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Regulation of Gene Expression in Stationary Phase of Bacillus Subtilis *Regulation of Gene Expression in Stationary Phase of Bacillus Subtilis* **Cell Cycle Phase Dependent Gene Expression and the Regulation of Cell Growth Phase Dependent Regulation of Gene Expression by Light** *The Effect of Stress Factors on Gene Expression in Higher Plants* **Control of M-G1 phase-specific expression in fission yeast Gene Expression at the Beginning of Animal Development** Two-Phase Clustering Strategy for Gene Expression Data Sets **Functional Discriminant Analysis and Time Dynamics of Microarray Gene Co-expression** Prokaryotic Gene Expression **Developmental Regulation of Plant Gene Expression** *Stress-induced Phase Separation as an Adaptive Strategy to Regulate Gene Expression* **Enhancers and Phase Separation in the Control of Gene Expression Gene Expression of Beta-defensins in Chicken White Blood Cells** *Characterization of Emergent Spatial-temporal Orders in Transcription Regulatory Networks Using Phase Locking Analysis Gas Phase Inductible and Repressible Gene Expression in Bioreactors on the Example of Human B-interferon* **Gene Expression in the Toxic Dinoflagellate, Alexandrium Fundyense** *Investigation of Growth Phase Infectivity and Gene Expression Signatures Important for Latent Mycobacterial Infection* **Phase Determination of Circadian Gene Expression in Synechococcus Elongatus PCC Seven Nine Four Two** Controlled Gene Expression Using Acute Phase Response Elements **Dynamics of Gene Expression During Vegetative Phase Change in Maize** *Cell Surface of Mycobacterium Smegmatis at the Stationary Phase* Insights Into Gene Regulation by Genome Structure, Phase Separation and Developmental Signaling **Developmental Regulation of Phase-I Drug Metabolizing Genes in Mouse Liver** *The Identification of New Regulators of Phase II Detoxification Gene Expression by a Genome-wide RNAi Screen in Caenorhabditis Elegans Genetics and Biotechnology of Bacilli Light Regulation of the Cell Cycle and Gene Expression in Euglena Gracilis Bacillaris* **Bacterial Transcription Factors and the Cell Cycle, 2nd edition Linking Gene Expression to Performance in a Fungal Vapor-phase Bioreactor Treating Ethylbenzene An Investigation of Immunological Markers and Gene Expression During the Manic Phase of Bipolar Mood Disorder Type 1 Acute phase response in dairy cows - focusing at the gene expression level The Impact, Pervasivity and Regulation of Two Phase-separating Entities** *Upstream Pathways Regulating Erythropoietin Gene Expression in the Liver During Acute Phase Response* **Regulation of Nuclear Phase of Eukaryotic Gene Expression by Ubiquitin-proteasome System** The Role of Chromosme Compaction in Phase Determination of Circadian Gene Expression Rhythms in the Cyanobacterium Synechococcus Elongatus **Analysis of Gene Expression in Cardiac Development and Disease** *Regulation of Gene Expression in Enteropathogenic Bacteria, Volume II* **Cell Cycle Regulation Molecular Aspects of Gene Expression in Plants** Basic Genetics

Developmental Regulation of Plant Gene Expression Apr 15 2022 The intricacies of plant growth and development present a fascinating intellectual challenge, and yet our understanding of the subject has increased relatively slowly, despite the application of many different experimental approaches. Now, however, the introduction of molecular methods, coupled with genetic transformation technology, has provided a change in pace, and fundamental advances are occurring rapidly. This volume, the second in our Plant Biotechnology series, shows how we are beginning to understand the molecular basis of plant growth and development, and are thus moving from the descriptive to the predictive stage. The ability, discussed in chapter one, to generate a fivefold change in plant height by overexpression of a single gene for the photoreceptor phytochrome heralds not only a new phase in plant photobiology but also highlights the close relationship between fundamental knowledge and commercial application. Other chapters review progress in our understanding of the molecular basis of hormone action and processes such as tuber development, seed protein synthesis and deposition, fruit ripening, and self-recognition during pollination. The successful uses of antisense genes to alter the colour and pattern of flowers and to change the enzymic composition of ripening fruit are also discussed, together with identification and down regulation of a gene involved in ethylene synthesis by antisense technology. Opportunities are considered for altering the composition and quality of harvested plant organs and for using plants to synthesise novel products.

