

POGIL - Gene Expression: Transcription

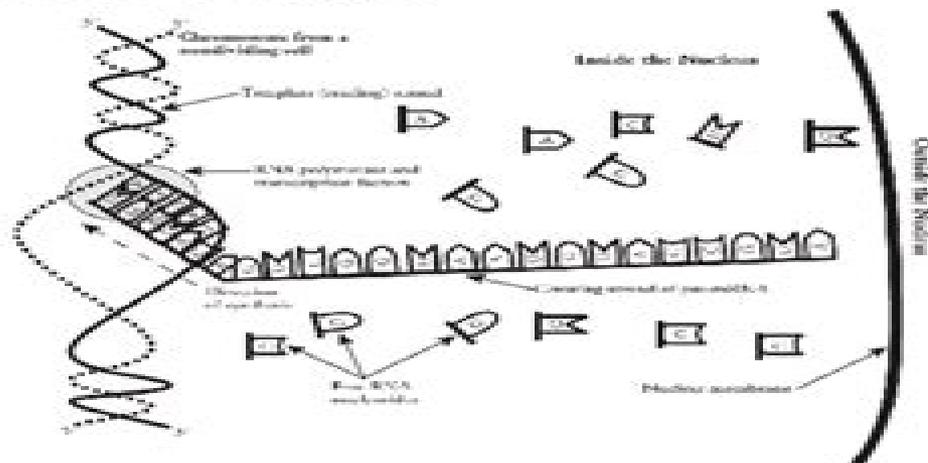
How is mRNA synthesized and what message does it carry?

Why?

Deoxyribonucleic DNA is often referred to as a genetic blueprint. In the same way that blueprints contain the instructions for construction of a building, the DNA found inside the nuclei of cells contains the instructions for assembling a living organism. The DNA blueprint carries its instructions in the form of genes. In most cases the genes direct the production of a polypeptide, from which other more complex proteins, such as enzymes or hormones, may be constructed. These polypeptides and other molecules run the organism's metabolism and, in multicellular

organisms, dictate what each cell's job is. So, what is the language of these instructions and how are they read and decoded by the cellular organelles? This activity will focus on the decoding of genes in eukaryotes.

Model 1 - Transcription



1. Consider the eukaryotic cell in Model 1.

a. Where in the cell is the DNA found?

b. Where in the cell does transcription take place?

2. Refer to Model 1.

a. What polymer is synthesized during transcription?

b. What monomers are used to construct this polymer and where are they found?

3. According to Model 1, what enzyme is required for transcription? (*Hint: Think about how enzymes are named. What ending is used for enzyme names?*)

4. Refer to Model 1.

a. What is the base-pair rule for a DNA strand matching an RNA strand?

b. Compare this base-pair rule with that of two DNA strands.

5. Which strand of the DNA contains the "blueprint" for the pre-mRNA?

6. Consider Model 1.

a. In which direction is the DNA molecule read? _____

b. The DNA strand and pre-mRNA strand are anti-parallel. With this in mind label the 3' and 5' ends of the pre-mRNA strand in Model 1.

c. In which direction is the pre-mRNA molecule constructed? _____

7. Before printing presses were available, books had to be transcribed in order to share the information

Pogil Gene Expression Translation Key

William Lewis Noderer



Poijl Gene Expression Translation Key:

Gene Expression, Translation and the Behavior of Proteins Lester Goldstein, 1980 **Translational Regulation of Gene Expression** J. Ilan, 2013-11-11 **Translational Control of Gene Expression** Nahum Sonenberg, John W. B. Hershey, Michael Mathews, 2000 There is fresh interest in protein synthesis and recognition of the key role of translational control mechanisms in regulating gene expression This new monograph updates and expands the scope of the 1996 publication *Translational Control* but it also takes a fresh look at the field In a new format the first eight chapters provide broad overviews while each of the additional twenty eight has a focus on a research topic of more specific interest The result is a thoroughly up to date account of initiation elongation and termination of translation control mechanisms in development in response to extracellular stimuli and the effects on the translational machinery of virus infection and disease This book is essential reading for students entering the field and an invaluable resource for investigators of gene expression and its control

