

Plant Functional Genomics

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Nucleotide sequencing of the *Arabidopsis* genome is nearing completion, sequencing of the rice genome has begun, and large amounts of expressed sequence tag information are being obtained for many other plants. There are many opportunities to use this wealth of sequence information to accelerate progress toward a comprehensive understanding of the genetic mechanisms that control plant growth and development and responses to the environment.

The recent completion of the genome sequences of a number of bacterial species and several eukaryotes (1) has demonstrated the feasibility and utility of sequencing large genomes. Most biologists now envision the day when the complete genome sequence of their favorite organisms, or a proxy thereof, will be available in powerful electronic databases. Access to this information, and new tools that exploit it, will profoundly alter the ways we select and approach questions in biology. This, in turn, will directly affect the application of genetic methods for improving economically important species. Although future developments in a rapidly emerging field are difficult to predict, we believe many of the major developments in genomics that will influence basic research in plant biology and plant improvement during the next decade can be anticipated. Some of these possibilities are summarized here as well as in recent articles (2, 3).

A DNA Sequence Transect

One of the first eukaryotic organisms that will be completely sequenced is the small mustard species *Arabidopsis thaliana* (4) (Fig. 1). During the past decade, *Arabidopsis* has emerged as one of the most widely used model organisms for studying the biology of higher plants. As a member of the mustard family, it is closely related to many food plants such as canola, cabbage, cauliflower, broccoli, turnip, rutabaga, kale, brussels sprouts, kohlrabi, and radish. It was chosen for sequencing because it has a highly compact genome of about 130 Mb with little interspersed repetitive DNA. Six research groups in Japan, Europe, and the United States are collaborating on the sequencing. About 59% of the genome sequence is currently available in public databases and a large proportion of the genes are also represented by partial cDNA sequences (4, 5). It is currently anticipated that the complete ge-

nome sequence of *Arabidopsis* will be available by the end of the year 2000.

Because *Arabidopsis* is only distantly related to the cereal crops that provide the bulk of the world's food supply, the genome of rice will also be sequenced during the next decade (6). Rice was chosen because, in addition to its importance as a food source for about one-quarter of the human population, it has one of the most compact genomes among the cereals. It contains about 3.5 times as much DNA as *Arabidopsis* but only about 20% as much DNA as maize and about 3% as much DNA as wheat (7). However, the genome organization of the cereals appears to be very highly conserved; rice, wheat, maize, sorghum, millet, and other cereals exhibit a high degree of synteny (8). The differences in genome size are primarily due to amplification of interspersed repetitive sequences (9); there is no evidence that angiosperms with large amounts of DNA per cell have substantially greater numbers of functional genes than

angiosperms with relatively small amounts of DNA. Because of extensive synteny among the cereal genomes, knowledge of gene order and organization in rice may be used to isolate and characterize the corresponding genes in other cereals (8, 10). Thus, for instance, if a genetic locus where a useful trait is encoded is mapped between a pair of closely linked molecular markers in wheat, it may be possible to identify candidate genes for the rice ortholog by analyzing the rice genome sequence located between the rice orthologs of the molecular markers.

The sequences of *Arabidopsis* and rice will provide two foci from which the genome contents of other higher plants can be extrapolated. It appears likely that, as the costs of DNA sequencing continue to decrease, additional plant genomes may eventually be sequenced. However, during the next decade additional complete plant genome sequences probably will not be publicly available because of the high cost of sequencing the whole genome of any of the major crops. For instance, the cost of sequencing the maize genome is expected to be about the same as the cost of sequencing the human genome. However, extensive partial cDNA sequence information will be publicly available for most of the genes from many important plant species (11). There are currently more than

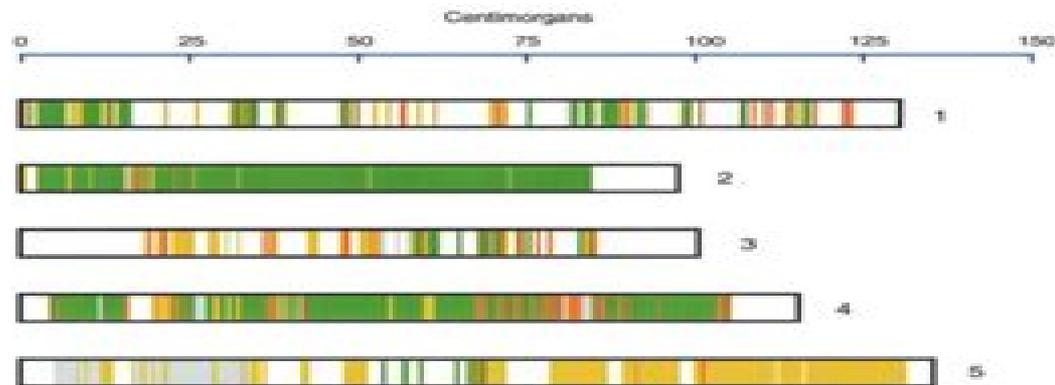


Fig. 1. Status of the *Arabidopsis* genome sequencing project. The five chromosomes are represented by rectangles; length is approximately to scale. Green regions represent annotated sequences available in GenBank; yellow represents regions completed and largely available in various databases; orange indicates regions that are currently being sequenced; gray indicates regions in preparation for sequencing. From the *Arabidopsis* database ATDB (<http://genome-www3.stanford.edu/cgi-bin/ATDB/Chr0m>) with permission.

