

Global rate variation in bony vertebrates

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Abstract

This study investigated long-term substitution rate differences using three calibration points, divergences between lobe-finned vertebrates and ray-finned fish, between mammals and sauropsids, and between holosteans (gar and bowfin) and teleost fish with amino acid sequence data of 625 genes for 25 bony vertebrates. The result showed that the substitution rate was two to three times higher in the stem branches of lobe-finned vertebrates before the mammal-sauropsid divergence than in amniotes. The rate in the stem branch of ray-finned fish before the holostean-teleost fish divergence was also a few times higher than the holostean rate, while it was similar to or somewhat slower than the teleost fish rate. The phylogenetic relationship of coelacanth and lungfish with tetrapod was difficult to determine because of the short interval of the divergences. Considering the high rate in the stem branches, the divergences of coelacanth and lungfish from the stem branch were estimated as 408 - 427 million years ago (Ma) and 399 - 414 Ma, respectively, with the interval of 9 - 13 million years. With the external calibration of the mammal-sauropsid split, the estimated times for ordinal divergences within eutherian mammals tend to be smaller than those in previous studies that used the calibration points within the lineage, with deeper divergences before the Cretaceous-Paleogene boundary and shallower ones after the boundary. In contrast the estimated times within birds were larger than those of previous studies, with the divergence between Galliformes and Anseriformes about 80 Ma and that between Galloanserae and Neoaves 110 Ma.