Regulation of Gene Expression in Stationary Phase of Bacillus Subtilis Feb 25 2023

Bacterial Transcription Factors and the Cell Cycle, 2nd edition Oct 29 2020 Analogous to the eukaryotic G1, S and M phase of the cell cycle, the bacterial cell cycle can be classified into independent stages. Slowly growing bacterial cells undergo three different stages, B-, C- and D-phase, respectively, while the cell cycle of fast-growing bacteria involves at least two independent cycles: the chromosome replication and the cell division. The oscillation in gene expression regulated by transcription factors, and proteolysis mediated by ClpXP, are closely correlated with progression of the cell cycle. Indeed, it has been shown that DnaA couples DNA replication initiation with the expression of the two oscillating regulators GcrA and CtrA, and the DnaA/GcrA/CtrA regulatory cascade drives the forward progression of the Caulobacter cell cycle. Furthermore, it has been found that: the DnaA oscillation in Eschericha coli and Caulobacter crescentus plays an important role in the cell cycle coordination; RpoS in Coxiella regulates the gene expression involved in the developmental cycle; the SigB and SinR transcription factors control whether cells remain in or leave a biofilm responding to metabolic conditions in Bacillus subtilis; similarly, BolA in most Gram-negative bacteria turns off motility and turns on biofilm development as a transcription factor; CtrA regulates cell division and outer membrane composition of the pathogen Brucella abortus; an essential transcription factor SciP enhances robustness of Caulobacter cell cycle regulation. Interestingly, transcription factors mediated metabolism fluctuations are also related to progression of the cell cycle. It has been shown that: CggR and Cra factors are involved in the flux-signaling metabolite fructose-1,6-bisphosphate; IclR mediates para-hydroxybenzoate catabolism in Streptomyces coelicolor; CceR and AkgR regulate central carbon and energy metabolism in alphaproteobacteria; and these metabolism changes affect cell growth. In line with the argument, AspC-mediated aspartate metabolism coordinates the E. coli cell cycle. However, the molecular mechanisms of maintaining the proper cell cycle progression through coordination of transcription factors mediated gene transcription oscillation, cellular metabolism with the cell cycle are not yet well-established. This Research Topic is intended to cover the spectrum of cell cycle regulatory mechanisms, in particular the coordination of transcription factor mediated gene transcription oscillations, and the cellular metabolisms associated with the cell cycle. We welcome all types of articles including Original Research, Review, and Mini Review. The subject areas of interest include but are not limited to: 1. Cell cycle coordination through gene expression and expression oscillation mediated by transcription factors. 2. Regulation of the cell cycle by proteolysis oscillation. 3. Coordination of the cell cycle with metabolism fluctuation. 4. DNA methylation fluctuation and the cell cycle. 5. Novel transcription factors and gene expression patterns associated with the cell cycle.

The Role of Chromosme Compaction in Phase Determination of Circadian Gene Expression Rhythms in the Cyanobacterium Synechococcus Elongatus Mar 22 2020

An Investigation of Immunological Markers and Gene Expression During the Manic Phase of Bipolar Mood Disorder Type 1 Aug 27 2020

Phase Determination of Circadian Gene Expression in Synechococcus Elongatus PCC Seven Nine Four Two Aug 07 2021

Enhancers and Phase Separation in the Control of Gene Expression Feb 13 2022 Gene regulation underlies the control of cell identity, development, and disease. Transcription of genes is regulated by DNA elements called enhancers, which are bound by transcription factors and coactivators, leading to the recruitment of RNA polymerase II and the production of RNA. Enhancers are thought to loop to specific gene promoters to stimulate transcription, but the mechanisms that cause enhancers to selectively loop to specific gene promoters is not well understood. In this thesis, I first describe new insights into enhancer-promoter loop specificity from studies examining the mechanisms that allow tumor-specific super-enhancers to loop to the MYC oncogene in diverse cancer types (Schuijers and Manteiga et al., 2018). While conducting these studies, it was proposed that super-enhancers and the factors associated with them form liquid-liquid phase-separated condensates. Following this proposal, I contributed to collaborative studies that strongly supported this model (Boija et al., 2018; Sabari et al., 2018, see Appendix I and II of this thesis).

This model of transcription led me to ask how key transcriptional components could be recruited into super-enhancer condensates. I performed studies showing that the interaction of RNA polymerase II with these condensates involves the large heptapeptide repeat of the C-terminal domain (CTD) of the enzyme. Furthermore, these studies provided evidence that phosphorylation of the CTD, which is associated with the initiation to elongation transition, weakens these interactions, thus facilitating the transition of RNA polymerase II into different condensates involved in co-transcriptional splicing of the nascent transcript (Guo and Manteiga et al., 2019). These studies provide new insights into the mechanisms of enhancer-promoter interaction, roles for the RNA polymerase II CTD in the enzyme's partitioning into nuclear condensates, and a role for phosphorylation in switching the nuclear condensate partitioning behavior of RNA polymerase II.

