New research shows how gene function drives natural selection in important class of genetic elements

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This is Regina Baucoma, genetics post-doctoral research assistant at UGA and lead author of the research. Credit: University of Georgia

Transposons are the Clark Kents of a genome. Apparently mild-mannered and inconsequential but with sudden bursts of activity, these free-floating bits of genetic material have for millions of years been sneaking into the genetic maps of plants and animals, dramatically increasing a genome's size.

For years, researchers thought that most of this DNA was passive "junk" and knew little about it. New findings, however, are peeling back the odd and baffling world of transposons. Now, researchers at the University of Georgia have just found that natural selection on gene

function is driving the evolution of one kind of transposable element called the LTR retrotransposon. (LTR refers to the "long terminal repeat"—a repetition of a recognizable sequence of nucleotides, the chemical bases that make up strands of DNA.)

"The lab of Professor Jeff Bennetzen at UGA discovered that this class of mobile DNA comprises more than half of most plant genomes and has led the way in determining the extraordinary rates of both amplification and removal of this type of repetitive element," said Regina Baucom, a genetics post-doctoral research assistant at UGA and lead author of the research.

Understanding the evolutionary pressures between host genome and transposable element will in the future be of interest to those studying retroviruses, which evolved from retrotransposons. There are a number of animal and human diseases caused by retroviruses including HIV/AIDS, avian leukosis and feline leukemia.

"Because LTR retrotransposons are abundant and impact host genomes, we wanted to determine the influence of natural selection on their evolution," said Baucom. "We find that the genes involved in their replication are subject to Darwinian evolution—the same evolutionary processes that affect species."

Other authors of the paper just published in the online version of the journal *Genome Research*, were Jeff Bennetzen, in whose genetics lab Baucom is a research associate; and James Estill and Jim Leebens-Mack in UGA's department of plant biology.

A "retrotransposon" is an element that copies itself and then pastes copies back into genomes at multiple places. It does this by initially copying itself into RNA, but this RNA element is then copied into DNA by an enzyme called reverse transcriptase.

"In this study, we specifically wanted to assess the pattern of selection on these elements—a pattern that could derive from the effect of the elements on the host genome, or the effect of host silencing mechanisms on the elements," Baucom said. "Our expectation was that if the elements are adapting to the host genome, we should see evidence of positive selection in the genes involved in transposition."

The researchers examined selection pressure on retrotransposons using Oryza sativa—rice—as a model plant genome. They analyzed more than 1,000 LTR retrotransposon sequences from 14 separate families that varied in both the dates they were inserted into the rice genome and the numbers of copies that were inserted.

"Overwhelmingly, we found that LTR retrotransposons are under significant evolutionary constraint, by finding strong purifying selection on genes involved in their replication and life-cycle, regardless of the family that any the LTR retrotransposon sequences might belong," says Baucom.

This evidence of so-called "purifying selection" across all gene regions is important in understanding how retrotransposons work. But the research also shows there are rare episodes of positive selection and even adaption to a host genome when these Clark Kents get busy.

It has been known for a long time that the insertion of transposable elements can harm the host, but few studies have been done to determine if there is evidence of selection pressure on LTR retrotransposons.

What the scientists found helps explain why these elements can, while lying quiet for millions of years, suddenly amplify within genomes while not causing more long-term harm than to take up space. And yet the observation that a tiny percentage of the elements actually become active parts of genomes provides an intriguing glimpse into how these twin

evolutionary pressures can, in rare cases, "sign an armistice."

Source: University of Georgia