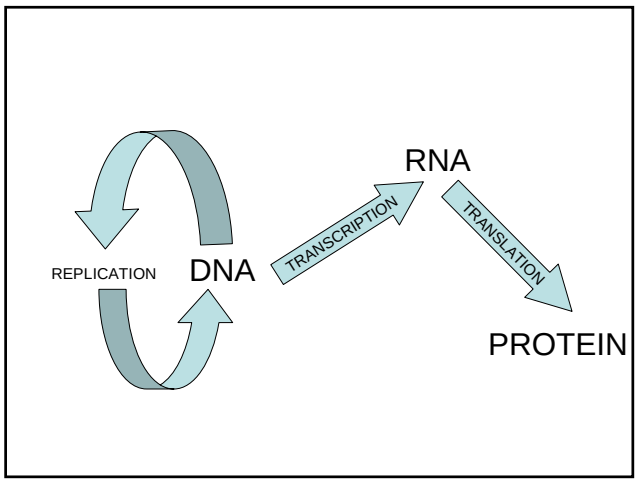
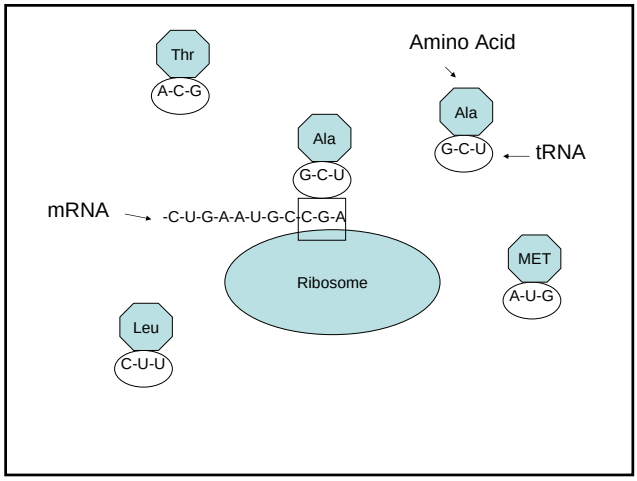
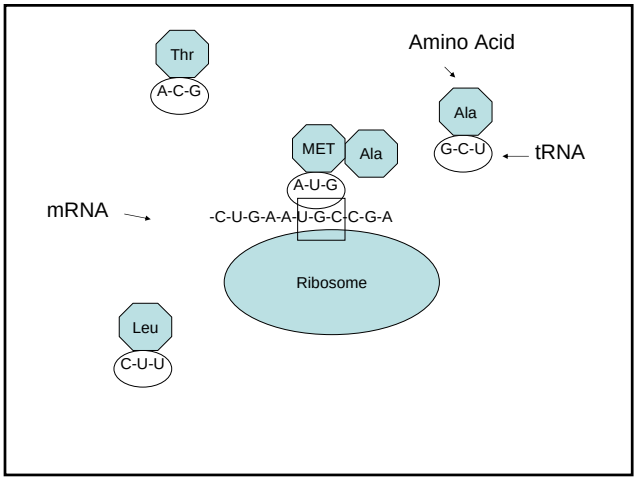
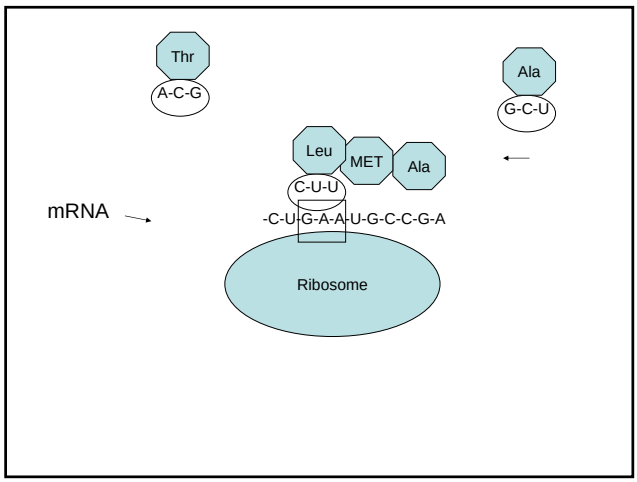


TRANSLATION

- 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

UUU = phe	UCU =ser	UAU =tyr	UGU=cys
UUC =phe	UCC =ser	UAC =tyr	UGC=cys
UUA = leu	UCA =ser	UAA =stop	UGA =stop
UUG =leu	UCG =ser	UAG =stop	UGG =trp

For rest of table see 175

64 codons but only 22 amino acids

Redundancy

Mutations

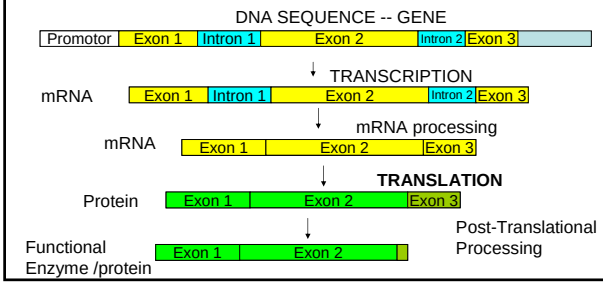
- Change in the sequence of DNA
- Four types
  - Single point
  - Frame shift
    - Deletion
    - Insertion
  - Transposition
    - Inversion
  - Chromosomal

Muatations

- 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 homozygoous
  - 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 protien
  - 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

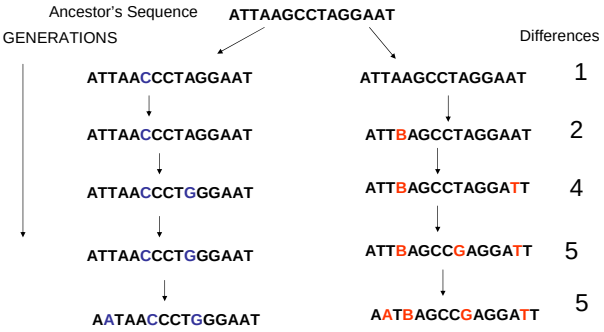
- If mutations occur at a constant rate (mutations/year is constant)
- And neutral mutations have no effect on the fitness of the organism.
- And if two individuals diverged from a common ancestor
- And if individuals inherited the mutated DNA from their parents
- Than the greater the amount of time 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) or T = K/(2*r)

Where: r= rate of evolutionary divergence
T = time
K = rate of neutral substitution

Molecular Clock Example



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