactions initially resulting in genomic and transcriptomic shock that must be resolved in a new polyploid lineage This process essentially acts as a reset button resulting in genomic changes that may ultimately promote adaptive speciation This book brings together for the first time the conceptual and theoretical underpinnings of polyploid genome evolution with syntheses of the patterns and processes of genome evolution in diverse polyploid groups Because polyploidy is most common and best studied in plants the book emphasizes plant models but recent studies of vertebrates and fungi are providing fresh perspectives on factors that allow polyploid speciation and shape polyploid genomes The emerging paradigm is that polyploidy through alterations in genome structure and gene regulation generates genetic and phenotypic novelty that manifests itself at the chromosomal physiological and organismal levels with long term ecological and evolutionary consequences

Polyploidy and Genome Evolution Pamela S. Soltis, Douglas E. Soltis, 2012-10-03 Polyploidy whole genome duplication WGD is a fundamental driver of biodiversity with significant consequences for genome structure organization and evolution Once considered a speciation process common only in plants polyploidy is now recognized to have played a major role in the structure gene content and evolution of most eukaryotic genomes In fact the diversity of eukaryotes seems closely tied to multiple WGDs Polyploidy generates new genomic interactions initially resulting in genomic and transcriptomic shock that must be resolved in a new polyploid lineage This process essentially acts as a reset button resulting in genomic changes that may ultimately promote adaptive speciation This book brings together for the first time the conceptual and theoretical underpinnings of polyploid genome evolution with syntheses of the patterns and processes of genome evolution in diverse polyploid groups Because polyploidy is most common and best studied in plants the book emphasizes plant models but recent studies of vertebrates and fungi are providing fresh perspectives on factors that allow polyploid speciation and shape polyploid genomes The emerging paradigm is that polyploidy through alterations in genome structure and gene regulation generates genetic and phenotypic novelty that manifests itself at the chromosomal physiological and organismal levels with long term ecological and evolutionary consequences

Evolutionary Biology: Genome Evolution, Speciation, Coevolution and Origin of Life Pierre Pontarotti, 2014-07-25 This book includes the most essential contributions presented at the 17th Evolutionary Biology Meeting in Marseille which took place in September 2013 It consists of 18 chapters organized according to the following categories Molecular and Genome Evolution Phylogeography of Speciation and Coevolution Exobiology and Origin of Life The

aims of the annual meetings in Marseille which bring together leading evolutionary biologists and other scientists using evolutionary biology concepts e.g. for medical research are to promote the exchange of ideas and to encourage interdisciplinary collaborations. Offering an overview of the latest findings in the field of evolutionary biology, this book represents an invaluable source of information for scientists, teachers and advanced students. *Polyploidy and its consequences* Yves Van de Peer, Andrew H. Paterson, Jonathan F. Wendel, 2023-09-28

Comparative and Evolutionary Genomics of Angiosperm Trees Andrew Groover, Quentin Cronk, 2017-11-21. Marking the change in focus of tree genomics from single species to comparative approaches, this book covers biological, genomic and evolutionary aspects of angiosperm trees that provide information and perspectives to support researchers broadening the focus of their research. The diversity of angiosperm trees in morphology, anatomy, physiology and biochemistry has been described and cataloged by various scientific disciplines, but the molecular genetic and evolutionary mechanisms underlying this diversity have only recently been explored. Excitingly, advances in genomic and sequencing technologies are ushering a new era of research broadly termed comparative genomics, which simultaneously exploits and describes the evolutionary origins and genetic regulation of traits of interest. Within tree genomics, this research is already underway as the number of complete genome sequences available for angiosperm trees is increasing at an impressive pace and the number of species for which RNAseq data are available is rapidly expanding. Because they are extensively covered by other literature and are rapidly changing technical and computational approaches such as the latest sequencing technologies are not a main focus of this book. Instead, this comprehensive volume provides a valuable broader view of tree genomics whose relevance will outlive the particulars of current day technical approaches. The first section of the book discusses background on the evolution and diversification of angiosperm trees as well as offers description of the salient features and diversity of the unique physiology and wood anatomy of angiosperm trees. The second section explores the two most advanced model angiosperm tree species, poplars and eucalypts, as well as species that are soon to emerge as new models. The third section describes the structural features and evolutionary histories of angiosperm tree genomes, followed by a fourth section focusing on the genomics of traits of biological, ecological and economic interest. In summary, this book is a timely and well-referenced foundational resource for the forest tree community looking to embrace comparative approaches for the study of angiosperm trees. **Evolution and Biodiversity of Wild Polyploids** Elvira Hörandl, Natascha D. Wagner, Karol Marhold, Christoph Oberprieler, 2021-09-28

The Brassica oleracea Genome Shengyi Liu, Rod Snowdon, Chittaranjan Koley, 2021-03-04. This book presents comprehensive information on genetics, genomics and breeding in Brassica oleracea, an agriculturally important species that includes popular vegetable crops such as cabbage, cauliflower, broccoli, Brussels sprouts, kale, collard greens, savoy, kohlrabi and gai lan. The content spans whole genome sequencing, assembly and gene annotation for this global vegetable species, along with molecular mapping and cloning of genes, physical genome mapping and analyses of the structure and composition.

