

## Pseudogenes and plastic trees

I enjoyed reading Rob Carter's book review on *Adam and the Genome* in issue 31(2). I'd like to comment on Rob's statement:

"I do not have a ready answer for why this gene family would fall into a nested hierarchy, but, from experience, I am deeply suspicious of the evolutionary claims (p. 43)."

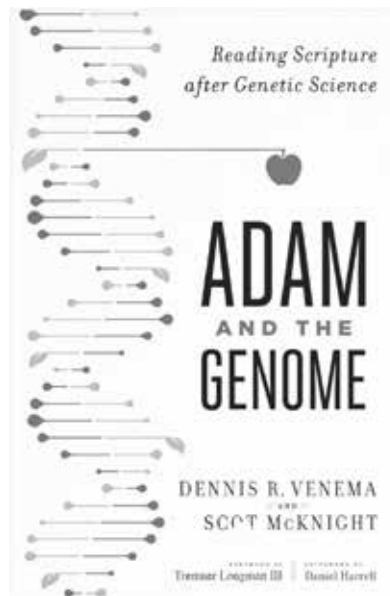
His suspicions are well founded. It appears this claim is the one posted on the *BioLogos* website on May 17, 2010, which I addressed in *Creation Matters*.<sup>1</sup> Essentially all one needs to do is read the open access article by Gilad *et al.*,<sup>2</sup> where they clearly state their methodology and the inferences they make.

Gilad *et al.*, first assumed the popular phylogeny where chimps are most closely related to humans, followed by gorillas, orangutans, and rhesus monkeys. Then they interpreted the data according to the tree:

"We inferred on which lineage each gene silencing event occurred by estimating the ancestral sequences of each node in a tree representing the phylogenetic relationships of the species (p. 3326)."

As Carter pointed out, olfactory receptor genes are believed to be among the most mutated genes known. When it appears that mutation has changed them to a pseudogene, often multiple frame-closing mutations are inferred. So how did Gilad *et al.* determine which one happened first?

"When more than one coding region disruption was identified in the same species, we inferred which occurred first by identifying disruptions shared between species. We considered only one disruption per gene to determine the gene silencing rate in each lineage (p. 3325)."



Could the data have fit as well or better in a different tree? Quite possibly, but that was not considered.

It is known that many genes in the gorilla are actually more similar to humans than those of the chimpanzee (Sally *et al.*).<sup>3</sup> So, some gene trees fit one phylogeny, and other gene trees fit a different phylogeny. It has been claimed that pseudogenes are better to use than ordinary genes because they have no function and only change by random mutation (i.e. no selection occurs). However, in the same issue of *J. Creation* where Carter's book review appears, there is an article discussing pseudogenes that are not really pseudogenes at all (pp. 10–12).

Nice book review!

### References

1. Lightner, J.K., Similarity and shared mistakes, *Creation Matters* 16(1):5–6, 2011.
2. Gilad, Y., Man, O., Pääbo, S., and Lancet, D., Human specific loss of olfactory receptor genes, *PNAS* 100(6):3324–3327, 2003.
3. Scally, A., Dutheil, J.Y., Hillier, L.W. *et al.*, Insights into hominid evolution from the gorilla genome sequence, *Nature* 483:169–174, 2012.

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