

Tzintar

Vijay Gahlaut,Abhishek Bohra,Dragan Perovic,Rajeev K. Varshney

High-Throughput Crop Phenotyping Jianfeng Zhou, Henry T. Nguyen, 2021-07-17 This book provides an overview of the innovations in crop phenotyping using emerging technologies, i.e., high-throughput crop phenotyping technology, including its concept, importance, breakthrough and applications in different crops and environments. Emerging technologies in sensing, machine vision and high-performance computing are changing the world beyond our imagination. They are also becoming the most powerful driver of the innovation in agriculture technology, including crop breeding, genetics and management. It includes the state of the art of technologies in high-throughput phenotyping, including advanced sensors, automation systems, ground-based or aerial robotic systems. It also discusses the emerging technologies of big data processing and analytics, such as advanced machine learning and deep learning technologies based on high-performance computing infrastructure. The applications cover different organ levels (root, shoot and seed) of different crops (grains, soybean, maize, potato) at different growth environments (open field and controlled environments). With the contribution of more than 20 world-leading researchers in high-throughput crop phenotyping, the authors hope this book provides readers the needed information to understand the concept, gain the insides and create the innovation of high-throughput phenotyping technology.

Genomic Designing for Abiotic Stress Resistant Vegetable Crops Chittaranjan Kole, 2022-08-21 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

Bioinformatics in Agriculture Pradeep Sharma, Dinesh Yadav, R.K. Gaur, 2022-04-28 Bioinformatics in Agriculture: Next Generation Sequencing Era is a comprehensive volume presenting an integrated research and development approach to the practical application of genomics to improve agricultural crops. Exploring both the theoretical and applied aspects of computational biology, and focusing on the innovation processes, the book highlights the increased productivity of a translational approach. Presented in four sections and including insights from experts from around the world, the book includes: Section I: Bioinformatics and Next Generation Sequencing Technologies; Section II: Omics Application; Section III: Data mining and Markers Discovery; Section IV: Artificial Intelligence and Agribots. Bioinformatics in Agriculture: Next Generation Sequencing Era explores deep sequencing, NGS, genomic, transcriptome analysis and multiplexing, highlighting practices for reducing time, cost, and effort for the analysis of gene as they are pooled, and sequenced. Readers will gain real-world information on computational biology, genomics, applied data mining, machine learning, and artificial intelligence. This book serves as a complete package for advanced undergraduate students, researchers, and scientists with an interest in bioinformatics. Discusses integral aspects of molecular biology and pivotal tool for molecular breeding Enables breeders to design cost-effective and efficient breeding strategies Provides examples of innovative genome-wide marker (SSR, SNP) discovery Explores both the theoretical and practical aspects of computational biology with focus on innovation processes Covers recent trends of bioinformatics and different tools and techniques

Parliamentary Papers Great Britain. Parliament. House of Commons, 1901

Marker-assisted selection (MAS) in crop plants Baohua Wang, Peng Chee, Ting Peng, Muhammad Kashif Riaz Khan, 2023-03-16

Ethnicity and Educational Policies in South Eastern Europe Nikolai Genov, 2005 The crosscutting area of interethnic relations and educational policies is the locus of most intriguing scientific and practical issues in South Eastern Europe. They concern economic, political and cultural dimensions of social action and social order, touch upon sensitive relationships between individual and collective human rights and imply integration or disintegration of societal systems.

Phospholipases in Physiology and Pathology Sajal Chakraborti, 2023-08-01 Phospholipases in Physiology and Pathology presents a comprehensive overview on the physiology and pathology of phospholipases. This seven-volume set considers the biochemical and molecular mechanisms of normal and abnormal cell function upon dysregulation of phospholipases in different diseases. Volumes cover signal transduction mechanisms, implications in cancer, infectious diseases, neural diseases, cardiovascular diseases and other diseases, implications in inflammation, apoptosis, gene expression and non-coding RNAs, the role of natural and synthetic compounds, and stem cell therapies, nanotechnology-based therapies, and more. Together, these volumes give researchers critical insight on the mechanistic and therapeutic aspects of phospholipases. Discusses the biochemical and molecular mechanisms of normal and abnormal cell function in different disease processes Covers a wide range of basic and translational research appropriate for scientists engaged in studying the regulation of phospholipases from interdisciplinary perspectives Features state-of-the-art chapter contributions from international leaders in the field

