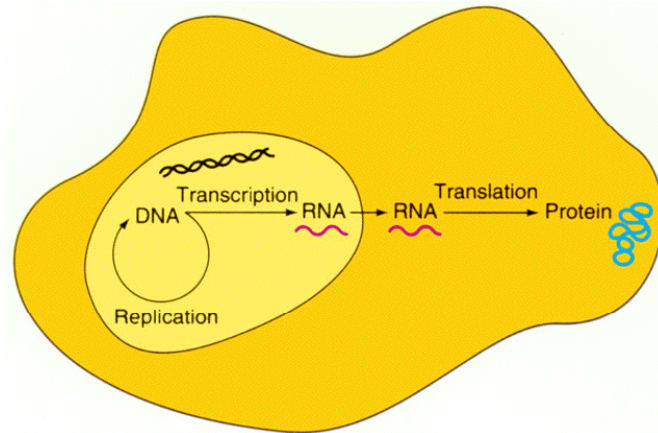


Information Transfer within a Cell and the Three Critical Processes that do this.

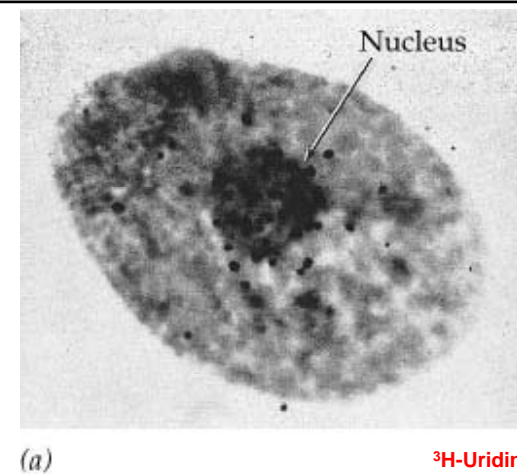
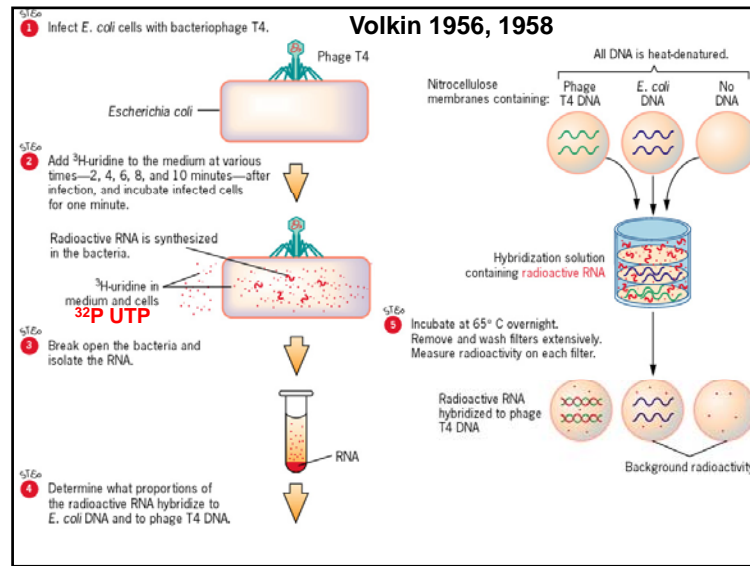


A. Crick postulated an intermediate that would have hydrogen bonding to the bases in the DNA and covalent bonding to amino acids (actually two intermediates necessary, mRNA and tRNA).

B. Volkin's Expt (base composition of RNA was similar to that of the DNA phage) shows intermediacy of RNA.

C. Pulse chase experiments and the movement of mRNA

D. Classes of RNA in prokaryotes; mRNA, tRNA, rRNA (23S, 16S, 5S in prokaryotes), snRNA, miRNA (RNAi).



Credit: From D. Prescott, "Cellular Sites of RNA Synthesis," *Prog. Nucleic Acid Res. Mol. Biol.* 3:33-57, 1964.

