

**Title: Rocks, Clocks, and Zombie Lineages: A literacy strategy based activity on the Tree of Life****Author(s):**

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**Abstract:**

This activity uses a recent popular-science article written for general audiences to discuss a specific example of evolutionary lineages. Using *The Guardian* article “The paleontology of rocks, clocks, and zombie lineages” by Elsa Panciroli, students will read an annotate a short article, then share and discuss the importance of evidence discussed in the article.

**Subject, Grade, Level:**

High school biology, honors level and above

**Learning objectives:**

By the end of this activity, students will be able to...

- ...read an annotate a newspaper article on scientific findings.
- ...compare provided examples with examples given during the “Tree Tender” video.
- ...discuss phylogenetic relationships in terms of common ancestors and evolution.

**Timeframe:**

Instructor preparation for this lesson is minimal. The teacher may choose to print article copies for all students (if annotating) or simply a class set (if taking notes).

This activity is best set midway or towards the end of a unit on evolutionary biology, phylogenetics, and The Tree of Life. Article annotation and question answering should be completed in a single 50 minute class period for advanced students.

**List of materials:**

Article available online here: <https://www.theguardian.com/science/2018/apr/11/the-palaeontology-of-rocks-clocks-and-zombie-lineages>

Printer friendly version of article at the end of this lesson plan.

**Procedure and general instructions (for instructor). REQUIRED.**

Ideally, the instructor should photocopy enough copies of the attached article for every student to have their own. Pass out articles to each student and tell them that they will be having a discussion in small groups regarding the phylogenetics of hedgehogs and related small mammals. Teachers can have students read the article and answer discussion questions as homework instead of a class discussion if time is an issue.

- **If annotating the article individually:** Students should read and annotate the article using the following parameters:
  - As you read, underline all main ideas. You should not underline more than 5-10 words at a time—these will help you find key topics as you’re reading back over the article later. Whole paragraphs that are important can be bracketed.
  - *Circle* any words, ideas, or concepts that you don’t understand and put a question in the margin. Record at least 10 vocabulary words that you can define in your article analysis.
  - Use *arrows* to connect ideas that are related from one paragraph or section to the next.
  - Draw *boxes* around any scientific language (for example, you may put a box around the word “phylogenetics” in the accompanying article). Words that you do not know you can serve as your vocab words for this article.
  - Write out in the margins of the article at least 10 thoughts you had while reading the article
  - Excellent article on annotations here:  
<https://biologycorner.com/worksheets/annotate.html>
- **If reading and discussing in class:** If time or photocopying resources prevents individual annotations, students can instead read a class set of the article and then discuss the questions below in pairs.
- **Suggested Discussion questions:**
  - How do paleontologists date the age of fossils found in the field?
  - How has molecular genetics impacted how scientists build phylogenetic trees?
  - Why is it important for scientists, engineers, and computer programmers to all work together when solving a scientific problem?
  - What is a solenodon and why are they important to phylogenetics?
  - What is a zombie lineage?
  - According to Professor Springer, “nothing in biology makes sense except in the light of phylogenetic trees. Phylogenetic trees provide a foundation for diverse areas of research in biology including genomics, ecology, and conservation genetics.” Do you agree with him? Why or why not?

### **Procedure and general instructions (for students).**

As you read through the article, complete the following:

- Underline all main ideas. You should not underline more than 5-10 words at a time—these will help you find key topics as you’re reading back over the article later. Whole paragraphs that are important can be bracketed.
- Use arrows to connect ideas that are related from one paragraph or section to the next.
- Write down and define at least 10 vocabulary words you don’t know the meaning of.

- Circle any words, ideas, or concepts that you don't understand and put a question in the margin.
- Draw boxes around any scientific language (for example, you may put a box around the word "phylogenetics" in the accompanying article). Words that you do not know you can serve as your vocab words for this article.
- Write out in the margins of the article at least 10 thoughts you had while reading the article
- Answer the provided questions *in complete sentences* on your own sheet of paper.

