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 Plant Genotyping

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SHYANNE SANTIAGO

Molecular Plant Taxonomy Springer Nature

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.

Genomic Designing of Climate-Smart Pulse Crops Springer Nature

Population genomics has revolutionized various disciplines of biology including population, evolutionary, ecological and conservation genetics, plant and animal breeding, human health, medicine and pharmacology by allowing to address novel and long-standing questions with unprecedented power and accuracy. It employs large-scale or genome-wide genetic information and bioinformatics to address various fundamental and applied aspects in biology and related disciplines, and provides a comprehensive genome-wide perspective and new insights that were not possible before. These advances have become possible due to the development of new and low-cost sequencing and genotyping technologies and novel statistical approaches and software, bioinformatics tools, and models. Population genomics is tremendously advancing our understanding the roles of evolutionary processes, such as mutation, genetic drift, gene flow, and natural selection, in shaping up genetic variation at individual loci and across the genome and populations; improving the assessment of population genetic parameters or processes such as adaptive evolution, effective population size, gene flow, admixture, inbreeding and outbreeding depression, demography, and biogeography; resolving evolutionary histories and phylogenetic relationships of extant, ancient and extinct species; understanding the genomic basis of fitness, adaptation, speciation, complex ecological and economically important traits, and disease and insect resistance; facilitating forensics, genetic medicine and pharmacology; delineating conservation genetic units; and understanding the genetic effects of resource management practices, and assisting conservation and sustainable management of genetic resources. This Population Genomics book discusses the concepts, approaches, applications and promises of population genomics in addressing most of the above fundamental and applied crucial aspects in a variety of organisms from microorganisms to humans. The book provides insights into a range of emerging population genomics topics including population epigenomics, landscape genomics, seascape genomics, paleogenomics, ecological and evolutionary genomics, biogeography, demography, speciation, admixture, colonization and invasion, genomic selection, and plant and animal domestication. This book fills a vacuum in the field and is expected to become a primary reference in Population Genomics world-wide.

The Duckweed Genomes Springer Nature

This book presents deliberations on molecular and genomic mechanisms underlying the interactions

of crop plants to the biotic stresses caused by different diseases and pests that are important to develop resistant crop varieties. Knowledge on the advanced genetic and genomic crop improvement strategies including molecular breeding, transgenics, genomic-assisted breeding, and the recently emerging genome editing for developing resistant varieties in cereal crops is imperative for addressing FHNEE (food, health, nutrition, energy, and environment) security. Whole genome sequencing of these crops followed by genotyping-by-sequencing has provided precise information regarding the genes conferring resistance useful for gene discovery, allele mining, and shuttle breeding which in turn opened up the scope for 'designing' crop genomes with resistance to biotic stresses. The eight chapters each dedicated to a cereal crop in this volume elucidate on different types of biotic stresses and their effects on and interaction with the crop; enumerate on the available genetic diversity with regard to biotic stress resistance among available cultivars; illuminate on the potential gene pools for utilization in interspecific gene transfer; present brief on classical genetics of stress resistance and traditional breeding for transferring them to their cultivated counterparts; depict the success stories of genetic engineering for developing biotic stress-resistant crop varieties; discuss on molecular mapping of genes and QTLs underlying stress resistance and their marker-assisted introgression into elite varieties; enunciate on different genomics-aided techniques including genomic selection, allele mining, gene discovery, and gene pyramiding for developing adaptive crop varieties with higher quantity and quality of yields, and also elaborate some case studies on genome editing focusing on specific genes for generating biotic stress-resistant crops.

