Chapter 21

Genomes and Their Evolution

Lecture Outline

Concept 21.5 Duplication, rearrangement, and mutation of DNA contribute to genome evolution.

- The earliest forms of life likely had a minimal number of genes, including only those necessary for survival and reproduction.
- The size of genomes has increased over evolutionary time, with the extra genetic material providing raw material for gene diversification.
- An accident in meiosis can result in one or more extra sets of chromosomes, a condition known as *polyploidy*.
- In rare cases, the polyploidy condition can facilitate the evolution of genes.
  - In a polyploid organism, one set of genes can provide essential functions for the organism.
  - The genes in the extra set may diverge by accumulating mutations.
  - These variations may persist if the organism carrying them survives and reproduces.
  - In this way, genes with novel functions may evolve.
- The accumulation of mutations may lead to the branching off of a new species, as happens often in plants.
- Scientists can compare the chromosomal organizations of many different species to make inferences about the evolutionary processes shaping chromosomes and possibly leading to speciation.
- Researchers performed a computer analysis of DNA sequences to reconstruct the evolutionary history of chromosomal rearrangements in eight mammalian species.
- The researchers found many duplications and inversions of large portions of chromosomes.
  - The rate of these events seems to have accelerated about 100 million years ago, around the time large dinosaurs became extinct and the number of mammalian species increased rapidly.
- Such chromosomal rearrangements are thought to contribute to the generation of new species.
  - Although two individuals with different arrangements could still mate and produce offspring, the offspring would have two nonequivalent sets of chromosomes, making meiosis inefficient or even impossible.
  - Due to chromosome rearrangements, the two populations could not successfully mate with each other, a step on their way to becoming two separate species.
- After the ancestors of humans and chimpanzees diverged as species, the fusion of two ancestral chromosomes in the human line led to different haploid numbers for humans ($n = 23$) and chimpanzees ($n = 24$).

- Another pattern with medical relevance was noted: The chromosomal breakage points associated with the rearrangements were not randomly distributed; specific sites were used over and over again.
    - A number of these recombination "hotspots" correspond to locations of chromosomal rearrangements within the human genome that are associated with congenital diseases.
- Errors during meiosis can lead to the duplication of smaller chromosomal regions, including segments that are about the length of individual genes.
- Unequal crossing over during prophase I can result in one chromosome with a deletion and another with a duplication of a particular gene.
- Transposable elements in the genome can provide sites where nonsister chromatids can cross over, even when their homologous gene sequences are not correctly aligned.
- Slippage during DNA replication can result in the deletion or duplication of DNA regions.
    - Such errors can lead to regions of repeats, such as simple-sequence DNA.
- Evidence that unequal crossing over and template slippage during DNA replication lead to duplication of genes is found in the existence of multigene families.
- Duplication events have led to the evolution of genes with related functions, such as the α-globin and β-globin gene families.
    - A comparison of gene sequences within a multigene family indicates that they all evolved from one common ancestral globin gene, which was duplicated and diverged about 450–500 million years ago.
    - Each of these genes was later duplicated several times, and the copies then diverged from each other in sequence, yielding the current family members.
    - The ancestral globin gene also gave rise to the oxygen-binding muscle protein myoglobin and to the plant protein leghemoglobin.
    - The latter two proteins function as monomers, and their genes are included in a "globin superfamily."
- After the duplication events, the differences between the genes in the globin family arose from mutations that accumulated in the gene copies over many generations.
    - The necessary function provided by an α-globin protein was fulfilled by one gene, while other copies of the α-globin gene accumulated random mutations.
    - Some mutations may have altered the function of the protein product in ways that were beneficial to the organism without changing its oxygen-carrying function.
- The similarity in the amino acid sequences of the various α-globin and β-globin proteins supports this model of gene duplication and mutation.
    - The existence of several pseudogenes among the functional globin genes provides additional evidence for this model.
    - Random mutations accumulating over time in the pseudogenes have destroyed their function.
- In other gene families, one copy of a duplicated gene can undergo alterations that lead to a completely new function for the protein product.
- The genes for lysozyme and α-lactalbumin are good examples.
- Lysozyme is an enzyme that helps prevent infection by hydrolyzing bacterial cell walls; α-lactalbumin is a nonenzymatic protein that plays a role in mammalian milk production.
- Both genes are found in mammals, but only lysozyme is found in birds.

