

Development and characterization of novel EST-microsatellites for the citrus red mite, *Panonychus citri* (Acari: Tetranychidae)

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Abstract

The citrus red mite, *Panonychus citri* (McGregor), is an economically important pest on citrus. To better understand the population structure of *P. citri*, we developed 15 novel polymorphic microsatellites derived from expressed sequence tags (EST). The new microsatellites were assessed in 32 female individuals sampled from Quanzhou (Fujian Province), China. The polymorphic information content (PIC) for each locus ranged from 0.305 to 0.726, with an average of 0.491. The number of alleles per locus ranged from 2 to 6, with an average of 3.8. The observed and expected heterozygosities ranged from 0.094 to 0.438 and from 0.345 to 0.764, respectively. Significant linkage disequilibrium was detected for three pairs of loci (*PC3* and *PC9*, *PC3* and *PC11*, *PC11* and *PC13*). Twelve of the 15 loci deviated significantly from Hardy-Weinberg equilibrium (*HWE*). The presence of null alleles, inbreeding and the Wahlund effect were considered potential sources of the deviations from *HWE*. The new polymorphic microsatellites provide a valuable resource for future population genetics studies and management of *P. citri*.

Key words: *Panonychus citri* (McGregor), citrus red mite, SSR, genetic diversity, genetic structure

Introduction

The citrus red mite, *Panonychus citri* (McGregor) is a polyphagous herbivore that attacks more than 100 different families of host plants (Migeon *et al.* 2010). In many countries such as China, Japan and Spain, it is regarded as one of the most important citrus pests (Yuan *et al.* 2010). It is mainly controlled with acaricides in recent years. Due to the abuse of acaricides, the acaricide resistance has become a problem in *P. citri* (Döker & Kazak, 2012). In addition to chemical control, biological control has been used to control the mite. Several predatory mites, including *Amblyseius swirskii*, *Agistemus exsertus* and *A. eharai* are considered as good candidates for controlling *P. citri* (Ji *et al.* 2013a, b). However, there is a long journey for commercializing these predatory mites and for replacing chemical control with biological control.

To better control *P. citri*, it is necessary to understand its population genetic structure, which can clarify population dynamics and identify management units (Palsboll *et al.* 2007; Porretta *et al.* 2007). To achieve this aim, a large number of highly polymorphic makers are needed. Previous population genetics studies of *P. citri* used allozyme (Osakabe & Komazaki 1996; Osakabe & Komazaki 1997), mitochondrial *COI* genes (Osakabe *et al.* 2005; Yuan *et al.* 2010) and internal transcribed spacer 1 (ITS1) sequences (Yuan *et al.* 2011). However, these markers are not good candidates for population genetics studies because of their low polymorphism, maternal inheritance or multiple copies in genome.