Evolution drives the diversity and unity of life. Supported by evidence from many scientific disciplines, Darwin’s theory of evolution states that heritable variations occur in individuals in a population; because of competition for resources, individuals with more favorable phenotypes are more likely to survive and reproduce, thus passing traits to offspring. The number of surviving offspring in a population is a measure of evolutionary success.

The long-term survival of a species depends on a diverse gene pool because the environment acts upon phenotypes through natural selection. Sources of genetic variations include mutations in DNA, recombination of genes during meiosis, and human-directed processes, such as artificial selection and genetic engineering. However, does genetic variation guarantee that a population will evolve? One way to test if a population is evolving is to apply mathematical procedures to calculate changes in allele and genotype frequencies.

According to the Hardy-Weinberg equilibrium principle, if a population meets certain requirements, the frequencies of alleles and genotypes will remain constant from generation to generation. By calculating the genetic makeup of a population that is not evolving, based on evidence of a certain gene locus, that scenario can be compared to data from a real population. Differences may suggest that the real population is evolving — and then the question is What is causing that evolution to occur?

One way to investigate evolutionary events is by comparing genome sequences from different species; more closely related species share more similarities in their DNA sequences. Phylogenetic trees and cladograms model evolutionary history, and represent traits that are either derived or lost because of natural selection. Cladograms can be constructed by using computer programs that measure relatedness among organisms and reflect current and emerging knowledge.

The suite of inquiry-based investigations in Big Idea 1 provides opportunities for students to ask questions, and explore answers, about evolution and the role of heritable information in the continuity of life (Big Idea 3).

**SYNOPSIS OF THE INVESTIGATIONS**

Students have limited opportunities to explore real-time natural selection with multicellular organisms, and many laboratory investigations that model the process are either computer-based or structured simulations.

**Investigation 1: Artificial Selection** provides an alternative for students to investigate artificial selection. Just as Darwin relied on artificial selection in domesticated farm animals to make his case in *On the Origin of Species*, students explore possible advantages or disadvantages that selected traits might confer on individuals in different environmental conditions. Because artificial selection experiments require a relatively large population with ample phenotypic variation, the first step of the investigation is conducted at the class level, and begins with questions that center on artificial selection in agricultural crops and well-known examples of natural selection.
and evolution, such as antibiotic resistance in bacteria (big idea 3). Once students identify the common features of these events (selection, rapid changes in populations, and genetic variations), they design and conduct a selection experiment based on observable traits in Wisconsin Fast Plants growing in the classroom. These quantitative traits include number of trichomes (plant hairs) and plant height. Students may benefit from having an understanding of evolution and natural selection prior to beginning this investigation.

**Investigation 2: Mathematical Modeling: Hardy-Weinberg** is a revision of Laboratory 8 (Population Genetics and Evolution) in the 2001 AP Biology Laboratory Manual. Students often find the study of population genetics challenging because most lab simulations in which students try to manipulate a population that is evolving are flawed, as the population is so small that genetic drift swamps any factors that promote evolution. Fortunately, the complexity of evolution in populations is illuminated by relatively simple mathematical equations, several of which are based on the Hardy-Weinberg (H-W) equilibrium formula. In this revised investigation, students manipulate data using a computer spreadsheet to build their own mathematical models derived from H-W to investigate allele inheritance patterns in a theoretically infinite population with inherent randomness. Students should begin this investigation after they have studied Mendelian genetics and have a solid understanding of alleles and genes, perhaps just as they start studying evolution.

In **Investigation 3: Comparing DNA Sequences to Understand Evolutionary Relationships with BLAST**, students use BLAST (Basic Local Alignment Search Tool) to compare several genes from different organisms, and then use the information to construct a cladogram (i.e., phylogenetic tree) to visualize evolutionary relatedness among species. The field of bioinformatics merges statistics, mathematical modeling, and computer science to analyze biological data; entire genomes can be compared quickly to detect genetic similarities and differences. Identifying the precise location and sequences of genes not only allows us to better understand evolutionary relationships among organisms, but it also helps us to better understand human genetic diseases. The investigation covers concepts that pertain to genetics (big idea 3), as well as evolution.