GUEST EDITORIAL

MAKING THE CONNECTION – GENETICS & EVOLUTION

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One of the most thought-provoking questions I ask my students is "What determines the order of nucleotides in your DNA?" Students are often not too clear on the different kinds of molecules, and I've gotten all kinds of answers like "the order of amino acids in your proteins" or something similar. It takes some discussion before they realize that the order of nucleotides in their DNA was determined by the order of nucleotides in their parents' DNA. The next question, of course, is what determined the order of nucleotides in their parents' DNA (grandparents, anyone?), and so on right back to the Universal Ancestor that lived some 3.5 billion years ago. Getting students to make the connection between their DNA and that of long-ago ancestors is one of the ways that teaching genetics can be used to enrich their understanding of evolution.

In the broadest sense, genetics should be taught hand-in-hand with evolution. All traits are inherited. Whenever we bring up a trait, we should ask when that trait evolved and place it on the appropriate phylogenetic tree. Very often, we don't know when a trait evolved, and this very uncertainty is important. It shows students that there are still unanswered questions in science, and it helps them define these unanswered questions. Figure 1 is a revised universal phylogenetic tree showing when many important traits evolved in the long history of life. This tree not only shows when certain traits evolved, but can also be used to infer who has them. For example, the Genetic Code evolved before the universal ancestor and is shared by all extant organisms. This tree can be used to show how our genetic (inherited) traits go back to the universal ancestor that lived 3.5 billion years ago and that all of today's genomes are the product of duplication and divergence, and exon shuffling from ~1200 ancestral genes present in that universal ancestral population. The evidence for the evolution can be read from our genomes. This tree can also be used to illustrate conserved core properties of various groups. The Genetic Code, DNA as hereditary material, and metabolic pathways such as glycolysis are conserved core properties of all life, having originated before the universal ancestor. Similarly, the cytoskeleton/endocytosis, nucleus, mitochondria, an endomembrane system, linear chromosomes with telomeres, and 9 + 2 cilia and flagella are conserved core properties of eukaryotes, having originated in the common ancestor of all eukaryotes. But watch out. As more DNA sequence data become available, the details, and even the outline, of this tree are likely to change in the next few years. What a great way to show students that a scientific theory is an intellectual framework that gives meaning to data (life can be organized into an evolution-based tree) and tells us what data we should be looking for, and also that a theory embodies the best we know now with the data available to us today.

A second way that we can enhance our teaching of genetics is to make the connection between Mendel's principles of heredity and DNA. Genes code for proteins and proteins determine phenotype. The more vividly we can make this connection to our students, the richer will be their understanding of both genetics and evolution. I find that concrete examples of mutations in DNA that change protein that, in turn, change phenotype is one of the best ways to make these connections.

We now understand some, but not all, of Mendel's traits at the molecular level. For example, Mendel found that tall pea plants are dominant to short pea plants. The "tall" gene codes for an enzyme required for synthesizing gibberellin, the plant hormone that promotes stem elongation. So why is this a dominant gene? A gene is dominant if it is expressed in the presence of a different gene. A heterozygote makes about half as much protein as a homozygote because the protein is being made from one copy of the gene

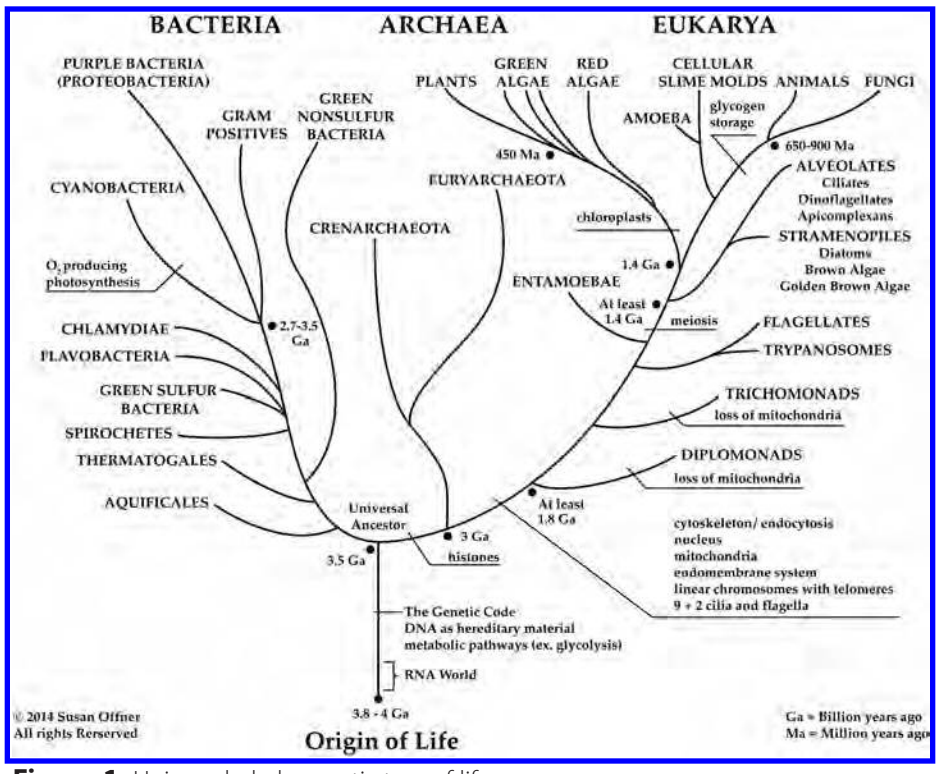

Figure 1. Universal phylogenetic tree of life.

rather than two. So if half as much protein is enough to give you the homozygous phenotype, the gene is dominant. In this case, one copy of the gene codes for enough enzyme so that enough gibberellin is produced in the heterozygous plant to make it as tall as the homozygous tall plant. If one copy of a gene does not code for enough protein to produce a homozygous phenotype, then the gene is either incompletely dominant or codominant. And it is the proteins that the genes code for that determine the phenotype – by acting as enzymes, serving as structural components of the cell or organism, or acting as a transcription factor that regulates the expression of another gene.

This issue of *ABT* contains more examples that enable you to connect classical and molecular genetics. Queen Victoria of England was a carrier of hemophilia, and her descendants passed this gene on to much of European royalty. Hemophilia is a sex-linked trait that for decades has been used to teach classical genetics. But now we know the molecular basis of this trait, and it is surprising. It is a point mutation, not in the coding part of the gene, but in the splice site of an intron that causes the exons to be spliced incorrectly – one base pair in 6 billion that changed the course of history. This is an excellent way to reintroduce molecular genetics during the unit on classical genetics, or vice versa if you teach classical genetics first.

It is hard not to be awed at how organisms function so intricately and so perfectly – well, not really perfectly, as anyone with back problems can tell you. Looking at the functioning of DNA, RNA, and protein in determining phenotype, students can begin to understand that they are the guardians of 3.5 billion years of evolution. And this provides motivation for taking care of our fragile planet that makes life possible. Isn't one of our jobs as teachers to nurture thoughtful and responsible citizens of the world?

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