Genotyping by Sequencing for Crop Improvement CABI

This volume explores a broad range of different genotyping techniques. Genotyping: Methods and Protocols consists of chapters that cover numerous topics such as: an overview of multiplexed microsatellite analysis; High Resolution Melt analysis and TaqMan-based assays; in situ analysis of variants in single RNA molecules; the MassARRAY system and Molecular Inversion Probes; Pulsed Field Gel Electrophoresis, Parologue Ratio Test, and Multiplex Ligation-Dependent Probe Amplification; long-range PCR combined with PacBio sequencing; Targeted Locus Amplification; Multilocus Sequence Typing and rapid SNP detection with pyrosequencing; and genotyping-by-sequencing for plant analysis. Finally, the volume concludes with a summary of pertinent points to describe genetic variation. Written in the highly successful Methods in Molecular Biology series format, chapters include introductions to their respective topics, lists of the necessary materials and reagents, step-by-step, readily reproducible laboratory protocols, and tips on troubleshooting and avoiding known pitfalls. Thorough and practical, Genotyping: Methods and Protocols is a valuable resource for anyone interested in learning more about the diverse field of genotyping.

Genomics of Plant Genetic Resources Springer Nature

This book presents an exciting collection of contributions based on the workshop "Bringing Maths to Life" held October 27-29, 2014 in Naples, Italy. The state-of-the art research in biology and the statistical and analytical challenges facing huge masses of data collection are treated in this Work. Specific topics explored in depth surround the sessions and special invited sessions of the workshop and include genetic variability via differential expression, molecular dynamics and modeling, complex biological systems viewed from quantitative models, and microscopy images processing, to name several. In depth discussions of the mathematical analysis required to extract insights from complex bodies of biological datasets, to aid development in the field novel algorithms, methods and software tools for genetic variability, molecular dynamics, and complex biological systems are presented in this book. Researchers and graduate students in biology, life science, and mathematics/statistics will find the content useful as it addresses existing challenges in identifying the gaps between mathematical modeling and biological research. The shared solutions will aid and promote further collaboration between life sciences and mathematics.

Molecular Breeding of Forage Crops Springer Science & Business Media

Forage plant breeding has entered the genome era. This timely book reviews the latest advances in the development and application of molecular technologies which supplement conventional breeding efforts for our major forage crops. It describes the plethora of new technologies and tools now available for high-throughput gene discovery, genome-wide gene expression analysis, production of transgenic plants, genome analysis and marker-assisted selection as applied to forage plants. Detailed accounts are presented of current and future opportunities for innovative applications of these molecular tools and technologies in the identification, functional characterisation, and use of valuable genes in forage production systems and beyond. This book represents a valuable resource for plant breeders, geneticists, and molecular biologists, and will be of particular relevance to advanced undergraduates, postgraduates, and researchers with an interest in forage legumes and grasses.

Single Nucleotide Polymorphisms John Wiley & Sons

The second edition of this volume focuses on applied bioinformatics with specific applications to crops and model plants. *Plant Bioinformatics: Methods and Protocols* is aimed at plant biologists who have an interest in, or requirement for, accessing and manipulating huge amounts of data being generated by high throughput technologies. This book would also be of interest to bioinformaticians and computer scientists who would benefit from an introduction to the different tools and systems available for plant research. Written in the highly successful *Methods in Molecular Biology* series format, chapters include introductions to their respective topics, lists of the necessary materials and software, step-by-step, readily reproducible protocols, and tips on troubleshooting and avoiding known pitfalls. Authoritative and thorough, *Plant Bioinformatics: Methods and Protocols* helps researchers with the increasing volume and diversity of data from different plants and also the integration of multiple diverse forms of data.

