**Roots: Exploring Our Distant Ancestry**
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**Summary**

This case study required you to think about your distant ancestors that (who? in some cases) lived more than a hundred million generations ago. In particular, it asked you to consider whether or not each item on a list of 13 anatomical, behavioral, or physiological characteristics that are not now characteristics of humans, were possessed by some distant human ancestor. After group discussion of each item, you were asked to research one characteristic for which there was disagreement or uncertainty and write a report supporting or refuting the hypothesis that the characteristic was possessed by some distant human ancestor.

As the initial course assignment, this exercise had several content purposes. It provided a context for you to review the history of life on Earth and review the diversity of organisms in an unusual, and hopefully interesting, context - human ancestry. It introduced the concepts of phylogeny and the logic by which evolutionary trees are constructed and used as hypotheses. And, it set the biological stage for the molecular and biochemical case studies to follow. This assignment had process objectives as well. It provided an opportunity to exercise and display your ability to locate relevant resources, assimilate information, and present that information in an organized and logical way. It also provided me with an early opportunity to establish my expectations and provide you with individual feedback on your work.

Normally "human evolution" refers to the last 5-7 million years since the human lineage diverged from our last common ancestor with chimpanzees. All but two of the thirteen characteristics being considered would not have been found among these "recent" ancestors. As many of you found, searching for *anaerobic, photosynthetic, scaly* or *egg-laying* human ancestors yielded little because the literature and research questions are not framed in that way. A better strategy involved identifying living species that possess these apomorphic or plesiomorphic characters, finding phylogenies that apply to them, and then comparing those phylogenies to the consensus human phylogeny to deduce when and where these characteristics arose or were lost. In some cases, it is necessary to consider multiple phylogenies because certain characters appear among several different groups of organisms, e.g. prehensile tails, flight, fossorial adaptations, and scales - examples of homoplasy.

Although the assignment did not specify the inclusion of a relevant title or diagrams of phylogenetic trees, these features definitely improved the quality of a report. I expected that the text of these reports would contain multiple citations to specific reliable sources listed in a reference section. While Internet sources can be excellent, they also can be poor. Primary references in the peer-reviewed literature are much more dependable than web-sites created by high school students for a science project. Also, in an area such as evolution, there is so much new information that older references may not reflect current thinking based on recent research.

The best reports began with a clear statement of the hypothesis and whether it would be supported or refuted by the evidence. The following effective discussions displayed phylogenetic trees obtained from reliable sources and related the characteristic of interest to the trees and the lineage leading to modern humans. While I looked for a conclusion consistent with contemporary thinking, I was most interested in a well-structured argument based on reliable evidence and scholarly research.