Cell Surface of Mycobacterium Smegmatis at the Stationary Phase May 04 2021 This book focuses on the intricate lipid rich cell wall which forms the first barrier for drug delivery with an emphasis on the cell surface antigenic glycolipids, the glycopeptidolipids. A detail account of their structure, biosynthetic pathway, intracellular function and their implications on biofilm formation has been provided. It highlights the changes in the cell surface of M. smegmatis at different ambience of growth. A chapter revisits the biosynthetic pathway of the glycopeptidolipids and justifies a need for a fresh perspective. The transcription apparatus and the regulation of gene expression in mycobacteria at different environmental condition and stages of growth are also discussed. The need for a detail investigation of the stationary phase induced changes in mycobacterial RNAP is stressed. The role of the mycobacterial principal like sigma factor, SigB, at the stationary phase of growth is addressed through expression proteomics. Undergraduate and graduate students investigating the lipid rich cell surface and transcription machinery, during the mycobacterial stationary phase of growth will be immensely benefited from this book.

Dynamics of Gene Expression During Vegetative Phase Change in Maize Jun 05 2021 As maize plants undergo vegetative phase change, they both exhibit heteroblasty, an abrupt change in pattern of leaf morphogenesis, and gain the ability to produce flowers. Both processes are under the control of microRNA 156, whose levels decline at the end of the juvenile phase. Gain of ability to flower is conferred by expression of miR156 targets that encode Squamosa Promoter-Binding (SBP) transcription factors, which in turn induce the expression of MADS-box transcription factors that promote maturation and flowering. What gene expression differences underlie heteroblasty, as well as what causes the reduction in miR156 levels, remain open questions. Here, we compare the gene expression in primordia that will develop into juvenile or adult leaves to identify genes that define these two developmental states and may influence vegetative phase change. In comparisons among successive leaves at the same developmental stage of plastochron 6, three-fourths of approximately 1,100 differentially expressed genes were more highly expressed in juvenile primordia. This juvenile set was enriched in photosynthetic genes, particularly those associated with cyclic electron flow at photosystem I, and genes involved in oxidative stress and retrograde redox signaling. Pathogen responsive pathways including jasmonic acid, salicylic acid, and benzoxazinoids were also up-regulated in juvenile primordia and indeed, we found that exogenous application of jasmonic acid, and hydrogen peroxide delays vegetative phase change in maize seedlings. These results suggest that the timing of vegetative phase change in maize is coordinated in part downstream of photo-oxidative stress signaling. Photo-oxidative stress during greening likely amplifies heterotrophic energy insufficiency. The successful amelioration of these stress signals may ultimately determine the duration of miR156-mediated juvenility.

Gene Expression at the Beginning of Animal Development Aug 19 2022 The beginning of life may be a miracle to some, and a mystery to others, but it is certainly one of the most exciting and perhaps controversial fields of scientific investigation in the 21st century. Among the metazoa, life begins when an egg is fertilized by a sperm. The sperm provides a genetic blueprint from the father and perhaps some critical proteins. The egg provides a genetic blueprint from the mother together with a large reservoir of mRNAs and proteins that are required for DNA replication, cell division and the onset of zygotic gene expression. All of the thousands of genes in these two mature gametes are transcriptionally silent and remain so until fertilization. This work focuses on three biological systems, providing the reader with a clear understanding of the current state of affairs, and the ability to identify common principles as well as critical differences that are responsible for beginning the process of animal development. The essays presented will be of practical value to all those who are interested in improving fertilization in vitro, in designing novel methods of contraception, in developing preimplantation genetic diagnosis for various diseases, in cloning animals by transplanting nuclei from adult cells to an enucleated egg, and in the application of embryonic stem cells to curing genetic diseases or replacing damaged tissues. But above all, this volume is offered to those who simply have an insatiable curiosity about life and its beginnings.

Basic Genetics Oct 17 2019 Basic Genetics is a concise introductory textbook that focuses not only on understanding and explaining the main points of genetics, but also upon covering the required essential traditional subjects in the field. The main goal of this textbook is to help first year students who are taking their first course in human genetics to understand the different topics within genetics. It is of particular interest for those who are preparing themselves to study medicine or other medical sciences. This textbook presents only the essential required information. Some of the different subjects included in the eight chapters are: cell cycle and cellular division, Mendelian principles of heredity, the molecular basis of genetic material, gene expression and gene expression control, genetic variations and genetic engineering, as well as human genetics. In addition, Basic Genetics contains multiple choice questions covering each topic and their answers. These questions are absolutely essential for students' self- assessment. These different topics of basic genetics have also been illustrated by simple diagrams in full color.

Gene Expression in the Toxic Dinoflagellate, Alexandrium Fundyense Oct 09 2021

The Effect of Stress Factors on Gene Expression in Higher Plants Oct 21 2022 The current work aimed at achieving a better understanding about the effect of stress factors on plant gene expression. In the first part a search for genes up-regulated in response to drought/osmotic stress was carried out by using a drought-tolerant wheat (Triticum aestivum L.) cultivar. Through a subtraction molecular approach differentially expressed genes were selected that could be further used in strategies for improving drought tolerance in crops. The second part of the work was focused on the regulation of alfalfa (Medicago sativa L.) B-type cyclin-dependent kinase (Medsa;CDKB2;1). A fragment from the kinase upstream gene region was cloned and shown to be sufficient to assure a cell cycle-dependent and G2/M-phase-specific gene expression, similarly to the endogenous CDKB2;1 kinase. Wounding and ethylene activated CDKB2;1 expression in a non cell cycle-dependent manner, which revealed the complex integration of a cell cycle phase-specific gene into the wound stress response. The study contributes to elucidation of the mechanism of environmental impact on plant development through transcription.

