



How hyenas decide whether to form a lion-fighting mob

Cooperative behaviour involves a trade-off between risks and rewards, and can provide benefits that are available only because of group action. Individual spotted hyenas (*Crocuta crocuta*) can join a group to take part in a mobbing behaviour (pictured) that drives away lions (*Panthera leo*) and might thereby provide access to carcasses of animals that have been killed by lions or hyenas.

Mobbing can deter lions as part of the battle between lions and hyenas for resources, but participating can be fatal for hyenas. The identification of factors that predict whether mobbing will occur sheds light on why

individuals cooperate in a complex society, as Montgomery *et al.* report in *Proceedings of the Royal Society B* (T. M. Montgomery *et al.* *Proc. R. Soc. B* **290**, 20231390; 2023).

The authors monitored wild spotted hyenas in a wildlife reserve in Kenya between 1988 and 2016. They found that the quest for food was not necessarily a key driver of mobbing. Lionesses were more likely to be mobbed than were male lions, and a high ratio of hyenas to lions was predictive of mobbing. Social ties between hyenas also boosted the chances of this behaviour occurring.

Mary Abraham

Evolution

Genes often uninformative for dating species' origins

Matt Pennell

The time frame of a species' origins provides context for evolutionary questions. However, dates from fossils are often inconsistent with estimates from genetic data. Emerging evidence points to a new explanation for this discrepancy.

The history of Earth is characterized by massive extinction events and the expansion of newly emerging groups of organisms. The timing of these extinctions is increasingly

well understood, but it has been difficult to pin down dates for the origin of many important groups, including animals, mammals, flowering plants and beetles. A large amount

of this uncertainty comes from the conflict between ages estimated solely from the fossil record and those derived from a combination of fossil data and the analysis of genetic differences between living species, known as the molecular clock. For example, analyses using molecular-clock methods date the origin of bilaterians – a group that includes whales, worms and humans – to between 688 million and 596 million years ago¹ but, when examining only the fossil record, the date is around 555 million years ago². Writing in *Systematic Biology*, Budd and Mann³ provide insights into why this time gap has remained so persistent.

The authors' analyses reveal that, paradoxically, the seemingly information-rich approaches that leverage several types of data for dating might not actually be using much information at all. Currently, molecular dating is done using a method called node dating, in which dates are estimated using what is known

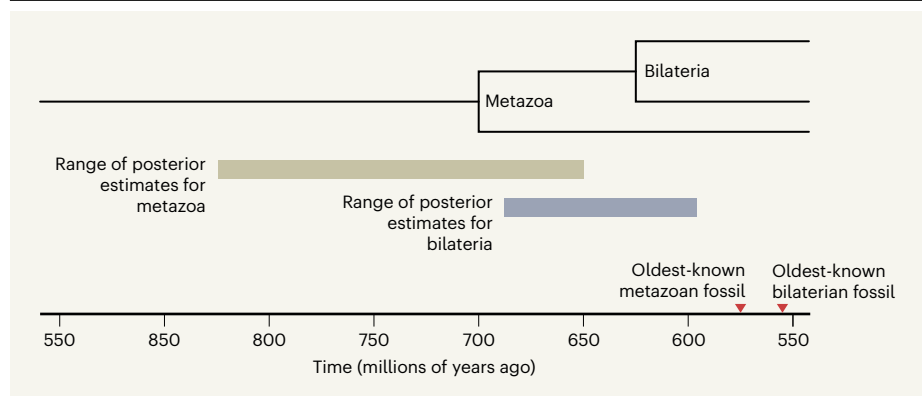


Figure 1 | Discrepancies between genetic and fossil data underpinning evolutionary trees. It can be difficult to assemble the branch points of a tree corresponding to the ancient origins of key groups, such as multicellular animals, termed metazoans, and the origins of a type of metazoa called bilateria (which includes humans). Assembly of such trees typically involves statistical analysis of genetic data to generate what are termed posterior estimates of probable origin dates. However, these dates are often substantially earlier than the oldest known fossils of the groups of interest. Budd and Mann³ provide an explanation for why these discrepancies occur. Data shown are from refs 1 and 3.

as a Bayesian approach⁴. All parameters in such Bayesian analyses need to have a prior probability (a reasonable distribution for the date of an event before looking at the data) assigned to them, for example, to estimate the ages of the branch points (nodes) of an evolutionary tree (Fig. 1). The posterior probabilities, which refer to the distribution of the estimated parameters, should reflect updates to this prior probability based on information obtained when the data are examined in depth.

