GENETIC CODE

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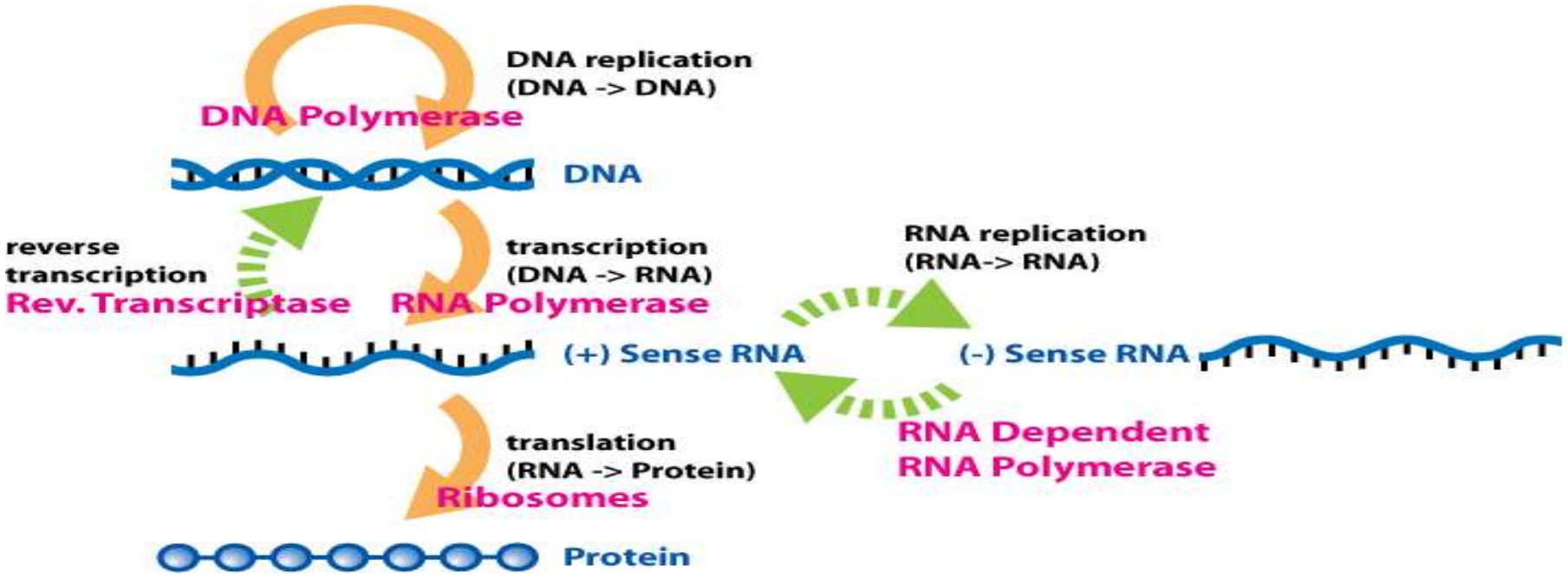
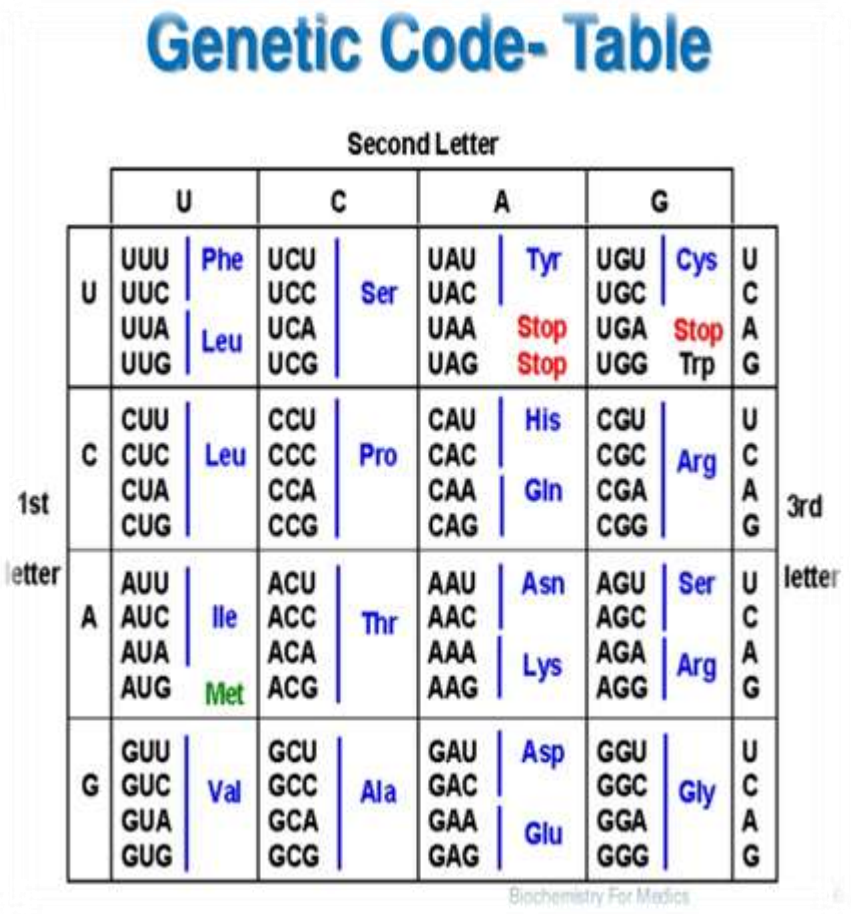
Central dogma of molecular biology