Genomic Designing for Abiotic Stress Resistant Vegetable Crops Springer

Biotic stresses cause yield loss of 31-42% in crops in addition to 6-20% during post-harvest stage. Understanding interaction of crop plants to the biotic stresses caused by insects, bacteria, fungi, viruses, and oomycetes, etc. is important to develop resistant crop varieties. Knowledge on the advanced genetic and genomic crop improvement strategies including molecular breeding, transgenics, genomic-assisted breeding and the recently emerging genome editing for developing resistant varieties in oilseed crops is imperative for addressing FPNEE (food, health, nutrition, energy and environment) security. Whole genome sequencing of these crops followed by genotyping-by-sequencing have facilitated precise information about the genes conferring resistance useful for gene discovery, allele mining and shuttle breeding which in turn opened up the scope for 'designing' crop genomes with resistance to biotic stresses. The eight chapters each dedicated to an oilseed crop in this volume elucidate on different types of biotic stress agents and their effects on and interaction with the crop plants; enumerate on the available genetic diversity with regard to biotic stress resistance among available cultivars; illuminate on the potential gene pools for utilization in interspecific gene transfer; present brief on the classical genetics of stress resistance and traditional breeding for transferring them to their cultivated counterparts; depict the success stories of genetic engineering for developing biotic stress resistant varieties; discuss on molecular mapping of genes and QTLs underlying biotic stress resistance and their marker-assisted introgression into elite varieties; enunciate on different emerging genomics-aided techniques including genomic selection, allele mining, gene discovery and gene pyramiding for developing resistant crop varieties with higher quantity and quality of yields; and also elaborate some case studies on genome editing focusing on specific genes for generating disease and insect resistant crops.

Plant Genotyping Springer

This book aims to help plant breeders by reviewing past achievements, currently successful practices, and emerging methods and techniques. Theoretical considerations are also presented to strike the right balance between being as simple as possible but as complex as necessary. The United Nations predicts that the global human population will continue rising to 9.0 billion by 2050. World food production will need to increase between 70-100 per cent in just 40 years. First generation bio-fuels are also using crops and cropland to produce energy rather than food. In addition, land area used for agriculture may remain static or even decrease as a result of degradation and climate change, despite more land being theoretically available, unless crops can be bred which tolerate associated abiotic stresses. Lastly, it is unlikely that steps can be taken to mitigate all of the climate change predicted to occur by 2050, and beyond, and hence adaptation of farming systems and crop production will be required to reduce predicted negative effects on yields that will occur without crop adaptation. Substantial progress will therefore be required in bridging the yield gap between what is currently achieved per unit of land and what should be possible in future, with the best farming methods and best storage and transportation of food, given the availability of suitably adapted cultivars, including adaptation to climate change. My book is divided into four parts: Part I is an historical introduction; Part II deals with the origin of genetic variation by mutation and recombination of DNA; Part III explains how the mating system of a crop species determines the genetic structure of its landraces; Part IV considers the three complementary options for future progress: use of sexual reproduction in further conventional breeding, base broadening and introgression; mutation breeding; and genetically modified crops.

The Radish Genome Springer Science & Business Media

Plant genetic resources provide a basis for food security, livelihood support and economic development as a major component of biodiversity. The Second Report on the State of the World's Plant Genetic Resources for Food and Agriculture demonstrates the central role plant genetic diversity continues to play in shaping agriculture growth in the face of climate change and other environmental challenges. It is based on information gathered from Country Reports, regional syntheses, thematic studies and scientific literature, documenting the major achievements made in this sector during the past decade and identifying the critical gaps and needs that should urgently be addressed. The Report provides the decision-makers with a technical basis for updating the Global Plan of Action on Conservation and Sustainable Use of Plant Genetic Resources for Food and Agriculture. It also aims to attract the attention of the global community to set priorities for the effective management of plant genetic resources for the future. Purchase a print copy.

The Potato Genome Food & Agriculture Org.

This book reviews the latest advances in multiple fields of plant biotechnology and the opportunities that plant genetics, genomics and molecular biology have offered for agriculture improvement. Advanced technologies can dramatically enhance our capacity in understanding the molecular basis of traits and utilizing the available resources for accelerated development of high yielding, nutritious, input-use efficient and climate-smart crop varieties. In this book, readers will discover the significant advances in plant genetics, structural and functional genomics, trait and gene discovery, transcriptomics, proteomics, metabolomics, epigenomics, nanotechnology and analytical & decision support tools in breeding. This book appeals to researchers, academics and other stakeholders of global agriculture.

