20.3A: Limitations to the Classic Model of Phylogenetic Trees

The concepts of phylogenetic modeling are constantly changing causing limitations to the classic model to arise.

LEARNING OBJECTIVES

Identify the limitations to the classic model of phylogenetic trees

KEY TAKEAWAYS

Key Points

• Charles Darwin sketched the first phylogenetic tree in 1837.
• A single trunk on a phylogenetic tree represents a common ancestor and the branches represent the divergence of species from this ancestor.
• Prokaryotes are assumed to evolve clonally in the classic tree model.
• Horizontal gene transfer is the transfer of genes between unrelated species and, as such, complicates the simple tree model.
• Ultimate gene transfer has provided theories of genome fusion between symbiotic or endosymbiotic organisms.

Key Terms

• **phylogenetic**: of, or relating to the evolutionary development of organisms
• **clonal**: pertaining to asexual reproduction
• **horizontal gene transfer**: the transfer of genetic material from one organism to another one that is not its offspring; especially common among bacteria

The concepts of phylogenetic modeling are constantly changing. It is one of the most dynamic fields of study in all of biology. Over the last several decades, new research has challenged scientists' ideas about how organisms are related. New models of these relationships have been proposed for consideration by the scientific community. Many phylogenetic trees have been shown as models of the evolutionary relationship among species. Phylogenetic trees originated with Charles Darwin, who sketched the first phylogenetic tree in 1837, which served as a pattern for subsequent studies for more than a century. The concept of a phylogenetic tree with a single trunk representing a common ancestor, with the branches representing the divergence of species from this ancestor, fits well with the structure of many common trees, such as the oak. However, evidence from modern DNA sequence analysis and newly-developed computer algorithms has caused skepticism about the validity of the standard tree model in the scientific community.

**Tree of life**: The (a) concept of the “tree of life” goes back to an 1837 sketch by Charles Darwin. Like an (b) oak tree, the “tree of life” has a single trunk and many branches.

Classical thinking about prokaryotic evolution, included in the classic tree model, is that species evolve clonally. That is, they produce offspring with themselves with only random mutations causing the descent into the variety of modern and extinct species known to science. This view is somewhat complicated in eukaryotes that reproduce sexually, but the laws of Mendelian genetics explain the variation in offspring, again, to be a result of a mutation within the species. The concept of genes being transferred between unrelated species was not considered as a possibility until relatively recently. Horizontal gene transfer (HGT), also known as lateral gene transfer, is the transfer of genes between unrelated species. HGT has been shown to be an ever-present phenomenon, with many evolutionists postulating a major role for this process in evolution, thus complicating the simple tree model. Genes have been shown to be passed between species which are only distantly related using standard phylogeny, thus adding a layer of complexity to the understanding of phylogenetic relationships. Finally, as an example of the ultimate gene transfer, theories of genome fusion between symbiotic or endosymbiotic organisms have been proposed to explain an event of great importance: the evolution of the first eukaryotic cell, without which humans could not have come into existence.