

Article

COI barcoding as a molecular assay for the identification of phyto-seiid mites

JIN-BO LI¹, YUAN-XI LI¹, JING-TAO SUN¹, XIAO-FENG XUE¹, XUE-NONG XU² & XIAO-YUE HONG^{1*}

¹Department of Entomology, Nanjing Agricultural University, Nanjing, Jiangsu 210095, China

²Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing 100193, China

* Corresponding author: E-mail: xyhong@njau.edu.cn

Abstract

Phytoseiid mites are the most studied family within the order Mesostigmata, especially because of their major interest for biological control programs. Phytoseiid mite species identification is essentially based on morphological characters. However, the development of faster and more accurate methods is under way. Molecular identification techniques, such as barcoding, are also used to improve mite diagnosis. The number of phytoseiid mite sequences used for diagnostic purpose has increased recently, but not all of them are reliable in the absence of voucher specimens or inaccurate taxonomy identification. In this study, we considered 14 common phytoseiid species collected from agricultural, urban, and wild ecosystems in different parts of China. We extracted genomic DNA from the mites and retained the mite specimens as vouchers to ensure the credibility of molecular data. Commonly used COI sequences were used as the most used barcoding marker. The results show that COI sequences are effective and capable of high-resolution molecular identification of the phytoseiid mite species herein considered.

Key words: Phytoseiid mites, barcoding, COI, voucher

Introduction

Phytoseiidae is a large family of predatory mites. There are more than 2,300 known species of phytoseiid mites placed in over 90 genera, though considerable synonymy is suspected (Moraes *et al.* 2004; Chant & McMurtry 2007; Beaulieu *et al.* 2011; Tixier *et al.* 2012b). Phytoseiidae is also the most studied family within the order Mesostigmata because of their major interest in biological control programs as predators of phytophagous mites on many crops (Gerson *et al.* 2003).

Phytoseiid mite species diagnosis is essentially based on morphological characters. This method has several advantages and good prospects for further development. However, in the process of phytoseiid mites resource development and application, there are some problems that have yet to be solved: (i) Phytoseiid species resources are still largely undeveloped; (ii) It is difficult to control the effective purity in mass production of phytoseiid mites. Predatory mites are very small and single species isolated feeding for long time is difficult because the mixtures and substitutions by exotic species are common and typical. (iii) It is difficult to evaluate the effect of predation of phytoseiid mites released on crops only with morphological identification system as it requires the expertise of a very capable taxonomist (Okassa *et al.* 2012). Indeed, morphologically cryptic mite species frequently coexist (Magalhães *et al.* 2007; Tixier *et al.* 2008; Kanouh *et al.* 2010). Three of the mite species herein studied, from the *largoensis* species group, *Amblyseius herbicolus* (Chant), *Amblyseius largoensis* (Muma), and *Amblyseius eharai* Amitai & Swirski are very similar in