^3H -Uridine in UTP

Fig 12.6a Autoradiographs demonstrating the synthesis of RNA in the nucleus and its subsequent transport to the cytoplasm.

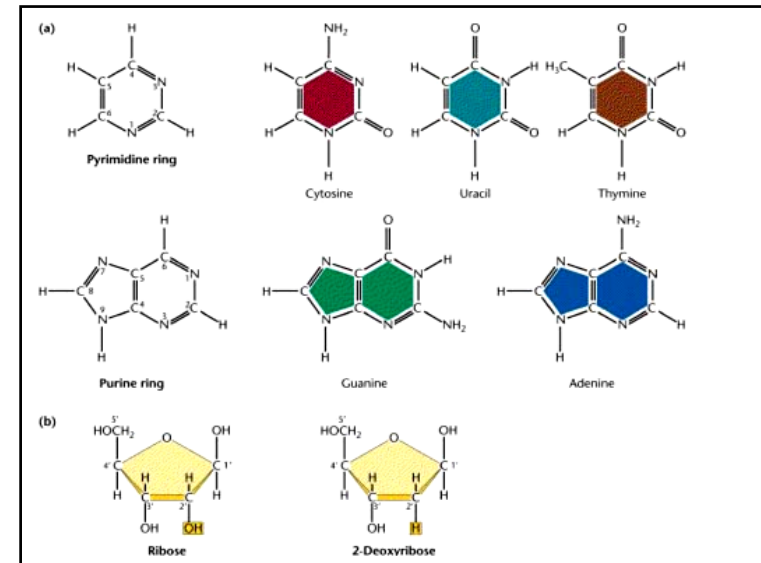
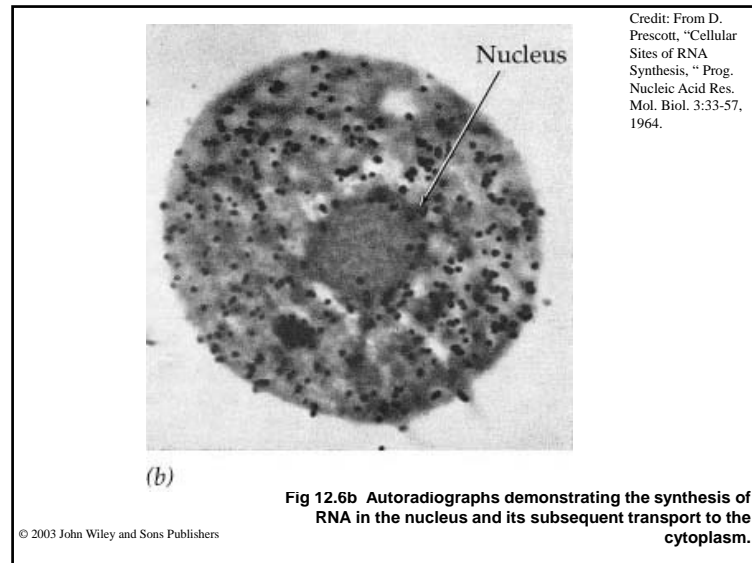


TABLE 10.4 RNA CHARACTERIZATION				
RNA Class	% Total RNA*	Components (Svedberg Coefficient)	Eukaryotic (E) or Prokaryotic (P)	Number of Nucleotides
Ribosomal (rRNA)	80	5S	P and E	120
		5.8S	E	160
		16S	P	1542
		18S	E	1874
		23S	P	2904
Transfer (tRNA)	15	4S	E	4718
Messenger (mRNA)	5	varies	P and E	75-90
				100-10,000

* In *E. coli*

Also

snRNAs (small nuclear RNAs)

miRNAs (microRNA & interfering RNA, RNAi)

Transcription

The Players:

RNA polymerase Synthesizes 5' to 3'

uses NTPs (ribose) not dNTP (deoxyribose)

uses UTP and not TTP

does not need primer, Why?