Physiological and Molecular Perspectives of Stress Tolerance in Vegetables Masayoshi Shigyo, Mostafa Abdelwahed Abdelrahman, Lam-Son Phan Tran, 2022-10-14

Compatible Solutes Engineering for Crop Plants Facing Climate Change Shabir Hussain Wani, Manu Pratap Gangola, Bharathi Raja Ramadoss, 2021-10-30 Plants, being sessile and autotrophic in nature, must cope with challenging environmental aberrations and therefore have evolved various responsive or defensive mechanisms including stress sensing mechanisms, antioxidant system, signaling pathways, secondary metabolites biosynthesis, and other defensive pathways among which accumulation of osmolytes or osmo-protectants is an important phenomenon. Osmolytes with organic chemical nature termed as compatible solutes are highly soluble compounds with no net charge at physiological pH and nontoxic at higher concentrations to plant cells. Compatible solutes in plants involve compounds like proline, glycine betaine, polyamines, trehalose, raffinose family oligosaccharides, fructans, gamma aminobutyric acid (GABA), and sugar alcohols playing structural, physiological, biochemical, and signaling roles during normal plant growth and development. The current and sustaining problems of climate change and increasing world population has challenged global food security. To feed more than 9 billion, the estimated population by 2050, the yield of major crops needs to be increased 1.1–1.3% per year, which is mainly restricted by the yield ceiling. A major factor limiting the crop yield is the changing global environmental conditions which includes drought, salinity and extreme temperatures and are responsible for a reduction of crop yield in almost all the crop plants. This condition may worsen with a decrease in agricultural land or the loss of potential crop yields by 70%. Therefore, it is a

challenging task for agricultural scientists to develop tolerant/resistant varieties against abiotic stresses. The development of stress tolerant plant varieties through conventional breeding is very slow due to complex multigene traits. Engineering compatible solutes biosynthesis by deciphering the mechanism behind the abiotic tolerance or accumulation in plants cell is a potential emerging strategy to mitigate adverse effects of abiotic stresses and increase global crop production. However, detailed information on compatible solutes, including their sensing/signaling, biosynthesis, regulatory components, underlying biochemical mechanisms, crosstalk with other signaling pathways, and transgenic development have not been compiled into a single resource. Our book intends to fill this unmet need, with insight from recent advances in compatible solutes research on agriculturally important crop plants.

Plant MicroRNAs and Stress Response Deepu Pandita, Anu Pandita, 2023-07-17 MicroRNAs (miRNAs) are small (20–24 nt), single stranded, regulatory RNA molecules or gene regulators of critical transcriptional or post-transcriptional gene regulation in plants in sequence-specific order that respond to numerous abiotic stresses and animals, non-coding, highly evolutionarily conserved and widely distributed throughout the plant kingdom. MiRNAs are master regulators of plant growth and development, development attenuation under various environmental stresses by stress-responsive miRNAs and plant stress responses and tolerance. Drought, salinity, heat, cold, UV radiation, heavy metal, pathogens, pests and other microbial infections affect survival, growth, development, quality, yield, and production of plants. Stress induced miRNAs down regulate their target miRNAs. This down regulation leads to the accumulation and function of positive regulators, highlighting their roles in stress responses and tolerance. Plant miRNA mediated modifications include overexpression or repression of stress-responsive miRNAs and/or their target complementary or partially complementary gene products, miRNA-resistant target genes, target-mimics and artificial miRNAs. Thus, miRNAs may serve as genomic gold mines, novel, potent and potential targets in plant genetic manipulations and miRNA-based biotechnology will aid plant improvement and crop-plant tolerance to different environmental stresses. This book reviews our recent understanding of plant microRNAs, biogenesis and functions, computational tools and bioinformatics, regulation of plant growth and development, expression studies, and the role of plant miRNAs in various biotic and abiotic stress-response regulation in plants.