Linking Gene Expression to Performance in a Fungal Vapor-phase Bioreactor Treating Ethylbenzene Sep 27 2020

The Identification of New Regulators of Phase II Detoxification Gene Expression by a Genome-wide RNAi Screen in Caenorhabditis Elegans Feb 01 2021

Upstream Pathways Regulating Erythropoietin Gene Expression in the Liver During Acute Phase Response May 24 2020

Stress-induced Phase Separation as an Adaptive Strategy to Regulate Gene Expression Mar 14 2022

Acute phase response in dairy cows - focusing at the gene expression level Jul 26 2020

Functional Discriminant Analysis and Time Dynamics of Microarray Gene Co-expression Jun 17 2022

Gene Expression of Beta-defensins in Chicken White Blood Cells Jan 12 2022 Infectious agents such as bacteria or viruses can grow rapidly. If a microorganism invades a host, it must be recognized rapidly and destroyed before it overwhelms the immune system. Limiting infection to a minimum in the early stage is critical for the outcome and the recovery from infection. The innate immune system has evolved to recognize a few highly conserved, constitutive structures present only in microorganisms, such as bacterial lipopolysaccharide (LPS), called pathogen-associated molecular patterns (PAMP). Toll-like receptors are the host receptors that recognize PAMP, ultimately activating a variety of transcription factors to induce expression of a wide spectrum of immune related genes, e.g. defensins. Defensins are antimicrobial peptides that play an important role in innate defense against microorganisms in plants and animals. Beta-defensins are the largest family of antimicrobial peptides, which can directly kill microorganisms and have regulatory effects on the immune system. Thirteen beta-defensins have been identified; however, the regulation of these genes has not been well-investigated in the chicken. The objective of this research was to understand constitutive and inducible gene expression of beta-defensins in chicken white blood cells. Real-time RT-PCR was used to quantify gene expression level before and after LPS stimulation. Transcription factor binding sites in the genes were identified to understand the gene expression regulation. From the expression profile results, most chicken beta-

defensins had induced gene expression by LPS stimulation in the early phase (0- to 3-hour) and reduced gene expression in the late phase (3- to 8-hour). As for the level of gene expression, the results show that the induced gene expression in the early phase corresponded to the higher levels of expression at 3-hours after LPS stimulation, and the reduced gene expression in the late phase corresponded to the lower levels of gene expression at 8-hours after LPS stimulation.

Light Regulation of the Cell Cycle and Gene Expression in Euglena Gracilis Bacillaris Nov 29 2020

Developmental Regulation of Phase-I Drug Metabolizing Genes in Mouse Liver Mar 02 2021

Analysis of Gene Expression in Cardiac Development and Disease Feb 19 2020 Large-scale partial sequencing of randomly selected cDNA clones to generate expressed sequence tags (ESTs) is an efficient means of discovering novel genes and characterizing transcription in different tissues. To characterize gene expression and its changes in cardiac development and disease, an EST project was initiated using adult and fetal human heart cDNA libraries. Generation of 3,874 ESTs from an adult heart library, representing the first catalogue of genes expressed in the cardiovascular system, revealed that approximately half of all transcripts represented genes of unknown function. Analysis of the remaining half of transcripts representing known genes demonstrated expression patterns consistent with physiologic function of the heart. Comparison of these patterns with those derived from 2,244 ESTs generated from fetal heart, and with patterns obtained from other tissues, found several differences in gene expression between fetal and adult heart suggestive of a rapidly growing, less differentiated phenotype in the fetal heart relative to the adult heart. Further acquisition of larger numbers of ESTs from nine cardiac cDNA libraries, coupled with development of new strategies for data analysis, allowed for detailed prediction of individual genes exhibiting differential expression in cardiac development and disease. These strategies were applied to analyze gene expression in hypertrophic failing heart, and to study the expression of cell cycle regulators in cardiac development and hypertrophy. In the former analysis, a total of 64 genes was predicted to be differentially expressed in cardiac hypertrophy. Supporting the validity of these predictions, RT-PCR analysis of 12 of these genes confirmed 11 to be differentially expressed. In the latter analysis, transcripts of cell cycle regulators were suggested to be differentially expressed between fetal and adult hearts. Subsequent ' in vitro' analyses confirmed down-regulation of S- and G2/M-phase regulators in adult heart relative to fetal heart, and also found re-induction of several S-phase (e.g., cyclin A, PCNA), but not G2/M-phase (e.g., cyclin B, cdc2), regulators in hypertrophy. These results extend, at a molecular level, current understanding of cardiovascular function, while suggesting several new avenues of investigation. Further, they demonstrate the power of EST-based expression analyses for exploring questions of cardiovascular biology and medicine.

