PSEUDOGENE SUITE
Lesson B: WHAT CAN PSEUDOGENES TELL US ABOUT COMMON ANCESTRY?

adapted for ENSIweb by L. Flammer
Macroevolution

A. SYNOPSIS:
Students compare the DNA sequence data for a portion of the rat GULO gene to the corresponding sequence in the inactive GULO gene (“pseudogene”) in humans, chimpanzees, orangutans, and crab-eating macaques by identifying the shared sequences in their alignment. They compare the pseudogene sequences and note a shared deletion. In addition, students do an alignment for the first 25 codons of the functional human beta globin gene and its pseudogene in humans, gorillas, and chimpanzees, then compare the pseudogenes and again note a shared deletion, as well as two other shared significant differences from the functional human sequence. Such shared deletions provide strong evidence for shared common ancestry (descent with modification), a natural process of macroevolution vs the more mysterious, vague, untestable “intelligent design” scenario.

B. MAIN CONCEPT:

Many features of modern organisms reflect the structure of their ancestors in ways that are not adaptive.

C. ASSOCIATED CONCEPTS:
1. Inactive DNA sequences that resemble the sequences of active genes are termed pseudogenes and can arise in one of three ways.
2. Descendants of a mutation-carrying individual may carry that same mutation.
3. Although single-base substitutions may undergo reverse mutation at a later time, deletions are unlikely to revert.
4. Independently occurring deletions are unlikely to occur at exactly the same site.
5. Shared deletions are strong evidence for shared common ancestry.
6. The existence of pseudogenes in genomes weighs heavily against the “intelligent design” idea.

D. ASSESSABLE OBJECTIVES: Having completed this activity, students should be able to:
1. Explain why shared deletions are strong evidence for common ancestry.
2. Describe at least two ways a pseudogene may arise.

E. MATERIALS: (click to get PDF files for downloading)

Student Handouts (Background and Worksheet) Genetic Code chart
green colored pencils or highlighters yellow colored pencils or highlighters

F. TIME: 45 minutes

G. PREPARATION:
1. This lesson assumes a basic understanding of enzyme structure/function and of gene expression (protein synthesis). It is intended to follow the first lesson (A) in this suite: “Why Do We Need Vitamin C In Our Diet?”
2. This lesson would fit nicely near the end of an introductory unit on DNA structure and function., or, in concert with the other two lessons in this suite, it would be appropriate in a unit on evolution, or classification and biological relationships.
3. Prepare enough copies of the Student Handout (unstapled) for every student or pair of students. The Worksheets (2 pages) should be printed back-to-back on a single separate sheet, for easy checking.

H. PROCEDURES: Students may work alone, or preferably in pairs.
1. Either present the background information included in the Introduction and second section of the Student Handout or pass out the Student Handout and have students read the background information.
2. Explain to students that they will be comparing a portion of the sequence of a functional gene to the corresponding portion of its pseudogene counterpart in a given set of species. (You may wish to point out that the choice of species was made by the researchers who conducted the study and that, for many species, sequence data is still not available.)