

Spider mite genome sequence establishes tools to tackle pest resistance

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(PhysOrg.com) -- The tiny two-spotted spider mite, *Tetranychus urticae* (only 0.3 mm in size) is a destructive worldwide pest that attacks more than 150 diverse crop plants, including tomatoes, peppers, strawberries, flowers, apples, pears, grapes, and soya. Among the most difficult pests to control, spider mites rapidly develop resistance to management pesticides.

Last year, the genome sequencing of the two-spotted spider mite was deciphered in a project led by researchers at Western University. In a new study, Western biology professor Miodrag Grbic and an international research team have exploited this genomic resource to identify both the mode of action of a major mite pesticide, as well as how mites have evolved resistance to the pesticide in field populations. The findings are published this week in [Proceedings of the National Academy of Sciences](#).

According to [Arthropod Pesticide Resistance Database](#), two-spotted [spider mites](#) have recorded an astonishing 389 cases of resistance, the highest amongst all arthropods (arthropods include both insects and mites). This means that spider mites often develop resistance to a pesticide within only two to four years of its introduction.

"The *T. urticae* genome sequence created unique resources that made this study possible," says Grbic, who leads Western's Genomics in Agricultural Pest Management project. "With the ability to produce large populations that segregate for resistance, we were able to

implement a new type of genetic mapping approach to locate pesticide resistance mutations to a specific gene. These mutations make mites immune to Etoxazole, a pesticide that is currently used worldwide and is at the forefront of controlling spider mites in agriculture."

A molecular understanding of how particular [pesticides](#) work is important because it may aid the development of improved pesticide compounds which are more effective and less toxic to other organisms.

"As hinted by earlier studies, we were able to show that Etoxazole inhibits chitin biogenesis in mites, thereby disrupting normal development. Because chitin is an essential component of the exoskeleton of insects and mites, but not vertebrates, it is an attractive target for pesticide development," says the study's lead author Thomas van Leeuwen from Belgium's Ghent University. "Our work proves that at least one specific chitin synthesis inhibitor acts by targeting a membrane protein that acts in the last step in chitin biosynthesis."

The study also illustrates the power of a new generation of sequencing and genetic analysis methods.

"Until now, lack of genomic resources have limited approaches to understand ecologically and economically important traits in arthropods, but our study brings hope that future progress can be greatly expedited with the judicious use of new technologies and novel genetic methods," says corresponding author Richard Clark from the University of Utah.

Major participants in the study included Miodrag Grbic (Western University), Thomas van Leeuwen (Ghent University, Belgium), Hans Merzendorfer (University of Osnabrück, Germany) and Richard Clark (University of Utah, USA). Canadian support for the study was from the Government of Canada through Genome Canada and the Ontario Genomics Institute and the Ontario Research Fund–Global Leadership in

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