TRANSLATION
- mRNA is synthesized in nucleus
- mRNA is the transferred to cytoplasm
- As the RNA is pulled past a ribosome
- tRNA carries amino Acids to bind with RNA
- A codon consist of three base pairs
- Each codon will attract a single amino acid-tRNA pair
**CODON AND AMINO ACIDS**

<table>
<thead>
<tr>
<th>Codon</th>
<th>Amino Acid</th>
</tr>
</thead>
<tbody>
<tr>
<td>UUU</td>
<td>phe</td>
</tr>
<tr>
<td>UUC</td>
<td>phe</td>
</tr>
<tr>
<td>UUA</td>
<td>leu</td>
</tr>
<tr>
<td>UUG</td>
<td>leu</td>
</tr>
<tr>
<td>UAU</td>
<td>tyr</td>
</tr>
<tr>
<td>UAC</td>
<td>tyr</td>
</tr>
<tr>
<td>UAA</td>
<td>stop</td>
</tr>
<tr>
<td>UAG</td>
<td>stop</td>
</tr>
<tr>
<td>UGU</td>
<td>cys</td>
</tr>
<tr>
<td>UGC</td>
<td>cys</td>
</tr>
<tr>
<td>UGA</td>
<td>stop</td>
</tr>
<tr>
<td>UGG</td>
<td>trp</td>
</tr>
</tbody>
</table>

For rest of table see 175

64 codons but only 22 amino acids

Redundancy

---

**Mutations**

- Change in the sequence of DNA
- Four types
  - Single point
  - Frame shift
    - Deletion
    - Insertion
  - Transposition
    - Inversion
  - Chromosomal

---

**Muation**

- Causes
  - UV light
  - Chemicals
  - Errors in replication
**Gene structure**

- **Introns** – A sequence of DNA in a gene that is not translated into protein.
- **Exons** – A sequence of DNA in a gene that is translated into protein.

**The Effects of Mutations**

- **Deleterious** – Decreases the fitness of the individual possessing the mutation.
  - Heterozygotes
    - Mutation be harmful if not recessive.
    - Mutation may decrease fitness because some offspring may be homozygous
  - Homozygotes – will always express deleterious mutation
- **Neutral**
  - Neutral single point substitution
  - Mutation is located in an intron or non transcribed region of the DNA
  - Mutation is not expressed because of post-translation modification of the protein
  - The mutation changes the sequence of amino-acids in the protein, but the new sequence is functionally identical to the old sequence.
- **Beneficial**
  - Mutation is expressed, does influences function and increases fitness

**Consequences of mutation**

- **Neutral**
- **Deleterious**
- **Beneficial**

**Molecular clock**

- If mutations occur at a constant rate (mutations/year is constant)
- And neutral mutations have no effect on the fitness of the organism.
- And if two individuals diverged from a common ancestor
- And if individuals inherited the mutated DNA from their parents
- Than the greater the amount of time since two individuals diverged from a common ancestor the less similar should be their sequences of DNA in non coding regions.
Estimating Time of Divergence

\[ r = K(2^T) \quad \text{or} \quad T = \frac{K}{2r} \]

Where:  
- \( r \) = rate of evolutionary divergence  
- \( T \) = time  
- \( K \) = rate of neutral substitution

Molecular Clock Example

<table>
<thead>
<tr>
<th>GENERATIONS</th>
<th>Ancestor’s Sequence</th>
<th>Differences</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>ATTAAGCCTAGGAAT</td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>ATTAACCCTAGGAAT</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>ATTAACCCTAGGAAT</td>
<td>2</td>
</tr>
<tr>
<td>4</td>
<td>ATTAACCCTGGGAAT</td>
<td>4</td>
</tr>
<tr>
<td>5</td>
<td>ATTAACCCTGGGAAT</td>
<td>5</td>
</tr>
<tr>
<td>5</td>
<td>AATAACCCTGGGAAT</td>
<td></td>
</tr>
</tbody>
</table>

Problems With Molecular Clock

- Are mutations rates constant?  
- Are the mutations really neutral?  
- Synonymous substitution

Conserved and non-conserved Genes

- The sequence of certain genes are close to identical for all organisms  
- These sequences are said to be “highly conserved”  
- Evidence supports that changing these sequences decreases the fitness of the organisms (ATP synthase example)  
- The sequence of other genes change rapidly
Similarities and differences in gene structure is consistent with Evolutionary theory

- Organism share some sequences because they inherit them from their parents
- When the cost of changing the sequence are high the mutated sequences are rare
- Sequences vary when the selective cost are low.

Gene sequences suggest that genes can be altered to serve new functions

- Many genes share similar structure (sequences) at crucial parts of the gene.
- Yet these genes may code for proteins that serve vastly different functions.
- Example LOV domains
  - Light, Oxygen, and Voltage sensitive proteins found in bacteria
  - Many other proteins share these same “domain” sequences within their genes and serve many different functions
  - Nerves, eyespots, pigments

Parsimony and Molecules

- Chance of any specific mutation occurring is small
- The probability of the same mutation occurring multiple times is even less
- The most parsimonious explanation of genes sharing the same sequence is that the mutation occurred once and was inherited by multiple offspring

Summary of Key Ideas for Molecular Evolution

- Mutation of DNA creates variation
- Some mutations are neutral and not selected for or against
- Other mutations are beneficial or deleterious and will therefore provide “fodder” for selection
- Parsimony can be used to analyze similarities of neutral sequences and make inferences of about descent and relatedness
- Analysis of shared conserved sequences allows inferences about the origins of function
- Genes may be co-opted to perform new functions
Topics you do not need to know from chapter 5

• Transposons and transposable elements
• Prokaryotic gene structure
• Retro Genes
• Protein Electrophoresis