

# Molecular characterization and detection of *Amblyseius andersoni* and *A. swirskii* (Acari: Phytoseiidae)

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## Introduction

Most of the predatory mites in the family Phytoseiidae are used as biological control agents for suppressing pest mites and preventing crop damage.

Some of them have been previously determined with molecular techniques, *vir. Neoseiulus californicus* (McGregor), *N. cucumeris* (Oudemans), *N. fallacis* (Garman), *Iphiseius degenerans* (Berlese) and *Phytoseiulus persimilis* (Athias-Henriot).

The aim of this research is to characterize two other species in this family, *Amblyseius andersoni* (Chant) and *A. swirskii* (Athias-Henriot). (Fig. 1)



Fig. 1: *A. swirskii* can not be distinguished from other predatory mites with the naked eye or with a magnifying glass.

## Methods

The polymerase chain reaction (PCR) was used to amplify ribosomal DNA fragments of *Amblyseius andersoni* and *A. swirskii*. These fragments contain the Internal Transcribed Spacers ITS1 and ITS2 and the entire 5.8S gene. Based on differences in these regions, species-specific primers have been developed and tested. (Fig. 2)

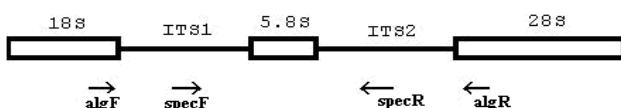


Fig. 2: Schematic representation of ribosomal genes containing the primer target areas.

## Results

The PCR results are consistent with studies based on morphology. (Fig. 3)

Phylogenetic relationship analysis of *Amblyseius andersoni* and *A. swirskii* with other members of the family Phytoseiidae based on rDNA sequences give better insight for discrimination. Both of them belong to the *Neoseiulus* cluster; therefore we prefer to use the name *Neoseiulus andersoni* and *N. swirskii*. (Fig. 4)

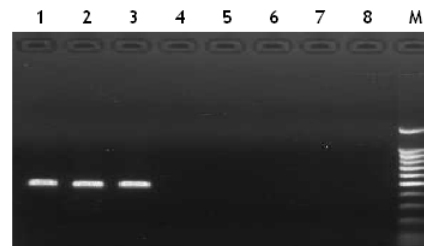


Fig. 3: PCR products amplified with specific primers for *Amblyseius andersoni*. Lane 1-3: *Amblyseius andersoni*; lane 4: *N. californicus*; lane 5: *N. fallacis*; lane 6: *N. cucumeris*; lane 7: *A. swirskii*; lane 8: water (negative control). M; 100bp Ladder (Promega).

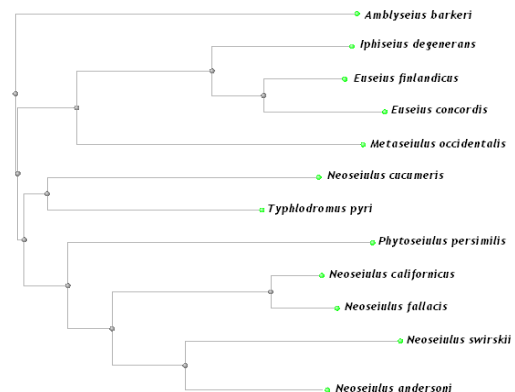


Fig. 4: A phylogenetic tree generated from an alignment of the nucleotide sequences of Internal Transcribed Spacers (ITS1 and ITS2) of *Amblyseius andersoni*, *A. swirskii* and other predatory mites of the family Phytoseiidae.