

Article

***Tetranychus urticae* (green form) on *Gossypium hirsutum* in China: two records confirmed by aedeagus morphology and RFLP analysis**

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Abstract

The two-spotted spider mite *Tetranychus urticae* Koch is a phytophagous spider mite that is now one of the most important pests of agricultural and economic crops worldwide. However, reports of *T. urticae* (green form) infection on cotton have been rare in China. Here we present two records of *T. urticae* (green form) on *Gossypium hirsutum* in China (Nanjing, Jiangsu Province and Shihezi, Xinjiang Uygur Autonomous Region). Because spider mites are difficult to identify, we confirmed the identification by both aedeagus morphology and PCR-RFLP (restriction fragment-length polymorphism) technology. These results also validate the usefulness of the RFLP technology for the identification of *T. urticae*.

Key words: Spider mites, *Tetranychus urticae*, identification, aedeagus, RFLP, cotton

Introduction

The phytophagous two-spotted spider mite *Tetranychus urticae* Koch is a ubiquitous crop pest (Bolland *et al.* 1998) feeding on more than 1000 different host plants (Migeon & Dorkeld 2006). *T. urticae* usually causes chlorotic spots on leaves and scarring of fruits, resulting in severe crop losses in many cases.

Tetranychus urticae in China was first reported in 1983 on *Salvia splendens* Ker-Gawl. and then expanded its distribution to many parts of the country including Gansu, Shandong and Hebei, mainly on apple trees (Cai & Cheng 2003; Zhu *et al.* 2013). Reports of *T. urticae* (green form) on cotton have been rare. *Tetranychus turkestanii* (Ugarov & Nikolskii 1937) is reported to be the dominant mite species on cotton in Xinjiang (Yuan *et al.* 2012). As far as we know, there have been no reports of *T. urticae* (green form) on cotton in Xinjiang.

Tetranychus species are very similar and have a limited number of diagnostic characters. As a result, identification of *Tetranychus* species is difficult and controversial. Nearly one third of the spider mite sequences in GenBank were unreliable due to misidentification (de Mendonca *et al.* 2011). Because morphological identification requires expertise and male individuals which are rare outdoors as a result of female-biased sex ratio of spider mites (Sabelis 1991), molecular techniques such as mtDNA barcoding (Ros & Breeuwer 2007), ITS-RFLP (Osakabe *et al.* 2008) and PGM method (Gotoh *et al.* 2007) have been advocated for the identification of the species in this genus.

In this study, we used both morphological and molecular methods to verify whether two green form samples we collected were *T. urticae*. We also examined the concordance between these two identification methods.