WHAT IS GENETIC CODE?



- The collection of base sequences(codons) that correspond to each **AMINO ACID** and to **TRANSLATION SIGNALS.**
- The genetic code is highly similar among all organisms and can be expressed in a simple table with 64 entries.
- The code defines how sequences of nucleotide triplets, called codons, specify which amino acid will be added next during **protein synthesis**. A three-nucleotide codon in a nucleic acid sequence that specifies a single amino acid.

The first CLUE

The Nirenberg and Matthaei experiment was a scientific experiment performed in 1961, by Marshall W. Nirenberg and his post doctoral fellow, J. Heinrich Matthaei. The experiment deciphered the first of the 64 triplet codons in the genetic code by using nucleic acid homopolymers to translate specific amino acids.

PROPERTIES OF THE GENETIC CODE

1. The code is a triplet codon:

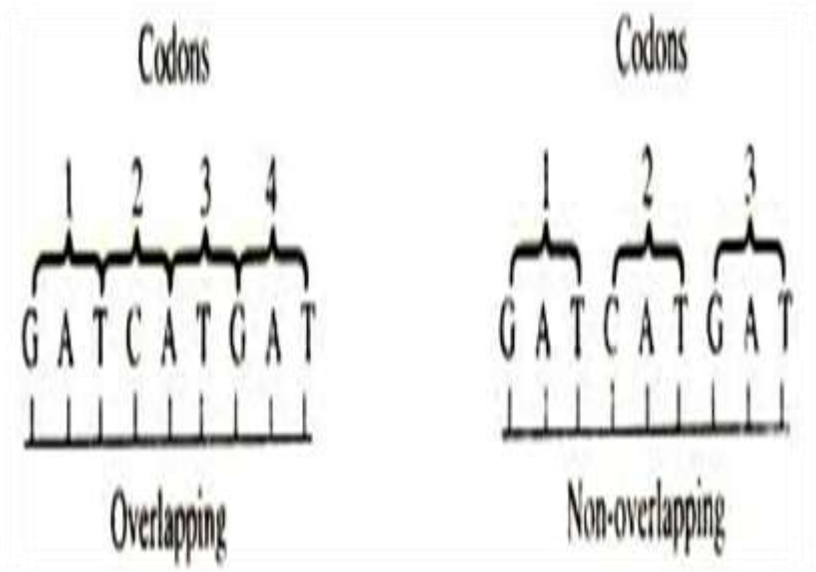
The nucleotides of mRNA are arranged as a linear sequence of codons, each codon consisting of three successive nitrogenous bases, i.e., the code is a triplet codon.

2. The code is non-overlapping:

In translating mRNA molecules the codons do not overlap but are "read" sequentially. Thus, a non-overlapping code means that a base in a mRNA is not used for different codons.

