Biology Supplementary Material Class 11 2015

Includes section "Books."

Topic Editor Prof. Ritva Tikkanen Receives Research Funding From Neurogene Inc. and GC Pharma for Studies Unrelated to the Subject. Topic Editor Prof. Carl Blobel is Co-Inventor on a Patent Describing a Method of Identifying Agents for Combination With Inhibitors of iRhoms. He and the Hospital for Special Surgery (New York, USA) are Investigating Suitable Approaches to Identify iRhom Inhibitors, and are Co-Founders of a Small Company Called SciRhom in Munich to Pursue These Efforts. Topic Editor Dr. Sylvia Fischer Declares no Competing Interests With Regards to the Research Topic Subject.

Emerging Therapeutic Targets in Brain Cancer

Systems Biology of Cell Signaling

Recent Developments in Cancer Systems Biology

BSCS Newsletter

The American Biology Teacher

This eBook presents all 10 articles published under the Frontiers Research Topic "Evolutionary Feedbacks Between Population Biology and Genome Architecture", edited by Scott V. Edwards and Tariq Ezaz. With the rise of rapid genome sequencing across the Tree of Life, challenges arise in understanding the major evolutionary forces influencing the structure of microbial and eukaryotic genomes, in particular the prevalence of natural selection versus genetic drift in shaping those genomes. Additional complexities in understanding genome architecture arise with the increasing incidence of interspecific hybridization as a force for shaping genotypes and phenotypes. A key paradigm shift facilitating a more nuanced interpretation of genomes came with the rise of the nearly neutral theory in the 1970s, followed by a greater appreciation for the contribution of nonadaptive forces such as genetic drift to genome structure in the 1990s and 2000s. The articles published in this eBook grapple with these issues and provide an update as to the ways in which modern population genetics and genome informatics deepen our understanding of the subtle interplay between these myriad forces. From intraspecific to macroevolutionary studies, population biology and population genetics are now major tools for understanding the broad landscape of how genomes evolve across the Tree of Life. This volume is a celebration across diverse taxa of the contributions of population genetics thinking to genome studies. We hope it spurs additional research and clarity in the ongoing search for rules governing the evolution of genomes.

A textbook on computer science

Integrative Genomics and Network Biology in Livestock and other Domestic Animals

Vascular Biology, Haemostasis and Extracellular Nucleic Acids in Vascular Diseases and Immunity. A Tribute to Klaus T. Preissner

Systems Biology and Omics Approaches to Understand Complex Diseases Biology

Multimedia and Web Technology

Twenty-fifth Annual Conference : Proceedings, November 1-4, 1995, Atlanta, Georgia ; Engineering Education for the 21st Century

The mononuclear phagocyte system (MPS) comprises dendritic cells (DCs), monocytes and macrophages (MØs) that together play crucial roles in tissue immunity and homeostasis, but also contribute to a broad spectrum of pathologies. They are thus attractive therapeutic targets for immune therapy. However, the distinction between DCs, monocytes and MØ subpopulations has been a matter of controversy and the current nomenclature has been a confounding factor. DCs are remarkably heterogeneous and consist of multiple subsets traditionally defined by their expression of various surface markers. While markers are important to define various populations of the MPS, they do not specifically define the intrinsic nature of a cell population and do not always segregate a bona fide cell type of relative homogeneity. Markers are redundant, or simply define distinct activation states within one subset rather than independent subpopulations. One example are the steady-state CD11b+ DCs which are often not distinguished from monocytes, monocyte-derived cells, and macrophages due to their overlapping phenotype. Lastly, monocyte fate during inflammation results in cells bearing the phenotypic and functional features of both DCs and MØs significantly adding to the confusion. In fact, depending on the context of the study and the focus of the laboratory, a monocyte-derived cell will be either be called "monocyte-derived DCs" or "macrophages". Because the names we give to cells are often associated with a functional connotation, this is much more than simple semantics. The "name" we give to a population fundamentally changes the perception of its biology and can impact on research design and interpretation. Recent evidence in the ontogeny and transcriptional regulation of DCs and MØs, combined with the identification of DC- and MØ-specific markers has dramatically changed our understanding of their interrelationship in the steady state and inflammation. In steady state, DCs are constantly replaced by circulating blood precursors that arise from committed progenitors in the bone marrow. Similarly, some MØ populations are also constantly replaced by circulating blood monocytes. However, others tissue MØs are derived from embryonic precursors, are seeded before birth and maintain themselves in adults by self-renewal. In inflammation, such differentiation pathways are fundamentally changed and unique monocyte-derived inflammatory cells are generated. Current DC, monocyte and MØ nomenclature does not take into account these new developments and as a consequence is quite confusing. We believe that the field is in need of a fresh view on this topic as well as an upfront debate on DC and MØ nomenclature. Our aim is to bring expert junior and senior scientists to revisit this topic in light of these recent

developments. This Research Topic will cover all aspects of DC, monocyte and MØ biology including development, transcriptional regulation, functional specializations, in lymphoid and non-lymphoid tissues, and in both human and mouse models. Given the central position of DCs, monocytes and MØs in tissue homeostasis, immunity and disease, this topic should be of interest to a large spectrum of the biomedical community.