Regulation of Gene Expression in Enteropathogenic Bacteria, Volume II Jan 20 2020 Following the success of this Research Topic http://journal.frontiersin.org/ researchtopic/3298/regulation-of-gene-expression-in-enteropathogenic-bacteria, we are happy to launch a second edition of the project. Pathogenic bacteria have evolved numerous strategies to survive in and to attack hosts, which can be reflected by transcriptional and posttranscriptional changes in specific genes especially including those encoding virulence determinants. Regulation of gene expression by regulatory proteins and non-coding RNAs enables the pathogens to adapt their metabolic needs and to coordinately express virulence determinants during different stages of infection.

Cell Cycle Regulation Dec 19 2019 Cell Cycle Regulation describes the interaction of the nuclear genome, the cytoplasmic pools, the organelles, the cell surface, and the extracellular environment that govern the cell cycle regulation. Comprised of 12 chapters, this book includes cell cycle regulation around nuclear chromatin modulation and some aspects of chromatin modification and its effects on gene expression. The opening chapters describe the macromolecular structure of chromatin subunits and the types and kinds of postsynthetic modifications occurring on histones, such as acetylation, methylation, and phosphorylation. The subsequent chapter deals extensively on histone phosphorylation, especially histone H1, H1M, H2A, and H3, during the cell cycle. Another chapter describes a selective histone leakage from nuclei during isolation accounting for the role of histone acetylation and phosphorylation in gene expression. This book goes on examining the assembly of microtubules and structural analysis on the regulatory role of calcium into a pattern for mitosis regulation. Other chapters discuss the methods used to measure intracellular pH changes as a function of the cell cycle of Physarum and the quantitative and qualitative changes taking place during the various phases of the cell cycle. The use of mammalian cell fusion to study cell cycle regulation and the protein synthesis regulation during the cell cycle in Chlamydomonas reinhardi are then discussed. The final chapters focus on the regulation of expression of an inducible structural gene during the cell cycle of the green alga Chlorella. The chapters provide evidence for a model of positive and negative oscillatory control of inducible gene expression. An analysis of the expression of cytoplasmic genes as a function of the cell cycle using pedigrees of a large number of individual yeast cells is also included. This book will appeal to a wide variety of life scientists and to molecular, cellular, and developmental biologists.

Gas Phase Inductible and Repressible Gene Expression in Bioreactors on the Example of Human B-interferon Nov 10 2021

The Impact, Pervasivity and Regulation of Two Phase-separating Entities Jun 24 2020 THE IMPACT, PERVASIVITY AND REGULATION OF TWO PHASE-SEPARATING ENTITIES: VTS1, A CONSERVED GENE EXPRESSION REGULATOR, AND, RUBISCO, AN ABUNDANT CARBON-FIXING ENZYME.

Characterization of Emergent Spatial-temporal Orders in Transcription Regulatory Networks Using Phase Locking Analysis Dec 11 2021 The study of gene regulatory networks (GRNs) is paramount for continued breakthroughs in understanding the genetic architecture of life and how alterations thereof contribute to disease. The complex spatio-temporal orders within GRNs are studied primarily through the modeling of time-course gene expression data. Recently, gene expression profiling technology has improved greatly in regards to accuracy and resolution, enabling novel methodology development and characterization of GRNs. Many methods have been utilized to model GRNs from gene expression data (correlational measures, time-warping, coherence, and/or causality, etc). In this study, we propose a new approach based on phase locking analysis that compliments existing methods by providing a fundamentally different metric, rooted in statistical physics, for GRN interaction inferences and analysis. Using high temporal resolution gene expression data of Saccharomyces cerevisiae (yeast) during cell cycle, we show that the phase locking metric is a great classifier for interaction and reveals subtle regulatory trends. First, a base-line was established by calculating all phase locking information (for up to 4:3 locking) for every possible gene pairing in the entire yeast genome. Using transcription factor (TF) binding data, we formed positive and negative control groups. We also constructed a high quality positive control group using an in-depth literature compilation and manual annotation by YoungLab at MIT. A sensitivity vs. specificity plot (for correct identification of interaction) was created. The area under the curve (a measure of accuracy) for the 1:1 phase locking index was 0.77 and 0.74 for the alpha factor and CDC28 data sets, respectively. Correlation coefficient yielded an AUC of 0.51. We also applied phase locking analysis to genes co-regulated by cell-cycle TFs and to all 13 3-node subgraphs (found via FANMOD) present within the yeast genome. The results revealed a trend in the locking profile of motif gene pairs, a trend in the locking as a function of number of edges for subgraphs, and a potential increase in multi-state stability for high edge number subgraphs. Our research has led to the conclusion that phase locking analysis shows great promise for GRN modeling and should be further explored by the systems biology community.

