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Response to Comment on "The Placental Mammal Ancestor and the Post–K-Pg Radiation of Placentals"

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Tree-building with diverse data maximizes explanatory power. Application of molecular clock models to ancient speciation events risks a bias against detection of fast radiations subsequent to the Cretaceous-Paleogene (K-Pg) event. Contrary to Springer *et al*., post–K-Pg placental diversification does not require "virus-like" substitution rates. Even constraining clade ages to their model, the explosive model best explains placental evolution.

Springer *et al*. (*1*) assume that nuclear DNA produces a "true" tree. The true tree is, however, unknown, and all data, including nuclear genes, show homoplasy. Even multinuclear gene data sets (*2*) fail to resolve the basal split within Placentalia, to recover Tethytheria, or to establish a sister taxon for Primates. Of higher-level mammalian crown clades accepted by (*2*), only five emerged from molecular phylogenetics, but 78% emerged from comparative phenomics [table 1 in (*3*)]. Interestingly, the combined tree of (*3*) is highly congruent with molecular topologies, but more phenomic than genomic characters are interpreted as homology on it [retention index (RI), phenomic partition (0.42632); RI, nuclear DNA (0.3960)].

It is contradictory for Springer *et al*. to calibrate molecular clocks with fossils (*2*) but to dismiss fossils in tree-building. A fossil can only calibrate a tree when placed on it using phenomic data. The use of "diachronous terminals" (fossil and living species) in tree-building is considered a strength by clock users (*4*), and varied tree-building methods showed that long-branch attraction did not compromise our analysis (*3*). Polyphyletic functional groups in Springer *et al*.'s figure 1 are a mere by-product of pruning fossils from a tree, not a result of reanalysis of the original data. Optimizations on this pruned tree are suspect because they discount fossil evidence. Characters with obvious functions can provide evidence of relationship (e.g., mammary glands). A priori deletion of data in Springer *et al*. is unjustified because it precludes discovery of homology and novel topologies (*5*).

Our hypothesis (*3*) of post–Cretaceous-Paleogene (K-Pg) placental diversification is derived from phylogenetic consideration of fossils, which provides a key test of molecular clock assumptions. Fossil ranges and ghost lineages provide minimum ages, but paleontologists have also searched extensively for Cretaceous crown clade placentals. Accumulated negative evidence indicates that such fossils are absent (*3*, *6*, *7*). The ancient Cretaceous divergence dates of (*2*) assume taphonomic bias exclusively against preservation of placentals because thousands of nonplacental Cretaceous fossils are known (*7*, *8*). Similar negative evidence indicates that nonavian dinosaurs are absent in Paleogene rocks, leading to the conclusion that dinosaur extinction occurred at or before the K-Pg boundary.

Basal branch lengths on the combined tree (*3*) suggest average nuclear DNA substitution rates of 0.12 to 0.14 substitutions per site per million years (s/s/My) over 200,000 years and 0.06 to 0.07 s/s/My over 400,000 years. These are higher-than-average substitution rates for mammalian nuclear DNA (*9*) but are orders of magnitude lower than average rates for viruses (*10*) (Fig. 1). If one selects extremely slowly evolving viruses, as Springer *et al*. do, then even average mammalian rates (*9*) can be called "virus-like." A hypothesized rate increase of as little as one order of magnitude during an adaptive radiation warrants consideration given that branch lengths of

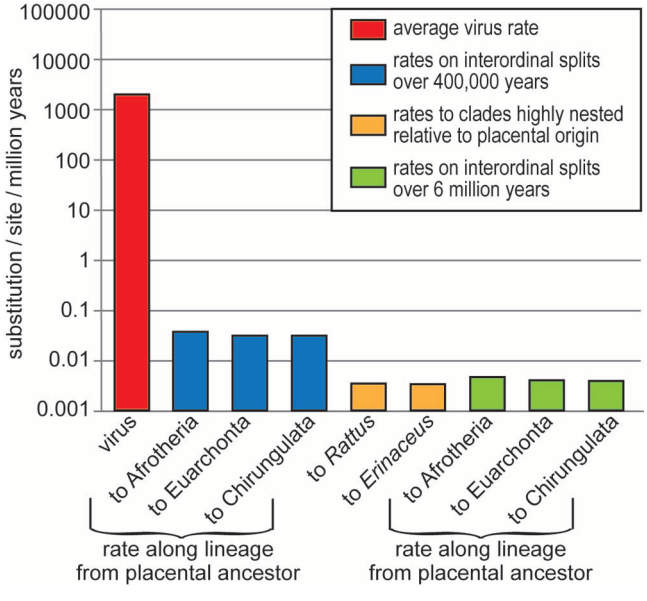

Fig. 1. Nuclear DNA substitution rates. Nuclear DNA substitution rates from maximum likelihood (ML) branch lengths on the combined data tree of (*3*) for key interordinal splits (Chirungulata is the common ancestor of Chiroptera and Euungulata and all of its descendants) compared to virus rates (*10*). Only 6 My is required to fit branch lengths to average rates.