Genomic Selection for Crop Improvement Springer

This book highlights modern methods and strategies to improve cereal crops in the era of climate change, presenting the latest advances in plant molecular mapping and genome sequencing.

Spectacular achievements in the fields of molecular breeding, transgenics and genomics in the last three decades have facilitated revolutionary changes in cereal- crop-improvement strategies and techniques. Since the genome sequencing of rice in 2002, the genomes of over eight cereal crops have been sequenced and more are to follow. This has made it possible to decipher the exact nucleotide sequence and chromosomal positions of agro-economic genes. Most importantly, comparative genomics and genotyping-by-sequencing have opened up new vistas for exploring available biodiversity, particularly of wild crop relatives, for identifying useful donor genes.

Plant Bioinformatics Springer

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 Genetics and Molecular Biology CABI

This book highlights modern strategies and methods to improve oilseed crops in the era of climate change, presenting the latest advances in plant molecular breeding and genomics-driven breeding. Spectacular achievements in the fields of molecular breeding, transgenics and genomics in the last three decades have facilitated revolutionary changes in oilseed- crop-improvement strategies and techniques. Since the genome sequencing of rice, as the first crop plant, in 2002, the genomes of about one dozen oilseed crops have been sequenced and more are to follow. This has made it possible to decipher the exact nucleotide sequence and chromosomal positions of agro-economic genes. Most importantly, comparative genomics and genotyping-by-sequencing have opened up new vistas for exploring available biodiversity, particularly of wild crop relatives, for identifying useful donor genes.

Plant Breeding: Past, Present and Future Springer Science & Business Media

The results obtained to date involving the use of in ~ methods to facilitate wide hybridization in plants are voluminous and impressive. The techniques of embryo culture, ovule culture, and in~ pollination and fertilization represent an extension of the normal sexual hybridization process. Successes recorded in obtaining hybrids stem largely from circumventing prezygotic or postzygotic hybridization barriers. Numerous recent successful hybridizations were possible because of the development of improved tissue and cell culture systems for crop plants and attention given to genotypes used in hybridization attempts. Interspecific and intergeneric hybridization utilizing the process of protoplast fusion will bypass the limits set by all sexual methods. In addition to combining complete genomes from two different species through protoplast fusion, this system affords unique opportunities for creating novel cytoplasmic combinations, transfer of individual chromosomes, transfer of cytoplasmic organelles, manipulation of male sterility, and for single gene transfer. Some caution must be noted with regard to the extent of hybridization possible between distantly related species. Although practically no limit exists to the physical fusion of protoplasts from widely divergent species, the restrictions imposed by somatic incompatibility have not been adequately addressed. Regeneration of plants from the protoplast or single heterokaryon level is still a major hurdle for many important crop species before somatic cell fusion can be exploited to produce interspecific and intergeneric hybrids. Identification and selection of hybrids is also a limitation to the efficient application of cell fusion methods.

The Second Report on the State of the World's Plant Genetic Resources for Food and Agriculture Woodhead Publishing