# The palaeontology of rocks, clocks and zombie lineages

By Elsa Panciroli

11 Apr, 2018



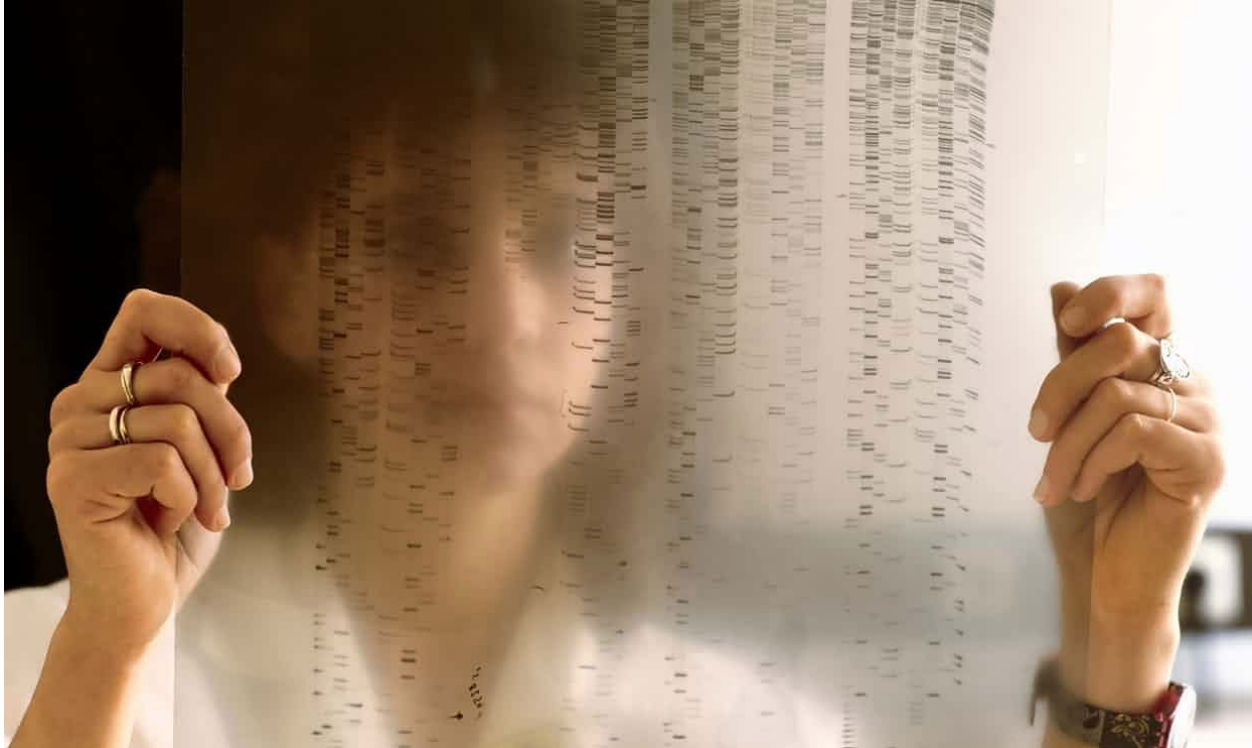
A rare Hispaniolan solenodon, *Solenodon paradoxus*. Photograph: Gregory Guida/PA Archive/Press Association Images

We can now extract DNA from pretty much anything. If US crime series are anything to go by (they are not), sequencing it only takes an afternoon at a desktop computer, and an expression of determination. DNA can not only help identify murderers, but tell us how animal groups are related to one another. In the last 50 years it has transformed scientific understanding of family trees and the evolution of life on earth.

With such technology at our fingertips, you may be left wondering: when it comes to understanding evolution, do we still need palaeontology? If I want to know if a hedgehog is more closely related to a shrew or a mole, I can just DNA test them, can't I?

It's a natural assumption that genetics beats comparative anatomy in the game of science top trumps. The [image of palaeontology](#) as dominated by foosty old white men rummaging in museum cupboards – or monumentally bearded ones wielding rock-hammers in the Badlands – may still be pervasive, but is far from an accurate reflection of modern palaeontological practice.

Thankfully, you are now as likely to have a background in computer programming or developmental biology, as in anatomy. Some of the greatest advances are being made by those who integrate the tools and techniques of multiple strands of science, engineering and computing into their research.



How can we combine the study of DNA and fossils to understand evolution? Photograph: Alamy

Before the science of genetics, animal relationships were worked out based solely on the intricacies of their anatomy. Natural scientists observed that you could identify and classify living things using even the smallest anatomical details, allowing great minds such as Sir Richard Owen to identify animals from only single teeth. In the last sixty years, our understanding of genes and molecules and their role in heredity, has added a new set of tools for scientists to trace animal lineages – using the ‘molecular clock’.

Professor Philip Donoghue, a molecular palaeobiologist from the University of Bristol, explained: “genetic differences arise as a consequence of copy errors, and they accrue over time. The number of differences in the same gene from different species is a factor of how much time has elapsed since those species last shared a common ancestor.” While a fossil tells us when an animal lived by the age of the rocks it is found in, it’s hard to know exactly when animal groups emerged from fossil evidence alone. “The molecular clock helps to narrow this range of uncertainty by estimating the rate at which genetic differences arise.”

The resulting trees combining molecules and fossils are called phylogenetic trees. Molecular biology undeniably transformed our understanding of evolution, but in the early days it led to a split among palaeontologists and biologists over how to reconstruct the tree of life. Should they

still rely on the rocks, or switch to the clocks? A recent paper reminds us that it shouldn't be either/or – the best science combines the best of both worlds.



Hedgehog, *Erinaceus euopaeus*, in Norfolk, UK. Photograph: Mike Powles

Most of us are familiar with hedgehogs. These little mammals are found across Europe, Asia and Africa, and are readily distinguishable by their body covering of spines. They are related to the equally familiar shrews and moles in a family called Eulipotyphla. But far fewer people are familiar with the other member of this group: the solenodon.

