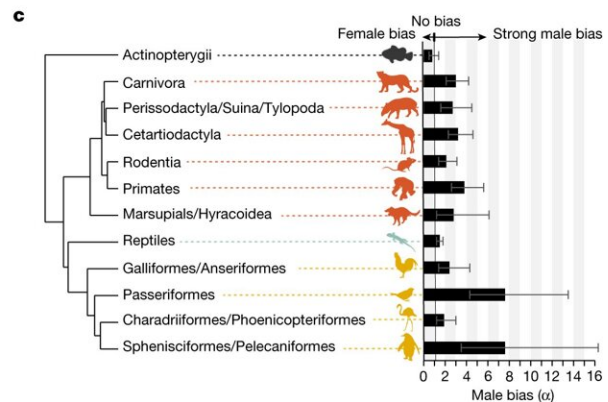
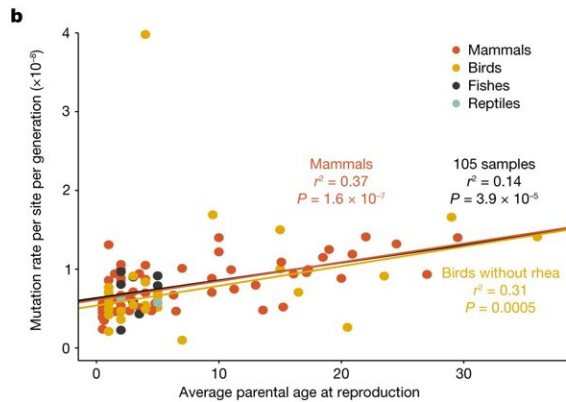
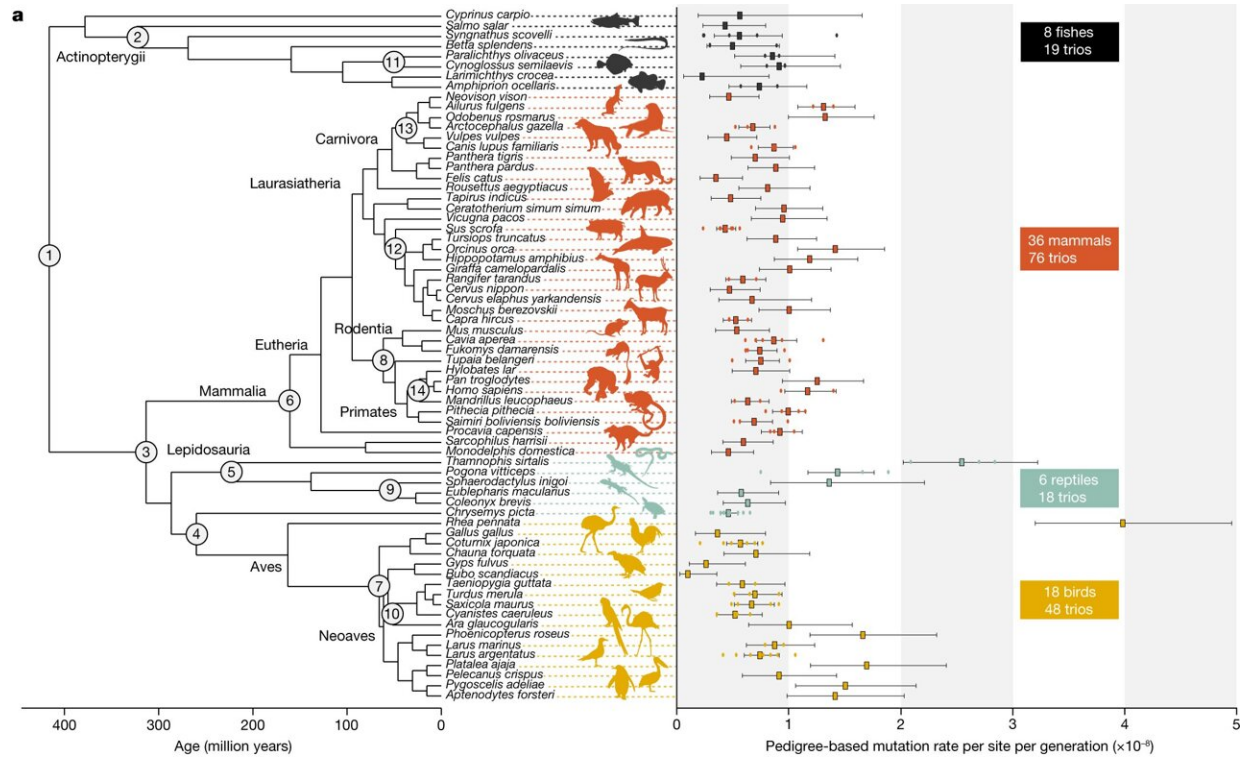