Biologically active small molecules have increasingly been applied in plant biology to dissect and understand biological systems. This is evident from the frequent use of potent and selective inhibitors of enzymes or other biological processes such as transcription, translation, or protein degradation. In contrast to animal systems, which are nurtured from drug research, the systematic development of novel bioactive small molecules as research tools for plant systems is a largely underexplored research area. This is surprising since bioactive small molecules bear great potential for generating new, powerful tools for dissecting diverse biological processes. In particular, when small molecules are integrated into genetic strategies (thereby defining "chemical genetics"), they may help to circumvent inherent problems of classical (forward) genetics. There are now clear examples of important, fundamental discoveries originating from plant chemical genetics that demonstrate the power, but not yet fully exploited potential, of this experimental approach. These include the unraveling of molecular mechanisms and critical steps in hormone signaling, activation of defense reactions and dynamic intracellular processes. The intention of this Research Topic of Frontiers in Plant Physiology is to summarize the current status of research at the interface between chemistry and biology and to identify future research challenges. The research topic covers diverse aspects of plant chemical biology, including the identification of bioactive small molecules through screening processes from chemical libraries and natural sources, which rely on robust and quantitative high-throughput bioassays, the critical evaluation and characterization of the compound's activity (selectivity) and, ultimately, the identification of its protein target(s) and mode-of-action, which is yet the biggest challenge of all. Such well-characterized, selective chemicals are attractive tools for basic research, allowing the functional dissection of plant signaling processes, or for applied purposes, if designed for protection of crop plants from disease. New methods and data mining tools for assessing the bioactivity profile of compounds, exploring the chemical space for structure–function relationships, and comprehensive chemical fingerprinting (metabolomics) are also important strategies in plant chemical biology. In addition, there is a continuing need for diverse target-specific bioprobes that help profiling enzymatic activities or selectively label protein complexes or cellular

compartments. To achieve these goals and to add suitable probes and methods to the experimental toolbox, plant biologists need to closely cooperate with synthetic chemists. The development of such tailored chemicals that beyond application in basic research can modify traits of crop plants or target specific classes of weeds or pests by collaboration of applied and academic research groups may provide a bright future for plant chemical biology. The current Research Topic covers the breadth of the field by presenting original research articles, methods papers, reviews, perspectives and opinions.

Plant Viruses, Volume II: Molecular Plant Virus Epidemiology and its Management

Plant RNA Biology

Dendritic Cell and Macrophage Nomenclature and Classification

Evolutionary Feedbacks Between Population Biology and Genome Architecture

Chemical Biology Tools for Peptide and Protein Research

T-cells are an essential component of the immune system that provide protection against pathogen infections and cancer and are involved in the aetiology of numerous autoimmune and autoinflammatory pathologies. Their importance in disease, the relative ease to isolate, expand and manipulate them ex vivo have put T-cells at the forefront of basic and translational research in immunology. Decades of study have shed some light on the unique way T-cells integrate extrinsic environmental cues influencing an activation program triggered by interactions between peptide-MHC complexes and the antigen-recognition machinery constituted of clonally distributed T-cell receptors and their co-receptor CD4 or CD8. The manipulation of these molecular determinants in cellular systems or as recombinant proteins has considerably enhanced our ability to understand antigen-specific T-cell activation, to monitor ongoing T-cell responses and to exploit T-cells for therapy. Even though these principles have given numerous insights in the biology of CD8+ T-cells that translate into promising therapeutic prospects, as illustrated by recent breakthroughs in cancer therapy, they have proven more challenging to apply to CD4+ T-cells. This Research Topic aims to provide a comprehensive view of the recent insights provided by the use of engineered antigen receptors and their ligands on T-cell activation and how they have been or could be harnessed to design efficient immunotherapies.

