

The Buzz on Bee Viruses

TECHNOLOGY DESIGNED FOR HUMAN
VIRUSES IS HELPING SOLVE A BEE RIDDLE.

In 2006, bee colonies started failing at a rate never seen before. Entire colonies died. Farmers feared a shortage of bees to pollinate their crops. The cause of this phenomenon, known as colony collapse disorder, remains a mystery despite intense effort. HHMI investigator Joe DeRisi is using his expertise on viruses to tackle the problem.

“Attempts to examine the cause of the bee colony collapses were confounded by the fact that very little was known about viruses in bees, period,” says DeRisi.

So DeRisi and his colleagues at the University of California, San Francisco, decided to follow a convoy of semitrailer trucks with 70,000 beehives as it drove around the country during its annual trek to pollinate crops. With the help of experienced commercial beekeepers, bee samples from 20 designated hives were collected each week throughout the year. Using a specially designed microarray that allows rapid screening for viruses and other pathogens of insects, they monitored pathogen incidence at different times of year in different hives.

“We were leveraging a lot of the same skills and technology that we use to look at human medicine and veterinary medicine,” says DeRisi, “and now applying that to insects.”

By the end of the year, the team had tracked all known bee viruses and identified four more, they reported in *PLoS One* on June 7, 2011. Two in particular stood out. The scientists named them Lake Sinai virus 1 and 2, after a South Dakota lake near where the bees were collected. Surprisingly, Lake Sinai virus 2 was found to be the most abundant pathogen in the bees, reaching levels of greater than 1 billion copies per bee in the winter.

The data collected by the DeRisi lab don’t solve the mystery of why bees are dying. But they offer a baseline for scientists who continue to track bee viruses. “This study provides a



Understanding the pathogens that normally inhabit beehives provides a baseline to look for the cause of colony collapse disorder.

foundation from which to work,” says DeRisi. Now the team can continue following bees and begin correlating viruses with colony collapse to better understand current and emerging threats. It’s a step toward keeping bees healthy.

■ -SARAH C.P. WILLIAMS

IN BRIEF

WHEN COPIES DON'T MATCH

For a cell to function properly, it needs to copy DNA—the most basic blueprint of proteins—to RNA strands that encode proteins. It’s long been assumed that RNA must code for the protein in exactly the same way as its complementary DNA for this process to work smoothly. Mistakes at any step were always thought to be detrimental—and rare. Now, new research suggests that DNA blueprints aren’t always followed to the letter.

“The idea that RNA and protein sequences are nearly identical to the corresponding DNA sequences has not been questioned in the past,” says Vivian Cheung, an HHMI investigator who led the study. To investigate this question, Cheung and her colleagues at the University of Pennsylvania School of Medicine analyzed the DNA and RNA sequences from B cells, a form of white blood cell, in 27 individuals.

The team found more than 10,000 differences in base pairs—the letters that make up genes—between the DNA and RNA. The RDDs (RNA-DNA differences) were found in about 40 percent of genes and often led to a change in protein

sequence. The researchers repeated the experiment in skin and brain cells of infants and adults to rule out the effect of age and cell type on the phenomenon. They found similar results, they reported May 19, 2011, in *Science Express*.

Known RNA-editing molecules could explain only about half of the RDDs the scientists found. Their next step is to explain how the rest arise, why the cell lets these sequence differences persist, and whether the RDDs in different individuals contribute to variations in disease susceptibility.

HOMING IN ON AUTISM GENES

A team of HHMI researchers has identified new gene mutations linked to cases of autism spectrum disorders (ASDs). The findings suggest that 20 percent of cases of sporadic autism—where neither parent of an affected child has a family history of the disorder—can be explained by spontaneous gene mutations.

ASDs cover a wide range of defects in language, social ability, and movement and vary widely in severity and symptoms, making them hard to study as a group. Scientists at the University of Washington

School of Medicine led by HHMI investigator Evan Eichler looked at 20 affected children in their latest study. They compared the genes of the children with those of their parents to find mutations that were unique to the child.

The team turned up 21 spontaneous mutations, 11 of which altered protein sequences. In four children, the researchers pinpointed severe mutations that have been linked to autism, intellectual disability, and epilepsy. The findings, published in the June 2011 issue of *Nature Genetics*, hint that the same mutations can manifest themselves in different ways in different individuals. They support the idea that having more than one mutation can change or worsen symptoms of ASDs.

“The idea that multiple genes are coming together in what’s called an oligogenic model of autism is, I think, an exciting but also daunting prospect,” says Eichler.

A DELICATE BALANCE PROTECTS AGAINST LEUKEMIA

When it’s turned up too high, the cellular Notch signaling pathway causes leukemia. Now, HHMI researchers have found