Determining the tempo of evolution across species

March 3 2023, by Justin Jackson



Variation in GMRs and their association with life-history traits across 68 vertebrate species. a, The phylogenetic tree of 68 species is based on UCE data and is calibrated with fossil data at 14 nodes. The average pedigree-based mutation rates per generation for each species, which are represented by the squares, show 40-fold variation among species. The 95% binomial confidence intervals are shown, and individual trios are represented by round points. b, The per-generation mutation rate is significantly associated with the average parental age at the time of offspring production across all individuals with known paternal age (105 trios), using linear regression. For birds, this relationship is statistically significant after removing a single outlier, the Darwin's rhea. c, The male-to-female contribution ratio (α) is estimated for groups of vertebrates having at least 30 mutations phased to their parents of origin in each group. The highest male bias (7.6:1) is found in two bird lineages, whereas fishes and reptiles show negligible male bias. The data are represented with 95% confidence intervals based on the binomial variance. The silhouette of *Syngnathus scovelli* was created by J.S. All other silhouettes are from PhyloPic (<http://phylopic.org>), except for one of the silhouettes of *Sarcophilus harrisii*, which was created by S. Werning, and the silhouette of *Pan troglodytes*, which was created by T. M. Keesey (vectorization) and T. Hisgett (photography); both are available under a [CC-BY 3.0 licence](https://creativecommons.org/licenses/by/3.0/). Credit: *Nature* (2023). DOI: 10.1038/s41586-023-05752-y

Scientists from Denmark and China have estimated germline mutation rates across vertebrates by sequencing and comparing genetic samples from 151 mother, father, and offspring trios from 68 species of mammals, fishes, birds and reptiles. A bioinformatics pipeline was designed to read, analyze and compare the genome mutations that occur yearly and between generations in each species.

The research was published March 1, 2023, in the journal *Nature*.

Knowing the germline mutation rate could allow a greater understanding of evolutionary drivers and be used to estimate when a species first

arose. Despite the variety of evolutionary paths seen in 68 different species, researchers found the germline mutation rate to be relatively conserved.

How fast a species evolves depends on the rate at which it accumulates mutations. Unlike [somatic mutations](#) that can occur in the DNA of any cell in the body but are never inheritable, germline mutations only occur in [reproductive cells](#) and are passed on to the next generation.

Individual germline mutation rates varied across all species in the study. While mutation rates per generation were found to be highest in reptiles, the difference between any of the four major classes of vertebrates was not statistically significant. Between species, birds had the most varied rates. More impactful was the amount of time between [generations](#), age at maturity, and reproduction rates.

Species with higher long-term effective population sizes tended to have lower mutation rates per generation, while those with longer generation intervals had higher per-generation mutation rates.

The father's age was the most significant explanatory variable of increased variants among mammals and birds. The researchers explained, "Although most birds and mammals produce sperm cells continuously through time, reptiles and fishes tend to be seasonal breeders, producing [sperm cells](#) during a limited period before the [mating season](#), which will tend to reduce differences in cell division numbers between males and females," allowing for less opportunity for [mutations](#) to occur.

While the germline mutation rates recorded the pace of species evolution, it is also an evolving parameter itself as life-history traits of the animals seem to play a role. With further research, scientists will continue to reveal the mechanisms that drive the tempo of evolution.

This latest study illustrates how much we can learn with a good design of experiments, robust access to [next-generation](#) gene sequencing machines, and a well-built bioinformatics pipeline to handle the tremendous amount of data required to thoroughly investigate even a small cross-section of evolving animals.

More information: Lucie A. Bergeron et al, Evolution of the germline mutation rate across vertebrates, *Nature* (2023). [DOI: 10.1038/s41586-023-05752-y](#)

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