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The genomics of herbivore-plant interaction: whole genome sequence of *Tetranychus urticae* provides novel genomic tools for dissecting plant-pest relationship

In response to herbivore attack, plants have evolved a variety of mechanisms to deter herbivore feeding, which prevent the herbivores from jeopardizing the plant's health, reproduction, and ultimately survival. Understanding the fundamental mechanisms of plant resistance to pest and interactions between plant and herbivores represent the basis for breeding of pest-resistant crops. The current need for novel methods of pest control coincides with unprecedented advances in genomic analyses of crop plants that open novel avenues for biotechnology. In contrast, genomic resources for pest species, necessary for the development of new control strategies, are lagging behind. Thus, the current gap in knowledge about pest genetics, genomics and genomics of plant-pest interactions is a major obstacle for the detailed understanding of plant-pest relationship.

The whole genome sequencing of the two spotted spider mite, *Tetranychus urticae* led by our group generated the first chelicerate whole genome and novel genomic resources in one of the major agricultural pests. *T. urticae* is a generalist herbivore and major agricultural pest that feeds on more than 1000 plant species (about 150 of which are of economic value). Conveniently, *T. urticae* develops on the model plant *Arabidopsis*, allowing utilization of the plethora of genomic tools available in this plant model species to dissect plant-pest interactions.

We characterized the differential resistance among natural *Arabidopsis* accessions to spider mite damage and isolated *Arabidopsis* accessions resistant and susceptible to *T. urticae*. In addition, we profiled the transcriptome of naturally resistant and susceptible *Arabidopsis* accessions upon spider mite feeding using ATH1 *Arabidopsis* microarray. In addition to plant response we analyzed the transcriptome of *T. urticae* feeding on resistant and susceptible plants using RNAseq technology. Our screen for natural variation of plant resistance and herbivore transcriptome profiling represents the first systematic step toward uncovering elements of plant-pest interaction on the genomic level. This approach has a potential to isolate plant and pest genes for breeding/biotechnological modification of crop plants for resistance against major pest in agriculture.