

# Creating the Tree of Life

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(PhysOrg.com) -- Imagine the wealth of information that would be at our fingertips if we could understand the genetic basis and evolutionary history that underlies the vast diversity in form and function seen within mammals.

An [international collaboration](#) including Conway Fellow, Dr Emma Teeling has created a phylogenetic framework using large genetic datasets to better understand the [evolutionary history](#) of mammalian families and the role of the environment and events in earth history in promoting living biodiversity.

Recently published in the journal *Science*, the findings of the Tree of Life consortium are the culmination of a five year project led by scientists at the University of California, Riverside (Prof. Mark Springer) and Texas A&M, USA (Prof. William Murphy). The study generated the largest DNA sequence alignment from more than 99% of mammalian families to build evolutionary trees that depict how different groups of mammals are related to each other and when they diverged from each other.

Dr Emma Teeling's research group, a Science Foundation Ireland funded team and members of the Tree of Life consortium, produced the majority of bat data in the project.

Explaining how the team produced reliable time estimates of when different mammal groups split, she said, "We used a 'relaxed clock' approach that enables rates of DNA to change across the tree of

mammals. We used a large collection of well established fossil mammals to estimate rates of change on different branches of the tree. This allowed us to convert the phylogentic tree of evolutionary relationships into a time-tree, in which the branches are scaled in proportion to time.

Using the time-tree, we were able to examine when different groups of mammals originated and diversified, and then associate factors that might have been responsible for these diversification events. For example, we observed a distinct pulse of diversification near the end of the Cretaceous Terrestrial Revolution (80-82 million years ago) when flowering plants started to diversify and when most of the mammalian orders began diverging from one another”.

This phylogeny also serves as a framework to understand the history of the unique changes in the genome underlying the vast morphological [diversity](#) observed in more than 5400 living species of [mammals](#).

Co-lead author on the publication, Professor Mark Springer from the University of California, Riverside said, “When you understand how taxa are related to each other... you can pinpoint key molecular changes that are associated with key morphological changes”.

For Emma Teeling’s research, this equates to changes at genomic level underpinning morphological and molecular changes associated with flight and echolocation in bats. “I personally will use this phylogeny to explore in more detail the evolution and genetic control of vision and hearing and how this relates to human disease”, she said.

She is excited about the possibilities that the framework offers biologists for comparative research in biomedicine, physiology and immunology. “Although the [Tree of Life](#) is currently a work in progress, it provides a benchmark that we can use into the future to decipher how our genome functions and has evolved”.

**More information:** Meredith et al. Impacts of the Cretaceous Terrestrial Revolution and KPg Extinction on Mammal Diversification. Science Express 22 September 2011. Page 1.

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[mammaltree.informatics.sunysb. ... du/investigators.htm](http://mammaltree.informatics.sunysb.edu/investigators.htm)

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