

CHAPTER 14:

THE EVOLUTION OF GENES AND

GENOMES

DEFINITIONS

1. **Copy number variation** – variation among conspecific individuals in the number of duplicates of a DNA sequence
2. **Polymorphism** – existence in a population of two or more genotypes
3. **Gene duplication** – process whereby new genes arise as copies of pre-existing gene sequences, resulting in gene family
4. **Gene family** – two or more loci with similar nucleotide sequences that have been derived from a common ancestral sequence
5. **Domains** – a small protein segment or module that can fold into specific three-dimensional structure independently of other domains
6. **Exon shuffling** – formation of new genes by assembly of exons from two or more pre-existing genes
7. **De novo genes** – coding DNA sequences that originate from noncoding DNA
8. **Paralogs** – two or more genes that originated by duplication
9. **Gene conversion** – process involving the unidirectional transfer of DNA information from one gene to another. A gene or part of a gene acquires the same sequence as the other allele at that locus or the same sequences as a different usually paralogous locus. A consequence may be homogenization of sequences among members of a gene family
10. **Concerted evolution** – maintenance of a homogenous nucleotide sequence among the members of a gene family, which evolves over time
11. **Neofunctionalization** – divergence of duplicate genes whereby one acquires a new function
12. **Subfunctionalization** – divergence of duplicate genes whereby each retains only a subset of the several functions of the ancestral gene
13. **Pseudogene** – a non-functional member of a gene family that has been derived from a functional gene
14. **Purifying selection** – elimination of deleterious alleles from a population (positive selection)
15. **Gene trafficking** – movement of a locus between locations that results when a gene is duplicated and the original copy is deleted or becomes a pseudogene
16. **Nonsynonymous change** – results in an amino acid substitution in protein product, also known as replacement substitution
17. **Synonymous change** – results in a change that does not alter the amino acid in the protein product of a gene, also known as a silent substitution

18. **Neutral theory of molecular evolution** – hypothesis that most alleles that are polymorphic within populations and that become fixed do not significantly alter fitness and evolve by genetic drift

19. **D_N/D_S ratio** – the ratio of the number of Nonsynonymous substitution per Nonsynonymous site (D_N) and the number of synonymous substitutions per synonymous site (D_S). Values of this ratio smaller than one are consistent with purifying selection, while values greater than one suggest the action of positive selection

20. **Codon bias** – non-random usage of synonymous codons to encode a given amino acid

21. **Operons** – segment of DNA containing multiple genes whose transcription is under the control of a single promoter

22. **Overlapping genes** – a gene whose coding region overlaps with another gene, transcribed in an alternate reading frame; thought to have evolved to aid in the timing and level of expression (sharing) and the streamline the genome

23. **Meiotic drive** – a form of segregation distortion that occurs during meiosis and causes an allele to have a greater than 50% chance of being transmitted to the gamete

24. **Transposable elements** – a DNA sequence, copies of which become inserted into various sites in the genome

- There is no correlation between complexity of an organism and the size of the genome
- To quantify the size of a genome, quantify the number of protein-coding genes an organism has
- Multicellular eukaryotes with tissue organization have more protein-coding genes than most unicellular and multicellular eukaryotes without distinct tissues

