

Geneious

Tony Silveira,Sandra Isabel Morena Abril,Mariana Härter Remiao,Caroline Gomes Lucas

CRISPR-Cas in Agriculture: Opportunities and Challenges Sandeep Kumar,Hiroshi Ezura,Vladimir Nekrasov,Linda Ann Rymarkis,2021-05-28

Application of Fishes as Biological Models in Genetic Studies Tony Silveira,Sandra Isabel Morena Abril,Mariana Härter Remiao,Caroline Gomes Lucas,2023-03-30 Although Gregor Mendel is considered the father of genetics, he has never taken the credit for his principles on heredity. Mendel's treatises, though they were part of the collection of the largest European libraries in the 19th century, were only rediscovered in 1900, 16 years after his death. Mendel's revolutionary ideas would have given greater strength to the formulation of Charles Darwin's ideas about common descent and gradual evolution through natural selection presented in 1859 in *The Origin of Species*. However, Darwin was not totally ignorant of the possibility of genetic heredity. He even described “invisible characters” emerging in atavistic situations and named his hypothetical particle of heredity as “gemmules.” It is remarkable that the “invisible characters” and “gemmules” referred by Darwin are what we now know as genes – a term coined in 1909 by Wilhelm Johannsen that was widely accepted. During the 1930s and 40s, the findings of great proponents of genetics and evolution such as Mendel, Darwin, Wallace, Fisher, Haldane, Wright, Dobzhansky, Mayr, and several others were brought together to form the neo-Darwinian synthesis. In addition, in the 40s, genetics started its molecular revolution, which in the late 70s, driven by sequencing technology, gave rise to the genomics era. It took approximately 100 years to formulate the theoretical foundations of genetics to understand how information is transmitted to the next generations. Now, less than 45 years after the beginning of the genomic era, science is fully capable of identifying complete genomes. Among animals, fishes are one of the most relevant groups in genetic studies. Although fish studies were important in applying and corroborating Mendel's findings in the first decades of the 19th century, these studies contributed little to the development of classical genetics. However, fish have been of great importance for the development of molecular genetics. Several species such as *Carassius auratus*, *Oryzias latipes*, and *Danio rerio* (among several others of productive interest such as *Salmo salar*, *Oreochromis niloticus*, and *Cyprinus carpio*) have been used around the world as biological models. These models can be used for the study of genes and genomes, epigenetics, and genetic expression. Genetic studies using fish, in addition to increasing genetic knowledge about the species, also serve for a better general understanding of the physiology of metabolic pathways, diseases, evolution, systematics, dispersion, creation, and selection of individuals and lineages. Considering this, this Research Topic aims to bring together studies that present applications of fish as targets in genetic studies.

Frontiers in global regulatory landscape of CRISPR-edited plants Aftab Ahmad,Neil E. Hoffman,Michael George Kepler Jones,Baohong Zhang,2024-02-07

Phylogenomic Discordance in Plant Systematics Stefan Wanke,Susann Wicke,2023-11-15 Phylogenetics often uncovers contradicting hypotheses regarding the relationships within the same group of organisms, a phenomenon known since the beginning of the molecular systematics era. While, historically, single marker-based analyses produced discordance, nowadays entire cellular genomes or portions of the same genomic compartment conflict with others or the rest, respectively. In contrast to the beginning of the molecular systematics era, when adding markers and taxa offered a way out of systematic errors, genome inference-based incongruences cannot be addressed and explained easily. Disagreeing phylogenomic hypotheses might originate from various evolutionary processes, including but not limited to hybridization or incomplete lineage sorting, thereby leading to gene tree-versus species tree-associated discrepancies. Today, this can be expanded to genome discordance, where phylogenomic signals of organellar genomes (plastid, mitochondrial) and the nuclear genome disagree due to intrinsically different coalescent paths or phenomena like organelle capture.

Paleoecology of Easter Island: Natural and Anthropogenic Drivers of Ecological Change Valentí Rull,Santiago Giralt,2018-09-04 After more than three decades of paleoecological research, the potential role of climatic and anthropogenic drivers on Easter Island's ecological and cultural change is still under discussion. This eBook aims to provide a synthetic view of the topic using evidence from different research fields such as paleoecology, archaeology, history and molecular phylogenetics. A holistic approach is provided to combine the results of these research fields into a comprehensive framework able to account for most of the available multidisciplinary evidence. This eBook is dedicated to the memory of John R. Flenley, the pioneer of paleoecological study of Easter Island, who passed away on June 22, 2018.

