

Article

Genetic variation among natural populations of *Euseius nicholsi* (Acari: Phytoseiidae) from China detected using mitochondrial *coxI* and nuclear rDNA *ITS* sequencesCHAO YANG¹, YUAN-XI LI¹, XIAN-MING YANG¹, JING-TAO SUN¹, XUE-NONG XU² & XIAO-YUE HONG^{1*}¹Department of Entomology, Nanjing Agricultural University, Nanjing, Jiangsu 210095, China²Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing 100193, China

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Abstract

Euseius nicholsi (Ehara *et* Lee) is an important indigenous predator of many species of pest mites and insects in China. In this study, the genetic diversity of *Euseius nicholsi* among ten populations was investigated using *coxI* and *ITS* sequences from 145 individuals. This indicated the existence of 33 and 16 haplotypes, respectively. Most of the populations studied showed high levels of haplotype and nucleotide diversity. In the *coxI* region, haplotype and nucleotide diversity varied among populations from 0.385 to 0.809 and from 0.00342 to 0.01111, respectively. In the *ITS* region they varied from 0.000 to 0.803 and from 0.00000 to 0.00185, respectively. For both gene regions, the highest haplotype and nucleotide diversities were detected in Chengdu (CD) and Chongqing (CQ) from southwestern China. The results of population differentiation suggested that *E. nicholsi* indicated at least three geographically approximate populations, the middle and lower reaches of the Yangtze River (WH, CS, JJ, NP, and NJ), southwestern China (CQ and CD), and southern China (NN, GZ, and SG). High levels of genetic diversity were observed in most populations. This study serves as an introductory probe into the genetic differentiation of *E. nicholsi*, for which little molecular information is available. Other genetic markers and intensive sampling in the following studies would be useful and necessary for more detailed classifications of this taxon.

Key words: Phytoseiidae, genetic variation, *Euseius nicholsi*, China, nuclear rDNA *ITS*, mtDNA cytochrome oxidase I

Introduction

Many species of Phytoseiidae are predators of mites and insects and are therefore widely used in biological control programs (Kostiainen & Hoy 1996; McMurtry & Croft 1997). Alien predator mites sometimes bring ecological risk (attack non-target insects) and genetic risk (affect the genetic integrity) into a new agroecosystem. Therefore, it is more secure and necessary to utilize indigenous predator mites, because their ecology and genetic background may be similar to the local population, and may more easily adapt to the local environment with fewer risks (Ito *et al.* 2011). The phytoseiid mite *Euseius nicholsi* (Ehara *et* Lee) (Arthropoda: Chelicerata: Acari), which is widely distributed across southern China, is an important natural indigenous enemy of many species of pest mites, such as *Tetranychus urticae* Koch, *Panonychus citri* (McGregor), *Eotetranychus kankitus* Ehara and *Polyphagotarsonemus latus* Banks (Wu *et al.* 2008). It also has been reported in Thailand (Charanasri & Kongchuensin 2000). It has been found to feed on pollen (Zhi *et al.* 1991). Morphological characteristics serve as the essential basis for the identification of *E. nicholsi*. The

on *coxI* data) and NJ (based on *ITS* data) clustered into southwestern populations (CD and CQ). At the same time, NN was far away from other populations, as indicated by *ITS* data. The possible major reason is that *ITS* and *coxI* belong to two different molecular markers. The former is located in the nuclear genome while the latter is on the mitochondrion in the cytoplasm. Because mitochondrion experienced the cytoplasmic inheritance, the genetic background of father exerted minor influence on it. What's more, the variation rates of them differ from each other so that their distinguish abilities in the genetic variation research are also different. And it has been proved that genetic diversity of mtDNA could be influenced by endosymbionts such as *Wolbachia* (Shoemaker *et al.* 2003; Yu *et al.* 2011). Thus those would be probed with more relevant researches in the future. The phylogenetic results suggested that the observed population structure was related to geographical distance. The F_{ST} value also supported this hypothesis. Environmental heterogeneity is a major factor in maintaining and structuring genetic diversity in natural populations. Subordinate factors, natural resources and climate, might have caused the differences among the hosts, as reported by Edelaar *et al.* (2012). Pronounced genetic differentiation between populations of *E. nicholsi* indicated a low or absent intra-population gene flow, in accordance with geographical isolation. Corresponding with this, the significant F_{ST} of both *coxI* and *ITS* values in the neighboring populations were also observed in comparisons such as GZ and SG population.

For small species that are classified using to minor morphological differences, the use of molecular tools to estimate genetic differentiation might detect in the presence of different genotypes. This has been accepted as one of criteria to judge the cryptic species (Canterino *et al.* 2000; Navia *et al.* 2005). The variations in mtDNA were more pronounced than the previously reported results. Cryptic species were possibly found to exist within the specimens identified as *E. nicholsi* based on the mtDNA data. There are some reports that mitochondrion of mites from Phytoseiidae may have high variation. In order to have a clear understanding of its truth, more data about morphology and cross experiments are needed. This study is the introductory probe in the genetic differentiation of *E. nicholsi*, for which limited molecular information is available. Research based on more genetic markers and specimens is necessary.

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