

# Environment drives genetics in 'Evolution Canyon'

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Interplay between genes and the environment has been pondered at least since the phrase "nature versus nurture" was coined in the mid-1800s. But until the arrival of modern genomic sequencing tools, it was hard to measure the extent that the environment had on a species' genetic makeup.

Now, researchers with the Virginia Bioinformatics Institute at Virginia Tech studying [fruit flies](#) that live on opposite slopes of a unique natural environment known as "Evolution Canyon" show that even with migration, cross-breeding, and sometimes the obliteration of the populations, the driving force in the gene pool is largely the environment.

The discovery in this week's [\*Proceedings of the National Academy of Sciences\*](#) shows that the animals genetically adapt depending on whether they live on the drier, hotter side of the canyon, or the more humid, cooler side.

"Despite complicating factors, such as likely gene flow between the two populations and changing demographics, the difference in the microclimate in this canyon apparently is so pervasive that it is sufficient to drive the genetic differences," said Pawel Michalak, an associate professor at the Virginia Bioinformatics Institute. "We don't have many examples of rapid environmental adaptation to stressful conditions from the field. We can simulate such conditions in a lab, but it is valuable to observe this actually happening in a natural system."

The two slopes of Evolution Canyon, which is located at Mount Carmel, Israel, are little more than two football fields apart at their bases, but the south-facing slope is tropical and may receive eight times as much sun, while the north-facing slope is more like a European forest.

Knowledge that climatic and environmental factors seem to exert a significant effect on the fruit-fly genome in spite of migration or repopulations adds to current understanding of the biodiversity, resilience, and ability of a species to adapt to [rapid climate change](#).

The native fruit fly in question—*Drosophila melanogaster*—is a well-studied laboratory animal and the source of the world's knowledge of how genetic information is packaged in chromosomes.

More than 65 percent of disease-causing genes in humans are believed to have functional counterparts in the fly, including many genes involved in certain cancers, Alzheimer's and Parkinson's diseases, heart disease, and other medical conditions.

Researchers used a technique known as whole genome sequencing to characterize the complete set of DNA in the total population of the fruit flies, noting differences in the [genetic makeup](#) between the populations on the opposing slopes.

The international team, which included scientists from the Institute of Evolution at Haifa University, the University of British Columbia in Vancouver, and Memorial Sloan-Kettering Cancer Center in New York, discovered 572 genes were significantly different in frequency between the populations, corroborating previous observations of differences in heat tolerance, life history, and mating behavior.

In addition, researchers discovered that genetic changes were accumulating in chromosomal "islands" in the north-facing-slope flies,

suggesting adaptive gene mutations would sweep through the population, given time.

Migration of flies between the slopes was confirmed by capturing and marking them with fluorescence.

"Although we were not correlating genetic change with [climate change](#), we were looking at heat-stress effects, which gives us an indirect understanding relevant to global climate changes," Michalak said. "We need some good indicators of genomic changes induced by climate changes. People have ways to cope unlike those of other organisms, but stress-resistance mechanisms are well-conserved in nature. The basic question of how organisms adapt to stressful environments is going to be more important in the years ahead. It affects us as a whole."

The research confirms that natural selection—the process in nature where organisms genetically adapt to their surroundings—is a powerful influence in the canyon.

"It is nice to see the molecular work finally completed, and that the molecular signal confirms the phenotypic data: There is divergence between the two slopes," said Marta L. Wayne, a professor of biology at the University of Florida and a member of the UF Genetics Institute, who was not involved in the research. "This is interesting because the slopes are close enough that we know animals travel between them, yet selection is so strong that there are differences between animals on the two slopes. This is really strong natural selection."

Provided by Virginia Tech

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