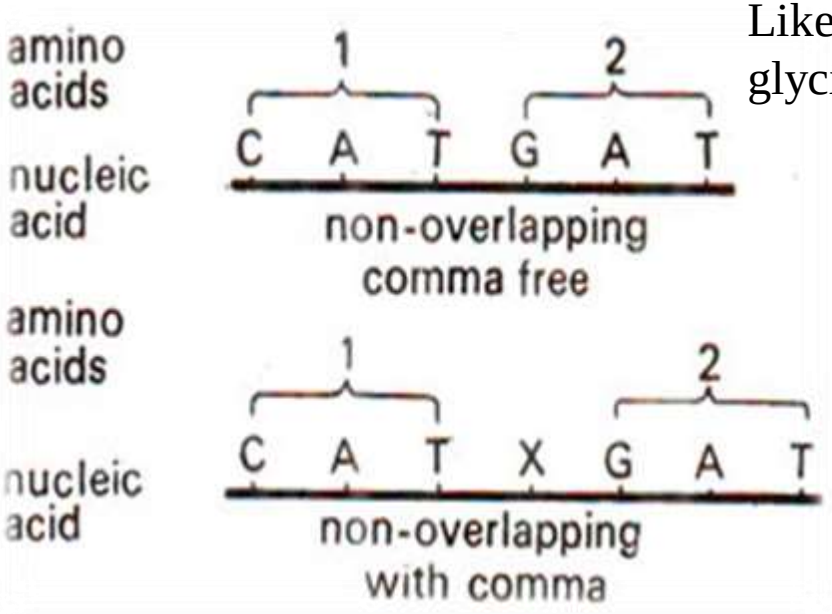
Second letter

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



3. The Genetic Code is 'commaless':

It means that after one amino acid is coded, the second amino acid will be automatically, coded by the next three letters and that no letters are wasted as punctuation marks.



4. The code is non-ambiguous:

Non-ambiguous code means that a particular codon will always code for the same amino acid. Generally, as a rule, the same codon shall never code for two different amino acids.

However, there are some reported exceptions to this rule: the codons AUG and GUG both may code for methionine as initiating or starting codon, although GUG is meant for valine. Likewise, GGA codon codes for two amino acids glycine and glutamic acid.

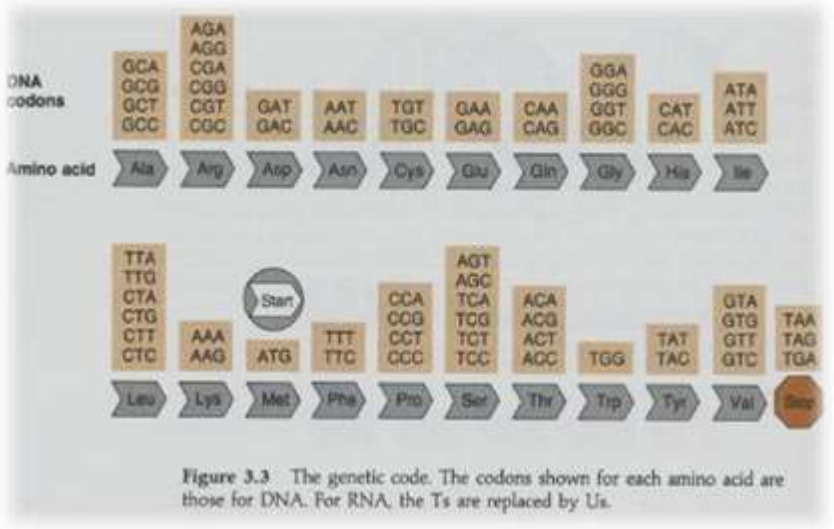
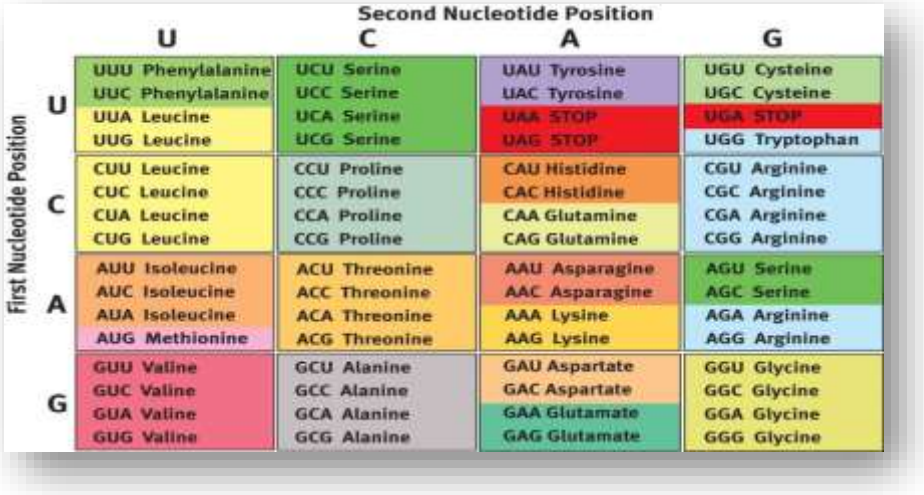


Figure 3.3 The genetic code. The codons shown for each amino acid are those for DNA. For RNA, the Ts are replaced by Us.

