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