Genetics of Translation Mick F. Tuite, Marguerite Picard, Monique Bolotin-Fukuhara, 1988 *Fidelity and Quality Control in Gene Expression*, 2012-01-25 The goal of this volume is to provide a comprehensive mechanistic and quantitative view of the processes that mediate or influence the quality control in translation In addition to discussing processes with direct contribution to translation fidelity such as aminoacylation of tRNAs and translation elongation itself special attention is given to other processes with impact on quality control detection and elimination of defective mRNAs recycling and translation re initiation mRNA editing and translational recoding through programmed frame shifting Provides a comprehensive mechanistic and quantitative view of the processes that mediate or influence the quality control in translation Special attention is given to other processes with impact on quality control detection and elimination of defective mRNAs recycling and translation re initiation mRNA editing and translational recoding through programmed frame shifting

Translation Mechanisms Jacques Lapointe, Lea Brakier-Gigras, 2003-07-31 *Translation Mechanisms* provides investigators and graduate students with overviews of recent developments in the field of protein biosynthesis that are fuelled by the explosive and synergic growth of structural biology genomics and bioinformatics The outstanding progress in our understanding of the structure dynamics and evolution of the prokaryotic and eukaryotic translation machinery as well as applications in medicine and biotechnology are described in 26 chapters covering recent discoveries on the subtleties of tRNA aminoacylation with natural and unnatural amino acids the control of mRNA stability a key step of gene regulation ribosome structure and function in the era of the atomic crystal resolution of the ribosome the regulation of the biosynthesis of the translational machinery components the action of a variety of inhibitors of translation and the prospect for clinical studies

Translation In Eukaryotes Hans Trachsel, 1991-07-24 This book presents an up to date review of the mechanisms and regulation of translation in eukaryotes Topics covered include the basic biochemical reactions of translation initiation elongation and termination and the regulation of these reactions under different physiological conditions and in

virus infected cells The book belongs on the shelf of everyone interested in translation in eukaryotes including students and researchers requiring comprehensive overviews of most aspects of translation and instructors who want to cover these topics at an advanced level

Control of Gene Expression Through Coupling of Transcription and Translation Flint Ruben Stevenson-Jones,2017
Gene Expression and Regulation Mr. Rohit Manglik,2024-06-24 Examines mechanisms of gene expression including transcription translation and epigenetic regulation with applications in molecular biology

Programmed Alternative Reading of the Genetic Code Philip J. Farabaugh,1997-03-15 2 The Translational Machinery 5 Translation Initiation in Prokaryotes 6 Translation Initiation in Eukaryotes 8 14 Translation Elongation Translation Termination in Prokaryotes 16 Translation Termination in Eukaryotes 17 Error Correction in Translation 18 A Structural Basis of Error Correction in Translation 20 Ribosome Editing A Failsafe Error Correction Mechanism 22 Conclusions 22 3 Errors During Elongation Can Cause Translational 29 Frameshifting Spontaneous Frameshifting Versus Programmed Frameshifting 30 Spontaneous Frameshifts Can Be Induced at Specific Codons 31 4 Programmed 1 Frameshifting 41 The pifE Gene of E coli 41 Using the pifE System to Study General Frameshifting in E coli 46 Ty Retrotransposons in Yeast 47 Frameshifting in Retrotransposon Ty1 Occurs by tRNA Slippage 48 Frameshifting in Retrotransposon Ty3 Occurs by Out of Frame Binding of tRNA 51 The Rat Ornithine Decarboxylase Antizyme Gene 56 Summary 62 5 Programmed 1 Frameshifting in Eukaryotes 69 Programmed 1 Frameshifting in Eukaryotes 69 1 Frameshifting Occurs on a Slippery Heptamer 71 The Simultaneous Slippage Model 72 of 1 Frameshifting by a Downstream Pseudoknot 77 Stimulation Does the Pseudoknot Only Block Passage of the Ribosome 79 Not All Pseudoknots Which Cause Ribosomes to Pause Can Stimulate 1 Frameshifting 84 Is There a Pseudoknot Recognizing Factor 88 Some Simultaneous Slippage Sites Do Not Include a Stimulatory Pseudo knot 91 Frameshifting Regulates a Morphogenetic Process 92 6 Programmed 1 Frameshift Sites in Prokaryotes 103 The dnaXGene 1 Frameshifting Stimulated by Both Upstream and Downstream Elements 103 Programmed 1 Frameshifts in Insertion Sequences Are Mechanistically Diverse In Vitro Transcription and Translation Protocols Martin J. Tymms,2008-02-02 Most laboratories conducting studies that use molecular biology techniques employ in vitro transcription and translation systems as a routine part of their day to day research The commercial availability of purified bacterial RNA polymerase and the availability of robust tra lation systems has made in vitro systems attractive not only as an alt native to the in vivo expression of genes but also as good model systems for studying specific aspects of transcription and translation Although fairly efficient eukaryotic translation systems have been established for a number of years reconstitution of transcription in vitro has proved to be more difficult Recent improvements in fractionation techniques and the cloning of proteins involved in transcription have made this a fast moving area of research Considerable progress has also been made in recent years in developing in vitro systems to study transcription and translation in chloroplasts and mitochondria together with systems for the study of protein import In Vitro Transcription and