Mechanisms of DNA Recombination and Genome Rearrangements: Intersection Between Homologous Recombination, DNA Replication and DNA Repair ,2018-03-06 Mechanisms of DNA Recombination and Genome Rearrangements: Intersection between Homologous Recombination, DNA Replication and DNA Repair, Volume 601, the latest release in the Methods in Enzymology series, continues the legacy of this premier serial with quality chapters authored by leaders in the field. Homologous genetic recombination remains the most enigmatic process in DNA metabolism. The molecular machines of recombination preserve the integrity of the genetic material in all organisms and generate genetic diversity in evolution. The same molecular machines that support genetic integrity by orchestrating accurate repair of the most deleterious DNA lesions, however, also promote survival of cancerous cells and emergence of radiation and chemotherapy resistance. This two-volume set offers a comprehensive set of cutting edge methods to study various aspects of homologous recombination and cellular processes that utilize the enzymatic machinery of recombination. The chapters are written by the leading researches and cover a broad range of topics from the basic molecular mechanisms of recombinational proteins and enzymes to emerging cellular techniques and drug discovery efforts. contributions by the leading experts in the field of DNA repair, recombination, replication and genome stability documents cutting edge methods

Recent Advances in Museomics: Revolutionizing Biodiversity Research Jonathan J. Fong,Anchalee Aowphol,Jimmy McGuire,Chirasak Sutcharit,Mozes Blom,Pamela Soltis,

Ecological, Behavioral and Genomic Consequences in the Rodent Family Sciuridae: Why Are Squirrels So Diverse? Toni Gossmann,Jane Waterman,John Lad Koprowski,Oleg Brandler,2021-11-29

Bovine Viral Diarrhea Virus and Related Pestiviruses Helle Bielefeldt-Ohmann,2020-12-03 The pestiviruses encompass some of the most economically important viral infections in the cattle, swine, and sheep industries worldwide. Discovered more than 70 years ago, bovine viral diarrhea virus (BVDV) and classical swine fever virus (CSFV) were long the main concern, but many new pestiviruses have emerged in recent years, which may also present additional threats to biosecurity and food safety. This issue brings together contributions from multiple disciplines – virology, immunology, veterinary clinical medicine, epidemiology, and pathology – on the subject of BVDV and related pestiviruses, and cover host-virus interactions, virus-cell interactions, cross-species transmission as well as the role of wildlife species as reservoirs of some of the pestiviruses.

Zoonotic Microorganisms and Spread of Acquired Polymyxin Resistance Determinants Alberto Quesada,Maria Jorge Campos,Azucena Mora Gutiérrez,2022-02-28

Rise to the challenges in plastome phylogenomics Wenpan Dong,Lianming Gao,Peter Poczai,Chao Xu,Yu Song,2023-06-23

Organelle Genetics in Plants Víctor Quesada,Pedro Robles,2021-09-02 Chloroplasts in photosynthetic organisms and mitochondria in a vast majority of eukaryotes, contain part of the genetic material of a eukaryotic cell. The organisation and inheritance patterns of this organellar DNA are quite different to that of nuclear DNA. Present-day chloroplast and mitochondrial genomes contain only a few dozen genes. Nevertheless, these organelles harbor several thousand proteins, the vast majority of them encoded by the nucleus. As a result, the expression of nuclear and organelle genomes has to be very precisely coordinated.

Contemporary Acarology Michael J. Skvarla,Ronald Ochoa,Jose Carlos Verle Rodrigues,H. Joel Hutcheson,2019-05-15 This book gathers papers presented at the annual meetings of the Acarological Society of America (ASA), jointly organized with the Entomological Society of America. The ASA plans to publish presentations from its annual meetings on a yearly basis; this book represents the first in the series.

Emerging Infectious Diseases ,2018

The Origin and Early Evolutionary History of Snakes David J. Gower,Hussam Zaher,2022-08-11 Snakes comprise nearly 4,000 extant species found on all major continents except Antarctica. Morphologically and ecologically diverse, they include burrowing, arboreal, and marine forms, feeding on prey ranging from insects to large mammals. Snakes are strikingly different from their closest lizard relatives, and their origins and early

diversification have long challenged and enthused evolutionary biologists. The origin and early evolution of snakes is a broad, interdisciplinary topic for which experts in palaeontology, ecology, physiology, embryology, phylogenetics, and molecular biology have made important contributions. The last 25 years has seen a surge of interest, resulting partly from new fossil material, but also from new techniques in molecular and systematic biology. This volume summarises and discusses the state of our knowledge, approaches, data, and ongoing debates. It provides reviews, syntheses, new data and perspectives on a wide range of topics relevant to students and researchers in evolutionary biology, neontology, and palaeontology.