A thorough understanding of pathogenic microorganisms and their interactions with host organisms is crucial to prevent infectious threats due to the fact that Pathogen-Host Interactions (PHIs) have critical roles in initiating and sustaining infections. Therefore, the analysis of infection mechanisms through PHIs is indispensable to identify diagnostic biomarkers and next-generation drug targets and then to develop strategic novel solutions against drug-resistance and for personalized therapy. Traditional approaches are limited in capturing mechanisms of infection since they investigate hosts or pathogens individually. On the other hand, the systems biology approach focuses on the whole PHI system,

and is more promising in capturing infection mechanisms. Here, we bring together studies on the below listed sections to present the current picture of the research on Computational Systems Biology of Pathogen-Host Interactions: - Computational Inference of PHI Networks using Omics Data - Computational Prediction of PHIs - Text Mining of PHI Data from the Literature - Mathematical Modeling and Bioinformatic Analysis of PHIs Computational Inference of PHI Networks using Omics Data Gene regulatory, metabolic and protein-protein networks of PHI systems are crucial for a thorough understanding of infection mechanisms. Great advances in molecular biology and biotechnology have allowed the production of related omics data experimentally. Many computational methods are emerging to infer molecular interaction networks of PHI systems from the corresponding omics data. Computational Prediction of PHIs Due to the lack of experimentally-found PHI data, many computational methods have been developed for the prediction of pathogen-host protein-protein interactions. Despite being emerging, currently available experimental PHI data are far from complete for a systems view of infection mechanisms through PHIs. Therefore, computational methods are the main tools to predict new PHIs. To this end, the development of new computational methods is of great interest. Text Mining of PHI Data from Literature Despite the recent development of many PHI-specific databases, most data relevant to PHIs are still buried in the biomedical literature, which demands for the use of text mining techniques to unravel PHIs hidden in the literature. Only some rare efforts have been performed to achieve this aim. Therefore, the development of novel text mining methods specific for PHI data retrieval is of key importance for efficient use of the available literature. Mathematical Modeling and Bioinformatic Analysis of PHIs After the reconstruction of PHI networks experimentally and/or computationally, their mathematical modeling and detailed computational analysis is required using bioinformatics tools to get insights on infection mechanisms. Bioinformatics methods are increasingly applied to analyze the increasing amount of experimentally-found and computationally-predicted PHI data.

Functional Imaging in living Plants - Cell Biology meets Physiology

Computational Systems Biology of Pathogen-Host Interactions

Biological and Ecological Studies on Marine Ichthyoplankton

Advances in Mathematical and Computational Oncology

Pseudomonas Aeruginosa, Biology, Genetics, and Host-pathogen Interactions

Topic Editor Prof. Xing is in collaboration with ATCC (https://www.atcc.org/) on testing some of their cell lines in research. All other Topic Editors declare no competing interests with regards to the Research Topic subject.

Functional Imaging in living Plants - Cell Biology meets PhysiologyFrontiers Media SA

School Science and Mathematics

When Chemistry Meets Biology – Generating Innovative Concepts, Methods and Tools for Scientific Discovery in the Plant Sciences

Proceedings of the 11th International Symposium on Aquatic Weeds, European Weed Research Society

Recent Advances in ?? T Cell Biology: New Ligands, New Functions, and New Translational Perspectives

Discoveries from the past decades revealed that RNA molecules are much more than inert intermediates between the coding DN sequences and their functional products, proteins. Today, RNAs are recognized as active regulatory molecules influencing gene expression, chromatin organization and genome stability, thus impacting all aspects of plant life including development, growth, reproduction and stress tolerance. Innovations in methodologies, the expanding application of next-generation sequencing technologies, and the creation of public datasets and databases have exposed a new universe of RNA-based mechanisms and le to the discovery of new families of non-coding RNAs, uncovered the large extent of alternative splicing events, and highlighted th potential roles of RNA modifications and RNA secondary structures. Furthermore, considerable advances have been made in identifying RNA-binding and processing factors involved in the synthesis and maturation of different forms of RNA molecules as well as in RNA processing, biochemical modifications or degradation. This Research Topic showcases the broad biological significance of RNAs in plant systems and contains eight original research articles, one review and four mini-reviews, covering various RNA-based mechanisms in higher plants. Emerging new technologies and novel multidisciplinary approaches are empowering the scientific community and will expectedly bring novel insights into our understanding of the mechanisms through which RNA is regulated and regulates biological processes in plant cells.