Allele Mining for Genomic Designing of Vegetable Crops Chittaranjan Kole, Tusar Kanti Behera, Prashant Kaushik, 2024-06-03 This book deliberates on the concept, strategies, tools, and techniques of allele mining in vegetable crops and its application potential in genome elucidation and improvement including studying allele evolution, discovery of superior alleles, discerning new haplotypes, assessment of intra- and interspecific similarity, and studies of gene expression and gene prediction. Available gene pools in global germplasm collections specifically consisting of wild allied species and local landraces for almost all major crops have facilitated allele mining. Development of advanced genomic techniques including PCR-based allele priming and Eco-TILLING based allele mining are being widely used now for mining superior alleles. Allele's discovery has become more relevant now for employing molecular breeding to develop designed crop varieties matching consumer needs and with genome plasticity to adapt the climate change scenarios. All these concepts and strategies along with precise success stories are presented in the chapters dedicated to the major vegetable crops. 1. The first book on the novel strategy of allele mining in vegetable crops for precise breeding 2. Presents genomic strategies for mining superior alleles underlying agronomic traits from genomic resources 3. Depicts case studies of PCR-based allele priming and Eco-TILLING based allele mining 4. Elaborates on gene discovery and gene prediction in major vegetable crops This book will be useful to the students and faculties in various plant science disciplines including genetics, genomics, molecular breeding, agronomy, and bioinformatics; the scientists in seed industries; and, the policymakers and funding agencies interested in crop improvement.

Sessional Papers Great Britain. Parliament. House of Commons, 1901

Commentaire théorique et pratique du Pacte de la Société des nations et des statuts de l'Union panaméricaine: Art. 18 à 26 Jesús María Yepes, 1934

Nitrogen Use Efficiency and Sustainable Nitrogen Management in Crop Plants Nandula Raghuram, Susanne Schmidt, Tariq Aziz, Surya Kant, Jianbin Zhou, 2022-04-26

Rhizobiology: Molecular Physiology of Plant Roots Soumya Mukherjee, František Baluška, 2021-12-07 This book discusses the recent advancements in the role of various biomolecules in regulating root growth and development. Rhizobiology is a dynamic sub discipline of plant science which collates investigations from various aspects like physiology, biochemistry, genetic analysis and plant-microbe interactions. The physiology and molecular mechanisms of root development have undergone significant advancements in the last couple of decades. Apart from the already known conventional phytohormones (IAA, GA, cytokinin, ethylene and ABA), certain novel biomolecules have been considered as potential growth regulators or hormones regulating plant growth and development. Root phenotyping and plasticity analysis with respect to the specific functional mutants of each biomolecule shall provide substantial information on the molecular pathways of root signaling. Special emphasis provides insights on the tolerance and modulatory mechanisms of root physiology in response to light burst, ROS generation, agravitrophic response, abiotic stress and biotic interactions. Root Apex Cognition: From Neuronal Molecules to Root-Fungal Networks and Suberin in Monocotyledonous Crop Plants: Structure and Function in Response to Abiotic Stresses” are available open access under a Creative Commons Attribution 4.0 International License via link.springer.com. Chapters “Root Apex Cognition: From Neuronal Molecules to Root-Fungal Networks and Suberin in Monocotyledonous Crop Plants: Structure and Function in Response to Abiotic Stresses” are available open access under a Creative Commons Attribution 4.0 International License via link.springer.com.

Cinémagazine, 1927

Plant Epigenetics Nikolaus Rajewsky, Stefan Jurga, Jan Barciszewski, 2017-04-27 This book presents, in 26 chapters, the status quo in epigenomic profiling. It discusses how functional information can be indirectly inferred and describes the new approaches that promise functional answers, collectively referred to as epigenome editing. It highlights the latest important advances in our understanding of the functions of plant epigenomics and new technologies for the study of epigenomic marks and mechanisms in plants. Topics include the deposition or removal of chromatin modifications and histone variants, the role of epigenetics in development and response to environmental signals, natural variation and ecology, as well as applications for epigenetics in crop improvement. Discussing areas ranging from the complex regulation of stress and heterosis to the precise mechanisms of DNA and histone modifications, it presents breakthroughs in our understanding of complex phenotypic phenomena.