of centromeres in the *B. oleracea* genome. The book also elaborates on asymmetrical genome evolution and transposable elements in the *B. oleracea*, describes gene family differentiation in comparison to other Brassica species, and structural and functional genomic resources and data bases developed for *B. oleracea*. Useful discussions on the impact of genome sequencing on genetic improvement in the species are also included. *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 Molecular Evolution* J.J. Doyle, Brandon S. Gaut, 2012-12-06. Plant molecular biology has produced an ever-increasing flood of data about genes and genomes. Evolutionary biology and systematics provides the context for synthesizing this information. This book brings together contributions from evolutionary biologists, systematists, developmental geneticists, biochemists, and others working on diverse aspects of plant biology whose work touches to varying degrees on plant molecular evolution. The book is organized in three parts, the first of which introduces broad topics in evolutionary biology and summarizes advances in plant molecular phylogenetics with emphasis on model plant systems. The second segment presents a series of case studies of gene family evolution, while the third gives overviews of the evolution of important plant processes such as disease resistance, nodulation, hybridization, transposable elements, and genome evolution and polyploidy. **Polyloid Population Genetics and Evolution - From Theory to Practice** Hans D. Daetwyler, Richard John Abbott, 2020-01-28. *The Evolution of the Genome* T. Ryan Gregory, 2011-05-04. The Evolution of the Genome provides a much-needed overview of genomic study through clear, detailed, expert-authored discussions of the key areas in genome biology. This includes the evolution of genome size, genomic parasites, gene and ancient genome duplications, polyploidy, comparative genomics, and the implications of these genome-level phenomena for evolutionary theory. In addition to reviewing the current state of knowledge of these fields in an accessible way, the various chapters also provide historical and conceptual background information, highlight the ways in which the critical questions are actually being studied, indicate some important areas for future research, and build bridges across traditional professional and taxonomic boundaries. The Evolution of the Genome will serve as a critical resource for graduate students, postdoctoral fellows, and established scientists alike who are interested in the issue of genome evolution in the broadest sense. Provides detailed, clearly written chapters authored by leading researchers in their respective fields.

Presents a much needed overview of the historical and theoretical context of the various areas of genomic study Creates important links between topics in order to promote integration across subdisciplines including descriptions of how each subject is actually studied Provides information specifically designed to be accessible to established researchers postdoctoral fellows and graduate students alike *The Sorghum Genome* Sujay Rakshit,Yi-Hong Wang,2017-01-18 This book provides insights into the current state of sorghum genomics It particularly focuses on the tools and strategies employed in genome sequencing and analysis public and private genomic resources and how all this information is leading to direct outcomes for plant breeders The advent of affordable whole genome sequencing in combination with existing cereal functional genomics data has enabled the leveraging of the significant novel diversity available in sorghum the genome of which was fully sequenced in 2009 providing an unmatched resource for the genetic improvement of sorghum and other grass species Cultivated grain sorghum is a food and feed cereal crop adapted to hot and dry climates and is a staple for 500 million of the world s poorest people Globally sorghum is also an important source of animal feed and forage an emerging biofuel crop and model for C4 grasses particularly genetically complex sugarcane

Phylogeny and Evolution of the Angiosperms

Douglas Soltis,Pamela Soltis,Peter Endress,Mark Chase,Steven Manchester,Walter Judd,Lucas Majure,Evgeny Mavrodiev,2018-01-24 Although they are relative latecomers on the evolutionary scene having emerged only 135 170 million years ago angiosperms or flowering plants are the most diverse and species rich group of seed producing land plants comprising more than 15 000 genera and over 350 000 species Not only are they a model group for studying the patterns and processes of evolutionary diversification they also play major roles in our economy diet and courtship rituals producing our fruits legumes and grains not to mention the flowers in our Valentine s bouquets They are also crucial ecologically dominating most terrestrial and some aquatic landscapes This fully revised edition of *Phylogeny and Evolution of the Angiosperms* provides an up to date comprehensive overview of the evolution of and relationships among these vital plants Incorporating molecular phylogenetics with morphological chemical developmental and paleobotanical data as well as presenting a more detailed account of early angiosperm fossils and important fossil information for each evolutionary branch of the angiosperms the new edition integrates fossil evidence into a robust phylogenetic framework Featuring a wealth of new color images this highly synthetic work further reevaluates long held evolutionary hypotheses related to flowering plants and will be an essential reference for botanists plant systematists and evolutionary biologists alike 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.

Polyploidy Yves Van de Peer, 2023-02-01 This volume provides protocols on evidence for polyploidy and how it can be unveiled. Chapters guide readers through evolutionary experiments, measure effects of polyploidy, evidence for remnants of ancient WGDs, models of chromosome number evolution, population genomics approaches to study polyploidy, analysing genetic data from polyploid populations, Phylogenetic and phylogenomic methods, gene expression, gene regulation, unicellular alga *Chlamydomonas* and a fast growing duckweed *Spirodela*. Written in the format of the highly successful *Methods in Molecular Biology* series, each chapter includes an introduction to the topic, lists necessary materials and reagents, includes tips on troubleshooting and known pitfalls, and step by step, readily reproducible protocols. Authoritative and cutting edge, *Polyploidy: Method and Protocols* aims to be of interest to experimental and computational evolutionary biologists, molecular biologists and biotechnologists.

