Lecture 11

- **11 Molecular phylogenetics.**

- **Using cladograms to understand evolution**
  - Mapping changes on a cladogram
    - If the cladogram is known, then the minimum number of transitions of a particular character can be inferred by using the principle of parsimony. The true number of transitions may be greater, but for many purposes the minimum number is sufficient.
    - Wings in mammals evolved only once. Characteristics associated with eating ants and termites evolved three times in mammals.
    - The number of times a character changes indicates how difficult it is for natural selection to cause that change. Wings in insects evolved only once. The loss of wings occurred independently in many groups, including fleas, stick insects, parasitic lice and many groups of cave-living insects.

- **Molecular phylogenetics can be used to understand recent evolutionary history.**
  - HIV
    - By assuming a molecular clock, the origin of HIV in humans is dated to the 1930s.
  - mtDNA
    - Because mtDNA is maternally inherited, the phylogeny of a sample of mtDNA is a tree that represents the ancestry of females.
  - Out-of-Africa.
    - The most recent common ancestor of all human mtDNA was present in a female who lived between 100,000 and 200,000 years ago, “mitochondrial Eve.” This female was not the only ancestor of modern humans at that time. Other individuals present at the same time were also ancestors but not of the mtDNA.
    - A phylogenetic tree of mtDNA from individuals from human populations shows that individuals from Africa are found throughout the tree, while individuals from other geographic regions are generally found in only small parts of the tree.
    - These two conclusions (the young age of the most recent common ancestor and the appearance of African mtDNA throughout the tree) together support the out-of-Africa theory, that all modern humans are descended from a population that lived in Africa less than 200,000 years ago and later dispersed to Europe, Asia and Australia in the past 100,000 years.
    - If the out-of-Africa theory is true, then populations of *Homo erectus* represented by fossils that are 500,000 to 1,000,000 years old (Peking Man, Java Man and others found throughout Europe and Asia) went extinct. Only the African population of *H. erectus* left descendants.
  - Neanderthals
    - Neanderthals (*Homo neanderthalensis*) lived in Europe and Asia from 300,000 years ago until 30,000 years ago. Between 60,000 and 30,000 years ago they lived in the same general areas as modern humans, *H. sapiens*, but there is no archaeological evidence of contact or interbreeding between the two species.
MtDNA from Neanderthals and humans had a common ancestor roughly 500,000 years ago. There is no Neanderthal-type mtDNA in any of the thousands of mtDNAs sampled from modern humans, so there is no evidence of gene flow from Neanderthals to modern humans.

Recently, approximately 1 mb of the nuclear genome of a Neanderthal bone from Croatia has been obtained. These sequences have confirmed the conclusion about the time of divergence of the human and Neanderthal lineages and still show no evidence of gene flow.

**Forensic use of phylogenetics**

In 2002, a doctor in Louisiana was accused of deliberately infecting someone with HIV by injecting blood from an HIV-positive patient. The victim developed AIDS and died. The doctor was convicted of second degree murder.

Part of the evidence used in the case was from phylogenetic analysis. HIV from the victim, from the patient alleged to be the source, and from HIV-positive people in the same community were sequenced and a phylogeny was inferred. HIV from the victim was shown to on the same part of the tree as HIV from the alleged source and quite separate from the HIV from other HIV-positive individuals in the community.

**Questions**

Which one of the following would you regard as the best evidence that there was substantial gene flow between Neanderthals and modern humans?

- a. The nuclear DNA of modern humans is similar to the mtDNA of modern humans.
- b. Some mtDNAs from modern humans are closer to the mtDNA of Neanderthals than they are to mtDNAs of other humans.
- c. There is less sequence variation among mtDNAs of modern humans than we previously thought.
- d. There is more sequence variation among mtDNAs of modern humans than has been found.
- e. There is more sequence variation among mtDNAs of Neanderthals than has been found.

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1. http://www.pnas.org/cgi/content/full/99/22/14292
In the above cladogram, the letters A-I represent species. Which one of the following are not monophyletic groups?

- a. A+B+C+F+G.
- b. B+C+F.
- c. A+B+C+F+G+I.
- d. D+E+H.
- e. All 4 are monophyletic.

Which statement best describes the evolution of wings in insects?

- a. Wings originated once and were lost many times.
- b. Wings originated many times and were lost many times.
- c. Wings originated many times and were lost only once.
- d. Wings in insects are homologous to wings in birds.
- e. None of the above.