

Rapidly evolving gene contributes to origin of species

February 5 2009

A gene that helped one species split into two species shows evidence of adapting much faster than other genes in the genome, raising questions about what is driving its rapid evolution.

The paper in today's issue of *Science* shows that the gene has connections to another previously identified "speciation gene." Both genes code for key proteins that control molecular traffic into and out of a cell's nucleus. The researchers believe an arms race of sorts inside the cell drives these genes to evolve rapidly—and as a consequence makes closely related species genetically incompatible with one another.

"When we cross two species of fruit fly, which had split from one another 3 million years ago, some of the hybrid offspring die," says Daven Presgraves, professor of biology at the University of Rochester and Grass Fellow at the Radcliffe Institute for Advanced Study at Harvard University. "This tells us that genes from one species are no longer compatible with genes from the other species. We've now found that a functionally related group of genes is responsible, with different versions of the genes having evolved in the two species. And just as Darwin predicted 150 years ago, they evolved by natural selection."

Presgraves has some ideas why two of the genes in particular, called Nup160 and Nup96, have evolved so quickly: they act as gatekeepers of a cell's nucleus, a favorite target for viruses and even malicious genes within the fly's own genome. Presgraves says that these genes probably experience constant assault and thus must constantly adapt. That these

genes also prevent genetic mixing between closely related species is incidental—the origin of new species is just a by-product of evolutionary arms races, he says.

When two populations become separated by a geographic barrier—a mountain range or an ocean—they evolve independently. Presgraves and his graduate student Shanwu Tang studied a fruit fly species from Madagascar that long ago become separated from its sister species in Africa. Separated by an expanse of the Indian Ocean, the two independently evolving species accumulated genetic differences. Tang and Presgraves's unexpected finding, however, was that in both species, the Nup160 and Nup96 genes became so different so quickly that they are no longer compatible.

"When the same genes in two different species evolve quickly, they become so different that they can be incompatible," says Tang. "The genes from one species can't talk to the genes in the other species any more."

Six years ago, Presgraves found that the Nup96 gene kills hybrid offspring between these fruitfly species. Since, two species can be separated by any number of incompatible genes with different functions, he and Tang were surprised when they found that Nup160 also kills hybrid offspring. Both genes encode parts of the same gatekeeping complex that regulates what gets in or out of a cell's nucleus.

"Shanwu and I were shocked," says Presgraves. "Only half a dozen such 'speciation genes' are known, so to find two of them that interact with one another as part of the same complex says that multiple parts of the same complex have evolved."

Presgraves and Tang are now investigating other genes that cause hybrid lethality, as well as trying to discern why natural selection has caused this

particular complex to evolve so quickly. Presgraves has said viruses could be responsible for the rapid evolution of the complex because viruses act by inserting their own DNA into a host cell's, which means getting their DNA through the gatekeeper complex. In a molecular arms race, the viruses constantly adapt to sneak through the gates, and the gatekeepers adapt to thwart the viruses.

Presgraves even suggests another, more exotic arms race. Certain genes in the fruitfly's own genome serve little purpose other than to replicate themselves. These selfish genes can also manipulate the gates for their own needs, requiring the gatekeepers to adapt to keep the selfish genes under control.

As a 2008-2009 Radcliffe fellow, Presgraves is focusing on the special role of sex chromosomes in speciation. He is combining genetic mapping and comparative genomics approaches to determine why the X chromosome is a hot spot for speciation genes in two closely related species of *Drosophila* fruit flies.

Source: University of Rochester

Citation: Rapidly evolving gene contributes to origin of species (2009, February 5) retrieved 2 May 2024 from <https://phys.org/news/2009-02-rapidly-evolving-gene-contributes-species.html>

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