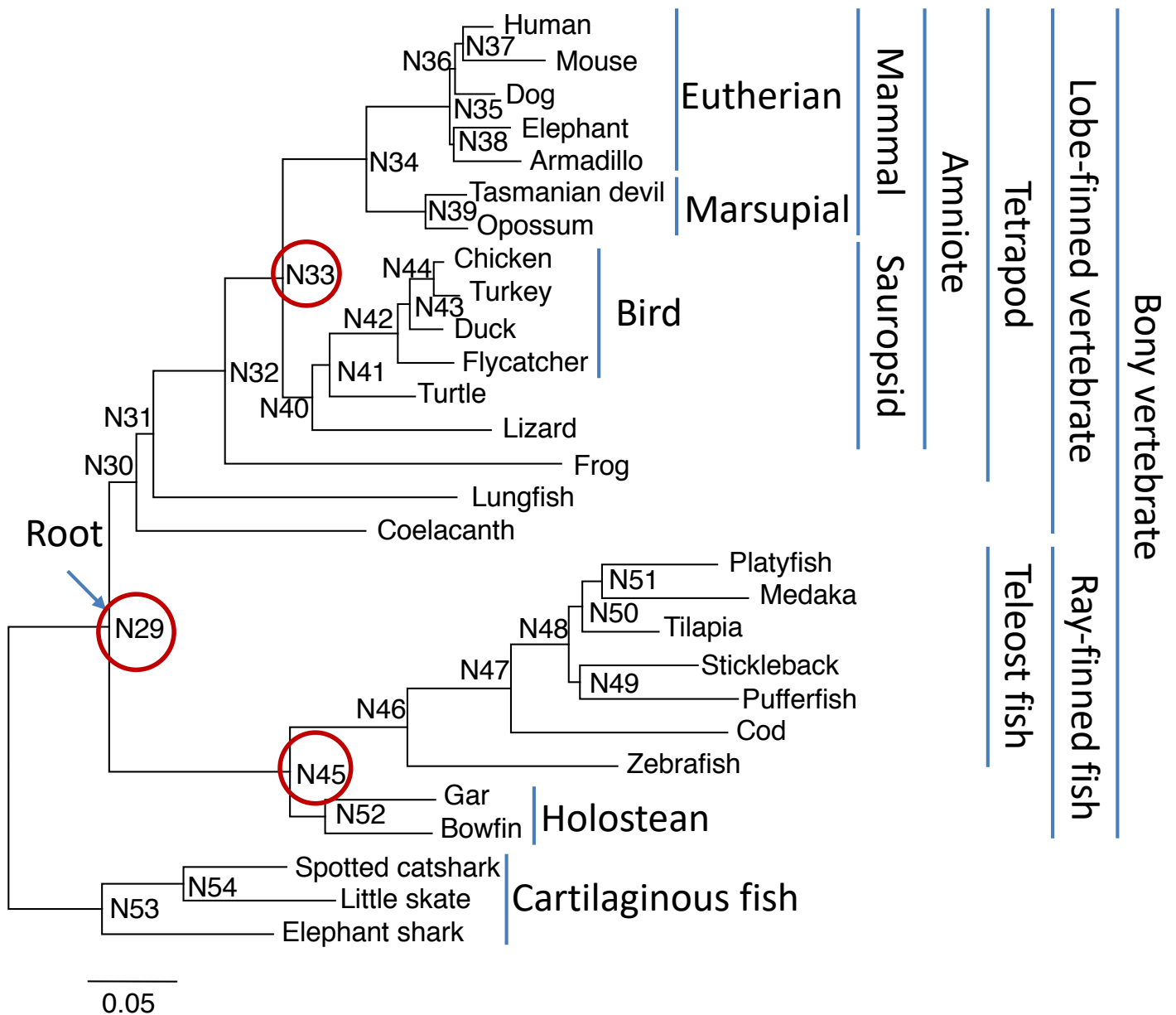


Figure 1. Phylogenetic tree of 28 vertebrate species. The tree topology is from Takezaki and Nishihara (2017). The branch lengths were estimated by the maximum likelihood method for each of 24 partitions obtained by PartitionFinder with BIC criterion and weighted averages were taken by excluding four partitions in which a single species had a long terminal branch (see Materials and Methods). Cartilaginous fish was used as outgroup. The numbers that follows N (N29 – N54) are those given to internal nodes. The three nodes marked with red circles are those used for calibration points: N29, 420.7 – 444.9 Ma, N33, 318 – 332.9 Ma, and N45, 250 – 331 Ma. Fossil ages are from Benton et al. (2015).

