The History in Our Genes

Molecules, Morphology & Molecular Clocks. Oh My!

Slide 1

Homology

- **Homology** is any characteristic of organisms that is derived from a common ancestor, for example: Hands, Wings
- Evidence that humans and birds share a common ancestor
What are Homologies?

- Homologies in DNA are similar genetic sequences inherited from common ancestors
- Over the past 20 years, evolutionary biologists learned to use DNA to construct evolutionary trees

Reading History in the Genes

- David Hillis study, 1992, UT-Austin
- Demonstrated how to read the history coded in genes - they tracked the evolution of a bacterial virus called T7 (bacteriophage)
Studying T7

- T7 infects *E. coli* (host)
- Using a single ancestor, created a T7 lineage
- Grew up billions of descendants
- Moved two of the viruses to new petri dishes of E.coli
- New lineages started

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T7 Experiment (continued)

- Viruses were allowed to replicate and mutate
- Offspring from the two petri dishes used to start four new populations
- Offspring of the four new populations used to start eight new petri dishes
T7 Experiment – Lineage Map

- Each of the 9 viruses produced can be considered as tips of an evolutionary tree
- Original virus is the root
- In each lineage, new mutations occurred
- New mutations were spread through natural selection and genetic drift
Experimental Meanings

• If a mutation occurred in the common ancestor, the two new lineages would inherit it
• Researchers were able to reconstruct the virus’s evolutionary tree by tracking the mutation
  – Differences in their DNA
• Relationships of species and other clades can be inferred from their DNA as well as their morphology
  – Clade: group of organisms that share a common ancestor
  – Morphology: form, shape, or structure of an organism

Species Trees & Gene Trees Using Bases

• Today, biologists can read individual bases of DNA
  – Adenine
  – Guanine
  – Thymine
  – Cytosine
• Human genome contains 3.5 billion base pairs
Species Trees & Gene Trees – Issues Using DNA

• There are problems using DNA
  – Decays
  – Disappears from fossils within a million years
• Most of the DNA used to study evolution comes from living organisms

Common Ancestors - Species Trees & Gene Trees

• Birds
  – Related to alligators and crocodiles
    • Don’t look alike
  – Share a common ancestor
    • Lived about 250 million years ago
• Once lineages diverged, underwent serious evolutionary changes
Species Trees & Gene Trees – some thoughts

• DNA tree includes **ONLY** living species
  – No details about how birds evolved from featherless reptiles
• Pieces of the puzzle are missing
• Trees can be drawn incorrectly
• Over hundreds of millions of years, many mutations can occur
• Some lineages will get the same mutation independently

Point Mutation - Species Trees & Gene Trees

• DNA is made up of only 4 bases
• A single point mutation can change a base to the same base more than once
  – Repeated mutation can make two species look to be more closely related than they really are
Matching Gene History Against Species History

- Another challenge is that the history of gene doesn’t always match the history of the species that carries it
  - Evolution of humans, chimpanzees, and gorillas

Why are There Issues Sometimes Matching Gene History Against Species History?

- Over the course of this evolution, new alleles evolved
- When the new species evolved, they inherited some of those alleles from the common ancestor
- They didn’t inherit others
- As the new species evolved, some of the alleles became less and less frequent and eventually disappeared
  - Others mutated and produced new alleles
Species Trees vs Gene Trees – Confusion?

• We can clear up any confusion between species trees and gene trees
  – Look at the history of many genes as opposed to just one

Species Trees & Gene Trees

• Phylogeny of a single segment of DNA may be different from the phylogeny of the species that carries it
  – Read pages 138-139 in your textbook
    • Work of Mark Batzer on the Alu elements
Molecules & Morphology

- Claim that closest living relatives of tetrapods are lobe-finned fishes
  - Coelocanths
  - Lungfish
- 30,000 species of fish
  - Prediction that only 6 should share a common ancestry with tetrapods

Molecules & Morphology

- Hallström and Janke (2008) analyzed hundreds of DNA segments
- Gathered DNA fragments from tetrapods and fishes
  - 12 species from lampreys to mammals
- Showed that lungfish were the closest relatives of tetrapods
  - Coelocanths shared ancestry with lungfishes and tetrapods
- Fossils made the prediction
  - DNA supported it
Molecules & Morphology - Humans

- Human evolution
- Oldest fossils closely related to *Homo sapiens* came from Africa ~200,000 years old
- Next oldest fossils relating to *H. sapiens* are from Israel, ~100,000 years old
- Even younger fossils relating to *H. sapiens* come from Europe, Asia, and Australia

Molecules & Morphology – Human Fossil Evidence

- Chris Stringer – Paleoanthropologist 1980s
- Argued these fossils were evidence humans originated in Africa
  - Spread out to other continents
  - Other hominid lineages became extinct
Human Fossil Evidence (cont...)

