

Bedbug genetic study finds possible pesticide-resistance genes

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Ohio State University entomologists have conducted the first genetic study of bedbugs, paving the road to the identification of potential genes associated with pesticide resistance and possible new control methods for the troublesome insect, whose sudden resurgence in the United States has led to a public health scare.

The discovery was reported Jan. 19 in the online journal [PLoS ONE](#).

"While [bedbugs](#) are poised to become one of the major household pests across the United States in the coming years, we know very little about their [genetic makeup](#) and their mechanisms of resistance to insecticides," said Omprakash Mittapalli, corresponding author of the study and an assistant professor of entomology with the university's Ohio Agricultural Research and Development Center in Wooster.

"This is the first study to elucidate the genetic make up of the insect and to obtain fundamental molecular knowledge regarding potential defense pathways and genes that may be involved in metabolic resistance to commonly used pesticides."

A minor nuisance since World War II as a result of the widespread use of DDT and other long-lasting residual insecticides, bedbug (*Cimex lectularius*) numbers have increased in the past decade as much as 500 percent in North America and other parts of the world — costing billions of dollars to homeowners and businesses annually and requiring the use of large quantities of pesticides, many of them ineffective.

Reasons behind the spike in bedbug infestations include a boom in international travel, increased exchange of used furniture, a shift from powerful but dangerous insecticides such as DDT to more selective control tactics, and the development of resistance among bedbug populations to currently used pesticides — pyrethroids in particular.

"The common assumption today is that pesticide resistance in bedbugs results from point mutations in certain genes," Mittapalli explained.

"However, the role of detoxification and antioxidant enzymes in pesticide resistance of bedbugs is poorly understood. Enzymes such as Cytochrome P450s and glutathione S-transferases (GSTs) have been shown in other insects to act as detoxification agents, allowing the insects to get rid of toxic compounds such as insecticides and not be killed by them. Our study looked closely at those groups of enzymes in bedbugs."

For the study, Mittapalli and his team employed 454 sequencing technology, which has recently enabled the application of functional genomics to a broad range of insect species previously unexplored at the molecular level. They analyzed both laboratory-reared bedbugs susceptible to insecticides (the Harlan strain) and pesticide-exposed bedbugs collected from a Columbus, Ohio apartment in 2009 and 2010.

This analysis led to the identification of 35,646 expressed sequence tags, or ESTs, which are instrumental in gene discovery and sequencing work. Before this study was conducted, less than 2,000 ESTs for *C. lectularius* had been filed in the National Center for Biotechnology Information (NCBI) databases. This information alone is expected to advance additional genetic studies of bedbugs and comparative molecular analyses of blood-feeding insects.

"From the database we created, we profiled the transcript level for a cytochrome P450 (CYP9) and a GST (Delta-epsilon) in different

developmental stages (early-stage nymphs, late-stage nymphs and adults) of pesticide-susceptible and pesticide-exposed bedbugs," Mittapalli said. "We found higher transcript levels for CYP9 in all developmental stages in pesticide-exposed populations compared to pesticide-susceptible populations. We also found higher transcript levels of Delta-epsilon in the late-instar nymphs of pesticide-exposed bedbug populations."

Further studies — including gene silencing, or "knocking down," the CYP9 and Delta-epsilon candidate genes to confirm that they are indeed involved in pesticide resistance — are still needed.

"The insecticides being used right now are based on the idea that resistance in bedbugs is caused by point mutations in genes," Mittapalli pointed out. "But we are finding out that the mode of resistance could be attributed to a combination of changes in the bug's genetic makeup (such as mutations) as well as transcriptomic adjustments leading to differential gene expression. Pinpointing such defense mechanisms and the associated genes could lead to the development of novel methods of control that are more effective."

More information: Bai X, Mamidala P, Rajarapu SP, Jones SC, Mittapalli O (2011) Transcriptomics of the Bed Bug (*Cimex lectularius*). PLoS ONE 6(1): e16336. doi:10.1371/ journal.pone.0016336

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