For some nodes in the tree, a plausible range of dates from a fossil ancestor can be used to calibrate the prior probabilities, or priors. However, for most of the nodes, such prior probabilities can be generated only by drawing from a model in which species are formed and go extinct at a clock-like rate; the rates of speciation and extinction have their own priors. There is also a prior for estimating how quickly genetic differences accumulate – the rate of molecular evolution – and in many current approaches, referred to as relaxed-clock methods, this rate can vary between different parts of the evolutionary tree.

Previous work has shown that, although a researcher can choose a prior distribution for any of the model's parameters, there is no way of knowing in advance whether these priors are in conflict with one another^{5,6}. A Bayesian algorithm can sample only internally consistent parameter sets – for example, the time point at which marsupials branched off from all other mammals must logically come after the emergence of the most-recent common ancestor of all mammals. The 'effective' (logically consistent) prior for the age of any node might be different from what is specified.

Budd and Mann found this method to be misleading for the two groups that they studied, animals and mammals. The effective prior for the age of bilaterians, for example, indicated that the chance of the date being within

20 million years of that of the oldest-known fossil is less than 5%; almost all of the estimated probable ages were considerably older than this oldest fossil. Strikingly, the effective prior indicated that the chance that the most-recent common ancestor of living placental animals emerged after the dinosaurs went extinct is less than one in one million, even though there are no undisputed fossils of this mammalian group that pre-date the extinction of dinosaurs.

In other words, Budd and Mann suggest that researchers think they are using the fossil data

“The fossil record cannot plausibly be as uncertain as suggested by the molecular-clock analyses.”

to generate baseline expectations and that they then update these expectations using molecular-clock data. However, scientists are actually setting up expectations that are wildly inconsistent with what is known from the fossil record and, after doing the analyses, they 'discover' that the molecular data happen to support these expectations.

This is particularly problematic for ancient nodes, because most genetic information corresponds to the present and such data become less useful as a resource at points further back in time – as such, the posterior probability tends to simply match the effective prior⁶. This is ironic, because the current Bayesian molecular theory was developed in part as a response to previous molecular-dating methods that were criticized for failing to properly convey uncertainty in the estimate provided⁷. If Budd and Mann's results are as general as they suggest, then the uncertainty around estimates of

ancient dates from the Bayesian approaches is artificial and does not represent their full uncertainty – it might even be barely informed by the actual data.

A study of the age of flowering plants⁶ yielded the same general conclusions as those of Budd and Mann. This prompted another group⁸ to suggest that researchers might have to come to terms with the idea that the timing of some of the biggest moments in the history of life might be fundamentally unknowable. Budd and Mann disagree. The fossil record provides strong and consistent evidence of when many of these events occurred.

Although there is some uncertainty in dates estimated using fossil evidence, simple models of speciation and extinction suggest that the fossil record cannot plausibly be as uncertain as suggested by the molecular-clock analyses. Budd and Mann propose instead that researchers using molecular clocks must accept the idea that, for extremely old splits in the evolutionary tree, their methods and their data are simply not as informative as they thought they were.

There is hope, however, because emerging dating models that more naturally integrate fossil observations with molecular data⁹ might mitigate these problems. But given that molecular-dating methods keep stumbling onto new versions of the same puzzles, researchers should approach this challenge with humility.

Matt Pennell is in the Department of Quantitative and Computational Biology and the Department of Biological Sciences, University of Southern California, Los Angeles, California 90089, USA.
e-mail: mpennell@usc.edu

1. dos Reis, M. *et al.* *Curr. Biol.* **25**, 2939–2950 (2015).
2. Budd, G. E. & Mann, R. P. *Interface Focus* **10**, 10201901 (2020).
3. Budd, G. E. & Mann, R. P. *Syst. Biol.* <https://doi.org/10.1093/sysbio/syad057> (2023).
4. dos Reis, M., Donoghue, P. C. J. & Yang, Z. *Nature Rev. Genet.* **17**, 71–80 (2016).
5. Rannala, B. *Phil. Trans. R. Soc. B* **371**, 20150134 (2016).
6. Brown, J. W. & Smith, S. A. *Syst. Biol.* **67**, 340–353 (2018).
7. Graur, D. & Martin, W. *Trends Genet.* **20**, 80–86 (2004).
8. Sauquet, H., Ramírez-Barahona, S. & Magallón, S. *J. Exp. Bot.* **73**, 3840–3853 (2022).
9. Heath, T. A., Huelsenbeck, J. P. & Stadler, T. *Proc. Natl Acad. Sci. USA* **111**, E2957–E2966 (2014).

The author declares no competing interests.
This article was published online on 22 November 2023.