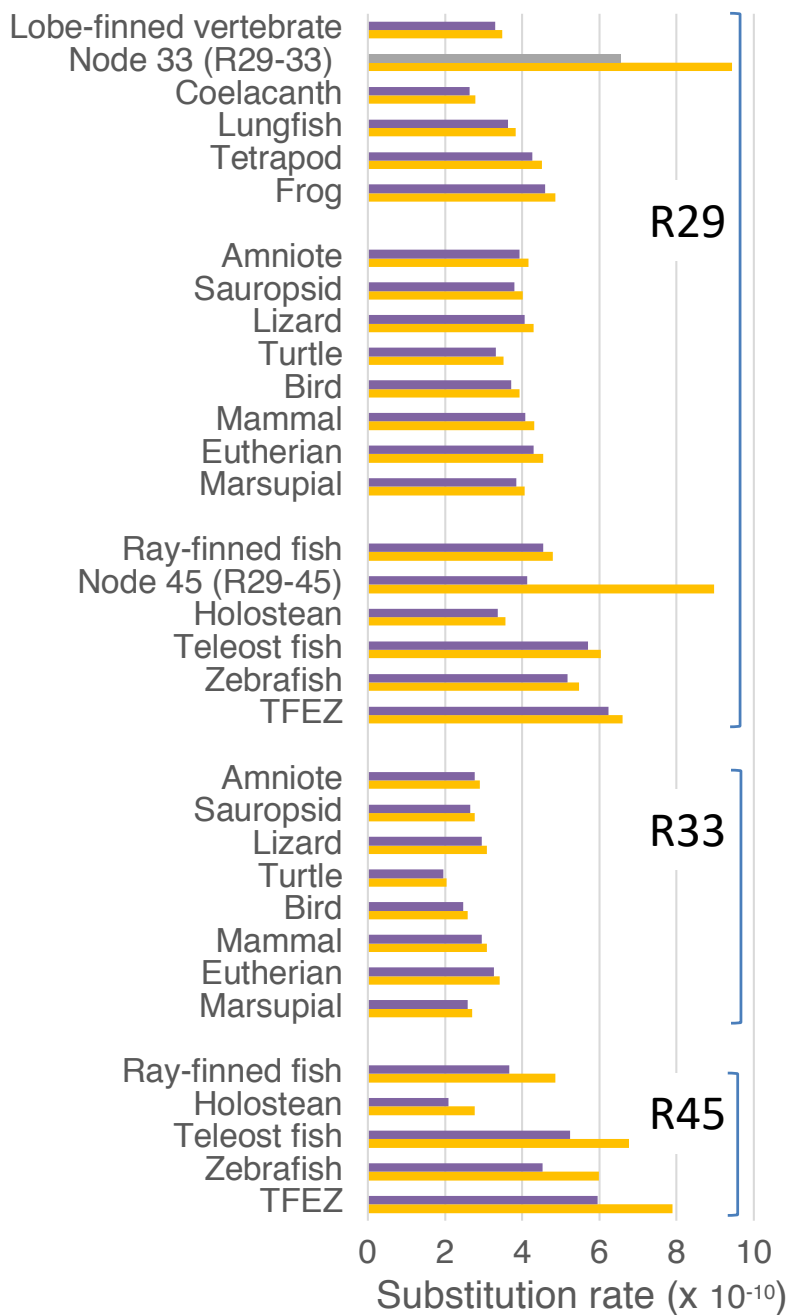


Figure 2. The substitution rates estimated by setting nodes 29, 33, 45 (N29, N33, N45) as calibration points (R29, R33, R45). Orange bars and gray bars indicate rates assuming minimum and maximum ages for the nodes, respectively. TFEZ: teleost fish excluding zebrafish. Holostean: gar and bowfin.

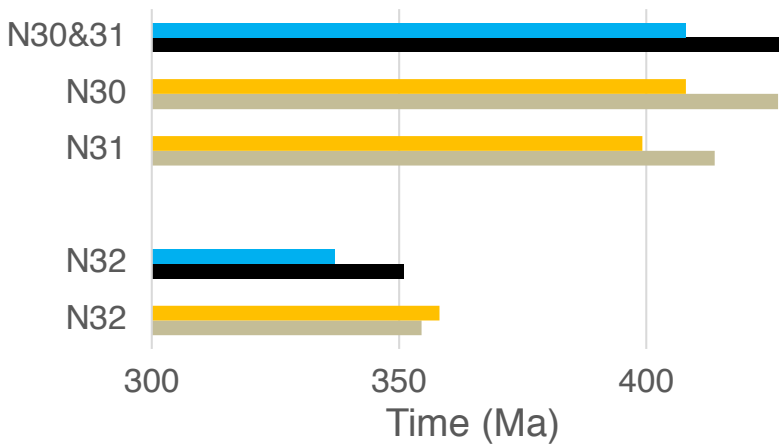


Figure 3. The fossil ages and estimated times at the stem branch of by setting N29 and N33 as calibration points. Blue and black bars indicate minimum and maximum ages of fossil ages, respectively. Orange and gray bars indicate estimated times by assuming the minimum and maximum time intervals (87.8 and 128 My) between N29 and N33.