Translation Protocols provides many detailed experimental procedures for prokaryotic transcription and translation systems together with protocols for many key techniques used in the analysis of eukaryotic transcription. In keeping with the successful format of preceding volumes of the Methods in Molecular Biology series, step by step instructions are provided together with extensive notes that cover troubleshooting and special tips considered important. Translation Factors in Control of Gene Expression, 1997. *A Multi-level Approach to Understanding the Regulation of Translation Initiation*. Heather Rochelle Keys, 2016. mRNA translation is an extremely complex process required for life. Translation consumes vast amounts of cellular resources and organisms have evolved tight regulatory mechanisms to control this process which are often deregulated in cancer and other disease states. Initiation as the rate limiting step in translation is particularly well regulated. Two kinase pathways that respond to cellular stresses, the GCN2 and mTORC1 pathways, sense amino acid insufficiency to inhibit translation initiation at distinct points. GCN2 is activated in response to amino acid deprivation and inhibits formation of the ternary complex comprising eIF2 GTP and the initiator methionyl tRNA which is required for recognition of the start codon. Although translation of most mRNAs is greatly suppressed when GCN2 is activated, mRNAs with certain cis elements escape inhibition. In contrast, the mTORC1 pathway is inhibited by the lack of amino acids which ultimately results in the disruption of eIF4F, a multiprotein initiation factor complex that coordinates the recruitment of the small ribosomal subunit to the 5' end of mRNA. Like a decrease in the amount of ternary complex, disruption of eIF4F also suppresses translation of most mRNAs, however, the translation of a subset of mRNAs harboring a 5' TOP motif is even more dramatically reduced when mTORC1 is inhibited. Here we describe the translational program downstream of amino acid insufficiency and present evidence of a novel uORF in murine ATF4 whose ribosome occupancy is regulated by the presence of amino acids. We identify the 4EBPs as the mTORC1 substrates that mediate the major effects of mTORC1 inhibition on translation of mRNAs, both globally and on 5' TOP mRNAs specifically. Although we cannot mechanistically explain the dependence of 5' TOP mRNA translation on mTORC1 activity, we uncover a surprising role of the cap proximal sequence in eIF4E recruitment. We systematically assess how the juxtacap sequence modulates eIF4E binding and translation and present a model whereby the juxtacap sequence dictates the cap proximal RNA secondary structure in an mRNA context dependent manner. *Translation Pausing*. Cameel H. Makhoul, 2002. Transcription and translation. U Satyanarayana, 2014-11-07. *Transcription and translation*. Post-transcriptional Control of Gene Expression. Orna Resnekov, Alexander von Gabain, 2011-10-12. Many important cellular processes rely on posttranscriptional control of gene expression. This book describes the mechanisms of gene expression at this level that occur in the cytoplasm of prokaryotes and eukaryotes. Several introductory chapters discuss the general principles of translation and mRNA stability. The interactions of mature mRNA with the translational machinery, the components of mRNA degradation and antisense RNA are surveyed. Subsequent chapters discuss protein folding, transport, modification and degradation. The book is an invaluable

source of information for both newcomers and those wishing an overview of the field