Genetics and Biotechnology of Bacilli Dec 31 2020 Genetics and Biotechnology of Bacilli, Volume 3 covers the proceedings of the Fifth International Conference on Genetics and Biotechnology of Bacilli, held on July 9-12, 1989 at the Asilomar Conference Center, Pacific Grove, California. It summarizes the remarkable progress made in the genetics and biotechnology fields of Bacilli. It is organized into four parts, encompassing 43 chapters, which focus on gene regulation and structure, enzyme structure, Bacillus thuringiensis toxins, and stationary phase gene regulation. Part I covers topics related to gene regulation and structure of Bacilli, such as control of gene expression, mutation, genetic organization, DNA sequence analysis, and identification of transcript units. It also discusses gene replication in Bacillus subtilis plasmids, levanase operon of B. subtilis, and characterization of global regulon in B. subtilis. The next part of this book focuses on the structure of various enzymes found in B. subtilis, including alpha amylases, subtilisin, alkaline phosphatase, and levansucrase. Part III discusses the generation of functional B. thuringiensis toxin hybrid genes, regulation of crystal protein gene promoters, toxicity of B. thuringiensis delta-endotoxin, and insecticidal activity of chimeric protoxins. The concluding part covers the aspects of signal transduction, regulation of differential gene expression during B. subtilis sporulation, and gene cloning and deletion for extracellular proteases of B. subtilis. It also discusses genetic and biochemical aspects of protein phosphorylation; properties of B. subtilis spores; control of stationary phase gene expression; and the novel regulatory gene, senS, of B. subtilis. This book is a valuable source of information for microbiologists, research biologists, and Bacilli enthusiasts.

Regulation of Gene Expression in Stationary Phase of Bacillus Subtilis Jan 24 2023

Investigation of Growth Phase Infectivity and Gene Expression Signatures Important for Latent Mycobacterial Infection Sep 08 2021

Controlled Gene Expression Using Acute Phase Response Elements Jul 06 2021

Molecular Aspects of Gene Expression in Plants Nov 17 2019 Nuclear DNA. RNA struture and metabolism. Protein syntesis. Nucleic acids and protein syntesis in chloroplasts and mitochondria. The cell cycle. Molecular aspects of differentiation. Plant growth substances.

Regulation of Nuclear Phase of Eukaryotic Gene Expression by Ubiquitin-proteasome System Apr 22 2020 Eukaryotic gene expression is a highly synchronized cellular process whose nuclear phase is comprised of transcription, and mRNA processing and export. Transcription can be further comprised of transcription initiation, and elongation. Regulation of transcription initiation, transcription elongation, and mRNA processing and export are crucial for normal cellular function, since misregulation of these processes are associated with various diseases including cancer. Many factors or proteins are associated with these cellular processes which are modulated by different regulatory processes to maintain normal cellular function. Ubiquitin-proteasome system (UPS) is one of the recently studied regulatory processes. Over the years, ubiquitin and 26S proteasome have emerged as important regulatory factors in coordination of transcription and coupled mRNA export. However, the mechanisms as to how the ubiquitin and 26S proteasome regulate transcription and coupled mRNA export have not been clearly elucidated. Therefore, my dissertation has focused on understanding the role of UPS in these important cellular processes: transcription initiation, transcription elongation and mRNA export. The results have shown the non-proteolytic role of 19S RP of 26S proteasome in regulation of transcriptional initiation of SAGA and TFIID-dependent PHO84 gene. It was found that 19S RP facilitates both SAGA- and NuA4-TFIID-dependent transcriptional initiations of PHO84 via increased recruitment of the coactivators SAGA and NuA4 HAT, which promote TFIID-independent and -dependent PIC formation in the presence and absence of an essential nutrient, Pi, in the growth media for transcriptional initiation, respectively. Next, our studies have uncovered the role of UPS in regulation of transcriptional elongation. It was found that E3 ubiquitin ligase, San1, mediated UPS regulation of transcription elongation factor, FACT is required for stimulating nucleosomal reassembly at the coding sequence of active genes for proper transcription elongation. We also found the interaction of FACT with another important transcription elongation factor, Paf1C via NTD (N-ter domain) of Cet1p (mRNA capping enzyme) to regulate transcription elongation. Subsequently, our results revealed a novel regulation of Paf1 component of Paf1C by UPS to regulate its abundance for proper cellular function. Transcription of genes could be blocked by DNA damage which can be repaired by transcription-coupled DNA repair (TCR) pathways. SUMOylation, another PTM (Post-translational modifications) like ubiquitination, is implicated in regulation of many DNA repair pathways including TCR, but it is not clearly understood how SUMOylation and associated enzymes are involved in regulation of such pathways. Here, we revealed the distinct role of SUMO ligases Siz1 and Siz2 in response to several DNA damaging agents such as UV, MMS (methyl methanesulfonate), HU (Hydroxyurea) and H2O2 (Hydrogen peroxide). Finally, we have extended our research works to understand the regulatory mechanisms of mRNA export by UPS. We found the interaction of TREX (Transcription/Export) component Sub2 with Mdm30 (F-box protein) for ubiquitination and proteasomal degradation of Sub2 in a transcription-dependent manner to regulate mRNA export. We also found the role CBC (Cap binding complex) in regulation of nuclear mRNA export. Collectively, the results of this study postulate a better understanding of regulation of transcription initiation, transcription elongation, and mRNA export by UPS.

