

# Gene Expression—Transcription

How is mRNA synthesized and what message does it carry?

## Why?

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



# Gene Expression Translation Pogil Answer

**Hamilton Courtney Hodges**



## Gene Expression Translation Pogil Answer:

**Gene Expression, translation and the behavior of proteins** Lester Goldstein, David Marshall Prescott, 1980

*Translational Control of Gene Expression* Nahum Sonenberg, John W. B. Hershey, Michael B. Mathews, 2001 Since the 1996 publication of *Translational Control* there has been fresh interest in protein synthesis and recognition of the key role of translation control mechanisms in regulating gene expression This new monograph updates and expands the scope of the earlier book 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 translation 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

*Translational Regulation of Gene Expression* J. Ilan, 2013-11-11      [Translational Regulation of Gene Expression 2](#) J. Ilan, 2012-12-06 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 mechanisms 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      [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

**Interaction of Translational and Transcriptional Controls in the Regulation of Gene Expression** Marianne Grunberg-Manago, Brian Safer, 1982 Interaction of Translational and Transcriptional controls in the regulation of gene Expression

**Inducible Gene Expression, Volume 1** P.A. Baeuerle, 1994-12-22 Cells have evolved multiple strategies to adapt the composition and quality of their protein equipment to needs imposed by changes in intra and extracellular conditions The appearance of proteins transmitting novel functional properties to cells can be controlled at a transcriptional posttranscriptional translational or posttranslational level Extensive research over the past 15 years has shown that transcriptional regulation is used as the predominant strategy to control the production of new proteins in response to extracellular stimuli At the level of gene transcription the initiation of mRNA synthesis is used most frequently to govern gene expression The key elements controlling transcription initiation in eukaryotes are activator proteins transactivators that bind in a sequence specific manner to short DNA sequences in the 5' of genes The activator binding sites are elements of larger proximity control units called promoters and enhancers which bind many distinct proteins These may synergize or negatively cooperate with the activators The de novo binding of an activator to DNA or if already bound to DNA its functional activation is what ultimately turns on a high level expression of genes The activity of transactivators is controlled by signalling pathways and in some cases transactivators actively participate in signal transduction by moving from the cytoplasm into the nucleus In this first volume of Inducible Gene Expression leading scientists in the field review six eukaryotic transactivators that allow cells to respond to various extracellular stimuli by the expression of new proteins

**Translation Factors in Control of Gene Expression**, 1997 **Inducible gene expression**, 1995 *Control of Gene Expression* Norman Maclean, 1976 The control of gene expression and its levels of action Gene expression in prokaryotes Experimental systems of differential gene function in eukaryotes systems involving one type of protein Experimental systems of differential gene function in eukaryotes systems of limited complexity Experimental systems of differential gene function in eukaryotes systems not well understood in molecular terms RNA involvement in gene expression General concepts of gene regulation

*Mechanisms Coupling Steps in Gene Expression* Jeanne Lynn Hsu, 2008 Eukaryotic gene expression is a multi step process beginning with transcription of pre mRNA in the nucleus The pre mRNA undergoes several processing steps including 5' capping splicing and 3' end processing Finally spliced mRNA is exported to the cytoplasm for protein synthesis Although each of these steps requires distinct machineries they are physically and functionally coupled to one another This dissertation focuses on understanding the coupling among steps in gene expression from transcription to translation In Chapter 2 I describe the development of a mini nuclear extract method combined with RNA interference to determine the functions of specific proteins in the coupled RNAP II transcription splicing reaction The feasibility of this method was demonstrated by knocking down two model proteins the conserved splicing factors U1C and Slu7 My data indicate that the

knockdown mini nuclear extract is a rapid and general in vitro strategy for determining the functions of specific proteins in gene expression as well as in other cellular processes In Chapter 3 I investigate the function of eIF4AIII a translation initiation like factor present in the nucleus My work showed that eIF4AIII is recruited to spliced mRNPs and is a component of the exon junction complex which is a protein complex recruited upstream of exon junctions during splicing In addition my work indicated that exon junction complexes are recruited to every exon junction present in the mRNA Finally eIF4AIII as well as a translation factor DDX3 co localizes with splicing factors in nuclear speckle domains Thus eIF4AIII and DDX3 may be recruited to mRNA during splicing in the nucleus and then function in translation related processes in the cytoplasm

