**Ch27**

**2. How Many Different mRNA Sequences Can Specify One Amino Acid Sequence?**

UUA-AUG-UAU

UUA-AUG-UAC

UUG-AUG-UAU

UUG-AUG-UAC

CUU-AUG-UAU

CUU-AUG-UAC

CUC-AUG-UAU

CUC-AUG-UAC

CUA-AUG-UAU

CUA-AUG-UAC

CUG-AUG-UAU

CUG-AUG-UAC

**3. Can the Base Sequence of an mRNA Be Predicted from the Amino Acid Sequence of Its Polypeptide Product?**

No, we can just predict one mRNA sequence that can be translated to the peptide. Because almost every amino acid can be translated by more than one codon, so we could not predict the certain mRNA which original translated to the peptide.

**4. Coding of a Polypeptide by Duplex DNA**

(a) (5’) CGA CGG CGC GAA GUG GGG UGU UAA G (3’)

(b) R-R-R-E-V-G-C

(c) The resulting amino acid sequence will be not the same as in (b). The complementary strand of the nontemplate DNA is also complementary to the initial mRNA. So, first, the direction is different from the RNA, also, because of the bases complementary to mRNA, every base in the new mRNA are different from before.

**8. Predicting Anticodons from Codons**

GGU: (3’-5’) CCA CCG CCI

GGC: (3’-5’) CCG CCI

GGA: (3’-5’) CCU CCI

GGG: (3’-5’) CCC CCU

(a) the 3’ position and the middle base are the primary determinants of their codon specificity in the case of glycine. The 5’ base is wabble.

(b) GGU-CCG GGU-CCI GGC-CCI GGA-CCI GGG-CCU

(c) CCA and CCC

**11. Basis of the Sickle-Cell Mutation**

GAA to GUA

GAG to GUG

Because these two mutations contain once base change.

**Extra questions:**

1. Based on what you now know about DNA and RNA, suggest why cells don’t use mRNA instead of DNA as the repository of genetic information, thus eliminating the need for a transcription step.

(a) In chemistry, DNA is more stable than RNA.

(b) DNA is double strain, whereas the RNA is single strain. In DNA, if there are wrongs in one strain, the other strain can provide the correct template for the repair.

(c) If the step of transcription is eliminated, it is hard to regulate the expression of protein precisely.

1. Which would you expect to be more critical to the production of a functional protein: the precise positioning of the initiation codon or the precise positioning of the termination codon?

I think the precise positioning of the initiation codon is more important. In the process of translation, every codon contains 3 bases without gaps or overlaps. If the position of initiation codon changes, the hole arrangement of codon would change and the protein will be totally different from the normal protein.