Solenodons are found on the islands of Cuba and Hispaniola. Once thought extinct, they were rediscovered a decade ago, and still teeter on the [red list](#). Their name may sound like a prehistoric reptile, but they are actually small nocturnal mammals – and as mammals go, they are some of the weirdest. Solenodons superficially resemble big shrews, around 30 cm in length. The nose of the Hispaniolan solenodon is not only long and pointed, but has a unique ball and socket joint at its base, giving it elephant-like flexibility. A groove in their bottom incisor teeth gives these feisty little animals a venomous bite – one of only a handful of mammals with this adaptation. They hunt by hearing and smell, eating insects, small reptiles, amphibians, and carrion.

Solenodons are unique among modern mammals, but the fossil record suggests they would have fitted right into the Mesozoic world, over 66mya. While all mammals have [ancestors reaching to the Triassic and beyond](#), most mammal groups have changed a great deal since the non-avian dinosaurs and marine and flying reptiles bit the asteroid dust at the end of the Cretaceous. Solenodons on the other hand, have held on to the winning body plan and venomous bite of their ancestors. This gives us a unique peek at what [early mammals](#) may have looked like.

The lineage of this singular animal confused scientists for decades. Multiple studies of solenodon genes in the last 15 years have helped figure things out: solenodons are the sister group of all of the other eulipotyphlans. Estimates suggest they split from the rest of the family in the Late Cretaceous, between 69 and 78 million years ago. This left scientists with a likely explanation for how the first solenodon ancestors reached their island homes: in the Cretaceous the land was connected to North America, making it possible for them to have lived there before tectonic movements carried them away from the mainland.

But [a paper in 2016](#) found an altogether different pattern in the eulipotyphlan tree. Sato and colleagues performed an analysis that found solenodons had only diverged from their common ancestor with hedgehogs, shrews and moles *after* the Cretaceous, just 58mya. This meant solenodons would have had to cross the Caribbean Sea to reach the Antilles. But more puzzling still, rather than a clear split from the rest of their relatives, Sato and colleagues' research suggested all the major families in Eulipotyphla had split at the same time, leaving no clear pattern to their family relationships. This situation is called a polytomy by scientists. It is considered highly unlikely to reflect real evolutionary relationships, instead usually resulting from problems with analysis or a lack of data.

So how did this team of scientists get such radically different results from everyone else? A [recent paper](#) led by Professor Mark Springer at the University of California, took this 2016 study and re-ran it to find out. The answer was *zombies*.

Springer explained that the first team's results were "in direct conflict with the fossil record. For example, the oldest 'hedgehog' fossils at around 62 million years are several million years older than Sato et al's estimate for the common ancestor of hedgehogs, moles, shrews, and solenodons. We refer to these discrepancies, where estimated ages are younger than minimum ages implied by the fossil record, as zombie lineages."



Fossils like this one of *Juramaia* from the Jurassic, provide oldest dates for groups of animals, and help calibrate the tree of life. Photograph: Mark Klingler/Carnegie Museum of Natural History

In Sato's study, the 58myo date for the split of Eulipotyphla was younger than the oldest fossil of the hedgehog ancestor, *Litolestes ignotus*. "We observed several more zombie lineages," Springer continued, "such as an estimated date for rodents to treeshrews of only around 36 million years, even though the fossil record mandates a minimum age of at least 61 million years."



Springer's team set about re-analysing the data. By adding the dates for the earliest fossils for hedgehogs, shrews, carnivorans and rodents, they were able to calibrate the previous analysis, rooting it in the fossil record. Doing this brought Sato's analysis into agreement with previous studies of these groups, and placed the solenodon split back in the Late Cretaceous, where it seems likely to belong. "This Cretaceous date is compatible with a plate tectonic origin for the presence of solenodons in the Greater Antilles," says Springer. Although he cautions that it doesn't rule out the possibility that solenodons crossed the sea at some point.

The combination of the data provided by molecules, and the solid evidence of fossils, not only gives us the most reliable results for our understanding of evolutionary relationships, but shows how palaeontology remains a vital discipline. While the separation between palaeontology and other sciences like molecular biology is maintained in common stereotype, it is seldom the reality.



The origin of bats, like this fruit bat, is one of the puzzles that fossil and molecular data has not yet solved. Photograph: Eureka/Alamy

"The molecular phylogenetic revolution has had a massive impact on our understanding of animal evolution," says Professor Donoghue "however, it never fails to surprise me how much of our understanding of animal phylogeny, based on the hierarchical similarities in the comparative anatomy of living and fossil beasts, has simply been confirmed by molecular data."

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Theodosius Dobzhansky, one of the 20<sup>th</sup> century's greatest evolutionary biologists, once said that nothing in biology makes sense except in the light of evolution. Professor Springer added: "nothing in biology makes sense except in the light of phylogenetic trees. Phylogenetic trees

provide a foundation for diverse areas of research in biology including genomics, ecology, and conservation genetics.”

So what questions remain unanswered in the study of animal evolution? I asked Professor Donogue – “many of the old unresolved controversies are no less controversial now, even with whole genome data,” he replied. “Like how are bats related to other mammals? And who has the faintest idea about the high-level relationships among teleost fish – even though we eat them regularly with chips?”

## References

Donoghue PC and Benton MJ. 2007. [Rocks and clocks: calibrating the Tree of Life using fossils and molecules](#). *Trends in Ecology & Evolution*, 22, 424-431.

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