Molecular basis of the nutritional regulation of gene expression via mRNA translation Jigna Vijay Patel,2002

**Inducible Gene Expression: Hormonal signals** Patrick Alexander Baeuerle,1995      Gene Expression Fumiaki Uchiumi,2022      *Single-Molecule Studies of Gene Expression* Hamilton Courtney Hodges,2009 During the twentieth century researchers made significant advances in understanding the biochemical basis for gene expression In the twenty first century the development of single molecule manipulation techniques allowed researchers for the first time to directly observe the activities of gene expression in real time In particular experiments involving single molecule visualization and manipulation have revealed the processes of gene expression to be stochastic events governed by the physics of the nanoscale Our investigation of eukaryotic transcription using single molecule optical trapping techniques has shown that RNA polymerase II is a type of molecular motor that periodically disengages its DNA substrate and freely diffuses along it resulting in transient pausing events The behavior of the polymerase during these pauses has turned out to be critical for understanding how the polymerase transcribes through nucleosomes In this dissertation I report that the nucleosome behaves as a fluctuating barrier that locally but dramatically affects the transcription dynamics of the polymerase The polymerase rather than actively separating DNA from histones functions instead as a ratchet that rectifies nucleosomal fluctuations We also obtained direct evidence that transcription through a nucleosome involves transfer of the core histones behind the transcribing polymerase via a transient DNA loop This work has significantly addressed how the interplay between polymerase dynamics and nucleosome fluctuations affects the dynamics of gene expression Using optical trapping techniques we also directly observed the process of translation by the E coli ribosome for the first time We observed that translation occurs through successive translocation and pause cycles The distribution of pause lengths indicated that at least two rate determining processes control each pause Additionally we have confirmed that each translocation step measures three bases one codon and observed that each step occurs in less than 0.1 s We also observed that translocation and RNA unwinding are strictly coupled ribosomal functions The emerging picture is that gene expression arises from the coordinated activities of specific macromolecular motors on their nucleic acid substrates Our observations of individual transcription and translation events support a detailed physical understanding of gene expression and its regulation      *Gene Transfer and Expression in*

*Mammalian Cells* S.C. Makrides, 2003-10-24 This volume provides a broad state of the art coverage of diverse technical topics in gene expression in mammalian cells including the development of vectors for production of proteins in cultured cells in transgenic animals vaccination and gene therapy progress in methods for the transfer of genes into mammalian cells and the optimization and monitoring of gene expression advances in our understanding and manipulation of cellular biochemical pathways that have a quantitative and qualitative impact on mammalian gene expression and the large scale production and purification of proteins from cultured cells

**From Gene to Protein: Information Transfer in Normal and Abnormal Cells** Thomas Russell, 2012-12-02 Miami Winter Symposia Volume 16 From Gene to Protein Information Transfer in Normal and Abnormal Cells presents the expression and processing of genetic information at the levels of both proteins and nucleic acids This book deals with the reassembly and mobilization of genetic information Organized into 105 chapters this volume begins with an overview of the discovery of the double helix and the search for the genetic code and the three dimensional structure of protein This text then examines the molecular mechanism by which steroid hormones regulate specific gene expression Other chapters consider the possible hazards inherent to hybrid DNA technology This book discusses as well the various problems of gene control in higher organisms which are illustrated by the changes that occur in the hemoglobin of mammals The final chapter deals with the characterization of adenovirus 2 mRNAs This book is a valuable resource for biochemists genetic engineers enzymologists scientists geneticists and molecular biologists

