

Female fly genomes also populated with de novo genes derived from ancestral sequences

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A presentation at Genetics Society of America's *Drosophila* Research Conference builds the case that de novo genes derived from ancestral non-coding DNA can spread through a species.

Earlier this year, researchers in David J. Begun, Ph.D.'s lab at UC Davis reported that they had uncovered 142 *de novo* genes that originated in the ancestral non-coding DNA sequences and are segregating in *Drosophila melanogaster* populations.

Dr. Begun and postdoctoral scientist Li Zhao, Ph.D., identified *de novo* genes by comparing the RNA transcripts of the testes of several wild-derived strains of *D. melanogaster* to the standard reference genome for this fly [species](#) and to the RNA transcripts and genomes of two other *Drosophila* species.

Their results suggested that these genes may play an important role in *Drosophila* male reproduction. The UC Davis scientists, who were the first to investigate whether *de novo* genes spread through a species, next turned their attention to females.

They conducted a systematic search for *de novo* genes that were expressed in female *Drosophila* flies and determined that these genes appear to derive primarily from ancestral intergenic sequences, which is similar to the case for male-biased *de novo* genes.

At the GSA *Drosophila* Research Conference, Dr. Zhao will report about

the female-expressed *de novo* genes. The population genetics and role of selection on these [genes](#) will also be discussed.

More information: Abstract: "Female-expressed de novo genes in *Drosophila*." Li Zhao, David J. Begun. [abstracts.genetics-gsa.org/cgi ...
il.pl?absno=14531505](https://abstracts.genetics-gsa.org/cgi-bin.pl?absno=14531505)

Provided by Genetics Society of America

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