

Highlight—Tiny, Unseeing Mite Defies Expectations

Danielle Venton*

*Corresponding author: E-mail: danielle.venton@gmail.com.

Accepted: April 12, 2016

For those who love and study insects and arachnids, they can see the underappreciated wonders of the biological realm. In the face of so much diversity, so much remains to be discovered.

A recent study in *Genome Biology Evolution* is a case in point. Researchers sequencing the genome of a mite have found what might seem stranger than fiction: a mite that has retained genes important to sight, despite having no eyes, and has spread genes important for the development of body segments all over its genome, in stark contrast to most organisms, keeps these genes close together in a tidy line.

Coauthor Stephen Richards, from the Baylor College of Medicine in Texas, says his “mind is still blown” when he reflects on this finding. “I always thought having the *Hox* genes all in a row was kind of important for animals, and apparently it’s not,” he says.

In other arthropods whose genomes have been examined, *Hox* genes are collinear, with few to no intervening genes. But in their examined mite, *Metaseiulus occidentalis*, the genes aren’t just spaced apart, they’re on completely different gene scaffolds.

In this mite, researchers also found an unusually high number of intron gains and losses, indicating that the evolutionary background of this arthropod (at least from a genome point of view) has been full of unexpected genetic gymnastics.

“It really makes me wonder what’s been happening in this lineage,” says Richards. It’ll take the sequencing of other related animals to determine if this mite started out with orderly *Hox* genes (which is assumed to be the historical arrangement). Or, Richards floats an alternate possibility, perhaps “it is more basal in the mites?”

A Mighty Important Mite

Marjorie Hoy has studied *M. occidentalis* for most of her career. It’s used in agriculture as a predator on mites that cause more trouble, including ones that feed on apples, grapes, peaches, almonds, cotton, and strawberries. Much

of Hoy’s focus is on trying to genetically improve this natural enemy to pests.

“I look on this sequence as the first step to the next phase of genetically improving this predator,” she says. “Now that we know how many genes it has and what they are, though we don’t know the function of many of them, we can investigate the gene function of interesting characteristics.”

She’s excited about using CRISPR gene editing in the future to take out, put in, or modify certain genes to boost the predatory effectiveness of this mite. In particular, she is interested in *M. occidentalis*’ sex ratio.

“It’s unusual,” she says. “It’s two and a half females for every male. The females are bigger and more effective predators. I would really like to have a strain developed that produces only female progeny.”

A big surprise for her, she says, was the finding that the mite has retained some genetic equipment that it seemingly can’t possibly use.

“This predator doesn’t have any eyes, yet we know that it can somehow detect light,” says Hoy. “But we don’t know how. One of the scientists on the project looked at what genes are present that are associated with light detection and this predator has them all!”

The researchers believe that, for actual hunting, this blind mite uses chemosensation. Yet, shortening daylengths will induce diapause in this mite (Hoy 1975). So somehow “despite having no eyes this mite seems to possess key eye developmental genes,” write the authors, “as well as all the major molecular components necessary for light perception.” Just one more mystery.

Purdue entomologist Jason Meyer (a former student of Hoy’s, not involved in this work) says the dataset published along with the article gives researchers many new opportunities to dissect mite biology.

In addition to biologists who would like to alter the mite in the name of agriculture, Hoy and Richards believe their paper will be of interest to those studying animal development (on account of the surprising arrangement of *Hox* genes).

“I’m always shocked by how many branches of the tree of life are understudied,” says Richards. Here, at last, is the opportunity to give at least one group of mites a very close look.

Literature Cited

Hoy MA, et al. 2016. Genome sequencing of the phytoseiid predatory mite *Metaseiulus occidentalis* reveals completely atomised Hox genes

and super-dynamic intron evolution. *Genome Biol Evol.* 8(6):1762–1775.

Hoy MA. 1975. Effect of temperature and photoperiod on the induction of diapause in the mite *Metaseiulus occidentalis*. *J Insect Physiol.* 21:605–611.

Highlights editor: George Jianzhi Zhang