5. The code has polarity:

The code is always read in a fixed direction, i.e., in the 5'→3′ direction. In other words, the codon has a polarity. If the code is read in opposite directions, it would specify two different proteins, since the codon would have reversed base sequence.

Codon :	UUG	AUC	GUC	UCG	CCA	ACA	AGG
Polypeptide:→	Leu	Ile	Val	Ser	Prof	Thr	Arg
	Val	Leu	Leu	Ala	Thr	Thr	Gly←



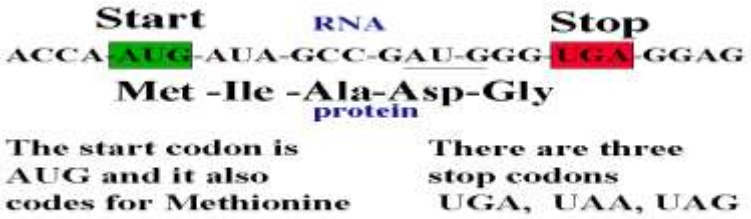
6. The code is degenerate:

More than one codon may specify the same amino acid; this is called degeneracy of the code.

- The amino acids Tryptophan and Methionine have one codon each coding for them (UGG & AUG).
- Nine amino acids namely, Phenylalanine, Tyrosine, Histidine, Glutamine, Asparagine, Lysine, Aspartic acid, Glutamic acid and Cysteine and 2 codons each coding for them.
- Isoleucine has 3 codons coding for it.
- Five amino acids namely Valine, Proline, Threonine, Alanine and Glycine have 4 codons each coding for them.
- Three amino acids, namely Leucine, Arginine and Serine, have 6 codons each.

7. Some codes act as start codons:

In most organisms, AUG codon is the start or initiation codon, i.e., the polypeptide chain starts either with methionine (eukaryotes) or N-formylmethionine (prokaryotes). Methionyl or N-formylmethionyl-tRNA specifically binds to the initiation site of mRNA containing the AUG initiation codon. In rare cases, GUG also serves as the initiation codon, e.g., bacterial protein synthesis. Normally, GUG codes for valine, but when normal AUG codon is lost by deletion, only then GUG is used as initiation codon



8. Some codes act as stop codons:

• Three codons UAG(amber), UAA(ochre) and UGA(opal) are the chain stop or termination codons. They do not code for any of the amino acids.

•These codons are not read by any tRNA molecules (via their anticodons), but are read by some specific proteins, called release factors (e.g., RF-1, RF-2, RF-3 in prokaryotes and RF in eukaryotes). These codons are also called nonsense codons, since they do not specify any amino acid.

• The UAG was the first termination codon to be discovered by Sidney Brenner (1965).

9. The code is universal:

• Same genetic code is found valid for all organisms ranging from bacteria to man.

• But recently, some differences have been discovered between the universal genetic code and mitochondrial genetic code.

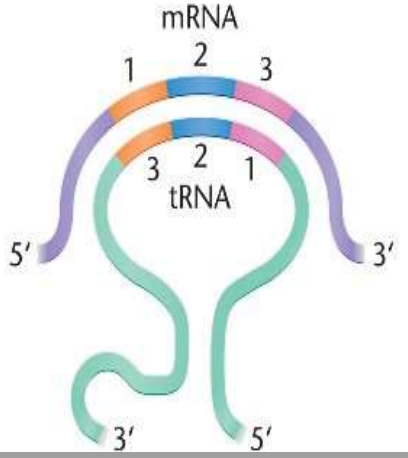
Codon	*Usual Use*	*Alternate Use*	*Where Alternate Use Occurs*
AGA AGG	Arg	Stop, Ser	Some animal mitochondria, some ptorozoans
AUA	Ile	Met	Mitochondria
CGG	Arg	Trp	Plant mitochondria
CUU CUC CUA CUG	Leu	Thr	Yeast mitochondria
AUU	Ile	Start(N-f Met)	Some prokaryotes[a]
CUG	Val		
UUG	Leu		
UAA UAG	Stop	Glu	Some protozoans
UGA	Stop	Trp Selenocysteine	Mitochondria, mycoplasmas *E.coli**

