

## After dinosaurs, mammals rise but their genomes get smaller

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(PhysOrg.com) -- Evidence buried in the chromosomes of animals and plants strongly suggests only one group -- mammals -- have seen their genomes shrink after the dinosaurs' extinction. What's more, that trend continues today, say Indiana University Bloomington scientists in the first issue of a new journal, *Genome Biology and Evolution*.

The scientists' finding might seem counter-intuitive, given that the last 65 million years have seen mammals expand in diversity and number, not to mention dominance in a wide variety of ecological roles. But it is precisely their success in numbers that could have led to the contraction of their genomes.

"Larger population sizes make natural selection more efficient," said IU Bloomington evolutionary biologist Michael Lynch, who led the study. "If we are correct, we have shown how to bring ancient genomic information together with the paleontological record to learn more about the past."

And the present. Lynch says the data he and his colleagues analyzed suggest human genomes are still undergoing a contraction -- though you shouldn't expect to see noticeable changes in our [chromosomes](#) for a few million years yet.

Lynch's group examined the genomes of seven mammals, eight non-mammalian animals and three plants, specifically with regard for the long terminal repeat (LTR) sequences of transposable elements, a

curious sort of "jumping" [genetic sequence](#) initially dropped into genomes by viruses. IU School of Informatics (Bloomington) bioinformaticians Mina Rho and Haixu Tang oversaw the survey of mammalian and non-mammalian genomes.

Transposable elements often lose their functionality soon after insertion but nevertheless are disturbingly common. In the human genome, for example, transposable elements constitute as much as 45 percent of an individual's total DNA. Long terminal repeat sequences, part of that figure, make up about 8 percent of humans' total DNA.

LTRs come in a range of sizes and ages, and it is the age distribution of LTRs that interested Lynch and his colleagues.

"This study started out as independent observations in the literature," Lynch said. "The data we saw suggested a bulge in age distribution of transposable elements in humans and mouse."

Left enough time, Lynch says, transposable elements are eventually lost from the genome, sometimes by accident and sometimes, perhaps, as the result of natural selection against excess DNA. An LTR is far more likely to survive a few years of cell divisions -- and the chance of obliteration via a DNA replication error -- than 10 million years of cell divisions. Plotting the full range of 17 species' LTRs, young and old, Lynch and his colleagues usually saw a descending curve with lots of new transposable elements and a dramatic drop-off in the number of older elements.

But not in most mammals. In humans, macaques, cows, dogs and mouse, Lynch's group observed a hill-shaped curve, with a peak of middle-aged LTRs and drop-offs both in the number of older and younger LTRs. The shape of the curve is consistent with previously published data for other types of so-called "junk" DNA elements.

The depressed numbers of very young LTRs, Lynch says, strongly suggests a contraction in overall genome sizes of the lineages of the mammals the scientists studied. That could come about in one of two ways, he says. One possibility is an increase in the efficiency of natural selection that accompanies population growth.

"We think that's the most likely explanation," Lynch said. "Another possibility is that natural selection was just stronger, but we doubt it. For that to be the case, [natural selection](#) would have to act in the same way on several lineages around the globe simultaneously."

More information: "Independent Mammalian Genome Contractions Following the KT Boundary," *Genome Biol. Evol.* 2009-0

Source: Indiana University ([news](#) : [web](#))

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