Probing Determinants of Start Codon Selection for Translation Initiation

Mohammed Husain Mohsin Bharmal, 2021 Bacterial translation comprising of three steps initiation elongation and termination is a highly energy intensive step of which translation initiation is very important for fidelity of gene expression This is because the canonical start codon AUG complements both initiator and elongator methionyl tRNAs making it important for ribosome to distinguish the start AUG codon from elongator AUG codons which is thought to be mediated by base pairing of the Shine Dalgarno SD sequence in the mRNA 5' UTR and the complementary anti SD sequence in the 16S rRNA of the 30S subunit of ribosome However this mechanism was proposed based on the sequence information of few E coli phage mRNAs and 16S rRNA sequence of E coli The complementary anti SD sequence was found to be present in E coli and few other bacteria of which 16S rRNA was later sequenced and therefore this mechanism was assumed to be present universally However with advancement in sequencing technologies several high throughput studies have showed that SD Anti SD base pairing is not essential for start codon selection and transcriptomics has revealed that non SD mRNAs which lack a SD sequence in the 5' UTR and leaderless mRNAs which completely lack any 5' UTR are broadly distributed across bacteria including the model organism *Caulobacter crescentus* which contains only 30% of mRNAs having SD and can initiate translation in the absence of the SD sequence Hence to explain how the mRNA translation initiates in the absence of SD sequence another mechanism 0 unique accessibility hypothesis0 which assumes that the TIRs are more accessible less RNA secondary structure as compared to the other regions of the mRNA has been proposed and tested computationally and experimentally in various organisms To test this hypothesis in *C. crescentus* we performed computational analysis to compute the accessibility of the TIRs and other regions of mRNAs using a metric 4Gunfold which revealed similar observations indicating importance of TIR accessibility for translation initiation and correct start codon selection Further to systematically test the effects of accessibility and other factors on leaderless start codon identity and presence of short leaders and leadered mRNA translation initiation presence of SD sequences which is not looked into synthetic in vivo translation initiation reporters were designed that ensured translation of the reporter gene only from the AUG codon in the TIR allowing the control of the TIR region Translation efficiency values calculated using RNA seq and ribosome profiling data were used to test the effect of these factors on translation initiation of natural mRNAs Using these data it was found that start codon accessibility is a key determinant in correct start codon selection and initiating translation from the TIR while leader length and start codon identity impacts leaderless mRNA translation initiation efficiency and presence of SD influences leadered mRNA translation initiation efficiency in bacteria

Translational Regulation of Gene Expression

2 J. Ilan, 2011-10-12 This book which results from the dramatic increase in interest in the control mechanism employed in gene expression and the importance of the regulated proteins presents new information not covered in *Translational Regulation of Gene Expression* which was published in 1987 It is not a revision of the earlier book

but rather an extension of that volume with special emphasis on mechanism. As the reader will discover there is enormous diversity in the systems employing genes for translational regulation in order to regulate the appearance of the final product the protein. Thus we find that important proteins such as protooncogenes, growth factors, stress proteins, cytokines, lymphokines, iron storage and iron uptake proteins, and a panorama of prokaryotic proteins as well as eukaryotic viral proteins are translationally regulated. Since for some gene products the degree of control is greater by a few orders of magnitude than their transcription, we can state that for these genes at least the expression is translationally controlled. Translational regulation of gene expression in eukaryotes has emerged in the last few years as a major research field. The present book describes mechanisms of translational regulation in bacteria, yeast, and eukaryotic viruses as well as in eukaryotic genes. In this book we try to provide in depth coverage by including important examples from each group rather than systematically including all additional systems not described in the previous volume.

Functional and Structural Mapping of 5' UTR Cis-regulatory Elements that Control Translation Gun Woo Byeon, 2021

Translation can be critically and pervasively regulated in a transcript specific manner to modulate protein synthesis. However, it is poorly understood which and how cis regulatory features of the messenger ribonucleic acid (mRNA) encode variable transcript specific translation rates to impact spatiotemporal gene expression patterns. Here I address the role of 5' untranslated 5' UTR in regulating mRNA translation in vertebrate species. In the first part of the dissertation I explore the phenomenon of extreme non coding sequence conservation in vertebrate genomes at the level of RNA function in 5' UTRs. Extreme conservation is a fascinating mystery in comparative genomics in which sequence conservation at levels often greater than coding regions with invariant polypeptide sequences stretches on for hundreds of nucleotides in the non coding regions of the genome. While extreme conservation has been extensively studied for its role in transcriptional regulation, its RNA level function in translational regulation remains largely unknown. This work reveals the role of extremely conserved 5' UTRs in translational regulation of genes linked to the emergence of essential developmental features in vertebrate species. Extremely conserved 5' UTRs are found to contain cis elements that promote cell type specific non canonical translation initiation. As these elements function as RNA molecules, an understanding of their structures is essential. To this end I develop in cell mutagenesis and map icM2, a methodology that maps RNA structure using high throughput mutational analysis inside cells. icM2 maps the ensemble of multiple conformations in an extremely conserved 5' UTR which is found to be important for its translational regulatory function. I find that active RNA structural remodeling inside cells by RNA helicase activity maintains the relative balance of the conformations. Furthermore, cellular structural remodeling occurs frequently in the most conserved regions of the 5' UTRs. I propose a structural explanation for extreme conservation at the level of RNA and highlight the importance of comparative genomics and of RNA structure in understanding 5' UTR function and evolution. In the second part of the dissertation I explore the genome wide role of mammalian ribosome expansion segments (ES) in interacting with 5' UTRs to regulate mRNA