- Used DNA to test this hypothesis
  - Used mitochondrial DNA
  - Analyzed DNA from Africans
  - Compared their DNA sequences to those of people from other parts of the world
- Found that Africans carry the biggest diversity of mitochondrial DNA
- Also belong to branches that split off very early from those of other humans

![Evolution tree of mitochondrial DNA gene](image)

Human Fossil Evidence (cont...)

- Mitochondrial DNA sequences of Asians, Europeans, and people from the New World are much more closely related to each
- Supports the hypothesis that *H. sapiens* first evolved in Africa and moved to other continents out from Africa

![Human migration map](image)
Human Fossil Evidence (cont...)

- This means ALL living humans can trace their ancestry to Africa. For example, here is a map showing Homo erectus locations

Natural Selection vs. Neutral Evolution

- Molecular phylogenies can help scientists figure out how evolution works
- Hardy-Weinberg Model folded mathematics and genetics into evolutionary biology
  - Hardy-Weinberg showed how natural selection can fix alleles in populations and produce new adaptations
- Other scientists didn’t believe that differences in DNA sequences automatically translated into differences in fitness
  - First clue came from early studies on hemoglobin
Natural Selection vs. Neutral Evolution

- Different animal species have slightly different amino acid sequences in their hemoglobin
- All use hemoglobin to store oxygen
  - Mutations altered the molecule’s structure
  - Didn’t change its ability to do its job

Natural Selection vs. Neutral Evolution

- These mutations were neutral
  - Had become fixed in certain species because of genetic drift
- Additional research showed there were other examples of neutral evolution
- Because multiple codons can code for the same amino acid (degenerate code), a mutation can alter a gene without changing the protein it makes
  - Silent substitution
Natural Selection – What Is It?

• Research has shown that much of the human genome has experienced neutral evolution
  – Caused by genetic drift
  – Mutations that don’t affect fitness
• The main point of the neutral evolution theory: when there are several versions of a gene in a population, it is likely that their frequencies are drifting around

Natural Selection vs. Neutral Evolution

• Neutral evolution enables scientists to estimate age of common ancestors by comparing mutations in a group of organisms
  – Still trying to figure out the exact relationship between natural selection and neutral evolution

The Molecular Clock

- Neutral mutations accumulate at a roughly constant rate (clock-like) rate
- Use this information to calculate time frames
- Example: sequence cytochrome c from a bird

Using The Molecular Clock

- Calculate the number of substitutions that separate its DNA sequence from ours
  - About 80 million years
- Scientists refer to this method of telling time by counting neutral mutations as the molecular clock
The Molecular Clock Details

• Reading the clock is not easy
• Neutral evolution runs at different rates in different lineages
  – Genes evolve at different rates
  – Molecular clock can speed up or slow down over millions of years
• Scientists use statistical methods to compensate for these challenges

Example Clock Calculation – HIV-1 Virus

• Age of HIV-1 virus
• Los Alamos National Laboratory
• 2000
• Compared RNA from 159 HIV-1 viruses
• Drew an evolutionary tree
Example Clock Calculation – HIV-1 Virus (cont...)

• Calculated the rate the viral genes mutated
  – Based on how different the viruses were from each
  – How old they were

Example Clock Calculation – HIV-1 Virus (cont...)

• Allowed the mutation rate to vary from branch to branch of the tree
• Allowed mutation rate to vary from site to site within the genes
  – Calculations required supercomputer at Los Alamos
Example Clock Calculation – HIV-1 Virus (cont...)

• Estimated the common ancestor of HIV-1 strains existed sometime between 1915 and 1941
• Calculations narrowed time frame to 1931

Example Clock Calculation – HIV-1 Virus (cont...)

• Verified estimate by looking at HIV-1 strain from 1959 that wasn’t used in the original research
• Counted mutations and used molecular clock to estimate first existence at 1959
The Molecular Clock

• Molecular clocks - a useful tool that can provide information on other events in evolution, taking place millions of years ago

Ancient Selection

• Read pages 148-151 in your text
Deciphering the Genome

• Read pages 151-153 in your text