- The two proteins are similar in their amino acids sequences and three-dimensional structures.

- Findings suggest that at some time after the bird and mammalian lineages had separated, the lysozyme gene underwent a duplication event in the mammalian lineage but not in the avian lineage.
- Subsequently, one copy of the duplicated lysozyme gene evolved into a gene encoding α-lactalbumin, a protein with a completely different function.
- Rearrangement of existing DNA sequences within genes has also contributed to genome evolution.
  - The presence of introns in eukaryotic genes may have promoted the evolution of new and potentially useful proteins by facilitating the duplication or repositioning of exons in the genome.
  - A particular exon within a gene could be duplicated on one chromosome and deleted from the homologous chromosome.
  - The gene with the duplicated exon would code for a protein with a second copy of the encoded domain.
  - This change in the protein's structure could augment its function by increasing its stability or altering its ability to bind a particular ligand.
- A number of protein-coding genes have multiple copies of related exons, which presumably arose by duplication and then diverged.
- The gene coding for collagen is a good example. Collagen is a structural protein with a highly repetitive amino acid sequence, which is reflected in the repetitive pattern of exons in the collagen gene.
- The mixing and matching of different exons within or between genes owing to errors in meiotic recombination is called *exon shuffling* and could lead to new proteins with novel combinations of functions.
  - The gene for tissue plasminogen activator (TPA), an extracellular protein that helps control blood clotting, has four domains of three types, each encoded by an exon; one exon is present in two copies.
  - Because each type of exon is also found in other proteins, the gene for TPA is thought to have arisen by several instances of exon shuffling and duplication.
- The persistence of transposable elements as a large percentage of eukaryotic genomes suggests that they play an important role in shaping a genome over evolutionary time.
- Transposable elements can contribute to the evolution of the genome by promoting recombination, disrupting cellular genes or control elements, and carrying entire genes or individual exons to new locations.
- The presence of transposable elements with similar sequence scattered throughout the genome allows recombination to take place between different chromosomes with homologous regions.
  - Most of these alterations are likely detrimental, causing chromosomal translocations and other changes in the genome that may be lethal to the organism.
  - Over the course of evolutionary time, however, an occasional recombination may be advantageous.
- The movement of transposable elements around the genome can have direct consequences.
  - If a transposable element "jumps" into the middle of a coding sequence of a protein-coding gene, it may prevent the normal functioning of that gene.

- If a transposable element inserts within a regulatory sequence, it may increase or decrease protein production.

- During transposition, a transposable element may transfer genes to a new position on the genome.
  - This process probably accounts for the location of the α-globin and β-globin gene families on different human chromosomes.

- A similar mechanism may insert an exon from one gene into another gene.
  - If the inserted exon is retained in the RNA transcript during RNA splicing, the protein that is synthesized will have an additional domain, which may confer a new function.

- Transposable elements can lead to new coding sequences when an *Alu* element hops into introns to create a weak alternative splice site in the RNA transcript.
  - Splicing usually occurs at the regular splice sites, producing the original protein.
  - Occasionally, splicing occurs at the new weak site.
  - In this way, alternative genetic combinations can be "tried out" while the function of the original gene product is retained.

- These processes produce either no effect or harmful effects in most individual cases.
- Over long periods of time, however, the generation of genetic diversity provides more raw material for natural selection to work on during evolution.

- The accumulation of changes in the genome of each species provides a record of its evolutionary history.
- Comparing the genomes of different species enables scientists to identify genomic changes and has increased our understanding of how genomes evolve.