

Lopez, John

From: [REDACTED]
Sent: Saturday, January 04, 2014 3:38 PM
To: Lopez, John
Subject: Heretofore Unadjudicated Factual Error in Pearson Texas Biology (2015)
Attachments: Cabill integrative annotation -2011 highlight.pdf; Ebersberger mapping human genetic ancestry highlight.pdf; Hangauer pervasive transcription journal.pgen.1003569 highlight.pdf; Hughes chimpanzee and human Y chromosomes highlight.pdf; Watanabe DNA sequence and comparative analysis highlight.pdf

Dear Mr. Lopez:

Pursuant to TEC Chapter 31, Subchapter B, Section 31.023(b) -- "Each instructional material on the list [of state-adopted instructional materials] must be free from factual errors." -- and to 19 TAC Chapter 66, Subchapter A, Section 66.10(d) -- "A penalty of \$5,000 shall be assessed for each failure to correct a factual error" -- we hereby petition TEA to direct Pearson to correct a previously-identified factual error in its just-adopted Texas Biology book. This factual error was not among those on the list of 17 submitted to the SBOE-appointed committee of 3 for arbitration in December. Specifically, the red-indicated portions of the following 2 passages of that text misstate the certainty and misrepresent the accuracy of overall chimp-human genetic similarities:

SE 767, par. 2, lines 8-9 -- "Recent DNA analyses confirm that, among the great apes, **chimpanzees are humans' closest relatives.**"

SE 767, par. 4, lines 1-2 -- "The brains of chimpanzees, **our closest living relatives,**"

These passages falsify known facts in 7 ways:

- (1) **RANK CHERRY-PICKING** In comparing chimp and human genomes, commonly-used "low-complexity sequence masking" excludes many non-aligning DNA segments, understating disparities between the two genomes.
- (2) **STATISTICAL SLANT** Focusing only on the most similar portions of chimp and human genomes exaggerates their total actual harmony.
- (3) **OVERRATED SYNC** The longer the DNA sequence segments compared, the lower the percentage of match-up between portions of chimp and human genomes.
- (4) **HIGH DISCREPANCY** 23% of chimp and human DNA sequences show no similarity. Chimp and human Y-chromosome DNA sequences differ by over 30%, or about as much as human and chicken autosomes differ. 83% of amino acid sequences in chimp chromosome 22 differ from those in its human chromosome 21 counterpart.
- (5) **CONFLICTING DESCENTS** Biochemical phylogenies of chimps, humans, gorillas, and orangutans contradict their standard anatomical phylogeny 40% of the time.
- (6) **BLOATED PERCENTAGE** Counting the gaps between closely aligning strands of chimp and human DNA sequences deflates the overall identity ratio between their respective genomes to 70-87%.
- (7) **RISKY SNAP JUDGMENT** Any assured correspondence between the two genomes is premature and arbitrary. Unacknowledged functions of now-omitted, non-aligning DNA sequence sections may revolutionize comparisons.

The 5 technical monographs here attached, with key passages highlighted in yellow, document most of the above points. In our recent written exchange with this text's co-author Kenneth Miller, he significantly failed to address, much less refute, any of these 7 objections. Yet Pearson refuses a fix. We therefore request TEA to require Pearson to correct these 2 factually-erroneous passages thus --

Revise SE 767, par. 2, lines 8-9, thus – "~~Recent DNA analyses confirm that, among the great apes, chimpanzees are humans' closest relatives~~ suggest no consistent pattern of evolutionary relationships among these hominoids."

Revise SE 767, par. 4, lines 1-2, to read – "The brains of chimpanzees, ~~our closest living relatives,~~ one of the hominoids,"

Both reasonable and judicious redactions exactly fit their respective contexts in sense, style, and space.

We sincerely appreciate TEA's attention to this important matter.

Neal Frey
Senior textbook analyst
Educational Research Analysts
Longview, Texas
Office phone [REDACTED]

cc: Barbara Cargill