

House fly sex may reveal one key to controlling them

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Close-up of the head of *Calliphora vomitoria*. Credit: Wikipedia.

The quest of University of Houston professor Richard Meisel to understand how and why males and females differ may one day lead to a more effective means of pest control - namely, the pesky house fly.

Meisel, an assistant professor in the UH Department of Biology and Biochemistry, collaborated with several scientists on sequencing the house fly genome. The results were recently published in the open-access journal *Genome Biology*.

"The house fly genome will be a useful resource for understanding how pest species are able to exist in their environment and for [pest control](#)," Meisel said. "We discovered many genes that are likely involved in the

ability to live in toxic environments, which could explain the pervasiveness of house flies in many habitats."

Meisel contributed to the project by analyzing genes that are expressed differentially between male and female house flies. These genes, he says, are likely responsible for differences between the sexes. He found that genes responsible for male traits evolve exceptionally fast and are gained and lost from the genome at a high rate.

"These results improve our understanding of how differences between the sexes evolve," Meisel said. "One promising avenue for pest control is wiping out one sex or making one sex sterile which would prevent the pest from reproducing. The house fly can be used as a model for this approach, and the genome will be an invaluable resource to those ends."

The process by which an individual fly decides whether it will develop into a male or female is known as [sex determination](#). The house fly has a highly variable sex determination system, and Meisel is using the species as a model for studying the genetics and evolution of it. Turning on or off genes involved in sex determination may allow scientists to develop pest control strategies that do not rely on chemical pesticides.

"We work a lot with flies collected from the wild. We then bring those flies into the lab and rear colonies of different isolates," he said. "This allows us to study natural variation in a laboratory setting. For the genome project, one strain was selected to have its genome sequenced and analyzed."

With much of his research addressing the genetics of how and why males and females differ in their anatomy and physiology, Meisel's lab is currently using this genome as a resource for studying other strains. Their goal is to understand how and why sex determination systems evolve.

"The house fly is one of the best models for understanding the evolution of sex determination," he said. "With a complete genome and growing genetic toolkit, the house fly is poised to be one of the most informative systems for studying this. I think this will inform how we apply techniques for the control of insect pests."

The effort of a global consortium of scientists, the fly genome sequencing project was coordinated and led by entomology professor Jeff Scott at Cornell University, and the [genome](#) was sequenced at Washington University. There were numerous other collaborators on the [genome project](#). Meisel, an evolutionary biologist and geneticist, continues to work with Scott and population geneticist Andy Clark and his lab at Cornell on house fly genomics projects.

Provided by University of Houston

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