

Geneticists discover genes that make fruit fly hybrids sterile

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While hybrids -- the result of the mating of two different species -- may offer interesting and beneficial traits, they are usually sterile or unable to survive. For example, a mule, the result of the mating of a horse and a donkey, is sterile.

Now, Cornell researchers have made the first identification of a pair of genes in any species that are responsible for problems unique to hybrids. Specifically, the researchers have found two genes from two fruit fly species (*Drosophila melanogaster* and *D. simulans*) that interfere with each other, thereby preventing the production of male offspring.

The finding may eventually shed light on what causes lethality or sterility in hybrids in general and, in a larger sense, offers clues to how species evolve from common ancestors.

The research, published in the Nov. 24 issue of *Science*, focuses on a rarely occurring mutation in a *D. melanogaster* gene called "Hmr" (Hybrid male rescue) and a similar mutation in a *D. simulans* gene called "Lhr" (Lethal hybrid rescue) that make these genes nonfunctional. When either of these genes is "turned off" and then crossed with the other fruit fly species, the males survive.

"We have found the first example of two genes that interact to cause lethality in a species hybrid," said the paper's senior author, Daniel Barbash, assistant professor in Cornell's Department of Molecular Biology and Genetics.

The finding supports the Dobzhansky-Muller model, a theory from the 1930s that suggests hybrid incompatibilities (such as death or sterility) are caused by genes that have evolved from a common ancestor but diverged in each of the species. More specifically, in the common ancestor, these genes may have worked perfectly well together. But, as each gene evolved in its own species, it began to code for proteins that no longer work in the other species.

In this case, when genes from each species were compared with each other, the Hmr gene in *D. melanogaster* and the Lhr gene in *D. simulans* each evolved much faster than most other genes and diverged due to natural selection, a genetic change due to a pressure that benefits the survival of a species. The researchers would like to learn what these genes normally do within their species in order to understand why they are evolving so fast.

The Dobzhansky-Muller model also proposes that these evolved genes depend on each other to cause hybrid incompatibilities.

However, when Barbash and his colleagues cloned each gene and inserted an Lhr gene from *D. simulans* into *D. melanogaster*, the two genes did not interfere with each other in the engineered *D. melanogaster* strain even though the Lhr and Hmr genes interfere with each other in hybrids.

"This tells us there must be other things involved in the hybrid" that impacts the incompatible pairing of these genes, said Barbash. In future work the researchers hope to determine whether the hybrids die because of additional genes like Hmr and Lhr, or because of more subtle differences between the chromosomes of these two species.

Source: Cornell University

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