ANSWERS to WS: Lesson B: What Can Pseudogenes Tell Us About Common Ancestry?

B-1: GULO Data:

2. 35 out of the 55 nucleotides are alike (64%); also, there are 3 big sequences: 2 with 9 bases, and 1 with 6 bases.

3. Human, chimp, and orangutan show about the same number of differences (8-9), mostly the same nucleotide bases.

4. Apes and humans had more differences (8-9) than shown by macaques (6).

5. Some nucleotide bases mutated, producing non-functional genes, but with sequences mostly identical to the functional rat gene. From this, we would infer that primate sequences were inherited by descent from a common ancestor to rats (not *from* rats). Primates had abundant access to fruits with vitamin C, therefore there was no selective advantage to retain the functional gene for making vitamin C, so random mutations over time would corrupt the gene, producing the non-functional "pseudogene" we find today.

6. Apes and humans are more closely related to each other (by a more recent common ancestry) than to macaques.

7. Apes and humans continued to evolve independently from macaques after their split from a common ancestor

To sum up the explanations (5-7): An evolutionary biologist would explain the similarities between the inactive GULO genes and the rat gene as evidence all the species in question have common ancestry and that the inactive gene arose through mutation of a functional GULO gene. The strong similarity among the pseudogenes would be interpreted as evidence of common ancestry among these species, while any differences (not indicated in this part of the sequence) would be interpreted as possibly being due to mutations that occurred since the species split.

Since a deletion is unlikely to occur independently at the same site in several species and is likely to persist once it occurs, a shared deletion is especially strong evidence for common ancestry.

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B-2: Psi Beta Hemoglobin Data:

8. [note highlighted nucleotides in codons 1, 3, 4, 5, 6, 7, 8, 10, 11, 12, 13, 14, 16, 17, 19, 20, 21, 22, 23, 24, 25 (namely, all codons except 2, 9, 15, and 18, which were identical in all four sequences).] 50 of the 75 nucleotides are different (67%).

9. a) the last G in TG**G** in the beta codon #16 was replaced with an A, creating the STOP codon TGA.
   b) the last G in GT**G** in the beta codon #21 was replaced with a deletion, causing a corruptive frame shift.

10. 25 of 75 (33%) are the same. This is a significantly higher match than would be expected if the sequences were independently produced, therefore suggesting that the psi beta gene arose by gene duplication.

11. All differences from the human beta are the same differences! This strongly suggests a fairly recent common ancestry of humans and apes.

12. There are NO differences in this sequence, therefore further confirming a recent common ancestry of apes and humans. Any differences would be interpreted as possibly being due to mutations that occurred since the species split.

13. A specific deletion, at a specific site, is extremely unlikely to happen, and then persist, by pure chance. This is especially strong evidence for common ancestry.

EXTENSION: Out of the entire 430 base pairs, the human and chimp sequences differ at only 6 positions, human and gorilla at only 3, and chimp and gorilla at only 7, an impressive degree of similarity since the human pseudogene differs from the human functional beta at over 25% of the positions. (The greater similarity of the human pseudogene to the gorilla pseudogene than of the human to chimp appears to contradict the widely supported hypothesis that the chimpanzee is our closest living relative but is not unexpected when comparing single genes for species for which the timing of branching is relatively close. Saitou and Nei estimated that comparison of close to 5000 base pairs would be needed in order to expect the molecular data to reflect the true phylogenetic relationship among 3 species that branched in a relatively short time interval.)

References (sources of sequences):

Chang, L.Y.; Slightom, J.:
Isolation and nucleotide sequence analysis of the beta-type globin pseudogene from human, gorilla, and chimpanzee.
J Mol Biol **180**:767-84, 1984. PubMed ID: 6098690

Ohta, Y; Nishikimi, M.:
Random nucleotide substitutions in primate nonfunctional gene for L-gulono-gamma-lactone oxidase, the missing enzyme in L-ascorbic acid biosynthesis.
Biochim Biophys Acta **1472**:408-11, 1999. PubMed ID: 10572964

Saitou, N; Nei, M.:
The number of nucleotides required to determine the branching order of three species, with special reference to the human-chimpanzee-gorilla divergence.
J Mol Evol **24**:189-204, 1986. PubMed ID: 3104615