Recent Advances on Nitrogen Use Efficiency in Crop Plants and Climatic Challenges Hamada Abdelgawad, 2023-08-25 Nitrogen (N) is a mineral nutrient that is essential for the normal growth and development of plants that is required in the highest quantity. It is an element of nucleic acids, proteins, and photosynthetic metabolites, therefore crucial for crop growth and metabolic processes. Recently, it was estimated that N fertilizers could meet the 48% demand of the world's population. However, overuse and misuse of N fertilizers raised environmental concerns associated with N losses by nitrous oxide (N₂O) emissions, ammonia (NH₃) volatilization, and nitrate (NO₃⁻) leaching. For instance, NH₃ is a pollutant in the atmosphere, N₂O is a greenhouse gas that has a warming potential 298 times higher than CO₂ and contributes to ozone depletion, and NO₃⁻ causes eutrophication of water bodies. Agricultural practices account for about 90% of NH₃ and 70% of N₂O anthropogenic emissions worldwide. The efficient use of N chemical fertilizers can be attained through cultural and agronomic practices. Nitrogen use efficiency (NUE) is an important trait that has been studied for decades in different crops. The grain production or economic return from the per unit supply of N fertilizer simply explained the NUE. Several definitions were suggested by different researchers. NUE can be defined as the product of N uptake efficiency (NUpE) and N utilization efficiency (NUE). An increase in NUE increases the yield, biomass, quality, and quantity of crops. N is generally applied as chemical

fertilizer to the soil, whereas a small amount is added to some crops like grain legumes through the fixation process. On the other hand, crop plants take N through the root system in the form of nitrate or ammonium which is thereby used in different metabolic processes. A number of studies have been conducted to increase the NUE in different crops and it has been indicated that NUE can be improved by agronomic, physiological, biochemical, breeding as well as molecular approaches. Nitrogen is the main limiting nutrient after carbon, hydrogen, and oxygen for the photosynthetic process, phyto-hormonal and proteomic changes, and the growth-development of plants to complete their lifecycle. Excessive and inefficient use of N fertilizer results in enhanced crop production costs and atmospheric pollution. Atmospheric nitrogen (71%) in the molecular form is not available for the plants. For the world's sustainable food production and atmospheric benefits, there is an urgent need to upgrade nitrogen use efficiency in the agricultural farming system. Nitrogen losses are too high, due to excess amount, low plant population, poor application methods, etc., which can go up to 70% of total available nitrogen. These losses can be minimized up to 15–30% by adopting improved agronomic approaches such as optimal dosage of nitrogen, application of N by using canopy sensors, maintaining plant population, drip fertigation, and legume-based intercropping. Therefore, the major concern of modern days is to save economic resources without sacrificing farm yield as well as the safety of the global environment, i.e. greenhouse gas emissions, ammonium volatilization, and nitrate leaching.

Genetics and epigenetics: Plausible role in development of climate resilient crops Vijay Gahlaut,Abhishek Bohra,Dragan Perovic,Rajeev K. Varshney,2023-04-13

Functional analysis of species-specific noncoding RNAs in plants Yuepeng Song,Mahmoud Yaish,Deqiang Zhang,Yun Zheng,Lianfeng Gu,Byeong-ha Lee,2023-02-01

This book delves into Tzintar. Tzintar is a crucial 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 Tzintar, encompassing both the fundamentals and more intricate discussions.

1. The book is structured into several chapters, namely:
 - Chapter 1: Introduction to Tzintar
 - Chapter 2: Essential Elements of Tzintar
 - Chapter 3: Tzintar in Everyday Life
 - Chapter 4: Tzintar in Specific Contexts
 - Chapter 5: Conclusion
2. In chapter 1, this book will provide an overview of Tzintar. The first chapter will explore what Tzintar is, why Tzintar is vital, and how to effectively learn about Tzintar.
3. In chapter 2, the author will delve into the foundational concepts of Tzintar. This chapter will elucidate the essential principles that need to be understood to grasp Tzintar in its entirety.
4. In chapter 3, this book will examine the practical applications of Tzintar in daily life. The third chapter will showcase real-world examples of how Tzintar can be effectively utilized in everyday scenarios.
5. In chapter 4, the author will scrutinize the relevance of Tzintar in specific contexts. The fourth chapter will explore how Tzintar is applied in specialized fields, such as education, business, and technology.
6. In chapter 5, the author will draw a conclusion about Tzintar. This chapter will summarize the key points that have been discussed throughout the book.
- The book is crafted in an easy-to-understand language and is complemented by engaging illustrations. It is highly recommended for anyone seeking to gain a comprehensive understanding of Tzintar.

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