



Identification and molecular phylogeny of agriculturally important spider mites (Acari: Tetranychidae) based on mitochondrial and nuclear ribosomal DNA sequences, with an emphasis on *Tetranychus*

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Abstract

Tetranychid mites are serious agricultural pests. Identification of species in the Tetranychidae is hampered by their close morphological similarities, especially for species within the genus *Tetranychus*. In this study, we examined the relationships of nine agriculturally important species in the Tetranychidae from China based on mitochondrial (*cytochrome c oxidase subunit 1*) and nuclear (*internal transcribed spacer 1 and 2* of ribosomal RNA gene) sequences. The results confirm the monophyly of the morphologically defined *Tetranychus*, *Panonychus*, *Amphitetranychus* and *Petrobia*. However the position of *Amphitetranychus viennensis* within the Tetranychidae needs to be confirmed. The genetic distances between *Tetranychus truncatus*, *T. turkestanii* and *T. urticae* that their taxonomy needs revision. In particular, both *cytochrome oxidase 1* and the *internal transcribed spacers 1 and 2* of rDNA sequences showed large geographical differences within *T. cinnabarinus*, suggesting the existence of cryptic species within this species.

Key words: *COI*, DNA barcoding, *ITS*, phylogeny, species identification, Tetranychidae

Introduction

The Tetranychidae are polyphagous pests that seriously damage vegetables, ornamentals, and agricultural crops throughout cold and temperate zones (Goka & Takafuji 1995). The damage caused by spider mites to agriculture has greatly increased during the past 60 years. Two species that have been given much attention worldwide are the two-spotted spider mite, *Tetranychus urticae* Koch, and the European red mite, *Panonychus ulmi* (Koch) (Helle & Sabelis 1985). The family Tetranychidae is subdivided into two subfamilies: Bryobiinae and Tetranychinae, each being further separated into tribes. The Bryobiinae encompass the tribes Bryobiini, Hystrichonychini and Petrobiini, whereas the Tetranychinae includes the tribes Eurytetranychini, Tenuipalpoidini and Tetranychini (Helle & Sabelis 1985). Morphological characters such as peritreme, aedeagus, tarsus claws and empodium, have been used to identify the species of Tetranychidae, and resolve their phylogenetic relationships.

Distinguishing tetranychid taxa is difficult because of their morphological similarity. In addition, both sexes of many species are often needed to make precise determinations (Ben-David *et al.* 2007). Species in the *Tetranychus* are especially difficult to identify. For example, the two-spotted spider mite *T. urticae* is considered a species complex (Navajas *et al.* 1998) and as many as 44 synonymous names are known (Bolland *et al.* 1998). The question whether red *T. urticae* mites should be considered as a separate species (*T. cinnabarinus* (Boisduval)) has been a subject of debate for many years (Dupont 1979; Gotoh & Tokioka 1996; Zhang & Jacobson 2000). In addition, *T. truncatus* Ehara and *T. turkestanii* (Ugarov & Nilolskii) can not be easily distinguished from *T. urticae* by molecular methods (Navajas *et al.* 2003; Ros & Breeuwer 2007). In this study, we provisionally consider *T. urticae*, *T. cinnabarinus*, *T. truncatus* and *T. turkestanii* as four different species.