

Rates of molecular evolution in mammals

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A growing wealth of sequence data is now available for mammals, both at the level of entire genomes (nuclear and mitochondrial) and for individual genes. Despite this fact, there is a clear gap in our knowledge regarding rates of molecular evolution in this group, and the variation in and the factors determining these rates. It is clear that, at best, only a local molecular clock exists and that the rate of evolution varies both between genes and between lineages. However, beyond this, much of the available information is largely dated, remains somewhat anecdotal (e.g., “fast rats” or the “hominid slowdown”), and is based on limited sequence information that was usually not analyzed in a robust phylogenetic framework.

To address this gap, I present a comprehensive, comparative investigation of rates of evolution in mammals and the variation therein at three (nested) levels: genes, individual branches, and clades. The analyses make use of the largest molecular data set yet compiled for mammals (44 genes comprising 35 427 bp distributed among 2111 species) in concert with a dated, species-level supertree for the group.

Nearly all genes had evolutionary rates on the order of 10^{-8} or 10^{-9} mutations per site per year. In line with expectations, mtDNA was found to evolve nearly an order of magnitude faster (8.9 x) than nDNA. However, there was no difference in rate between tRNA genes and other mtDNA genes, belying the evolutionarily more conservative reputation of the former. Similarly, 18S rDNA was found to be the fastest evolving of all 44 genes, again in contrast to its conservative reputation.

Branch- and clade-specific rates of evolution showed that most mammalian lineages have “slow” rates of molecular evolution in that most genes are evolving slower along a given branch or within a given clade than their average across all mammals. Only restricted groups with rodents and, to a lesser degree, bats, primates, and cetartiodactyls show a noticeable speedup. Apes do indeed show a reduced rate compared to other Primates (which is among the fastest of all orders), with the branch leading to humans being even slower still, thereby confirming the existence of the “hominid slowdown”. Rodents are the fastest of the major mammalian orders, thereby supporting the “fast rat” hypothesis, although many lineages within this order do exhibit significant slowdowns.

Future work will extend these observations to look for mutational hotspots within individual genes and to characterize codon-specific rates of evolution.