DNA template (Promoter)

How is the information of the genes converted into the production of different proteins?

RNA was shown to be an intermediate (Crick's prediction).
What are the characteristics of this code?

Since mRNA is made of 4 bases, how many bases would be needed to code for the 20 amino acids?

-- If each base coded for one amino acid, how many amino acids could be encoded in mRNA?

Answer: 4

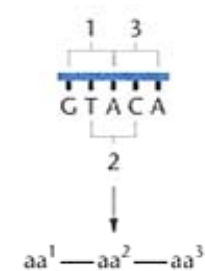
-- If two bases coded for each amino acid?

Answer: Doublet code $4^2=16$ words (still not enough)

1) Deductive reasoning also lead to speculation of triplet code: $4^3=64$ words.

2) Single base pair changes generally changed one amino acid in a protein.

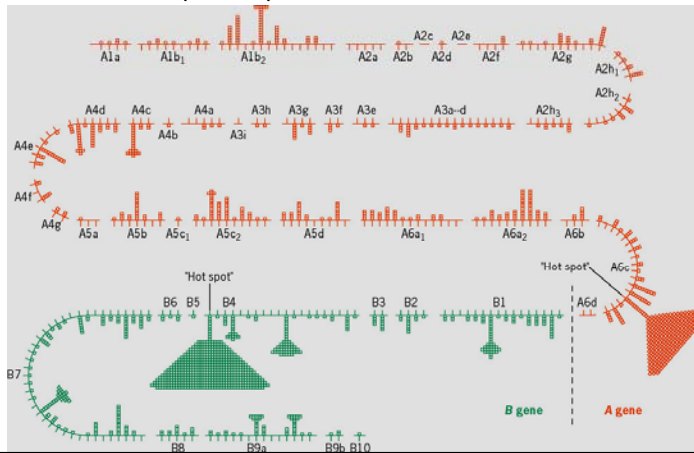
Conclusion: Code probably not overlapping.



A base substitution would often change 3 aa at once if code was overlapping.

What else can we deduce?

With **Benzer's** map, researchers could look to see what each mutation did to the protein product!!

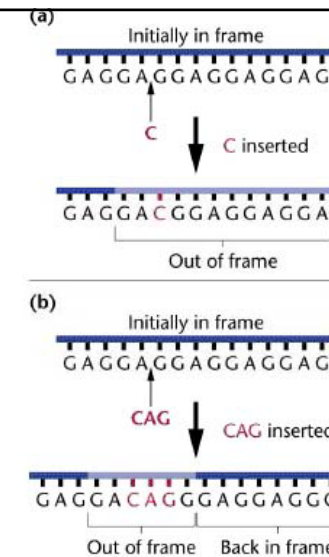


Benzer had used Proflavin as a mutagen that induces insertions and deletions

How do insertions and deletions affect the message?

1 or 2 bp insertions or deletions puts message out of frame.

Multiples of 3 bp changes keeps the message in frame.



What is happening?

THE FAT CAT ATE THE BIG RAT
 THE FAT ATA TET HEB IGR AT
 THE FAT ATA ATE THE BIG RAT
 *Suppressor Mutation

Delete C
 Insert A

Delete 3 bases THE FAT ATE THE BIG RAT

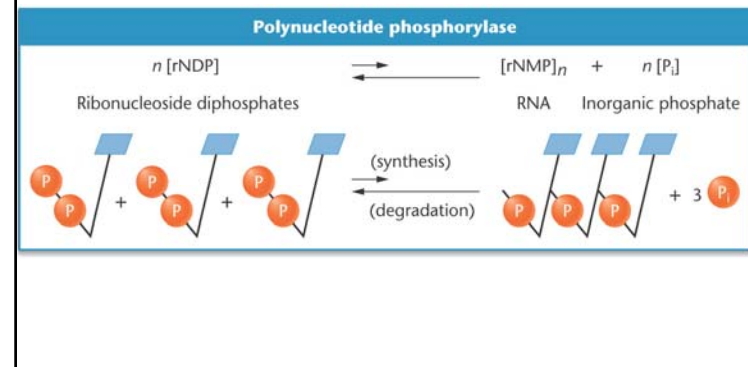
We "know"

- 1) triplets – deductive reasoning and experimental 3 bp deletions
- 2) non overlapping – 1 base substitution → 1 aa change
- 3) no punctuation – 1 base insertion/deletion affects all subsequent aa in the message (frameshift)

What are all the extra triplets for?
 Degeneracy?