Two-Phase Clustering Strategy for Gene Expression Data Sets Jul 18 2022

Insights Into Gene Regulation by Genome Structure, Phase Separation and Developmental Signaling Apr 03 2021 Proper regulation of gene expression is essential to the developmental processes that give rise to hundreds of different cell types with unique cellular identities. Regulation of protein-coding and long non-coding RNA genes by RNA polymerase 11 is carried out by the coordinated action of transcription factors and cofactors. Transcription factors can be cell-type specific and bind cell-type specific gene regulatory regions called enhancers, which can be located far upstream or downstream from the gene they activate. The enhancer-bound factors can loop to the promoters of cell-type specific genes to enhance the levels of transcription of these genes, and studies described in this thesis have provided new insights into the factors that contribute to this looping process (Weintraub et al., 2017). Recent studies have revealed that super-enhancers, which contribute to regulation of genes with prominent roles in cell identity, form phase-separated condensates that compartmentalize and concentrate the transcription apparatus at these genes. This insight led us to test the idea that signaling factors, which bring information regarding the developmental environment of cells to the transcription apparatus, might preferentially interact with super-enhancers through condensate interactions that were not considered in previous studies of signaling. Our studies confirmed that super-enhancer condensate do indeed facilitate the preferential localization of signaling factors to genes with prominent roles in cell identity (Zamudio et al., 2019). Thus, the studies described in this thesis provide new insights into gene regulation by genome structuring, phase separation and developmental signaling.

Cell Cycle Phase Dependent Gene Expression and the Regulation of Cell Growth Dec 23 2022

Control of M-G1 phase-specific expression in fission yeast Sep 20 2022 The mitotic cell cycle underlies propagation of eukaryotic cells, continually duplicating and dividing. The past few years have seen major advances in understanding of the regulatory mechanisms that impose on the cell cycle to tightly co-ordinate progression through its individual phases, safeguarding the timing and integrity of its hallmark events, DNA synthesis and mitosis. Transcription is prominent among these processes, manifesting its importance for cell cycle controls by the large number of eukaryotic genes that are expressed at specific cell cycle times. Certain genes are cell cycle regulated in a number of organisms, suggesting that their phase-specific transcription is important for all eukaryotic cells. The budding and fission yeasts, Saccharomyces cerevisiae and Schizosaccharomyces pombe, have been used extensively as model organisms for the study of the eukaryotic cell cycle and cell cycle-regulated transcription, because the cell cycle machinery is conserved among eukaryotes and they are experimentally tractable. Recent microarray analyses have shown that cell cycle-specific expression is a frequent theme in the two yeasts, identifying consecutive, inter-dependent, waves of transcriptional activity, coinciding with the four main cell cycle transitions; G1-S, S, G2-M and M-G1 phases. Each phase-specific transcriptional wave corresponds to at least one group of co-regulated genes, sharing common cis- and trans- acting elements. The work presented in this thesis delves into the regulatory network that drives phase-specific gene expression during late mitosis-early G1 phase in fission yeast. During this late cell cycle stage, fission yeast and, indeed, every eukaryotic cell, undergo major changes; each completes mitosis and cytokinesis, partitioning its duplicated genetic and cytoplasmic material into two progeny cells, which then themselves prepare for a new round of mitotic cell division. Consistent with their periodic pattern of expression, most of the genes transcribed during the M-G1 interval in S. pombe encode proteins that execute important functions during late mitosis and cytokinesis. A DNA sequence promoter motif, the PCB (Pombe cell cycle box), has been identified in fission yeast that confers M-G1 specific transcription, and is bound by the PBF (PCB binding factor) transcription factor complex. PCB promoter motifs are present in several M-G1 transcribed genes, including cdc15, spo12, sid2+, fin1+, slp1+, ace2+, mid1+/dmf1+ and plo1+, the latter encoding a Polo-like kinase that also regulates M-G1 gene expression and influences the PCB-dependent binding properties of PBF. Three transcription factors, Sep1p and Fkh2p, both forkhead-like transcription factors, and Mbx1p, a MADS-box protein, have been implicated in M-G1 specific gene expression and are thought to be components of PBF. Consistent with Fkh2p and Sep1p regulating M-G1 specific transcription, forkhead-related sequences are present in the genes' promoters. Notably, fkh2+ contains both PCB and forkhead promoter sequences and is transcribed during the M-G1 interval, implying that Fkh2p and Plo1p regulate gene transcription during late mitosis and ensuing passage through cytokinesis via feedback loops. This study provides further evidence about transcriptional regulation late in the fission yeast cell cycle, revealing that the PCB sequence is crucial for M-G1 specific transcription, with forkhead-associated DNA motifs playing a parallel but smaller regulatory role. Consistent with this hypothesis, work here and elsewhere shows that both Fkh2p and Sep1p control phase-specific expression of their co-regulated genes through the PCB and forkhead sequences. Notably, data in this thesis reveal that these two forkhead transcription factors associate with each other in vitro and in vivo and bind in vivo to the PCB promoter regions of M-G1 transcribed genes, including cdc15+ and plo1+, in a cell cycle specific manner, consistent with Fkh2p repressing and Sep1p activating transcription. Furthermore, Fkh2p contacts its own promoter, suggesting that it regulates its own expression via a negative feedback mechanism. The Plo1p kinase is shown here to bind in vivo to Mbx1p throughout the cell cycle and in a manner that requires both its kinase and polo-box domains. In agreement with this observation, Plo1p can phosphorylate in vitro Mbx1p, itself known to become phosphorylated during late mitosis. This is the first time that a Polo-like kinase has been shown to bind and phosphorylate a MADS-box protein in any organism. Moreover, in concert with Plo1p binding and phosphorylating Mbx1p, ChIP assays here reveal that this kinase interacts in vivo with the PCB promoter DNA of M-G1 expressed

