

Dramatically dynamic genomic evolution of a mighty mite

March 10 2016



Female *Metaseiulus occidentalis*, Credit: Aaron Pomerantz

Sequencing and comparative analysis of the genome of the Western Orchard predatory mite has revealed intriguingly-extreme genomic evolutionary dynamics through an international research effort co-led by scientists from the University of Geneva and the SIB Swiss Institute of Bioinformatics. In a study published in the journal *Genome Biology and Evolution*, the researchers detail the initial insights into several remarkable features of the genome of this agriculturally important mite that is widely employed to control plant pests, with thousands shipped to fruit growers every day.

As a major natural enemy of several damaging agricultural pests, the predatory mite *Metaseiulus occidentalis* is used in many agricultural settings as an effective biological control agent. Some of its favourite

prey include spider mites that feed on and destroy various fruits including strawberries, apples, peaches and grapes. "I have been studying the behaviour, ecology, and molecular biology of these mites for more than 40 years," said Prof. Marjorie Hoy lead author from the University of Florida USA, "so I was very keen to sequence the [entire genome](#) to reveal the full catalogue of [genes](#)." To explore the unique biology of this agriculturally important predator the researchers focused their studies on genes putatively involved in processes linked to paralysis and pre-oral digestion of prey species and its rather rare parahaploid sex determination system, as well as how it senses chemical cues from its surroundings and defends itself from infections.

Compared with other arthropod species, the evolutionary history of this mite's [genome](#) has been particularly dynamic. For example, the team's analyses revealed remarkably more intron gains and losses than in other arthropods. "The dynamic gains and losses of introns in the genes of this mite are in stark contrast to its closest relative with a draft genome assembly, the Ixodes tick" described Dr Robert Waterhouse, lead author from the University of Geneva and the SIB Swiss Institute of Bioinformatics. They identified five copies of Dicer-2, a gene found almost exclusively in single-copy in other arthropods, suggesting a possible rewiring of RNA processing pathways. The Hox genes, which are important for determining animal body plans and are located in a cluster of neighbouring genes in almost all species examined to date, were found to be completely dispersed across the mite's genome. "This raises questions about how regulatory programmes that turn Hox genes on and off during the coordinated development of complex body plans can be achieved even when the genes are no longer physically close to each other in the genome" explained Dr Waterhouse.

"These resources greatly improve the genomic sampling of chelicerates, a group of arthropods that has so far been poorly represented mainly due to challenges associated with their often very large genomes" said Prof.

Stephen Richards from the Baylor College of Medicine USA, where the genome sequencing was performed. Indeed, results from the study's phylogenomic analyses question the relationships amongst some of the major chelicerate groups of mites, ticks, and spiders, further emphasising the need for improved genomic sampling in this clade. This reference genome assembly therefore provides valuable new high-quality resources for future functional genomic and taxonomic analyses of this family of predatory mites and other arachnids.

More information: Marjorie A. Hoy et al. Genome sequencing of the phytoseiid predatory mite reveals completely atomised genes and super-dynamic intron evolution , *Genome Biology and Evolution* (2016). [DOI: 10.1093/gbe/evw048](https://doi.org/10.1093/gbe/evw048)

Provided by Swiss Institute of Bioinformatics

Citation: Dramatically dynamic genomic evolution of a mighty mite (2016, March 10) retrieved 20 April 2024 from

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