



Transcriptome analysis in spider mite *Tetranychus turkestanii* doubly infected with *Cardinium* and *Wolbachia**

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Endosymbiotic bacteria *Cardinium* and *Wolbachia* play an important role in the growth and development of mites. However, the mechanisms of their reproductive manipulations in host mites, especially inducing cytoplasmic incompatibility (CI), is still unclear. In the study, transcriptional responses of a spider mite, *Tetranychus turkestanii*, jointly infected with *Cardinium* and *Wolbachia*, were analyzed based on RNA-Seq. Potential target genes of reproductive regulation and inducing CI were identified with functions and metabolism pathways, especially detoxification metabolic processes, redox processes, as well as reproductive and immune-related pathways, while the mites uninfected with *Cardinium* and *Wolbachia* were used as the control for comparative transcriptome analysis. Our transcriptional outputs provide a rich resource for the mechanisms of double infection on reproduction manipulation of mites, and can be explored in detail in symbiotic interactions between microbes and their multicellular hosts.

Keywords: *Cardinium*, *Wolbachia*, *Tetranychus turkestanii*, double infection, transcriptome