Today's biodiversity is the spectacular product of hundreds of millions of years of evolution. Understanding how this diversity of living organisms appeared is one of the most intriguing and challenging question in biology. Because organismal morphology is established during embryonic development, and because morphological traits diversified from ancestral forms during evolution, it can be inferred that changes in the mechanisms controlling embryonic development are instrumental for morphological evolution. This syllogism lies at the very heart of a new discipline called Evo-Devo which is centered in the identification of the cellular and genetic mechanisms that, through modifications in developmental programmes, were at the base of morphological innovations during evolution. After the discovery of the broad conservation of gene content and regulatory networks in the animal kingdom, as well as in plants, Evo-Devo is orienting towards the study of differences through experimental and functional approaches. Given the wide range of species, gene families, and developmental processes considered, a concerted effort is still required to shed light on the genetic, cellular and molecular mechanisms involved in phenotypic evolution. It is a particularly exciting time for this field of evolutionary developmental biology, as the advent of novel imaging, genome editing and sequencing technologies allows the study of almost any organism in ways that were unthinkable only a few years ago. Therefore, the aim of this Frontiers Research Topic is to gather an original collection of experimental approaches, concepts and hypotheses reflecting

the current diversity of the Evo-Devo field. We have organized the articles according to the mechanistic depth with which they tackle specific evolutionary issues. Hence, comparisons of expression patterns have been grouped in Chapter 1, changes in regulatory interactions and gene networks are presented in Chapter 2, while Chapter 3 focuses on the evolution of developmenta processes and biological patterns.

The Biological and Clinical Aspects of HLA-G

New Trends in Biology Teaching. Tendances Nouvelles de L'Enseignement de la Biologie

Integrative Computational Systems Biology Approaches in Immunology and Medicine

Explainable Intelligent Processing of Biological Resources Integrating Data, Information, Knowledge, and Wisdom

Biological Drivers Of Vector-Pathogen Interactions

This book constitutes the proceedings of the 11th International Conference on Computational Methods in Systems Biology, CMSB 2013, held in Klosterneuburg, Austria, in September 2013. The 15 regular papers included in this volume were carefully reviewed and selected from 27 submissions. They deal with computational models for all levels, from molecular and cellular, to organs and entire organisms.

The loss to national economies resulting from excessive plant biomass has been appreciable and has put pressure on water managers to develop weed control procedures. The results from the most up-to-date research activities and field trials of leading aquatic plant scientists and managers in all five continents, aimed at resolving these weed problems, has been drawn together in this volume.

Macrophytes in Aquatic Ecosystems: From Biology to Management

11th International Conference, CMSB 2013, Klosterneuburg, Austria, September 22-24, 2013, Proceedings

The Journal of Experimental Biology

In Silico Methods for Drug Design and Discovery

Computational Methods in Systems Biology

The study of plant cell physiology is currently experiencing a profound transformation. Novel techniques allow dynamic in vivo imaging with subcellular resolution, covering a rapidly growing range of plant cell physiology. Several basic biological questions that have been inaccessible by the traditional combination of biochemical, physiological and cell biological approaches now see major progress. Instead of grinding up tissues, destroying their organisation, or describing cell- and tissue structure, without a measure for its function, novel imaging approaches can provide the critical link between localisation, function and dynamics. Thanks to a fast growing collection of available fluorescent protein variants and sensors, along with innovative new microscopy technologies and quantitative analysis tools, a wide range of plant biology can now be studied in vivo, including cell morphology & migration, protein localization, topology & movement, protein-protein interaction, organelle dynamics, as well as ion, ROS & redox dynamics. Within the cell, genetic targeting

of fluorescent protein probes to different organelles and subcellular locations has started to reveal the stringently compartmentalized nature of cell physiology and its sophisticated spatiotemporal regulation in response to environmental stimuli. Most importantly, such cellular processes can be monitored in their natural 3D context, even in complex tissues and organs – a condition not easily met in studies on mammalian cells. Recent new insights into plant cell physiology by functional imaging have been largely driven by technological developments, such as the design of novel sensors, innovative microscopy & imaging techniques and the quantitative analysis of complex image data. Rapid further advances are expected which will require close interdisciplinary interaction of plant biologists with chemists, physicists, mathematicians and computer scientists. High-throughput approaches will become increasingly important, to fill genomic data with 'life' on the scale of cell physiology. If the vast body of information generated in the -omics era is to generate actual mechanistic understanding of how the live plant cell works, functional imaging has enormous potential to adopt the role of a versatile standard tool across plant biology and crop breeding. We welcome original research papers, methodological papers, reviews and mini reviews, with particular attention to contributions in which novel imaging techniques enhance our understanding of plant cell physiology and permits to answer questions that cannot be easily addressed with other techniques.

