

PSEUDOGENE SUITE

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

by Mary Ball and Steve Karr of Carson-Newman College
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.)

3. Using the GULO alignment (Part B-1), have students use a green colored pencil or highlighter to mark the positions in the partial rat sequence and the corresponding pseudogene sequences given in the Student Handout in terms of which are identical across all five species.
4. Using the GULO alignment, have students use a yellow colored pencil or highlighter to mark any shared differences among the pseudogenes.
5. Students then answer the questions asked (2-7).
6. Using the beta globin data (Part B-2), have students use a green colored pencil or highlighter to mark positions at which all four sequences are identical and a yellow colored pencil or highlighter to mark the shared differences among the pseudogenes.
7. Students then answer the questions asked (9-13).

I. DISCUSSION:

Lead a discussion in which teams share their answers to the questions in the Student Handout. (Refer to the Answer Key.)

Note (if not discussed with Lesson A): Students may have the misconception that any nonfunctional genes should, over generations, be somehow “removed” by Natural Selection. If this point should come up, remind students that for Natural Selection to be able to select against a nonfunctional gene, there would have to be individuals in the population **lacking** that **nonfunctional** gene AND these individuals would need to be **more** likely to survive and reproduce as a result. Although one could argue that having useless DNA imposes a metabolic burden, such a difference for just one gene is expected to be extremely slight, so once a gene is inactivated, it is likely to persist in its inactive state. (If some individuals lack the gene, then it might, over generations, be lost solely by chance.)

J. ASSESSMENT & EVALUATION:

1. Check student worksheets to determine whether they were able to color-code the sequences correctly.
2. Ask students to explain why a shared deletion is strong evidence for common ancestry.
3. Ask students to propose a biologically reasonable explanation for why the human GULO pseudogene shares a deletion with the GULO pseudogenes of certain primates and why the human psi beta pseudogene shares a deletion with the psi beta pseudogenes of certain primates.

K. EXTENSIONS & VARIATIONS:

1. This lesson was meant to follow lesson A: “Why Do We Need Vitamin C in Our Diet?”
2. The data from which these partial sequences were taken consists of the complete coding sequence corresponding to rat exon 10 from the rat, human, chimpanzee, orangutan, and crab-eating macaque and from the complete coding sequences for the beta globin gene and pseudogenes. This data is available through Biology Workbench for computer manipulation. (See lesson C: “Exploring Primate Pseudogenes With Biology Workbench”).
3. The comparison of different species in the two examples reflects the gaps in our knowledge of gene sequences across species. An extension of the activity would be to have students research currently accepted phylogenetic trees for a “favorite” or suggested species and predict, on the basis of the inferred relationships, other species in which the same shared deletions will someday be found.
4. Do the “Polar Bear / Giant Panda Ancestry” lesson, by Caroline Maier, in which DNA sequence data are used for building phylogenetic trees. This lesson will soon be added to this ENSI site. It can be found in *The American Biology Teacher* journal of November/December 2001 (**63**(9):642-646).

L. ATTRIBUTIONS:

This activity was developed by Mary Ball and Steve Karr of Carson-Newman College for use in a high school biology course or a college-level introductory biology course. References used as a source of information, ideas, and sequences are listed on the References page. (The actual articles were not consulted. The abstracts and data were accessed through PubMed.)