translation ESs are eukaryote specific insertions to the ribosomal ribonucleic acid rRNA They are positioned mostly at the exterior surface of the ribosome structure extending from the core of the ribosome like flexible tentacles It has been recently shown that the mammalian ES9S in 18S rRNA directly interacts with a Hox gene 5 UTR element to promote its translation Direct rRNA mRNA interaction is not a widely recognized paradigm for translation initiation in eukaryotes However addressing the potential genome wide significance of such a mechanism mediated by ribosome ESs and mRNA 5 UTRs is challenging Since rRNAs are transcribed from tandem repeats of ribosomal DNA units that can range up to hundreds of thousands of copies it has not been possible to directly manipulate ESs in most species To solve this problem I develop VELCRO IP RNA seq variable expansion segment ligand chimeric ribosome immunoprecipitation RNA sequencing VELCRO IP RNA seq interrogates the interaction of a ribosome ES with mRNA elements genome wide by combining yeast genetics in vitro biochemical pull down and high throughput sequencing By applying VELCRO IP RNA seq on mammalian ES9S hundreds of mRNA regions that interact with the ribosome via specific interaction with the ES are identified Furthermore the 5 UTR targets of ES9S are found to promote non canonical translation A number of short k mers that have Watson Crick complementary to ES9S subsequences are overrepresented in its targets suggesting potential importance of canonical base pairing These results provide evidence for the usage of direct mRNA rRNA interaction as a mechanism of translation initiation on a wider scale than previously imagined for vertebrate species Finally in the last chapter I discuss how my findings can shape future investigations into the remaining unanswered questions on 5 UTR regulation of translation Altogether this dissertation takes us a step closer to the ultimate goal of deciphering the code for translational regulation

Quantitative Analysis of Mammalian Translation Initiation William Lewis Noderer, 2014 A fundamental goal of biology is to predict the protein expression from a genomic sequence Any such quantitative proteomic prediction must account for the process of translation initiation which defines the translational reading frame and directly affects the protein synthesis rate In the eukaryotic scanning ribosome model the small ribosomal subunit traverses the mRNA starting from the 5 cap in search of a start codon which is typically an AUG The likelihood of a ribosome recognizing and initiating at any given start codon is defined as the translation initiation site TIS efficiency It is known that the mRNA sequence surrounding the start codon interacts with the scanning ribosome and impacts the TIS efficiency The goal of this work is to quantitatively predict the efficiency of initiation for every possible translation initiation site that contains an AUG start codon In order to analyze the large number of possible TIS sequences we could not rely on traditional laboratory methods but instead had to develop a new technique called FACS seq which combines high throughput cell sorting and next generation DNA sequence We applied the FACS seq method to a genetic fluorescence reporter representing all 65 536 possible TIS sequences spanning the 6 bases upstream and 2 bases downstream of the start codon From our FACS seq data we found the TIS motif RYMRMVAUGGC to have the highest translation efficiency where R A or G Y C or U M A or C and V A C or G However by

fitting a dinucleotide position weight matrix to the TIS efficiency data it was shown that dinucleotide interactions which cannot be conveyed in a single TIS motif significantly impact the initiation efficiency Here FACS seq was applied to the study of translation initiation but in principle the method could be applied to any genetic library that uses a fluorescence reporter The FACS seq dataset combined with modeling enabled the prediction of translation initiation efficiency for any mRNA transcripts based solely on the sequence We first investigated how mutations near an annotated start codon altered gene expression thereby causing disease A collection of somatic TIS mutations found in tumor samples were screened to identify mutations that altered gene expression in a manner consistent with known tumor expression patterns Therefore the identified TIS mutations potentially drove the tumor formation by altering the protein synthesis rate Next we considered how leaky scanning past low efficiency TISs allows for initiation at down stream alternative sites Similar to transcriptional isoforms the translational isoforms resulting from alternative initiation sites expands the proteomic diversity with important biological consequences A quantitative leaky scanning model was used to predict mRNA transcripts with in frame alternative initiation sites which would generate truncated protein isoforms These predictions were supported experimentally by ribosome footprint profiling data In conclusion the extensive analysis of the TIS sequence space using FACS seq has improved our ability to quantitatively predict the efficiency and location of translation initiation

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