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Plant Functional Genomics

Erich Grotewold



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Plant Functional Genomics Erich Grotewold, 2008-02-03 Functional genomics is a young discipline whose origin can be traced back to the late 1980s and early 1990s when molecular tools became available to determine the cellular functions of genes Today functional genomics is perceived as the analysis often large scale that bridges the structure and organization of genomes and the assessment of gene function The completion in 2000 of the genome sequence of *Arabidopsis thaliana* has created a number of new and exciting challenges in plant functional genomics The immediate task for the plant biology community is to establish the functions of the approximately 25 000 genes present in this model plant One major issue that will remain even after this formidable task is completed is establishing to what degree our understanding of the genome of one model organism such as the dicot *Arabidopsis* provides insight into the organization and function of genes in other plants The genome sequence of rice completed in 2002 as a result of the synergistic interaction of the private and public sectors promises to significantly enrich our knowledge of the general organization of plant genomes However the tools available to investigate gene function in rice are lagging behind those offered by other model plant systems Approaches available to investigate gene function become even more limited for plants other than the model systems of *Arabidopsis* rice and maize [The Handbook of Plant Functional Genomics](#) Guenter Kahl, Khalid Meksem, 2008-09-08 In this incisive concise overview of this booming field the

editors two of the leading figures in the field with a proven track record combine their expertise to provide an invaluable reference on the topic Following a treatment of transcriptome analysis the book goes on to discuss replacement and mutation analysis gene silencing and computational analysis The whole is rounded off with a look at emerging technologies Each chapter is accompanied by a concise overview helping readers to quickly identify topics of interest while important carefully selected words and concepts are explained in a handy glossary Equally accessible to both experienced scientists and newcomers to the field

Plant Functional Genomics Fatemeh Maghuly,2024-04-24 This detailed book gathers hands on techniques to characterize identify localize profile and determine genome functions in plants Volume 1 opens with a section exploring protocols to advance our understanding of plant genetics and ecology via phenomics and it continues with chapters on plant genetics transcriptomics and proteomics to unravel plant protein structures and functions bridging proteomics and phosphoproteomics Written for the highly successful Methods in Molecular Biology series chapters include introductions to their respective topics lists of the necessary materials and reagents step by step and readily reproducible laboratory protocols and tips on troubleshooting and avoiding known pitfalls Authoritative and comprehensive Plant Functional Genomics Methods and Protocols serves as an ideal guide to the immense promise of functional genomics spanning from fundamental evolutionary studies to practical advancements in crop improvement

The Handbook of Plant Functional Genomics Guenter Kahl,Khalid Meksem,2008-07-21 In this incisive concise overview of this booming field the editors two of the leading figures in the field with a proven track record combine their expertise to provide an invaluable reference on the topic Following a treatment of transcriptome analysis the book goes on to discuss replacement and mutation analysis gene silencing and computational analysis The whole is rounded off with a look at emerging technologies Each chapter is accompanied by a concise overview helping readers to quickly identify topics of interest while important carefully selected words and concepts are explained in a handy glossary Equally accessible to both experienced scientists and newcomers to the field

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springer com *CRISPR and Plant Functional Genomics* Jen-Tsung Chen,2024-05-08 CRISPR is a crucial technology in plant physiology and molecular biology resulting in more sustainable agricultural practices including outcomes of better plant stress tolerance and crop improvement CRISPR and Plant Functional Genomics explores ways to release the potential of plant functional genomics one of the prevailing topics in plant biology and a critical technology for speed and precision crop breeding This book presents achievements in plant functional genomics and features information on diverse applications using the emerging CRISPR based genome editing technologies producing high yield disease resistant and climate smart crops It also includes theories on organizing strategies for upgrading the CRISPR system to increase efficiency avoid off target effects and produce transgene free edited crops Features Presents CRISPR based technologies releasing the potential of plant functional genomics Provides methods and applications of CRISPR Cas based plant genome editing technologies Summarizes achievements of speed and precision crop breeding using CRISPR based technologies Illustrates strategies to upgrade the CRISPR system Supports the UN s sustainable development goals to develop future climate resilient crops CRISPR and Plant Functional Genomics provides extensive knowledge of CRISPR based technologies and plant functional genomics and is an ideal reference for researchers graduate students and practitioners in the field of plant sciences as well as agronomy and agriculture

