



Dynamics of transcriptome-based gene expression across spider mite life cycle induced by *Wolbachia**

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Wolbachia are maternally transmitted endosymbionts which cause an array of effects on hosts reproduction, fitness, immunity etc. To better understand *Wolbachia*-associated effects on their hosts, we identified gene expression profilings for a spider mite, *Tetranychus turkestanii*, across the entire life cycle by transcriptome sequencing. Dynamic changes of mites at different developmental stages, including eggs, larvae, nymphs and adults were analyzed. We found that quite a few host genes exhibited stage- or sex-specific expression differences across the mite life cycle. Most metabolism processes were affected by *Wolbachia*, such as detoxification, redox, reproduction and immunity pathways. Differentially expressed genes of detoxification metabolism included ABC transporters, cytochrome P450, glutathione-S-transferase and carboxylesterase. Differentially expressed genes of reproduction included cathepsin B, histone acetyltransferase KAT7, Juvenile hormone binding, histone H2B etc. Our work provides comprehensive insights into the developmental dynamics of differential gene-expression for a mite associated with an intracellular bacterium, and shows that public gene expression data harbor rich resources to probe the functional basis of the *Wolbachia*-mite symbiosis.

Keywords: *Wolbachia*, *Tetranychus turkestanii*, symbiosis, transcriptome