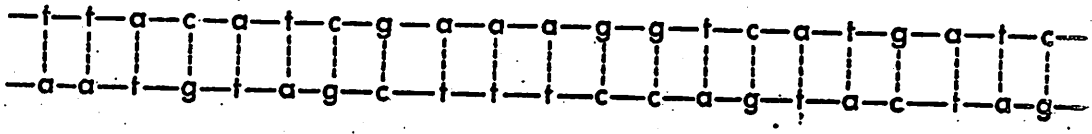
THE GENETIC CODE AND GENE MUTATION

INTRODUCTION

Knowing now something of the way in which the structure of DNA molecules is related to the structure of protein molecules, it is possible for you to understand more clearly what is meant by gene mutations. You can most easily arrive at such understanding by working out with paper and pencil some hypothetical examples.

Figure 17 • 32



PROCEDURE

Assume that the above diagram represents a part of a DNA molecule. The whole molecule is much longer, and the strands of deoxyribose and phosphate groups have been omitted. The key to the bases is:

a = adenine, c = cytosine,
t = thymine, g = guanine.

Assume that the lower strand is the one from which a messenger RNA strand is copied. • Using paper and pencil, write the sequence of bases in an mRNA strand that would be formed on the DNA strand. (Remember that in RNA, uracil—symbolized by u—replaces thymine.)(1)

Reading from left to right, divide your sequence of mRNA bases into code triplets *(codons)*. • Then, using Figure 17 • 33, construct the protein segment—the chain of amino acids—that is specified by your sequence of mRNA codons.(2)

The dictionary of RNA codons provided here does not include all the amino acids. Even if it did, you would find that there are many more possible codons than there are amino acids. Might there be more than one codon for some of the amino acids—as "cat" and "kat" are different spellings for the same sound? Assume that by X-radiation a geneticist deletes (that is, destroys and thus removes) the left-most base pair of the DNA molecule shown above. • To discover the effect of this kind of mutation, construct the mRNA chain indicated by the remaining letters, starting at the new left-hand base.(3) • Again using the chart, construct the chain

RNA CODON	AMINO ACID
aag	lysine
auc	isoleucine
aug	methionine
cau	histidine
cga	orginine
gaa	glutamic acid
gga	glycine
guc	voline
uac	tyrosine
uca	serine
uga	none
uua	leucine

Figure 17 • 33
An incomplete chart of codons.

of amino acids specified by the complete codons of the new mRNA.(4) • What has happened to the codon on the right end?(5) The codon that does not appear in the chart specifies arginine. Thus you see that a single amino acid can be specified by more than 1 codon. • Does the deletion in the DNA molecule change the resulting protein? If so, in what way?(6)

One codon (uga) in the altered mRNA

does not specify an amino acid. Codons of this sort specify the ends of protein molecules.

Assume now that X-radiation deleted the first 3 base pairs on the left instead of just the first one. • Would this kind of deletion have more or less effect on an amino-acid sequence than deletion of a single base pair? Explain.(7)

Occasionally, errors in DNA replication occur—apparently without environmental causes. For example, at rare intervals adenine pairs with cytosine instead of thymine. The consequence of this error is as follows:

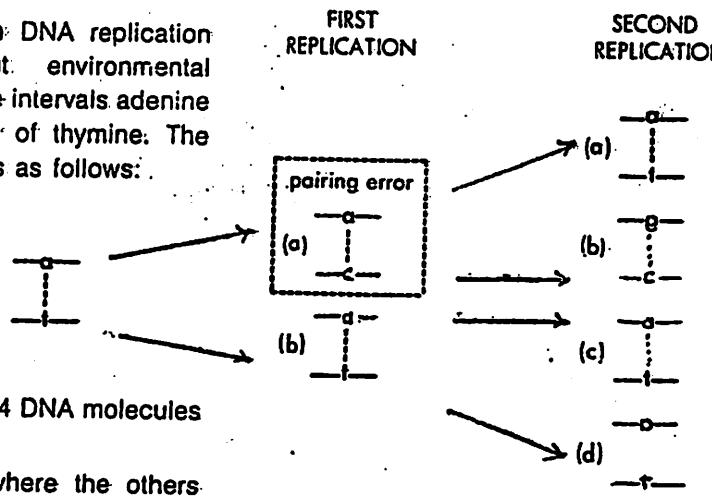


Figure 17 • 34

After 2 replications, 1 of the 4 DNA molecules

$$\begin{matrix} -g- \\ \vdots \\ -c- \end{matrix}$$

(IIIb) has the base pair $\begin{matrix} -a- \\ \vdots \\ -t- \end{matrix}$ where the others have the original . An error of this sort, if it had occurred in the DNA molecule diagramed at the beginning of this investigation, would substitute c for t at some point in the DNA strand. Assume such a substitution occurs at the 3rd base pair from the right. • Show how this changes the mRNA.(8) • Show how it changes the amino-acid chain.(9)

One of the changes known to occur in this way involves the substitution of glycine for glutamic acid at 1 site within the protein molecule. • Can you deduce an error in the normal DNA molecule that would account for this mutational change? If so, what is it?(10)

SUMMARY

Studies of amino-acid sequences in hemoglobins show that the only difference between normal Hb^A and sickle-cell Hb^S hemoglobins is the substitution of one amino acid (valine) for another (glutamic acid) in a polypeptide chain approximately 150 amino acids long! • According to the codon chart above, how many changes in base pairs would be necessary to specify this substitution in amino acids?(11) Because there are 4 codons for valine (guu, guc, gua, gug) and 2 for glutamic acid (gaa, gag), the change can be made by a mutation in only 1 base pair. • What are the possibilities for such a change?(12) • Which possibility is more likely: that the mutation involves changes at 2 base pairs simultaneously or a change at just 1 pair?(13) From such a small genotypic difference arise the great phenotypic differences between persons with and those without sickling disease!

mRNA LAB ACTIVITY **NAME:**_____
ANSWER SHEET

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(2) _____

(3) _____

(4) _____

(5) _____

(6) _____
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(7) _____
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(8) _____
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(9) _____

(10) _____
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(11) _____
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(12) _____
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(13) _____