Wobbles Hypothesis

- In 1965, Dr. F.H.C. Crick proposed a hypothesis called wobbles hypothesis to explain the phenomenon of the same transfer-RNA recognizing more than one codons.
- The third base of the codon is not so specific in its base pairing and may wooble(loosly pair).
- He discovered that if U is present at the first position of the anticodon, it can pair with either A or G, respectively, in the third position of the codon .similarly G at the 1st position of the anticodon could pair with C or U.
- Inosine can pair with either A,U or C.

ANTICODON–CODON BASE-PAIRING RULES

Base at first position (5′ end) of tRNA	*Base at third position (3′ end) of mRNA*
A	U
C	G
G	C or U
U	A or G
I	A, U, or C



CODON BIAS

1. Codon usage bias refers to differences in the frequency of occurrence of synonymous codons in coding DNA. A codon is a series of three nucleotides (a triplet) that encodes a specific amino acid residue in a polypeptide chain or for the termination of translation (stop codons).
2. There are 64 different codons (61 codons encoding for amino acids plus 3 stop codons) but only 20 different translated amino acids. The overabundance in the number of codons allows many amino acids to be encoded by more than one codon. Because of such redundancy it is said that the genetic code is degenerate. The genetic codes of different organisms are often biased towards using one of the several codons that encode the same amino acid over the others—that is, a greater frequency of one will be found than expected by chance.

Codon for	*E. coli*	*Yeast*	*Euglena chloroplast*
Arginine (6)*	CGC	AGA	CGU/CGC/AGA
Leucine (6)	CUG	UUG	UUA/UUG/CUU
Serine (6)	UCU/UCC/AGC	UCU/UCC	UCU/UCA/AGU
Proline (4)	CCG	CCA	CCU/CCA
Tyrosine (4)	UAC	UAC	UAU/UAC
Lysine (2)	AAA	AAG	AAA

REFERENCES

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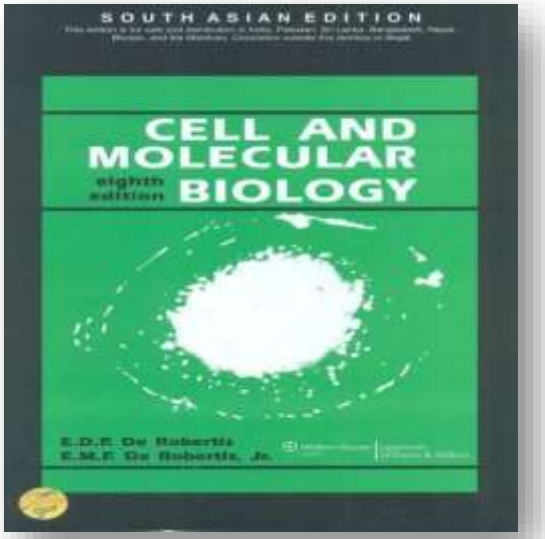
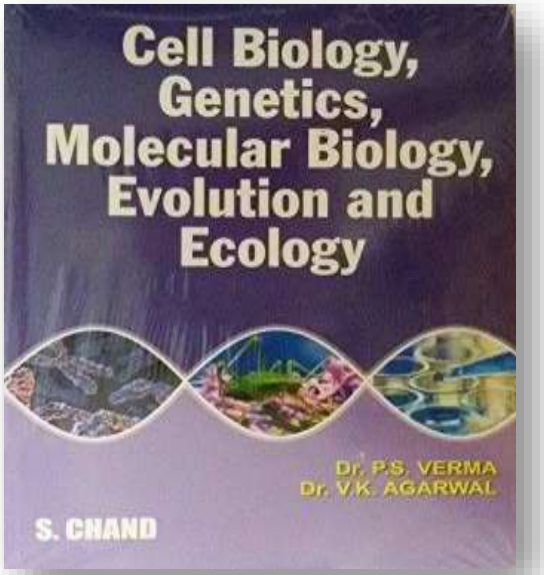


BIOLOGY DISCUSSION
DISCUSS ANYTHING ABOUT BIOLOGY

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