RNA-Based Technologies for Functional Genomics in Plants Guiliang Tang,Sachin Teotia,Xiaoqing Tang,Deepali Singh,2021-04-11 This book offers a unique and comprehensive overview of key RNA based technologies as well as their development and applications for the functional genomics of plant coding and non coding genes It focuses on the latest as well as classical RNA based techniques used for studies on small RNAs long non coding RNAs and protein coding genes These techniques chiefly focus on target mimics TMs and short tandem target mimics STTMs for small RNAs and artificial microRNAs amiRNAs RNA interference RNAi and CRISPR Cas for genes Furthermore the book discusses the latest trends in the field and various modifications of the above mentioned approaches and explores how these RNA based technologies have been developed applied and validated as essential technologies in plant functional genomics RNA based technologies their mechanisms of action their advantages and disadvantages and insights into the further development and applications of these technologies in plants are discussed These techniques will enable the users to functionally characterize genes and small RNAs through silencing overexpression and editing Gathering contributions by globally respected experts the book will appeal to students teachers and scientists in academia and industry who are interested in horticulture genetics pathology entomology physiology molecular genetics and breeding in vitro culture genetic engineering and functional genomics

[Plant Functional Genomics](#) R. A. S. Tomar,2014 [Plant Functional Genomics for Abiotic Stress Resilience](#) Sanjib Kumar Panda,Mather A. Khan,2025-10-24 The book provides a comprehensive overview of the functional genomics to develop a stress resilience crop The book will be helpful to students doing their Master s Ph D postdoc and the scientific community in the fields of molecular biology biotechnology and crop improvement The individual chapters of the

proposed book will demonstrate a comprehensive understanding of the molecular mechanism which is yet to be characterized for improving stress tolerance. Abiotic stresses such as drought, high soil salinity, heat, cold, oxidative stress, and heavy metal toxicity are common adverse environmental conditions that affect and limit crop productivity worldwide. Understanding the molecular basis of plant response to these environmental conditions has been a major focus of recent research. Abiotic stress is a complex trait which is governed by multiple genes. Functional Genomics, which aims to identify genes and determine their functions, has progressed to a high throughput stage. The various parameters for developing abiotic stress resilience plants can be studied using transcriptomics, proteomics, metabolomics, and phenomics. OMICS. As a result, the study of functional genomics is critical in the development of crop production and meeting the demands of the world's ever-increasing population. This book is aimed at students, teachers, and scientists in academia and relevant private companies who are interested in the fields of crop improvement, horticulture, genetics, breeding, physiology, molecular genetics, genomics, in vitro culture, and genetic engineering and structural functional genomics. Specially, this book is intended to provide a comprehensive understanding of plant stress tolerance with a focus on abiotic stress resilience in order to improve crop yield. The primary audience for this book includes those seeking to deepen their knowledge of the biological process underlying plant stress tolerance and to apply this knowledge to the development of novel strategies for enhancing crop productivity.

Functional Plant Genomics J F Morot-Gaudry, P Lea, J.F. Briat, 2007-01-06. The openings offered by functional genomics reconcile organism biology and molecular biology in order to define an integrative biology that should allow new insights about how a phenotype is built up from a genotype in interaction with its environment. This book covers a wide area of concepts and methods in genomics. This range from international genome sequencing projects to invaluable bioinformatics tools, analytical methods of gene expression including final metabolic products and their specific tissue to cellular compartmentalization. This new knowledge enables readers to understand the integration of basic physiological functions and developmental programs. Also, the establishment of tight relationships between genomics and genetics and plant breeding reveals synergies for exploiting molecular markers for analysing genetic variation or for studying quantitative traits. The integration that is now feasible by these new approaches also affects ecophysiology and opens up new perspectives for the us.

Transgenic Plants as a Tool for Plant Functional Genomics Inna Abdeeva, 2012. **Transgenic Plants as a Tool for Plant Functional Genomics**

From Functional Genomics to Biotechnology in Ornamental Plants Swee-Suak Ko, Akira Kanno, Raquel Sánchez-Pérez, Hsin-Hung Yeh, Annette Hohe, Mariana Mondragón-Palomino, 2019-07-12. For centuries, plants of a broad taxonomical background have been bred and commercialized because of the beauty of their flowers. However, until recently, genomic analyses of ornamentals remained a challenge because of their large genome sizes and high ploidy levels. In the last decade, increasingly affordable sequencing technologies and powerful bioinformatic approaches resulted in the complete sequencing of several horticultural species genomes and the characterization of their

transcriptomes These developments enabled research on many challenging topics This Research Topic gives you a primer into them by featuring a broad range of original research contributions on some of the most active areas of ornamental plant research the genetic basis of flower morphology scent and color the genetic regulation of physiology as well as the epigenetic factors affecting vegetative development In this context one of the most significant hurdles to functional genetic studies in ornamentals is achieving efficient genetic transformation Several articles in this Research Topic describe strategies to tackle this challenge and present insights into the way transgene activity renders novel flower phenotypes