Applied plant genomics and biotechnology reviews the recent advancements in the post-genomic era, discussing how different varieties respond to abiotic and biotic stresses, investigating epigenetic modifications and epigenetic memory through analysis of DNA methylation states, applicative uses of RNA silencing and RNA interference in plant physiology and in experimental transgenics, and plants modified to produce high-value pharmaceutical proteins. The book provides an overview of research advances in application of RNA silencing and RNA interference, through Virus-based transient gene expression systems, Virus induced gene complementation (VIGC), Virus induced gene silencing (Sir VIGS, Mr VIGS) Virus-based microRNA silencing (VbMS) and Virus-based RNA mobility assays (VRMA); RNA based vaccines and expression of virus proteins or RNA, and virus-like particles in plants, the potential of virus vaccines and therapeutics, and exploring plants as factories for useful products and pharmaceuticals are topics wholly deepened. The book reviews and discusses Plant Functional Genomic studies discussing the technologies supporting the genetic improvement of plants and the production of plant varieties more resistant to biotic and abiotic stresses. Several important crops are analysed providing a glimpse on the most up-to-date methods and topics of investigation. The book presents a review on current state of GMO, the cisgenesis-derived plants and novel plant products devoid of transgene elements, discuss their regulation and the production of desired traits such as resistance to viruses and disease also in fruit trees and wood trees with long vegetative periods. Several chapters cover aspects of plant physiology related to plant improvement: cytokinin metabolism and hormone signaling pathways are discussed in barley; PARP-domain proteins involved in Stress-Induced Morphogenetic Response, regulation of NAD signaling and ROS dependent synthesis of anthocyanins. Apple allergen isoforms and the various content in different varieties are discussed and approaches to reduce their presence. Euphorbiaceae, castor bean, cassava and Jatropha are discussed at genomic structure, their diseases and viruses, and methods of transformation. Rice genomics and agricultural traits are discussed, and biotechnology for engineering and improve rice varieties. Mango topics are presented with an overview of molecular methods for variety differentiation, and aspects of fruit improvement by traditional and biotechnology methods. Oilseed rape is presented, discussing the genetic diversity, quality traits, genetic maps, genomic selection and comparative genomics for improvement of varieties. Tomato studies are presented, with an overview on the knowledge of the regulatory networks involved in flowering, methods applied to study the tomato genome-wide DNA methylation, its regulation by small RNAs, microRNA-dependent control of transcription factors expression, the development and ripening processes in tomato, genomic studies and fruit modelling to establish fleshy fruit traits of interest; the gene reprogramming during fruit ripening, and the ethylene dependent and independent DNA methylation changes. provides an overview on the ongoing projects and activities in the field of applied biotechnology includes examples of different crops and applications to be exploited reviews and discusses Plant Functional Genomic studies and the future developments in the field explores the new technologies supporting the genetic improvement of plants

Genomic Designing for Biotic Stress Resistant Oilseed Crops Humana Press

This book presents deliberations on molecular and genomic mechanisms underlying the interactions

of crop plants to the abiotic stresses caused by heat, cold, drought, flooding, submergence, salinity, acidity, etc., important to develop resistant crop varieties. Knowledge on the advanced genetic and genomic crop improvement strategies including molecular breeding, transgenics, genomic-assisted breeding, and the recently emerging genome editing for developing resistant varieties in vegetable crops is imperative for addressing FHNEE (food, health, nutrition, energy, and environment) security. Whole genome sequencing of these crops followed by genotyping-by-sequencing has provided precise information regarding the genes conferring resistance useful for gene discovery, allele mining, and shuttle breeding which in turn opened up the scope for 'designing' crop genomes with resistance to abiotic stresses. The nine chapters each dedicated to a vegetable crop or crop group in this volume elucidate on different types of abiotic stresses and their effects on and interaction with the crop; enumerate on the available genetic diversity with regard to abiotic stress resistance among available cultivars; illuminate on the potential gene pools for utilization in interspecific gene transfer; present brief on classical genetics of stress resistance and traditional breeding for transferring them to their cultivated counterparts; depict the success stories of genetic engineering for developing abiotic stress-resistant crop varieties; discuss on molecular mapping of genes and QTLs underlying stress resistance and their marker-assisted introgression into elite varieties; enunciate on different genomics-aided techniques including genomic selection, allele mining, gene discovery, and gene pyramiding for developing adaptive crop varieties with higher quantity and quality of yields, and also elaborate some case studies on genome editing focusing on specific genes for generating abiotic stress-resistant crops