Insect Molecular Genetics Marjorie A. Hoy, 2013-04-09 Insect Molecular Genetics, Third Edition, summarizes and synthesizes two rather disparate disciplines—entomology and molecular genetics. This volume provides an introduction to the techniques and literature of molecular genetics; defines terminology; and reviews concepts, principles, and applications of these powerful tools. The world of insect molecular genetics, once dominated by *Drosophila*, has become much more diverse, especially with the sequencing of multiple arthropod genomes (from spider mites to mosquitoes). This introduction includes discussion of honey bees, mosquitoes, flour beetles, silk moths, fruit flies, aphids, house flies, kissing bugs, cicadas, butterflies, tsetse flies and armyworms. This book serves as both a foundational text and a review of a rapidly growing literature. With fully revised and updated chapters, the third edition will be a valuable addition to the personal libraries of entomologists, geneticists, and molecular biologists. Up-to-date references to important review articles, websites, and seminal citations in the disciplines Well crafted and instructive illustrations integral to explaining the techniques of molecular genetics Glossary of terms to help beginners learn the vocabulary of molecular biology

Proceedings of the 3rd International Conference on Biology, Science and Education (IcoBioSE 2021) Muhyiatul Fadilah, D. Rahmawati, Reki Kardiman, Rijal Satria, 2023-05-20 This is an open access book. ICoBioSE stands for International Conference on Biology, Science and Education. ICoBioSE is the international conference held by the Biology Department and Master Program of Biology Education, Faculty of Mathematic and Sains, Universitas Negeri Padang. The aim of this international conference is to facilitate scientific publications of lecturers, biologists and biology education experts, diploma, master, and doctoral students and natural science experts. The scope of conference are botany, zoology, ecology, microbiology, genetics, molecular biology, bioinformatics, biochemistry, biophysics, environmental health, conservation and biology education.

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

Phylogeography and Population Genetics in Crustacea Christoph Held, Stefan Koenemann, Christoph D. Schubart, 2016-04-19 Recently, technological progress and the rise of DNA barcoding efforts have led to a significant increase in the availability of molecular datasets on intraspecific variability. Carcinologists and other organismal biologists, who want to use molecular tools to investigate patterns on the scale of populations, face a bewildering variety of genetic markers, analytical methods, and computer programs from which to choose. A modern overview of population genetic and phylogeographic studies, *Phylogeography and Population Genetics in Crustacea* offers insights to guide research on intraspecific genetic variation in crustaceans. Combining theory and case studies of current best practices, the book helps researchers select methods of analysis and interpret their results. The theoretical chapters discuss the potential of currently used and upcoming molecular markers in the context of marine non-model species. They also gather practical tips and address the effect of seldom-discussed sources of error, such as spatial and temporal variation, stochasticity, and choice of statistical parameters. Case studies of marine and limnic crustaceans from around the world highlight the importance and diversity of sources of population structure in intraspecific variation. Written by an international team of 46 leading experts, the book showcases the use and analysis of molecular markers, including mitochondrial and nuclear DNA sequence data, coding and non-coding sequences, microsatellites, and cytogenetics. It gives researchers and students a valuable summary of current knowledge on the processes that shape genetic variability and geographic distribution patterns in space and time.

Viral Metagenomics Vitantonio Pantaleo, Laura Miozzi, 2023-12-07 This second edition volume expands on the previous edition with discussions about the latest viral metagenomics aspects covering a range of different specimens such as soil, freshwater, wastewater, fecal samples, blood plasma, clinical tissues, fungi, and herbarium samples. Chapters also look at different viral groups including archaeal viruses, eukaryotic viruses, phages, mycoviruses, and circular DNA viruses. Techniques required for studying the three viral metagenomic steps of samples processing, library construction, and analysis of data are also discussed. 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. Authoritative and cutting-edge, *Viral Metagenomics: Methods and Protocols*, Second Edition is a valuable resource for researchers who are interested in learning more about this important and developing field.

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