OK, now we know some of the characteristics of the code, but...What is the code?????

Race was on to decipher it. One method was to create synthetic mRNA and see what polypeptide it would make.



Cracking the Code

1) Nierenberg and Matthaei 1962: Homopolymers
 Results: UUU phenylalanine
 CCC proline
 AAA lysine
 GGG -----

2) Mixed/Random Copolymers

3) Repeating Copolymers. Gobind Khorana 1967 (Nobel Prize) he generated short nucleotides (di, tri tetra) and then linked them.

Mixture of
 5 parts C:
 1 part A

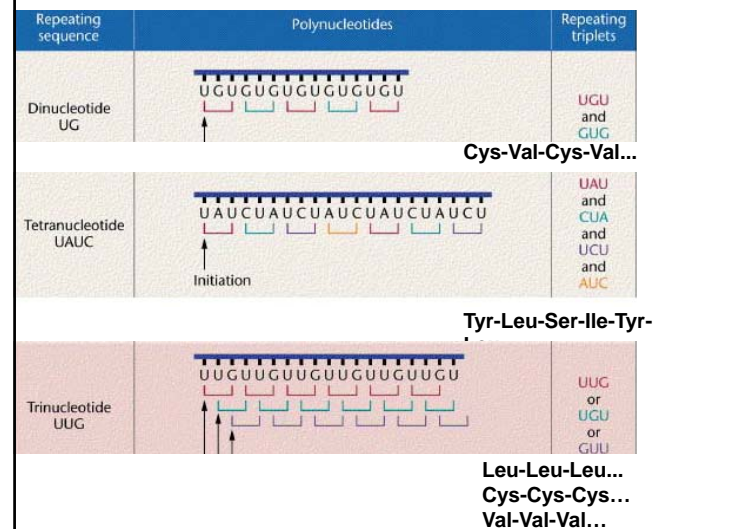
Possible compositions	Probability of occurrence of any triplet	Possible triplets	Final %
3A	$(1/6)^3 = 1/216 = 0.4\%$	AAA	0.4
1C:2A	$(5/6)(1/6)^2 = 5/216 = 2.3\%$	AAC ACA CAA	$3 \times 2.3 = 6.9$
2C:1A	$(5/6)^2(1/6) = 25/216 = 11.6\%$	ACC CAC CCA	$3 \times 11.6 = 34.8$
3C	$(5/6)^3 = 125/216 = 57.9\%$	CCC	57.9
			100.0

Chemical synthesis of message
 ↓
 CCCCCCCCCACCCCCCAACCAACCCCCCAACCCCCCAACCCAA RNA

Translation of message
 ↓

Percentage of amino acids in protein	Probable base-composition assignments
Lysine <1	AAA
Glutamine 2	1C:2A
Asparagine 2	1C:2A
Threonine 12	2C:1A
Histidine 14	2C:1A, 1C:2A
Proline 69	CCC, 2C:1A

Repeating Copolymers



Repeating Copolymers (continued)

[illegible]

What polypeptide was translated from this message?

ZIPPO, NADA, NONE!!!

