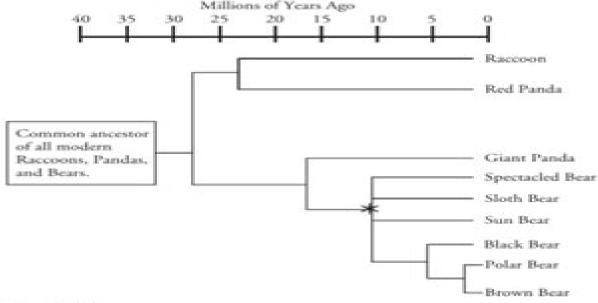
Phylogenetic Trees

How do the changes in gene sequences allow us to reconstruct the evolutionary relationships between related species?

Why?

The saying "Don't judge a book by its cover." could be applied to the topic of evolution. For example, humans share 75% of their DNA with chickens. Biologists point to this as evidence that humans and chickens once shared a common ancestor. The advent of DNA technology has given scientists the tools with which to examine how closely related certain species are. DNA analysis allows scientists to construct phylogenetic trees whose branches link together the relatedness of different organisms.

Model 1 - Phylogenetic Trees



- 1. Refer to Model 1.
 - a. How long ago did the common ancestor of all the organisms on this phylogenetic tree exist?
 - b. Which two lines diverged 30 million years ago?
 - c. List all modern descendants of the organism that was alive at the point indicated by the asterisk.

Model Phylogenetic Trees Answer Key

Michael J. Benton, David A. T. Harper

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also included on animals harbouring their own variants of HIV such as cats non human primates and bovines Other retrovirus models including lentivirus viruses like Equine Infectious Anemia Virus EIAV Visna Maedi Simian Retrovirus SRV and Feline Leukemia Virus FeLV are discussed The book also deals with the biohazard aspects of working with these viruses the comparative value of the models and their relation with AIDS in humans Examples of the applications of these models in the development of antiretroviral agents and vacines are given

Australian Systematic Botany, 2007

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