genes, including cdc15+ and fkh2+, in a cell cycle-dependent manner with a timing that coincides with low levels of expression, but follows promoter binding by Fkh2p. Given that Plo1p has previously been shown to positively influence M-G1 dependent transcription, its cell cycle pattern of promoter contact suggests that this Polo-like kinase functions at the genes' promoters, most-likely via binding and phosphorylation of Mbx1p, to re-stimulate transcription, following repression by Fkh2p. In parallel, these findings suggest that Plo1p regulates its own expression via a positive feedback loop. Overall, the work presented in this thesis unravels crucial regulatory aspects of the transcriptional network that drives M-G1 specific transcription in S. pombe: it suggests an important role for the PCB promoter motif in transcriptional regulation; it proposes that Fkh2p acts as a repressor while Sep1p as an activator of late mitotic transcription; it reveals and proposes novel functions for Plo1p, a conserved Polo-like kinase family member, involving its association with Mbx1p, a MADS box protein, and its cell cycle specific recruitment to PCB promoters of M-G1 transcribed genes. As transcriptional systems, encompassing homologues of most of the components of this S. pombe M-G1 specific transcriptional network operate both in S. cerevisiae and humans, this demonstrates their importance for mitotic cell cycle progression. Thus this work potentially offers new insights into M-G1 specific gene expression in all eukaryotes.

Phase Dependent Regulation of Gene Expression by Light Nov 22 2022

Prokaryotic Gene Expression May 16 2022 Prokaryotic gene expression is not only of theoretical interest but also of highly practical significance. It has implications for other biological problems, such as developmental biology and cancer, brings insights into genetic engineering and expression systems, and has consequences for important aspects of applied research. For example, the molecular basis of bacterial pathogenicity has implications for new antibiotics and in crop development. Prokaryotic Gene Expression is a major review of the subject, providing up-to-date coverage as well as numerous insights by the prestigious authors. Topics covered include operons; protein recognition of sequence specific DNA- and RNA-binding sites; promoters; sigma factors, and variant tRNA polymerases; repressors and activators; post-transcriptional control and attenuation; ribonuclease activity, mRNA stability, and translational repression; prokaryotic DNA topology, topoisomerases, and gene expression; regulatory networks, regulatory cascades and signal transduction; phosphotransfer reactions; switch systems, transcriptional and translational modulation, methylation, and recombination mechanisms; pathogenicity, toxin regulation and virulence determinants; sporulation and genetic regulation of antibiotic production; origins of regulatory molecules, selective pressures and evolution of prokaryotic regulatory mechanisms systems. Over 1100 references to the primary literature are cited. Prokaryotic Gene Expression is a comprehensive and authoritative review of current knowledge and research in the area. It is essential reading for postgraduates and researchers in the field. Advanced undergraduates in biochemistry, molecular biology, and microbiology will also find this book useful.

- Analysis Of Gene Expression In Cardiac Development And Disease
- Regulation Of Gene Expression In Enteropathogenic Bacteria Volume II
- Cell Cycle Regulation
- Molecular Aspects Of Gene Expression In Plants
- Basic Genetics