Genetic variation in the predacious phytoseiid mite, *Amblyseius swirskii* (Acari: Phytoseiidae): Analysis of specific mitochondrial and nuclear sequences

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ABSTRACT

Patterns of polymorphism of two DNA fragments with contrasted modes of evolution, mitochondrial DNA (mtDNA) and nuclear ribosomal DNA (rDNA), were used to study population structure and taxonomy of the predacious mite, Amblyseius swirskii Athias-Henriot. A fragment in the mitochondrial gene coding for cytochrome oxidase subunit I (COI) and the region of the internal transcribed spacers (ITS) of rDNA were amplified, from the total genomic DNA, using polymerase chain reaction (PCR). The PCR-amplified products were purified and sequenced. The results indicated that sequence analysis combined with morphological characters can be used for identification of various species of phytoseiid mites and the biotypes of the same species.

Key words: *Amblyseius swirskii, COI gene, ITS, mtDNA, rDNA.*

INTRODUCTION

The application of molecular techniques to the study of mites has recently yielded new insights into their population structures and taxonomic relationships. Population variations and interspecific divergence have been studied in the *Tetranychidae* (Navajas *et al.,* 1994; 1998; Toda *et al.,* 2000), *Eriophydae* (Fenton *et al.,* 1995), and *Phytoseiidae* (Navajas *et al.,* 1999; Yli-Mattila *et al.,* 2000).

The methods applied to study mites have much in common and successfully facilitating the identification of taxonomically difficult species (Japanese *Panonychus* species; Toda *et al.,* 2000), understanding population structure and elucidating phylogenetic relationships, (Cassava green mite, *Monochellus progresivies* Dorsta; Navajas *et al.,* 1994). Morphological description has been widely used for classification of mites, although the advantage of molecular techniques has generated the potential to study DNA at the individual base-pair indicating a direct way of measuring and quantifying the genetic variation within and between species. The DNA fragments amplified by polymerase chain reaction (PCR) can be analyzed for polymorphism by obtaining the nucleotides sequence that provides access to details of variation in DNA.

Different genomic regions would be analyzed depending on the problem concerned. The most popular markers used for studying molecular evolution are mitochondrial DNA (mtDNA) and nuclear ribosomal DNA (rDNA). Several genes of the mitochondrial