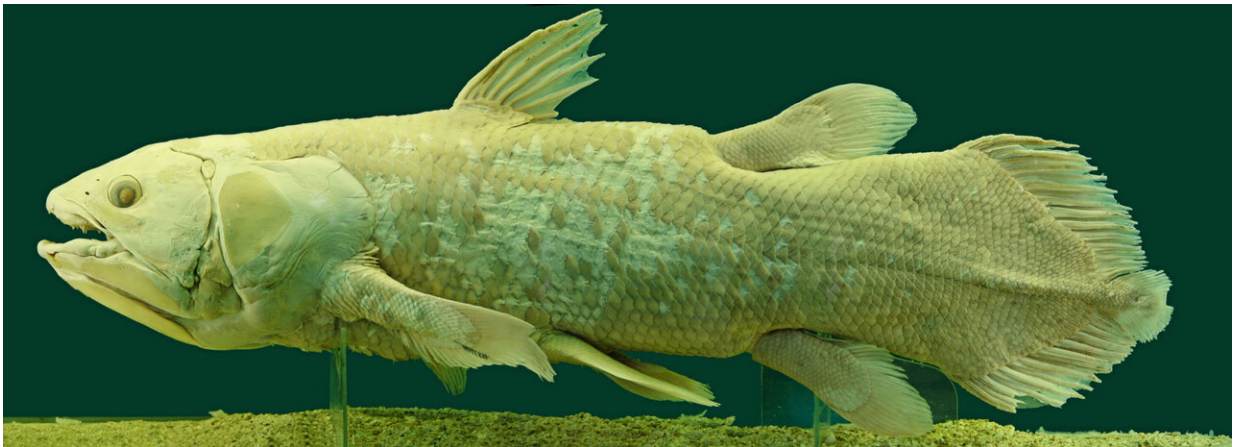


Not a living fossil: How the Coelacanth recently evolved dozens of new genes

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Coelacanths have an undeserved reputation as living fossils and the study adds to the growing body of research showing widespread evolution at the genome level. Credit: Alberto Fernandez Fernandez via Wikimedia Commons

The capture of the first living Coelacanth, a mighty ocean predator, off the coast of South Africa caused quite a stir in 1938, 65 million years after its supposed extinction. It became known as a "living fossil" owing to its anatomy looking almost identical to the fossil record. But while the Coelacanth's body may have changed little, its genome tells another story.

Toronto scientists have now revealed that the African Coelacanth, *Latimeria chalumnae*, gained 62 [new genes](#) through encounters with

other [species](#) 10 million years ago. Their findings are reported in the journal *Molecular Biology and Evolution*.

What's even more fascinating is how these [genes](#) came about. Their sequences suggest they arose from transposons, also known as "[selfish genes](#)". These are parasitic DNA elements whose sole purpose is to make more copies of themselves, which they sometimes achieve by moving between species.

The findings show the dramatic effect traveling transposon DNA can have on the creation of genes and provide a glimpse into some of the forces that shaped the genome of one of the most ancient and mysterious organisms.

"Our findings provide a rather striking example of this phenomenon of transposons contributing to the [host genome](#)," says Tim Hughes, senior study author and a professor of molecular genetics in the Donnelly Centre for Cellular and Biomolecular Research at the University of Toronto.

"We don't know what these 62 genes are doing, but many of them encode DNA binding proteins and probably have a role in gene regulation, where even subtle changes are important in evolution," says Hughes, who is Canada Research Chair in Decoding Gene Regulation and John W. Billes Chair of Medical Research at the Temerty Faculty of Medicine at U of T.

Transposons are sometimes also called "jumping genes" because they switch location in the genome, thanks to a self-encoded enzyme that recognises and move its own DNA code via "cut and paste" mechanism. New copies can arise through serendipitous jumps during cell division when the whole genome is replicated.

Over time, the enzyme's code drifts into disrepair and the jumping ceases. But if the altered sequence confers even subtle selective advantage to the host, it can begin new life as a bona fide host gene.

There are myriad examples of transposon-derived genes across species, but the Coelacanth stands out for the sheer scale of it.

"It was surprising to see coelacanths pop out among vertebrates as having a really large number of these transposon-derived genes because they have an undeserved reputation of being a living fossil," says graduate student Isaac Yellan who spearheaded the study.

"The Coelacanth may have evolved a bit more slowly but it is certainly not a fossil," he says.

Yellan made the discovery while looking for counterparts in other species of a human gene he was studying. He knew that the gene, CGGBP1, had arisen from a particular type of transposon in the common ancestor of mammals, birds and reptiles. It was named after the protein it encodes, which binds CGG-containing DNA sequences, but it was difficult to study partly because it has no counterpart in other commonly researched species, such as fruitfly.

After scanning all available genomes, Yellan was able to find related genes, but their distribution across species was patchy and not what you'd expect from common ancestry. In addition to the single CGGBP-like gene in all mammals, birds and reptiles, Yellan found copies in some, but not all, fish he looked at, as well as in lamprey, a primitive vertebrate, and a type of fungus. Worms, molluscs, and most insects had none. And then there were 62 in the Coelacanth, whose genome became available in 2013.

With common ancestry ruled out, it appears instead that the transposons

came into various lineages at different times by being carried between species through what is known as [horizontal gene transfer](#).

"Horizontal gene transfer fuzzies up the picture of where the transposons came from but we know from other species that it can occur via parasitism," says Yellan. "The most likely explanation is that they were introduced multiple times throughout evolutionary history."

It remains unclear what the genes are doing but several lines of evidence point to a finely-tuned role in [gene regulation](#). Computational modeling and test tube experiments established that the genes' products are proteins which bind unique sequence signatures on the DNA, suggests a role in gene expression, similar to the human counterpart. Furthermore, the genes are varyingly switched on across dozen or so Coelacanth organs for which data exist, suggesting finely-tuned roles that are tissue-specific.

Where the genes originally came from and what they're doing in the Coelacanth may well remain a mystery. Research specimens are only occasionally pulled up by fishing boats and it took until 1998 to discover the other known living species, *Latimeria menadoensis*, in an Indonesian fish market.

The species split before the new genes appeared, ruling them out from driving speciation. Still, they might have shaped the African Coelacanth we know today whose majestic armor of royal blue scales throws shade on its brownish-coloured relative, said Yellan noting that this is pure speculation.

Alas, we may never find out.

"The Coelacanths are extremely rare," says Yellan. "And they're very good at hiding."

Provided by University of Toronto

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