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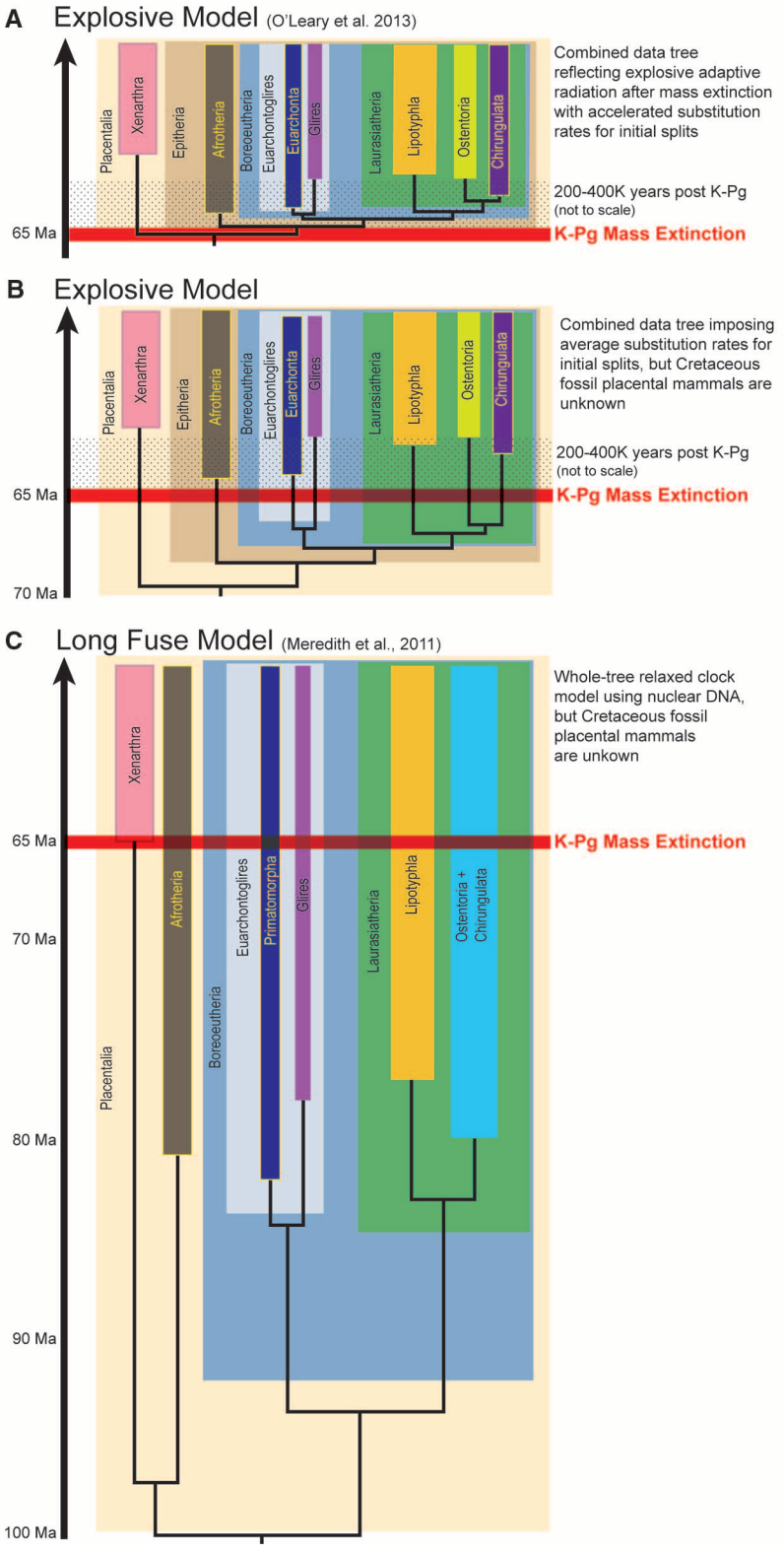

Fig. 2. Diversification scenarios. Diversification scenarios for Placentalia (*12*). (**A**) Explosive model supported by (*3*). (**B**) Explosive model based on (*3*) with basal splits strictly scaled to average substitution rates, differing from (**C**), the long-fuse model (*2*) from a relaxed clock with ancient Cretaceous divergences.

the genes used vary by three orders of magnitude. Moreover, the range of rates of nuclear gene substitutions is treated as if a constant (*9*) by Springer *et al*., when the studies on which they are based (*9*) removed the most variable genes, and used older fossil calibrations than in (*3*), potentially biasing estimated rates toward invariance and slowness.

Hypotheses regarding mammalian mutation rates are currently derived from only ~0.1% of the mammalian genome. Generalizations about rates of molecular evolution, and what they imply about speciation, derived from such a limited sample may be premature. Cichlid fishes have been estimated to produce new species every 43 years (*11*). Thus, the <10 speciation events needed for interordinal splits in 200,000 to 400,000 years (*3*) do not outstrip known rates.

Finally, if one recalculates clade ages on the combined evidence tree (*3*) while imposing a gamma-corrected general time-reversible substitution model, as preferred by Springer *et al*., results still fit the explosive model that we supported (*3*), described as placentals radiating "within a very short interval of about 10 million years, mainly following the K-T boundary" [p. 111, figure 2 in (*12*)]. These rates can be accommodated by extending interordinal diversification just 6 million years into the Cretaceous (Fig. 2). The 101 Ma age for crown Placentalia from clocks (*2*) would then be off by at least 30 My, and the attendant scenario of a "Cretaceous Terrestrial Revolution" tied to continental fragmentation is unsupported.

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