Abiotic Stress Signaling in Plants: Functional Genomic Intervention Girdhar K. Pandey, Manoj Prasad, Amita Pandey, Maik Boehmer, 2016-08-08 Abiotic stresses such as high temperature low temperature drought and salinity limit crop productivity worldwide Understanding plant responses to these stresses is essential for rational engineering of crop plants In Arabidopsis the signal transduction pathways for abiotic stresses light several phytohormones and pathogenesis have been elucidated A significant portion of plant genomes Arabidopsis and rice were mostly studied encodes for proteins involves in signaling such as receptor sensors kinases phosphatases transcription factors and transporters channels Despite decades of physiological and molecular effort knowledge pertaining to how plants sense and transduce low and high temperature low water availability drought water submergence microgravity and salinity signals is still a major question for plant biologist One major constraint hampering our understanding of these signal transduction processes in plants has been the lack or slow pace of application of molecular genomic and genetics knowledge in the form of gene function In the post genomic era one of the major challenges is investigation and understanding of multiple genes and gene families regulating a particular physiological and developmental aspect of plant life cycle One of the important physiological processes is regulation of stress response which leads to adaptation or adjustment in response to adverse stimuli With the holistic understanding of the signaling pathways involving not only one gene family but multiple genes or gene families plant biologist can lay a foundation for designing and generating future crops which can withstand the higher degree of environmental stresses especially abiotic stresses which are the major cause of crop loss throughout the world without losing crop yield and productivity Therefore in this e Book we intend to incorporate the contribution from leading plant biologists to elucidate several aspects of stress signaling by functional genomics approaches

Transgenic Plants as a Tool for Plant Functional Genomics Inna Abdeeva, Eleonora Piruzian, Rustam Abdeev, Sergey Bruskin, 2012

Elucidation of Abiotic Stress Signaling in Plants Girdhar K. Pandey, 2015-05-30 Abiotic stresses such as high temperature low temperature drought and salinity limit crop productivity worldwide Understanding plant responses to these stresses is essential for rational engineering of crop plants In Arabidopsis the signal transduction pathways for abiotic stresses light several phytohormones and pathogenesis have been elucidated A significant portion of plant genomes most studies are Arabidopsis and rice genome encodes for proteins involves in signaling such as receptor sensors kinases phosphatases transcription factors and transporters channels Despite decades

of physiological and molecular effort knowledge pertaining to how plants sense and transduce low and high temperature low water availability drought water submergence and salinity signals is still a major question before plant biologists One major constraint hampering our understanding of these signal transduction processes in plants has been the lack or slow pace of application of molecular genomic and genetics knowledge in the form of gene function In the post genomic era one of the major challenges is investigation and understanding of multiple genes and gene families regulating a particular physiological and developmental aspect of plant life cycle One of the important physiological processes is regulation of stress response which leads to adaptation or adjustment in response to adverse stimuli With the holistic understanding of the signaling pathways involving not only one gene family but multiple genes or gene families plant biologists can lay a foundation for designing and generating future crops that can withstand the higher degree of environmental stresses especially abiotic stresses which are the major cause of crop loss throughout the world without losing crop yield and productivity Therefore in this proposed book we intend to incorporate the contribution from leading plant biologists to elucidate several aspects of stress signaling by functional genomic approaches

Functional Plant Genomics J F. Morot-Gau,2013 Plant Genomics Ralph Quatrano,2001 **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 **Plant Comparative and Functional Genomics** ,2015 Plants form the foundation for our global ecosystem and are essential for environmental and human health An increasing number of available plant genomes and tractable experimental systems comparative and functional plant genomics research is greatly expanding our knowledge of the molecular basis of economically and nutritionally important traits in crop plants Inferences drawn from comparative genomics are motivating experimental investigations of gene function and gene interactions In this special issue aims to highlight recent advances made in comparative and functional genomics research in plants Nine original research articles in this special issue cover five important topics 1 transcription factor gene families relevant to abiotic stress tolerance 2 plant secondary metabolism 3 transcriptomebased markers for quantitative trait locus 4 epigenetic modifications in plant microbe interactions and 5 computational prediction of protein protein interactions Finally we studied the plant species in these articles which include model species as well as nonmodel plant species of economic importance e g food crops and medicinal plants

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