

In fly DNA, the footprint of a fly virus

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Drosophila yakuba is one of several fruit fly species whose DNA appears to harbor genetic material from a virus, according to a new University at Buffalo study. Credit: Photo courtesy of D.J. Obbard, University of Edinburgh

(Phys.org) -- In a curious evolutionary twist, several species of a commonly studied fruit fly appear to have incorporated genetic material from a virus into their genomes, according to new research by University at Buffalo biologists.

The study found that several types of fruit fly -- scientific name *Drosophila* -- harbored <u>genes</u> similar to those that code for the sigma virus, a fly virus in the same family as rabies. The authors believe the <u>genetic information</u> was acquired during past <u>viral infections</u> and passed on from fruit fly parent to offspring through many generations.

The discovery could open the door for research on why flies and other



organisms selectively retain viral genes -- dubbed "fossil" genes -through evolution, said lead author Matthew Ballinger, a PhD candidate in UB's Department of <u>Biological Sciences</u>.

One hypothesis is that viral genes provide an anti-viral defense, but scientists have had trouble testing this theory because viral genes found in animals are often millions of years old -- ancient enough that the genes' genetic sequence differs significantly from that of modern-day viruses.

The new study, in contrast, uncovered a <u>viral gene</u> that appears to be relatively young, with genetic material closely mirroring that of a modern sigma virus.

"We don't know that these genes have an anti-viral function, but it's something we'd like to test," Ballinger said. "It's tempting to think that these genes are retained and express RNA because there's some kind of advantage to the host."

He and his co-authors -- Professor Jeremy Bruenn and Associate Professor Derek Taylor in UB's Department of Biological Sciences -reported their results online on June 26 in the journal *Molecular Phylogenetics and Evolution*. The research, supported in part by UB's Center for Advanced <u>Molecular Biology</u> and Immunology, will also appear in a forthcoming print edition of the journal.

"Our findings establish that sigma virus-like (genes) are present in *Drosophila* species and that these infection scars represent a rich evolutionary history between virus and host," the researchers wrote in their paper.

Another important contribution the study makes is advancing our understanding of how flies and other organisms acquire copies of virus-



like genes in the first place.

The sigma virus belongs to a class of RNA viruses that lack an important enzyme, reverse transcriptase, that enables other viruses to convert their <u>genetic material</u> into DNA for integration into host genomes.

Given this limitation, how did sigma virus genes get into fly genomes?

The new study supplies one possible answer, suggesting that viruses may use reverse transcriptase present in host cells to facilitate incorporation of viral genes into host DNA.

In the genome of one fly, the researchers found a sigma fossil gene right in the middle of a retrotransposon, a genetic sequence that produces reverse transcriptase for the purpose of making new copies of itself to paste into the genome.

The position and context of the viral gene suggests that the retrotransposon made a copying error and copied and pasted virus genes into the fly genome. This is the clearest evidence yet that non-retroviral RNA virus genes naturally enter host genomes by the action of enzymes already present in the cell, Ballinger said.

The study builds on prior research by Taylor and Bruenn, who previously co-authored a paper showing that bats, rodents and wallabies harbor fossil copies of genes that code for filoviruses, which cause deadly Ebola and Marburg hemorrhagic fevers in humans.

The next step in the research is to continue exploring how and why flies and other organisms acquire copies of virus genes. To find out whether sigma virus-like genes have an anti-viral function in <u>fruit flies</u>, scientists could splice the genes into flies that can contract modern sigma viruses, or introduce modern <u>sigma</u> viruses into flies that already harbor the



genes.

Provided by University at Buffalo

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