

Publisher Response to Errors Reported by Biology Panel
 Holt McDougal, a division of Houghton Mifflin Harcourt

Item	Panel Description of Error	Holt McDougal Response
7A Applying Darwin's Ideas	<p>Based on Epigenetic studies, it is not appropriate to assume that "... if species have changed over time, the genes that determine their characteristics should also have changed". It would be better worded if the 'should have changed' were changed to 'might have changed'.</p> <p>And a second related comment: "For example, if species have changed over time, the genes that determine their characteristics should also have changed." Change "should" to "might." Epigenetic adjustments can cause changes in species WITHOUT changing genes. A good example is the lizard, <i>Podarcis sicula</i>.</p>	<p>We believe the current wording is appropriate because the preceding sentence makes clear that this an example of a testable prediction (so the use of "should" is in fact scientifically necessary to create a truly testable prediction.) It is also true that epigenetic phenomena lead to differences in traits through environmental influences on gene expression, but these mechanisms such as DNA methylation and histone modification are typically studied in upper level university courses not in first year high school biology. In general, the current statement is still correct.</p>
7G Complexity of Cells	<p>The red blood cell is referred to as a simple eukaryotic cell, but it has no nucleus, no organelles, and no membranes in its cytoplasm. Therefore, it cannot be referred to as a eukaryotic cell.</p>	<p>The red blood cell is indeed a highly derived eukaryotic cell. Red blood cells, or erythrocytes, form from eukaryotic progenitor cells that do have a nucleus, organelles, and cytoplasmic membranes. These structures are extruded from erythrocytes during the course of their development from the progenitor cells.</p>

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7A Comparing Hominoid Skulls	<p>- Lab activity: comparing hominoid skulls: 2010 research confirms humans and chimps differ by 30%. This fact is not discussed in the lab activity. The human/chimp skull homology does not match the genetic homology. Including the human skull leads students to a conclusion that differs from 21st century scientific research that is testable and repeatable, and should be removed from the activity. "The difference in MSY gene content in chimpanzee and human is more comparable to the difference in autosomal gene content in chicken and human, at 310 million years of separation." The similarities in human skulls with other hominids may be convergent evolution, but it is erroneous to pretend that common ancestry is the cause.</p>	<p>There is no error with this Virtual Lab. The comment from the panel appears to refer to a research paper published in the January 28, 2010, issue of <i>Nature</i>: Hughes et al., "Chimpanzee and human Y chromosomes are remarkably divergent in structure and gene content." The study found a 30 percent difference in the genetic makeup of the male-specific region of the Y chromosome (MSY). This region accounts for a tiny percentage of the overall genome in humans and chimps, which the paper explicitly refers to as "our closest living relative." In the sentence immediately preceding the one quoted in the panel comment, the researchers point out that "in the remainder of the genome, comparison of chimpanzee draft sequence with human reference sequence suggests that the gene content of the two species differs <1%." The researchers conclude that the major difference in MSY sequence indicates rapid evolution during the 6 million years since humans and chimps diverged from a common ancestor. Thus the article itself does not support the assertions made in the panel comments.</p>

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7A Applying Darwin's Ideas, Figure 7	<p>- Whale evolution- 4 fossils is hardly a "transition". 400 intermediates would work. Also, research has shown that there is no reason to believe</p>	<p>There is no scientific basis to the assertion that hundreds of intermediates would be required to establish a transition in the fossil</p>
	<p><i>Pakicetus</i> was ever anything but a land mammal. Also, no complete skeletons have been found, but the picture shows a full skeleton, which a major factual error. It is erroneous to include it in this example. <i>Ambulocetus</i> also shows a full skeleton, which is another major factual error, since no complete <i>Ambulocetus</i> skeletons have been found.</p>	<p>record. Four forms are shown here as a representative sample to illustrate the transition. There are, in fact, many more species in the fossil record linking the earliest forms in the lineage to modern cetaceans.</p> <p>The text in this figure explicitly states that <i>Pakicetus</i> was a land-dwelling mammal. However, the panel's comment that "research has shown that there is no reason to believe <i>Pakicetus</i> was ever anything but a land mammal" is not quite accurate. Research suggests that it was mainly a land animal living in seasonally flooded marshes and likely feeding in aquatic systems by wading and possibly paddling. The ear structure shows it as a taxa near the base of the lineage leading to modern whales. It should be no surprise that basal members of the group would not be aquatic animals, since cetaceans are derived from terrestrial ancestors.</p> <p>It is true that no complete skeletons have been found of <i>Pakicetus</i> and <i>Ambulocetus</i>, but extensive sets of fossil evidence do exist. See the attached photo of fossil bones for a single specimen of <i>Ambulocetus</i>, which shows a nearly complete reconstruction of the skeleton. (Source: website of Dr. Hans Thewissen, leading expert in cetacean evolution) In fact, complete skeletons are rarely found for any species in the fossil record, but it is not necessary to have a complete skeleton to make strong deductions about the form of an animal, how it lived, and its evolutionary relationships.</p>