Mechanisms of Translation Initiation Mediated by mRNA Structure Wan-Jung Christine Lai, 2019 The initiation of translation is a critical process that controls gene expression in all cells Dysregulation of translation initiation contributes to the development of pathological conditions including cancer diabetes and obesity Despite the fundamental importance of translation initiation the essential mechanisms that underlie this process are still unknown This thesis combines in vitro in vivo and in silico approaches to test a hypothesis that mRNA secondary structure is a major determinant that governs translational initiation Using FRET we show that mRNAs and long noncoding RNAs lncRNAs have an intrinsic propensity to fold in the absence of proteins into structures in which the 5' end and 3' end are 7 nm apart irrespective of RNA length In addition single molecule FRET measurements demonstrate that instead of adopting a single structure each mRNA folds into a dynamic ensemble of structures with multiple end to end distances that are within just a few nanometers Computational estimates suggest that the inherent proximity of the ends is a universal property of most mRNA and lncRNA sequences Only guanosine depleted RNA sequences with low sequence complexity are unstructured and exhibit end to end distances expected for the random coil conformation of RNA Based on these observations we propose a novel model that explains how the universally conserved eukaryotic initiation factor 4G eIF4G poly A binding protein PABP interaction stimulates translation initiation in eukaryotes We hypothesize that PABP binding to the poly A tail can facilitate the recruitment of the cap binding protein complex eIF4E eIF4G to the 5' end of the mRNA since the 5' and 3' ends of mRNA are intrinsically close Therefore the

eIF4G PABP interaction enhances translation by exploiting the intrinsic closeness of mRNA ends Our data showed that replacing the natural 3' UTR in model mRNAs with intrinsically unstructured sequences decreases mRNA translation efficiency We also found that the synergy between the 5' mRNA cap and 3' poly A tail in protein synthesis is reduced by the introduction of unstructured sequences into the 3' UTR of mRNA Gel mobility shift assays show that eIF4E eIF4G PABP binding to mRNA is promoted by mRNA secondary structure suggesting that the synergistic enhancement of translation by the 5' cap and 3' poly A tail is mediated through the intrinsic proximity of mRNA ends In conclusion our results provide strong evidence that mRNA secondary structure plays a critical role in protein synthesis by facilitating translation initiation through a previously unidentified mechanism Our studies provide the basis for measuring computing and manipulating end to end distances and secondary structure in mRNAs in research and biotechnology

*Applications of Chimeric Genes and Hybrid Proteins* Jeremy W. Thorner, Scott Emr, John Abelson, Jeremy Thorner, 2000

**Controlling Protein Translation** Angavai Swaminathan, 2015

The control of mRNA translation is one of the many mechanisms utilized by cells to regulate gene expression How well an mRNA is translated is often determined by codes within the 3' untranslated region 3' UTR Regulatory molecules RNA and or proteins can bind these codes to influence when where and how often mRNA is translated One way in which the translational output of individual mRNA can be graded is by regulated change in the poly A tail length A long poly A tail is generally correlated with high translational efficiency whereas mRNA having a short poly A tail are poorly translated Moreover as a further level of control recent work shows more than 50% of eukaryotic transcripts undergo condition dependant alternative 3' end processing referred to as Alternative Polyadenylation APA This generates mRNA isoforms with differing 3' UTR lengths and can result in the gain or loss of the regulatory elements Variation of the position at which the pre mRNA 3' UTR is cleaved and polyadenylated can thus provide a mechanism by which the level of protein translation can be regulated That is a long 3' UTR isoform might contain multiple regulatory elements that silence translation whereas a short isoform may be translationally deregulated The translation of mRNA can be conveniently determined by its degree of association with ribosomes Actively translating mRNA show better ribosomal association than silent or poorly translating mRNA This study hypothesize that the deadenylation rate of mRNA poly A tail is specified by proteins that bind to the 3' UTR of specific transcripts and thereby regulate translational repression However it remains unresolved whether the poly A tail shortening is a direct cause or indirect consequence of translational repression In order to address this as well as to explore the functional consequence of APA a ribosome affinity isolation assay has been established which traps mRNA with translating ribosomes The subsequent comparison between ribosome enriched RNA and the total RNA within the sample serves as a surrogate read out of mRNA translation at steady state In addition to investigate if any adenylation state modulators are responsible for differential translation using reporters differing in their 3' UTRs a classic growth based assay was designed This was based on modification of the HIS3 gene locus such that life on media lacking histidine depends on the

stabilization of the HIS3 mRNA poly A tail and thus increased His3p protein expression However this study revealed an unappreciated complexity in the control of 3 UTR dynamics in the endogenous genomic context that is not easily predicted or overcome by standard genetic engineering methodologies Overall this thesis will provide mechanistic insight into the 3 end mediated control of mRNA translation



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