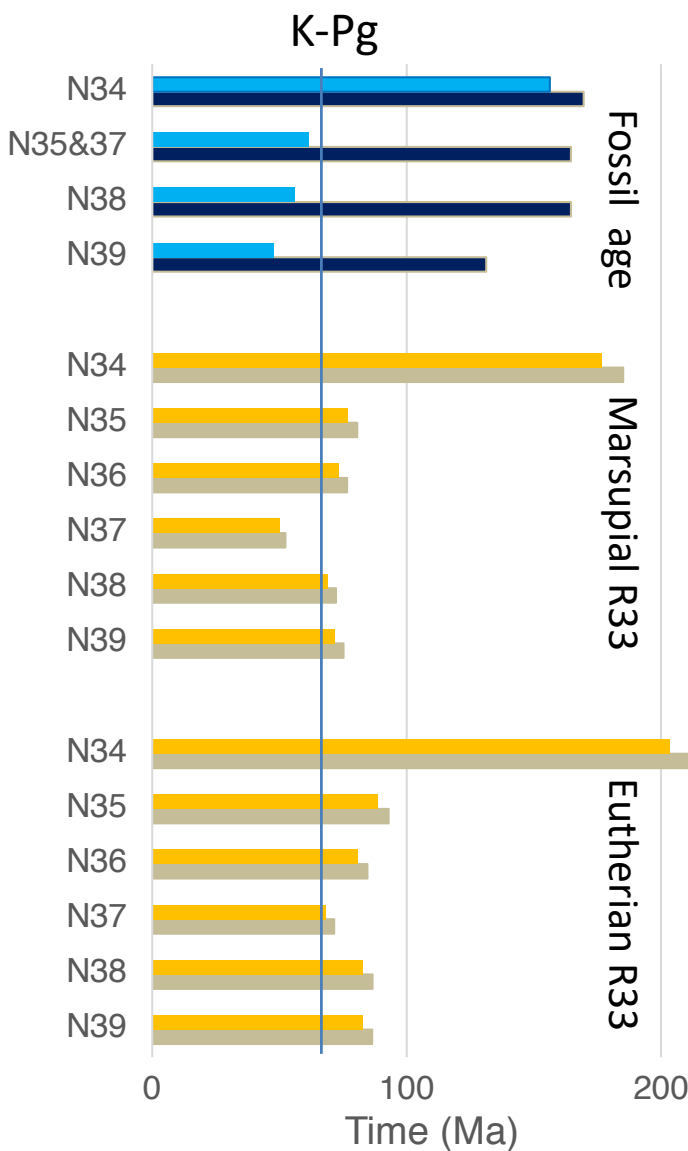


Figure 4. The fossil ages and estimated times within mammals by setting N33 as a calibration point. Blue and black bars indicate minimum and maximum ages of fossil ages, respectively. Orange and gray bars indicate estimated times by setting the minimum and maximum fossil ages of N33 as calibration points. The solid vertical line indicates K-Pg boundary (66 Ma).

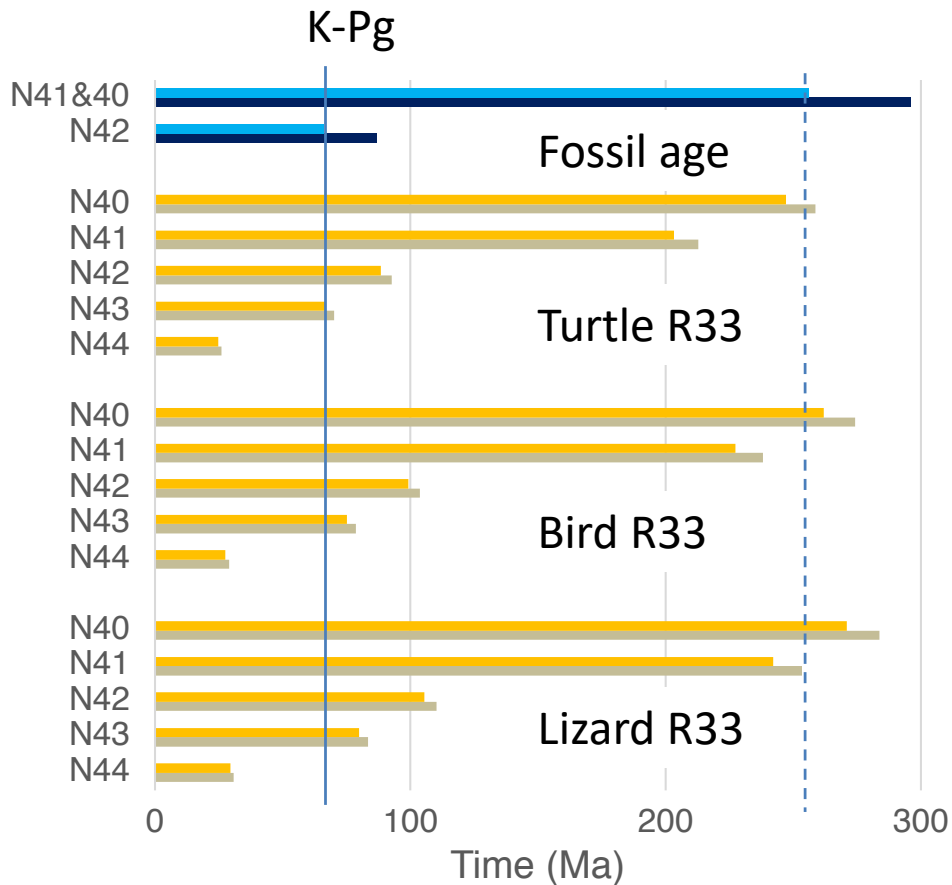


Figure 5. The fossil ages and estimated times within sauropsids by setting N33 as a calibration point. Blue and black bars indicate minimum and maximum ages of fossil ages, respectively. Orange and gray bars indicate estimated times using the minimum and maximum fossil ages of N33 as calibration points. The solid vertical line indicates K-Pg boundary (66 Ma). The dotted vertical line indicates the minimum fossil age of N40 and N41.