

Article

Effects of *Wolbachia* on rDNA-ITS2 variation and evolution in natural populations of *Tetranychus urticae* Koch

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Abstract

In this study, rDNA-ITS2 was sequenced and analyzed to investigate the effect of *Wolbachia* on the rDNA of four populations of *Tetranychus urticae* Koch. The result showed that all four populations of *T. urticae* were infected with two strains of *Wolbachia*. They are wUrtOri1 (HM486515–HM486517) and wUrtCon1 (HM486518), belonging to the Ori group and Con group of B supergroup, respectively. There was one mutation site among 645 sites for the ITS2 fragments. All the sequenced ITS2 were classified into two haplotypes. The diversity analysis of ITS2 sequences of individuals showed that infection by *Wolbachia* did not significantly change the diversity of rDNA. A neutrality test using ITS2 indicated that the population of *T. urticae* has remained stable during evolution and is not off the Hardy-Weinberg equilibrium.

Key words: *Tetranychus urticae* Koch, *Wolbachia*, rDNA diversity, neutrality test

Introduction

The two-spotted spider mite, *Tetranychus urticae* Koch (Acari: Tetranychidae), is an important agricultural pest that can feed on about 1200 host plant species, among which more than 150 are economically important (Badawy *et al.* 2010). It mainly damages vegetables, fruit trees, cotton, soybean, maize and ornamental crops worldwide (Miao *et al.* 2006; Badawy *et al.* 2010). Its high reproductive potential and short life cycle allow it to quickly develop resistance to many acaricides (Nicastro *et al.* 2010). It is estimated that *T. urticae* has developed resistance to more than 80 acaricides in 60 countries (Badawy *et al.* 2010). It is the most damaging mite species on agricultural crops and fruit trees (Miao *et al.* 2006).

Wolbachia is a very common cytoplasmic symbiont and is maternally inherited (Zhou *et al.* 1998; Hurst *et al.* 1999). It can infect insects, crustaceans, filarial nematodes and mites at rates of 16% to 76% (Miao *et al.* 2006). *Wolbachia* has evolved a large scale of host manipulations such as parthenogenesis induction (Stouthamer *et al.* 1993; Arakaki *et al.* 2001), feminization (Bouchon *et al.* 1998; Hiroki *et al.* 2002), male killing (Hurst *et al.* 1999) and crossing incompatibility which is the most common effect between infected males and uninfected females (Perrot-Minnot *et al.* 1996; Breeuwer 1997; Dobson *et al.* 2001). *Wolbachia* can affect the development and propagation of arthropod hosts (Wang *et al.* 2010).

Both mitochondrial DNA (mtDNA) and nuclear ribosomal DNA (rDNA) are widely used for population genetic studies. Hillis & Dixon (1991) were the first to use rDNA for phylogenetic analysis, subsequently rDNA was widely used in many studies on evolution and taxonomy for