A Guide to QTL Mapping with R/qtl Springer Science & Business Media

This book describes the concepts, strategies and techniques for pulse-crop improvement in the era of climate change, highlighting the latest advances in plant molecular mapping and genome sequencing. Genetic mapping of genes and QTLs has broadened the scope of marker-assisted breeding and map-based cloning in almost all major pulse crops. Genetic transformation, particularly using alien genes conferring resistance to herbicide, insects and diseases has facilitated the development of a huge number of genetically modified varieties of the major pulse crops. Since the genome sequencing of rice in 2002, genomes of over 7 pulse crops have been sequenced. This has resulted in the possibility of deciphering the exact nucleotide sequence and chromosomal positions of agro-economic genes. Most importantly, comparative genomics and genotyping-by-sequencing has opened up a new vista for exploring wild crop relatives for identification of useful donor genes.

The Handbook of Plant Genome Mapping Springer Nature

This book tells the story behind the first Spirodela genome sequencing project. Further, it describes the current genomics applications of these findings, and efforts to sequence new genomes within the family. The closing chapters address the sequencing of the over 1 Gigabase Wolffia genomes, which could have major impacts on genome evolution and agricultural research. The duckweed or

Lemnaceae family is a collection of 5 genera and 37 species of the smallest, fastest-growing flowering plants. Many of these aquatic monocotyledonous plants can grow all over the world, in a variety of climates. Given their simplified and neotenous morphology, duckweeds have been researched for several decades as a model species for plant physiology and ecotoxicological research, contributing to our understanding e.g. of flowering response, plant circadian systems, sulfur assimilation pathways and auxin biosynthesis. In addition, duckweed-based treatment has been a favorite and feasible means, especially in developing countries, of removing phosphorus and pharmaceutical chemicals from sewage and wastewater. With a dry annual mass yield per hectare of up to 80 tonnes (equivalent to 10 tonnes of protein), duckweed is also a promising aquatic crop in new modern and sustainable agriculture. Besides being an excellent primary or supplemental feedstock for the production of livestock and fish, duckweed biomass can be utilized as a potential resource for human nutrition, biofuel, or bioplastics, depending on water quality as well as protein or starch accumulating procedures. These academic and commercial interests have led to international efforts to sequence the Spirodela polyrrhiza genome, the smallest and most ancient genome in the family.

Applied Plant Genomics and Biotechnology Karger Medical and Scientific Publishers

This book presents abiotic stresses that cause crop damage in the range of 6-20%. Understanding the interaction of crop plants to the abiotic stresses caused by heat, cold, drought, flooding, submergence, salinity, acidity, etc., is important to develop resistant crop varieties. Knowledge on the advanced genetic and genomic crop improvement strategies including molecular breeding, transgenics, genomic-assisted breeding, and the recently emerging genome editing for developing resistant varieties in cereal crops is imperative for addressing FPNEE (food, health, nutrition, energy, and environment) security. Whole genome sequencing of these crops followed by genotyping-by-sequencing has facilitated precise information about the genes conferring resistance useful for gene discovery, allele mining, and shuttle breeding which in turn opened up the scope for 'designing' crop genomes with resistance to abiotic stresses. The nine chapters each dedicated to a cereal crop in this volume are deliberate on different types of abiotic stresses and their effects on and interaction with crop plants; enumerate on the available genetic diversity with regard to abiotic stress resistance among available cultivars; illuminate on the potential gene pools for utilization in interspecific gene transfer; are brief on the classical genetics of stress resistance and traditional breeding for transferring them to their cultivated counterparts; elucidate on the success stories of genetic engineering for developing abiotic stress-resistant crop varieties; discuss on molecular mapping of genes and QTLs underlying stress resistance and their marker-assisted introgression into elite varieties; enunciate on different emerging genomics-aided techniques including genomic selection, allele mining, gene discovery, and gene pyramiding for developing adaptive crop varieties with higher quantity and quality, and also elaborate some case studies on genome editing focusing on specific genes for generating abiotic stress-resistant crops.