Item	Panel Description of Error	Holt McDougal Response
7A Applying Darwin's Ideas, p. 384	<p>"... A comparison of DNA or amino-acid sequences shows that some species are more genetically similar than others. These comparisons, like those in anatomy, are evidence of hereditary relationships among the species. For example, comparing one kind of protein among several species reveals the pattern shown in Figure 10. The relative amount of difference is consistent with hypotheses based on fossils and anatomy." Correct by saying "... A comparison of DNA or amino acid sequences shows that some species are more genetically similar than others. These comparisons may suggest patterns of descent inconsistent with expectations based on comparative anatomy. For example, comparing two proteins among various species reveals discrepancies shown in Figure 10. In comparative biochemistry, anatomical homologies may not be evidence of close common ancestry."</p>	<p>This panel comment and the following one are closely related. Any phylogeny is a hypothesis, whether based on morphological or molecular evidence. Not all phylogenies based on molecular evidence are consistent with phylogenies based on anatomy. However, in the preponderance of cases there is congruence between molecular and morphological data. In the case of inconsistencies, there are a variety of well-established factors consistent with evolutionary dynamics that can lead to such incongruencies.</p>
7A Applying Darwin's Ideas, Figure 10	<p>- "Figure 10: Scientists have compared the amino acids that make up hemoglobin proteins in several species. Organisms that have fewer differences are more likely to be closely related. How does this pattern relate to genetic change?" To Correct, add a second table to Figure 10 entitled "Insulin Comparison" showing that compared to mice, the percentage of insulin amino acid sequence differences in Chickens, Ducks and Turkeys (birds) is 20%; in Rattlesnakes (reptiles) is 27%; in Bonito (fish) and Cod (fish) are 28% and 31% respectively; in Tuna (fish) and Angler fish are 33%; and in Guinea pig and Coypu (mammals) are 35% and 38% respectively. Revise the Figure 10 caption to read: "A phylogeny is an evolutionary tree showing descent from common ancestors. How would a phylogeny based on the insulin comparison differ from a phylogeny based on the hemoglobin comparison?" "Teaching Notes," "Reading: What Darwin Explained," "Answers – Caption Questions ... Figure 10 "Genes change (by mutation) over time;"</p>	<p>The panel comment does not identify the source of insulin data cited, but these data seem to be consistent with the fact that the structure of insulin has been strongly conserved across the course of vertebrate evolution. Because there are only minor differences in insulin structure among the various vertebrate taxa, molecular data for insulin would be a poor choice for constructing a phylogeny.</p>
Item	Panel Description of Error	Holt McDougal Response
7A Animation:	- "Student Resources, "Animation:	The current wording is correct and

<p>Similarities in Macromolecules (Student Resources)</p>	<p>Similarities in Macromolecules" "Darwin observed anatomical features of organisms and hypothesized that organisms that appear similar have a more recent common ancestor than do</p>	<p>will remain. As noted above, in most cases phylogenies based on molecular evidence are congruent with ones based on morphological evidence. Cases in which there are</p>
	<p>organisms that do not appear similar. Modern biology proves on the molecular level what Darwin noticed on the anatomical level. The number of amino acid differences in homologous proteins of different species is proportional to the length of time that has passed since the two species shared a common ancestor. Thus, the more similar the homologous proteins are in different species, the more closely related the species are thought to be." Revise "Student Resources, "Animation: Similarities in Macromolecules," as follows: "Darwin observed anatomical features of organisms and hypothesized that organisms that appear similar have a more recent common ancestor than do organisms that do not appear similar. Yet modern biochemical phylogenies often contradict Darwin's anatomical phylogenies. Phylogenies b</p>	<p>incongruencies can be accounted for by factors consistent with evolutionary dynamics.</p>

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7A Animation: Similarities in Macromolecules (Teacher Resources)	<p>- "Teacher Resources," "Audiovisual: Similarities in Macromolecules – Teach from Visuals" "Remind students that molecular homologies can provide evidence of common ancestry. Ask If the amino acid sequences of homologous proteins in three organisms are known, how could it be determined which two of the organisms shared the most recent common ancestor? (The two organisms with the least amount of difference between their amino acid sequences have the most recent common ancestor.) How is the evidence from macromolecules different from Darwin's evidence of common ancestry? (Darwin observed anatomical features of organisms. He did not use evidence on the molecular level.)"Revise "Teacher Resources," "Audiovisual: Similarities in Macromolecules – Teach from Visuals," to state: "Remind students that a phylogeny shows evolutionary relationships among life forms based either on their anatomical or their biochemical similarities and differences. Ask:Do phylogenies based on comparative anatomy and comparative biochemistry always agree with each other? (No) How does 'convergent evolution' address discrepancies between anatomical and biochemical phylogenies? (It postulates that more closely related life forms evolved traits like those of less closely related life forms.) How does 'convergent evolution' often weaken homologies as evidence of close common ancestry? (It claims that close common ancestry is often not the source of homologies.)Do fewer transitional forms in the fossil record enhance or reduce the evidence for 'convergent evolution'? (They reduce it.)"</p>	<p>The current text is correct and will remain. Note that there is no coverage of the concept of convergent evolution in this animation, and so it would not be instructionally appropriate to pose questions about it at this point.</p>