BIO 311C Spring 2010

Lecture 35 – Monday 26 Apr.

Illustration of Information Flow in Prokaryotic and Eukaryotic Cells

Textbook Fig. 17.3, p. 329



eukaryotic cell

Nuclear envelope DNA TRANSCRIPTION Pre-mRNA RNA PROCESSING mRNA Ribosome TRANSLATION Polypeptide

All information flow in prokaryotic cells occurs in the cytoplasmic matrix. Relatively little processing of information molecules occurs in prokaryotic cells.

Information flow and processing in eukaryotic cells is partitioned between the nucleoplasm and the cytoplasmic matrix.

Additional systems of information flow in eukaryotes occur within the matrix of mitochondria and in the stroma of plastids (not shown in these illustrations). These organellar systems of information flow are very similar to the information flow systems in prokaryotic cells.

Flow of Information in Cells



Use of the Genetic Code



portion of a molecule of messenger RNA

Second mRNA base								Key	to t	he	genetic
13		U		С		A		G			
FIRST MKINA Dase (5' end)	U	υυυ ⁻ υυς _	Phe	ucu ⁻ ucc	Ser	UAU UAC	Tyr	UGU UGC	Cys Stop	U C	
		UUA -	Leu	UCA		UAA	Stop	UGA		Α	
		UUG _		UCG _		UAG	Stop	UGG	Trp	G	
	с	cuu -	Leu	ccu -	Pro	CAU -	Hie	CGU -	Arg	U	
		CUC		ccc		CAC	1113	CGC		с	(pr
		CUA		CCA		CAA		CGA		А	(3' er
		CUG _		ccg _		CAG _	Gin	CGG _		G	base
	A	AUU -	lle	ACU -	Thr	AAU	Asn	AGU -	Sor	U	RNA
		AUC		ACC		AAC	ASI	AGC	361	С	m pr
		AUA _		ACA		AAA ⁻		AGA	Arg	A	μ
		AUG	Met or start	ACG _		AAG _	Lys	AGG _		G	
	G	GUU -	Val	GCU -	Ala	GAU -	Asp	GGU -	Gly	U	
		GUC		GCC		GAC		GGC		С	
		GUA		GCA		GAA	Glu	GGA		Α	Textbo
		GUG		GCG		GAG		GGG		G	p. 330

Use of the genetic code makes it possible to determine the sequence of amino acids in a polypeptide chain by knowing the sequence of nucleotides in a molecule of mRNA.

codon 1 codes for the amino acid "trp". Can you use the code to determine the amino acids generated by codons 2, 3 and 4?

Textbook Fig. 17.5, p. 330

code



By knowing the information content of a portion of any one information molecule, it is possible to deduce the information content of the corresponding portion of any of the other information molecules.



In order to deduce the information content of all other information molecules corresponding to the content of any one molecule, it is necessary to know:

- a. the nucleotide base-pairing rules.
- b. the genetic code,

Sequence of Events in Information Flow (1. Information stored as double-helix DNA)



Sequence of Events in Information Flow (2. Information transcribed as mRNANA)



Sequence of Events in Information Flow (3. Information translated as a polypeptide chain)



Often when the sequence of a gene that codes for a protein is presented, only the sequence of the minus strand is displayed, shown left-to-right from the 5' end to the 3' end of the gene. That sequence corresponds to the sequence of nucleotides in transcribed RNA, only with T substituted for U.

units of coded information shown in boxes

Example:

If this region of DNA codes for a portion of a polypeptide chain, then can you deduce, from the table shown in slide 7, the amino acid sequence that would be derived from this minus-strand sequence of nucleotides?

from plus strand

Methods are currently available to determine the sequences of large expanses of DNA from any organism in a very short time.

The complete DNA sequences of many organisms, including humans, have been determined.

Proteins are the central molecules of cell (and by extension organism) functions.

Thus, it appears that it might be possible to determine functions of a cell simply by knowing the DNA content of the cell.