CONCLUSION: One of the triplets codes for a STOP

		Second letter				
		U	C	A	G	
First (5') letter	U	UUU } Phe UUC } UUA } Leu UUG }	UCU } UCC } Ser UCA } UCG }	UAU } Tyr UAC } UAA Ochre (terminator) UAG Amber (terminator)	UGU } Cys UGC } UGA Opal (terminator) UGG Trp	U C A G
	C	CUU } CUC } Leu CUA } CUG }	CCU } CCC } Pro CCA } CCG }	CAU } His CAC } CAA } Gln CAG }	CGU } CGC } Arg CGA } CGG }	U C A G
	A	AUU } AUC } Ileu AUA } AUG Met (initiator)	ACU } ACC } Thr ACA } ACG }	AAU } Asn AAC } AAA } Lys AAG }	AGU } Ser AGC } AGA } Arg AGG }	U C A G
	G	GUU } GUC } Val GUA } GUG }	GCU } GCC } Ala GCA } GCG }	GAU } Asp GAC } GAA } Glu GAG }	GGU } GGC } Gly GGA } GGC }	U C A G
						Third (3') letter

= Polypeptide chain initiation codon
 = Polypeptide chain termination codon

*Each triplet nucleotide sequence or codon refers to the nucleotide sequence in **mRNA** (not DNA) that specifies the incorporation of the indicated amino acid or signals polypeptide chain termination.

Differences Between Human and Yeast Mitochondrial Genetic Codes

CODON ^a	AMINO ACID		
	NUCLEAR CODE	MITOCHONDRIAL CODE	
		MAMMAL	YEAST
UGA	Termination	Tryptophan	Tryptophan
AUA	Isoleucine	Methionine	Isoleucine
CUN ^b	Leucine	Leucine	Threonine
AGG, AGA	Arginine	Termination	Arginine
CGN ^b	Arginine	Arginine	Termination?

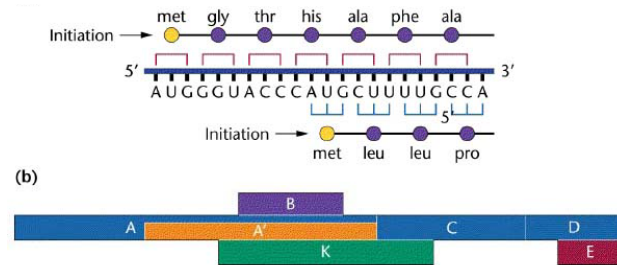
^aAll sequences read 5' to 3'.

^bN = any one of the four bases A, G, U, and C.

Similar to Table 14.5

Once the Code was cracked, small genome organisms were examined to count the genes and identify the spaces between genes.

ϕ X174 5386 nucleotides 1795 aa?
Adding up the length of its proteins 2300+ aa



Genes can be overlapping!! (The code is NOT overlapping).

		Second letter				
		U	C	A	G	
First (1 st) letter	U	UUU } Phe UUC } UUA } Leu UUG }	UCU } UCC } Ser UCA } UCG }	UAU } Tyr UAC } UAA } Ochre Bermutator UAG } Amber Bermutator	UGU } Cys UGC } UGA } Opal Bermutator UGG } Trp	U C A G
	C	CUU } CUC } Leu CUA } CUG }	CCU } CCC } Pro CCA } CCG }	CAU } His CAC } CAA } Gln CAG }	CGU } CGC } Arg CGA } CGG }	U C A G
	A	AUU } AUC } Ileu AUA } AUG } Met (Initiator)	ACU } ACC } Thr ACA } ACG }	AAU } Asn AAC } AAA } Lys AAG }	AGU } Ser AGC } AGA } Arg AGG }	U C A G
	G	GUU } GUC } Val GUA } GUG }	GCU } GCC } Ala GCA } GCG }	GAU } Asp GAC } GAA } Glu GAG }	GGU } GGC } Gly GGA } GGG }	U C A G

Third (3rd) letter

Repeating Copolymer

5'-
GUGUGUGUG..

..

A) his-his-his...
B) thr-his-thr-his...
C) cys-cys-cys...
D) cys-val-cys-val...
E) val-val-val...

*Each triplet nucleotide sequence or codon refers to the nucleotide sequence in mRNA (not DNA) that specifies the incorporation of the indicated amino acid or signals polypeptide chain termination.