4.4 3 Roles of RNA in Translation (p. 119-125)

1. triplet code
2. 1 codon = 1 amino acid
3. START and STOP codons
4. reading frame
5. aminoacyl-tRNA synthetases
6. tRNA acceptor arm and anticodon
7. "wobble"
8. 20 a.a., 20 a.a.-tRNA synthetases
The code is “degenerate”

<table>
<thead>
<tr>
<th>First Position (5' end)</th>
<th>Second Position</th>
<th>Third Position (3' end)</th>
</tr>
</thead>
<tbody>
<tr>
<td>U</td>
<td>C</td>
<td>A</td>
</tr>
<tr>
<td>Ala</td>
<td>Cys</td>
<td>U</td>
</tr>
<tr>
<td>Leu</td>
<td>Arg</td>
<td>Ile</td>
</tr>
</tbody>
</table>

Fig. 4-20

**What polypeptide is encoded by the 2nd mRNA on the previous slide?**

What polypeptide would be encoded by Frame 3?

How about “Frame 4?”
Proofreading: if wrong a.a. is attached to the tRNA, the synthetase removes it.

20 aminoacyl tRNA synthetases
50-100 tRNAs
61 codons for a.a.

If cell has less than 61 tRNAs, how are all the codons read?
Nonstandard base-pairing permitted at the wobble position.

Fig. 4-23

If the anticodon of a tRNA is 5'GAU3', what are all the possible mRNA codons that can be recognized?

*I = inosine (modified adenine)

Wobble positions from 5' end of RNAs:
- 1st in tRNA anticodon
- 3rd in mRNA codon

Fig. 4-23

4.5 Stepwise synthesis of proteins on ribosomes (p.125-131)

1. ribosomal subunits
2. initiation
3. elongation
4. termination
5. translation efficiency

Eukaryotic Ribosomes

Fig. 4-24
The initiating activated tRNA

tRNA\textsubscript{Met}:
• recognizes AUG (START)
• different tRNA than the tRNA\textsubscript{Met} used for internal a.a. incorporation
• only tRNA that “fits” into P site

Translation Initiation

1. eIF2\textsuperscript{GTP} + Met-tRNA\textsubscript{Met} (ternary complex)
2. Preinitiation complex
3. Translation Initiation
   - m\textsuperscript{7}Gppp
   - AUG - (AAA)\textsubscript{n}
   - 2’ structure unwinding, scanning, and start site recognition
   - 5’ AUG - (AAA)\textsubscript{n}, 3’
Translation Initiation

- Met AUG
- 60S subunit-elf6, elf5-GTP
- elf6, elf5-GDP + P_i
- 80S ribosome (AAA)_n 3'

Translation Elongation

The tRNA sites:
E = exit
P = peptide
A = aminoacylated
- GTP hydrolysis, ribosome conformational change
- Peptide bond formation
- Peptidyltransferase catalyzed by large rRNA
- only if correct codon-anticodon pairing

Fig. 4-26
Translation Translocation

Ribosome translocation

1. Multiple ribosomes/mRNA

Efficiency of Translation

2. Recycling via circularization

Translation Termination

Release Factors:
- RF1 - shaped like tRNA; binds "A" site of STOP codons
- RF3 - GTP hydrolysis results in peptide cleavage from tRNA and complex dissociation