Since all body cells of a living organism contain the same content of DNA, it appears that it might be possible to know the functions of an entire living organism by knowing the DNA content of any one of its cells.

Yet, only a small portion of cell functions, and an even smaller proportion of wholeorganism functions, have been accurately predicted by DNA sequences alone.

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Illustration of a transcription unit within a DNA polynucleotide chain



A transcription unit is a stretch of nucleotides in a molecule of DNA that is used as a template to produce a molecule of RNA with a complementary sequence of nucleotides. Most transcription units are somewhere between a few hundred and a few thousand nucleotides long.

Often a segment of DNA of interest is shown inscribed in a box, as illustrated here with the red box.

Requirements for the Start of Transcription



The enzyme that catalyzes the synthesis of a new molecule of RNA from a DNA template is called RNA polymerase.

A specific sequence of DNA immediately upstream of the transcription unit on the + (plus) strand of DNA is called a promoter. The promoters for most transcription units are a few dozen nucleotides long. RNA polymerase, a large enzymatic protein, binds to this site and then catalyzes the process of transcription.

The unit of transcription is a structural gene while the promoter is a regulatory gene.

Regulation of Transcription



A unit of regulated synthesis of RNA includes a promoter and a transcribed unit of DNA. In prokaryotes this unit is called an operon. One or more proteins may regulate the rate of RNA synthesis by binding to the promoter site and either inducing (speeding up) or repressing (slowing down) transcription.

In eukaryotes other proteins, called transcription factors, also bind to the promoter site and influence the ability of RNA polymerase to bind to the promoter site and begin to synthesize RNA.

In eukaryotes, other proteins (not shown here) can influence the effectiveness of RNA polymerase in less direct ways. Enhancers interact with transcription factors to enhance the efficiency of transcription. Suppressors function similarly, except they suppress transcription efficiency. Silencers are proteins that modify histones and thereby altering the structure of nucleosomes, which then deny access of RNA polymerase to the promoter.

Initiation of Transcription



See Textbook Fig. 17.7, p. 332

Elongation of the RNA Transcript



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Termination of Transcription



The recently synthesized molecule of RNA is called a primary transcript.

Many primary transcripts can be used to fulfill their function in a cell without any modification. However, some primary transcripts (especially in eukaryotes) must be modified before they can be utilized. This modification is called RNA processing. Since the processing happens after transcription, but before the RNA is utilized to perform its function, it is called post-transcriptional processing.

Elongation of a Molecule of RNA During Transcription



From textbook Fig. 17.7, p. 332

A second reaction coupled to this reaction is:

$$\mathbb{P} \sim \mathbb{P} + H_2O \xrightarrow{pyrophosphatase} 2 P_i$$

The two coupled reactions form a very exergonic metabolic pathway.

Energetics of the Ligase Function of RNA Polymerase

Note: these reactions are virtually identical to the ligase reactions of DNA polymerase (Lecture 34 presentation slides)

1.
$$(\text{polynucleotide})_n + \text{NTP} \xrightarrow{\text{RNA polymerase}} (\text{polynucleotide})_{n+1} + (P) \sim (P)$$

 $\Delta G^{\circ} \approx -15 \text{ kJ/mole}$
2. $(P) \sim (P) + H_2O \xrightarrow{\text{pyrophosphatase}} 2 P_i$
 $\Delta G^{\circ} \approx -30 \text{ kJ/mole}$

Sum: $(polynucleotide)_n + NTP + H_2O \xrightarrow{RNA polymerase}{pyrophosphatase} (polynucleotide)_{n+1} + 2 P_i$ $\Delta G^{\circ} \approx -45 \text{ kJ/mole}$

Thus, \approx 45 kJ/mole of energy is released for each nucleotide inserted into the growing polynucleotide chain, making the ligation reaction virtually irreversible.

Expression of Structural Genes



synthesis of polypeptide chains

Some Major Functions of RNA in Cells



Each cell makes thousands of different primary transcripts, most of which (in eukaryotes) are processed. Each processed transcript serves only one specific function.