

THE GENETIC CODE

By the early 1960s the details of the genetic code were worked out and the amino acid specified by each triplet codon of mRNA was determined. Remarkably, the code has turned out to be the same for organisms ranging from bacteria to humans. The table of codons on this plate displays the complete code.

Color the heading mRNA Bases and titles and structures A, C, G, and U. Then use the same colors to color the letter symbols for those bases marked A, C, G, and U at the top and the two sides of the table.

The table displays all the possible codons that can be formed using the four bases found in messenger RNA. Since there are four choices for the first base, four choices for the second base, and four choices for the third, the total number of such combinations is $4 \times 4 \times 4$, or 64. Three of these are stop codons, and 61 actually code for amino acids. Only 20 amino acids are used to make proteins, however, so the code is redundant (or degenerate, as some biologists put it). That is, some amino acids are coded by more than one codon. This is feasible because some amino acids have more than one kind of tRNA that will transfer them, each with a different anticodon, and some other tRNAs have modified bases in their anticodons and require precise base-pairing of only the first two bases of the codon. This phenomenon, referred to as "wobble" in the code, means that one particular kind of tRNA will recognize more than one codon.

Color the heading Amino Acids and the title for the first amino acid, alanine (B). (We start labeling these with B because we already used A for adenine. C, G, and U will be skipped for the same reason.) Color the heading First mRNA Base, Second mRNA Base, and Third mRNA Base around the edges of the table. Then color the boxes labeled B near the bottom of the plate.

Obviously, four different codons code for *alanine*. You will notice that all of them have G as the first base and C as the second base. The third base can be any one of the four; alanine will still be added to the growing polypeptide chain at that point.

Continue coloring the remainder of the table in the same fashion. Color the amino acid name first, then color the codon(s) for that amino acid.

In completing the plate you will find that some amino acids have as many as six codons that code for them while others have four, two, or only one. *Leucine*, which has six codons, is very likely to have more than one kind of tRNA that binds to it.

It is easy to see from this code how a mutation in the DNA would exert its effect. If an error occurs in the usually precise process of DNA replication or if a DNA molecule is damaged and a repair enzyme repairs it incorrectly, one or several of the bases will be the wrong ones. That error will then be perpetuated in all the subsequent generations of cells descending from the one with the changed DNA. Because of the redundancy of the code, that could result in a new codon that happens to code for the same amino acid, and there would then be no change at all in the protein coded for. Such a mutation is generally called a "silent mutation" because we have no easy way of knowing that it has happened.

On the other hand, if the new codon codes for a different amino acid, a different amino acid will be inserted into the protein when it is synthesized. If that amino acid is in some unimportant place on the protein molecule, the substitution may cause little or no change in function. But if it is at an important place, such as the active site of an enzyme, the resulting protein may not function at all or may function improperly. It is well established, for example, that sickle-cell anemia (Plate 74) is the result of a single substitution of the amino acid *valine* for *glutamic acid* in the sixth position of the two beta chains of the hemoglobin molecule. Only 2 amino acids are wrong out of a total of 574, but the consequences are devastating for any person unfortunate enough to have this error on both of the DNA molecules (genes) coding for hemoglobin.

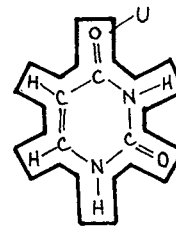
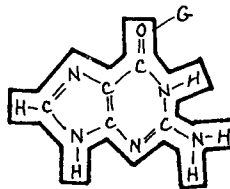
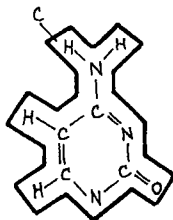
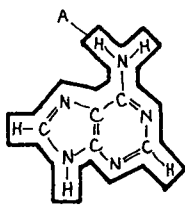
Color the remainder of the plate.

The short sentence at the bottom of the plate illustrates the nature of the damage done when a base is *deleted* (a similar distortion occurs when a base is added). Since the mRNA has no "punctuation" and the ribosome "reads" it in a "reading frame" of three bases at a time, any deletion (or insertion) that is not in some multiple of three results in a shift in the "reading frame," and the code becomes complete nonsense. The second version of the sentence on the plate is the same as the first except for deletion of the sixth letter. If it is read in a reading frame of three letters at a time, all the rest of the sentence becomes nonsense.

THE GENETIC CODE.

mRNA BASES★

- ADENINE_A
- CYTOSINE_C
- GUANINE_G
- URACIL_U



AMINO ACIDS★

- ALANINE_A
- ARGININE_R
- ASPARAGINE_E
- ASPARTIC ACID_F
- CYSTEINE_H
- GLUTAMINE_G
- GLUTAMIC ACID_D

GLYCINE_K

HISTIDINE_L

ISOLEUCINE_M

LEUCINE_N

LYSINE_K

METHIONINE_P

PHENYLALANINE_O

PROLINE_R

SERINE_S

THREONINE_V

TRYPTOPHAN_W

TYROSINE_X

VALINE_Y

SECOND mRNA BASE★

STOP CODON_Z

FIRST mRNA BASE★

	U ^{-U'}	C ^{-C'}	A ^{-A'}	G ^{-G'}	
U ^{-U'}	UUU Q	UCU S	UAU X	UGU H	U ^{-U'}
	UUC Q	UCC S	UAC X	UGC H	C ^{-C'}
	UUA N	UCA S	UAA Z	UGA Z	A ^{-A'}
	UUG N	UCG S	UAG Z	UGG W	G ^{-G'}
C ^{-C'}	CUU N	CCU R	CAU L	CGU D	U ^{-U'}
	CUC N	CCC R	CAC L	CGC D	C ^{-C'}
	CUA N	CCA R	CAA I	CGA D	A ^{-A'}
	CUG N	CCG R	CAG I	CGG D	G ^{-G'}
A ^{-A'}	AUU M	ACU V	AAU E	AGU S	U ^{-U'}
	AUC M	ACC V	AAC E	AGC S	C ^{-C'}
	AUA M	ACA V	AAA O	AGA D	A ^{-A'}
	AUG P	ACG V	AAG O	AGG D	G ^{-G'}
G ^{-G'}	GUU Y	GCU B	GAU F	GGU K	U ^{-U'}
	GUC Y	GCC B	GAC F	GGC K	C ^{-C'}
	GUA Y	GCA B	GAA J	GGA K	A ^{-A'}
	GUG Y	GCG B	GAG J	GGG K	G ^{-G'}

THIRD mRNA BASE★

ORIGINAL MESSAGE_{AA}

THE BIG DOG BIT TED AND RAN OFF

DELETION AND FRAME SHIFT_{BB}

THE BID OGB ITT EDA NDR ANO FF

↑
DELETION

AA

BB