

Genetic Relationship between the Carmine Spider Mite *Tetranychus cinnabarinus* (Boisduval) and the Two-spotted Mite *T. urticae* Koch in China Based on the mtDNA COI and rDNA ITS2 Sequences

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Abstract

The population structure of the Chinese carmine spider mite *Tetranychus cinnabarinus* (Boisduval) was investigated by amplifying and sequencing a portion of the mitochondrial DNA gene coding for cytochrome oxidase I (COI, 453bp) and a portion in the second internal transcribed spacer (ITS2, ~645bp) of rDNA. Nineteen *T. cinnabarinus* populations of various geographical origins were sampled from all over China. Intraspecific variation analysis showed that 81 nucleotide positions (17.9% of the total length) were found polymorphic in COI sequences, of which 88.9% were silent substitutions. Compared with COI sequences, there were only 11 differences (five transversions, five transitions and one 2bp insertion/deletion) in the ITS2 sequences among these populations. We argue that the reasons for less ITS2 divergences might be that ancestral polymorphism was generally lower for ITS2 than for COI. From the trees established by MEGA based on Kimura-2-parameter distance, we found that the phylogenetic relationships inferred from COI and ITS2 sequences approximately accorded with their geographical relationships. It has long been considered in China that *T. cinnabarinus* and *T. urticae* are two independent species. However, the molecular phylogeny obtained by mtDNA and rDNA analyses indicated that *T. cinnabarinus* and *T. urticae* from China were not clearly distinguished from each other.

Key words: *Tetranychus cinnabarinus*, *Tetranychus urticae*, mitochondrial DNA, cytochrome oxidase subunit I (COI), ribosomal DNA, the second internal transcribed spacer (ITS2), phylogenetic analysis

Introduction

The carmine spider mite *Tetranychus cinnabarinus* is closely related to the two-spotted spider mite *T. urticae* Koch. The separation of *T. cinnabarinus* from *T. urticae* was proposed by Boudreaux (1956) based on morphological characters such as the shape of male aedeagus, the shape of dorsal integumentary lobes and the color of live summer females and newly laid eggs as well as the breeding experiments. The separation was supported by Parr and Hussey (1960), van de Bund and Helle (1960), Jordaan (1977), Brandenburg and Kennedy (1981), Kuang and Cheng (1990), and Zhang and Jacobson (2000), but rejected by Dupont (1979), Mollet and Sevacherian (1984), Meyer Smith (1987), Ehara (1999), Baker and Tuttle (1994) and Bolland et al. (1998). In fact, it is very difficult to differentiate *T. cinnabarinus* and *T. urticae* using morphological characters because both species are polymorphic and there is significant intraspecific variation among populations on different host plants and from different geographic locations (van de Bund and Helle 1960; Wang 1981; Zhang and Jacobson 2000). In China, acarologists believe that *cinnabarinus* and *urticae* are separate species just because they have different colors in adult stages (red for *cinnabarinus* and green for *urticae*) and they do not mate with each other naturally (Kuang and Cheng 1990; Liu and Sun 1998). However, biochemical and molecular studies demonstrate that the two species have homogeneity or a great degree of similarity, which