Polyplodization and Cancer Randy Y.C. Poon, 2011-01-11 Limiting genome replication to once per cell cycle is vital for maintaining genome stability. Although polyploidization is of physiological importance for several specialized cell types, inappropriate polyploidization is believed to promote aneuploidy and transformation. A growing body of evidence indicates that the surveillance mechanisms that prevent polyploidization are frequently perturbed in cancers. Progress in the past several years

has unraveled some of the underlying principles that maintain genome stability This book brings together leaders of the field to overview subjects relating to polyploidization and cancer Genome Evolution Axel Meyer,Yves van de Peer,2011-06-28 In the years since the publication of Susumu Ohno s 1970 landmark book Evolution by gene duplication tremendous advances have been made in molecular biology and especially in genomics Studies of genome structure and function prerequisite to testing hypotheses of genome evolution were all but impossible until recent methodological advances This book evaluates newly generated empirical evidence as it pertains to theories of genomic evolutionary patterns and processes Tests of hypotheses using analyses of complete genomes interpreted in a phylogenetic context provide evidence regarding the relative importance of gene duplication The alternative explanation is that the evolution of regulatory elements that control the expression of and interactions among genes has been a more important force in shaping evolutionary innovation This collection of papers will be of interest to all academic and industry researchers working in the fields of molecular biology biotechnology genomics and genome centers *Evolutionary Diversity as a Source for Anticancer Molecules* Akhileshwar Kumar Srivastava,Vinod Kumar Kannaujiya,Rajesh Kumar Singh,Divya Singh,2020-09-21 Evolutionary Diversity as a Source for Anticancer Molecules discusses evolutionary diversity as source for anticancer agents derived from bacteria algae bryophytes pteridophytes and gymnosperms The book goes over the isolation of anticancer agents and the technologyenabled screening process used to develop anticancer drugs The book also includes discussion of the nutraceuticals and natural productsderived from invertebrates that can be used as part of cancer treatment Evolutionary Diversity as a Source for Anticancer Molecules also deals with some of the current challenges in the prevention of cancer as well as the side effects of conventional drugs used for cancer patients This book is a valuable resource for cancer researchers oncologists biotechnologists pharmacologists and any member of the biomedicalfield interested in understanding more about natural products with anticancer potential Discusses the application of natural products in place of conventional drugs to minimize the side effects in cancer treatment Explains the relation between evolutionary mechanisms and climate change for production of secondary metabolites **The Brassica napus Genome** Shengyi Liu,Rod Snowdon,Boulos Chalhoub,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

Polyploidy: Recent Trends and Future Perspectives Tanvir-Ul-Hassan Dar, Reiaz-Ul Rehman, 2017-10-31 This is the first book to present consolidated up to date information regarding recent trends and future perspectives of polyploidy a phenomenon that has played a pivotal role in the evolution of domesticated plants and a research area that has been given new impetus thanks to advances in plant biology techniques integrated with bioinformatics tools The book emphasizes the tremendous potential of polyploidy in plant breeding to improve existing crops and develop new ones to cater for the needs of an ever increasing human population It is divided into 8 chapters each including an introduction and references and complemented with plentiful illustrations figures and tables The chapters cover all facets of polyploidy from its origin occurrence recent polyploidization formation pathways artificial induction criteria for detection and its significance in the contexts of genomic changes and the changing environment as well as future perspectives The book discusses at length the aspects of polyploidy that need to be understood for a thorough comprehension of this biologically important subject It also highlights the recent techniques involved in polyploidy research Further it provides a detailed account with suitable examples of the different genetic and epigenetic changes that occur in polyploids to help their survival A timely publication it serves as an excellent single source textbook It is a valuable resource for students research scholars and teachers of biological sciences in particular and to plant breeders cytologists geneticists and molecular biologists in general

This book delves into Polyploidy And Genome Evolution. Polyploidy And Genome Evolution is an essential topic that needs to be grasped by everyone, from students and scholars to the general public. The book will furnish comprehensive and in-depth insights into Polyploidy And Genome Evolution, encompassing both the fundamentals and more intricate discussions.

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Polyploidy And Genome Evolution Introduction

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web from the examples $a = \{2, 4, 8\}$ $b = \{x, y, z\}$ $c = \{5, 7\}$ we see that $n_p a = 8$ $n_p b = 8$ each of the set a and b has three elements and $n_p c = 4$ c has two elements if we take the number of elements as k in each set then $p_s n = 2k$ for $n_p a = k = 2 \cdot 2 = 4$ a has three elements so $k = 3$ similarly $n_p b = 2k = 2 \cdot 3 = 6$ b also has three elements

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