Title: Genetic Similarity

Title Slide

Narrator: Welcome to this presentation on genetic similarity.

Slide 2

Title: Underlying the Outwardly Visible Similarities, We Find Genetic Homology

Slide Content:
Text: Tracing arm bones from fish to humans

Image: Comparison of arm bones on animals and humans

Narrator: Up to this point, our discussion has focused on anatomical structures as the markers of interrelatedness and decent with modification. However, technological advances are opening another powerful avenue of comparison: DNA sequences.

Slide 3

Title: A Little Primer on Genetics Is Needed First

Slide Content:
Text:

- The genetic code:
  - Adenine, Cytosine, Guanine, Thymine
  - Arranged linearly
    **e.g.,** ACGGCCATATTTTGCCTGATGCTGATAAGCTCCC

- Code for proteins or RNA
- Like words in a sentence, the order and identity of the nucleotides matter

Image: None

Narrator: Before we get started discussing just how DNA can be used in this way, we need to establish at least a minimal foundation. Each of your cells contains copies of information bearing molecules called Deoxyribonucleic Acids or DNA. DNA is a polymer made up of monomers called nucleotides. There are 4 different types of nucleotide found in DNA: Adenine, Cytosine, Guanine, and Thymine symbolized by As Cs, Gs, and Ts respectively. These nucleotides are connected to one another in a linear sequence that is millions of nucleotides long. The nucleotide sequence is a code specifying the construction of RNA and protein. If the sequence is altered, that is mutated, a different product or no product may result.
Slide 4

Title: This Code Is Passed to Descendants

Slide Content:
Text:
- Copies of the genes are carried by sperm and egg.
- So, if the sequence ACGGCCATATTTTGCTGATAGCTGATAAGCTCCC is found in a parent, then we would not be surprised when the exact same sequence ACGGCCATATTTTGCTGATAGCTGATAAGCTCCC is found in the offspring.
- So certain are we that this indicates relationships that this is the basis of modern paternity testing.

Image: None

Narrator: This DNA is replicated and packaged into eggs and sperm before sexual reproduction. This replication of DNA is accomplished mostly without errors. So, the nucleotide sequence found in a parent is likely to be found in their offspring. We are so confident in the reliability of replication and inheritance that DNA sequence comparison is the basis of modern paternity testing. It is also a powerful tool that can ensure the conviction or exoneration of many accused criminals.

Slide 5

Title: Genetic Sequences Remarkably Conserved Between Species

Slide Content:
Text:
- That's right, different species share identical sequences of DNA!
  - e.g., humans and chimpanzees have 95-98.5% identical gene sequences

Image: None

Narrator: Just as we see homologous anatomy between species, genetic sequences are also shared by species. Closely related species, like chimpanzees and humans, have nearly identical nucleotide sequences (95-98.5% identical) whereas more distantly related species share fewer sequences. Even distantly related species have some genetic similarity; for example, jellyfish and man share some similar sequences.
A common target of scientific interest is a type of DNA sequence known as a pseudogene. Pseudogenes are non-functional versions of genes. There are various reasons for these sequences to be nonfunctional, but usually a mutation has changed the code in such a way that it no longer codes for a protein. Once the gene is made non-functional, that is, made a pseudogene, further changes to its sequence will have no effect on the organism. These sequences are then, essentially, inert series of nucleotides. Nonetheless, they are replicated and passed through sperm or egg to offspring.

Consider a hypothetical 60-nucleotide sequence. Haphazardly choose 7 positions in the sequence where a mutation occurs. At these 7 positions exchange the existing nucleotide for any one of the other three nucleotides, for example, G to an A or T or C. Pause the recording until you have noted the position of each change and the new nucleotide found at each position.
Slide 8

Title: A Thinking Exercise

Slide Content:
Text:
Original: GGAGAAGACCAAGGAGGCCCTACTGGAGCTAAAGGCCATGCTGGAGGCCCACCCCAAAGT

Copy with Mutations: AA---------C--------G---------G---------------------------------------------G—G--

Did you get the same result? Are you surprised?
The likelihood of independently selecting the same seven locations and making the same mutations is 1.12 out of 10,000,000,000,000,000 (that’s 10 quadrillion)

Image: None

Narrator: Compare your results with mine. In this illustration, a dash indicates no change from the original sequence. A letter indicates the newly substituted nucleotide. Did you make all of your changes at the same positions that I did? Did you substitute the same nucleotides at those positions? I would be shocked if you did. The likelihood of independently selecting the same seven locations and making the same mutations is 1.12 out of ten quadrillion. The likelihood would have been diminished if a whole gene containing thousands of nucleotides were used instead of just 60.

So?

Slide 9

Title: Some Additional Information...

Slide Content:
Text: None

Image: Chart comparing the pseudogene sequences of a rat, human, chimp, orangutan, and a macaque.

Narrator: So, this sequence is a small part of a pseudogene found in primates. It is a nonfunctional homolog of a functional gene in rats. First, notice the incredible similarity (indicated by dashes) between the rat sequence and the primate sequences. Why would this be?
Slide 10

Title: Some Additional Information…

Slide Content:
Text: None

Image: Chart comparing the pseudogene sequences of a rat, human, chimp, orangutan, and a macaque.

Narrator: Notice that many of the differences between the primates’ sequences and the rats’ are shared by the primates. For example, the first two positions have an As instead of the Gs the rat has. Compare the chimpanzee and the orangutan sequence. Remember, these represent random changes to a non-functional gene. What are the odds that these changes occurred independently in the chimpanzee and orangutan in such a way that all seven of the highlighted positions were changed and that they were changed to the same alternative nucleotides? Remember the previous hypothetical example 1.21 out of 10 quadrillion. If you argue that the chimpanzee and orangutan sequence are designed that way, my questions would be 1) Why design a gene so that it is non-functional and 2) Why make it non-functional in such a similar fashion when any mutations would do? Evolutionary biologists would suggest instead, that the highlighted mutations occurred in the common ancestor to all of the primates. The other mutations occurred after these primates diverged from that common ancestor and stopped interbreeding. By considering even more of this gene (not shown here), scientists have been able to reconstruct the evolutionary history or “family tree” of these primates.

Slide 11

Title: Remarkable Consensus

Slide Content:
Text: None

Image: An amino acid, DNA, and morphological chart, each constructed by different scientists, yet illustrating the same results

Narrator: The interesting thing is that this tree constructed using this pseudogene is in agreement with others constructed by independent teams of scientists employing different comparisons. For example, the new trees shown here were constructed using skeletal anatomy and amino acid structure.
Title: Homology Supports Darwin’s Concept

Image: The first tree that Darwin drew

Narrator: Homology, whether molecular or anatomical, is further evidence for Darwin’s idea of descent with modification.