Gamma/delta (γδ) T-cells are a small subset of T-lymphocytes in the peripheral circulation but constitute a major T-cell population at other anatomical localizations such as the epithelial tissues. In contrast to conventional α/β T-cells, the available number of germline genes coding for T-cell receptor (TCR) variable elements of γδ T-cells is very small. Moreover, there is a prefential localization of γδ T-cells expressing given Vgamma and Vdelta genes in certain tissues. In humans, γδ T-cells expressing the Vg9Vd2-encoded TCR account for anywhere between 50 and >95% of peripheral blood γδ T-cells, whereas cells expressing non-Vd2 genes dominate in mucosal tissues. In mice, there is an ordered appearance of γδ T-cell „waves" during embryonic development, resulting in preferential localization of γδ T-cells expressing distinct VgammaVdelta genes in the skin, the reproductive organs, or gut epithelia. The major function of γδ T-cells resides in local immunosurveillance and immune defense against infection and malignancy. This is supported by the identification of ligands that are selectively recognized by the γδ TCR. As an example, human Vgamma9Vdelta2 T-cells recognize phosphorylated metabolites („phosphoantigens") that are secreted by many pathogens but can also be overproduced by tumor cells, providing a basis for a role of these γδ T-cells in both anti-infective and anti-tumor immunity. Similarly, the recognition of endothelial protein C receptor by human non-Vdelta2 γδ T-cells has recently been identified to provide a link for the role for such γδ T-cells in immunity against epithelial tumor cells and cytomegalovirus-infected endothelial cells. In addition to „classical" functions such as cytokine production and cytotoxicity, recent studies suggest that subsets of γδ T-cells can exert additional functions such as regulatory activity and – quite surpisingly – „professional" antigen-presenting capacity. It is currently not well known how this tremendous extent of functional plasticity is regulated and what is the extent of γδ TCR ligand diversity. Due to their non-MHC-restricted recognition of unusual stress-associated ligands, γδ T-cells have raised great interest as to their potential translational application in cell-based immunotherapy. Topics of this Research Focus include: Molecular insights into the activation and differentiation

requirements of γδ T-cells, role of pyrophosphates and butyrophilin molecules for the activation of human γδ T-cells, role of γδ T-cells in tumor immunity and in other infectious and non-infectious diseases, and many others. We are most grateful to all colleagues who agreed to write a manuscript. Thanks to their contributions, this E-book presents an up-to-date overview on many facets of the still exciting γδ T-cells. Dieter Kabelitz & Julie Déchanet-Merville

Evolution of Organismal Form: From Regulatory Interactions to Developmental Processes and Biological Patterns

Curriculum Applications In Microbiology: Bioinformatics In The Classroom

Proteomics and its Applications in Cancer

Autoantibodies

Tools, Techniques, and Strategies for Teaching in a Real-World Context With Microbiology

This book includes original research articles and reviews to update readers on the state of the art systems approach to not only discover novel diagnostic and prognostic biomarkers for several cancer types, but also evaluate methodologies to map out important genomic signatures. In addition, therapeutic targets and drug repurposing have been emphasized for a variety of cancer types. In particular, new and established researchers who desire to learn about cancer systems biology and why it is possibly the leading front to a personalized medicine approach will enjoy reading this book.

The opportunistic pathogen Pseudomonas aeruginosa offers a rich variety of biologically relevant topics to explore and serves as a model system to understand the interactions of Gram-negative bacteria with human hosts. The organism adapts readily to most environments. It has a large and variable genome with a great deal of metabolic potential. P. aeruginosa encodes a variety of regulatory systems to fine tune gene expression and integrate environmental signals. This organism can infect both plants and animals and produces a plethora of enzymes and factors that can overcome host defenses. Moreover, it has the ability to change between the states of a sedentary colonizer to an invasive and highly motile organism. Clinically, the bacterium is resistant to many antibiotics making it difficult to treat and impossible to eradicate from the lungs of patients with cystic fibrosis. Intrinsic antibiotic resistance combined with an armamentarium of tissue degradative enzymes makes it imperative to possess a comprehensive understanding of the biology, genetics and pathogenesis of this organism so that novel therapeutics based on virulence product neutralization can be designed and implemented. This Research Topics issue will be devoted to updating the current understanding of P. aeruginosa systems as they relate to its different lifestyles in different environments. The underlying theme is to provide broad overviews and to integrate protein structure-function and gene regulation as it relates to the biology of this bacterium.

Investigating and harnessing T-cell functions with engineered immune receptors and their ligands

Frontiers in Education 1995

Resources in Education