

The First Record in Turkey of *Pachycrepoideus vindemmiae* as a parasitoid of *Ceratitis capitata*: Molecular identification

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Short Report

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Abstract

Ceratitis capitata Wied. (Diptera: Tephritidae) is a polyphagous species and a serious pest worldwide. In the present study, surveys for associated *C. capitata* parasitoids were conducted in the Adana province of Turkey. Our finding represents the first record in Turkey of *Pachycrepoideus vindemmiae* Rondani (Hymenoptera: Pteromalidae) as a parasitoid of *C. capitata*.

Introduction

Tephritid flies, also known as fruit flies, are one of the most damaging groups of insect pests that infest economically significant fruit and vegetable. Among fruit flies, *Ceratitis capitata* (Diptera: Tephritidae) infest more than 300 hosts, with worldwide losses amounting to several billion USD (Liquido et al., 1990; Szyniszewska & Tatem, 2014; Satar & Tireng, 2016; Tiring & Satar, 2017; 2021).

C. capitata control management in Turkey is most of based on the use of insecticides. Nevertheless, safe eco-friendly strategies such as mass trapping are being applied. Other eco-friendly control systems like Biological Control have been conducted the several studies. However, biological control potential has been inspected in only a few species (Hepdurgun et al., 2009). Here we report the first record of a pupae parasitoid from *C. capitata* in Turkey.

Materials And Methods

Sample collection and DNA isolation

Surveys for associated medfly parasitoids were carried out between June and July in 2021 in Adana (37°03' 98.21"N, 35°36' 05.73"E), Turkey. These specimens were collected from loquat fruits. Surveys for *C. capitata* parasitoids were conducted on both infested fruits and pupae that dropped into the soil. The infested fruits and pupae samples were transferred to the Citrus Pest Laboratory at Cukurova University. Infested fruits were maintained in plastic trays at 24 ± 1°C and 65–80% RH until the emergence of adult *C. capitata* and parasitoids. The emerged parasitoids were stored in 96% ethanol for preservation. DNA was isolated from *C. capitata* parasitoids using the standard extraction kit and protocol provided by DNeasy Blood and Tissue Kit (QIAGEN, Hilden, Germany).

Pcr Amplification

Approximately 630 bp of the barcoding region of the mtCOI gene was amplified using the primers LC01490 (5'-GGT CAA CAA ATC ATA AAG ATA TTG G-3') and HCO2198 (5'-TAA ACT TCA GGG TGA CCA AAA AAT CA-3') (Folmer et al., 1994). Amplification was conducted in 50 µl with the containing 2x Master Mix (containing Tris-HCl pH 8.5, (NH₄)₂SO₄, 3 mM MgCl₂, 0.2% Tween 20, 0.4 mM of each dNTP, Taq DNA Polymerase), 10 µM primer, 50 ng DNA template and added PCR grade H₂O to a final volume. The thermocycler conditions were: 5 min at 94°C for pre-denaturation, followed by 35 cycles at 94°C for 1 min,

50°C for 1 min, at 72°C for 1 min, and a final period at 72°C for 7 min. All the PCR products were confirmed electrophoretically using 1% agarose gel, stained with ethidium bromide, and viewed with a gel imaging system before two-way sequencing by a commercial company (Macrogen, Amsterdam, Netherlands).

Data analysis

The sequences were edited using FinchTV (version 1.4.0) and aligned by CLUSTAL W that had been integrated with MEGA7 software (Tamura et al., 2013). The MEGA 7 software was also used to create maximum likelihood (ML) trees, with 1000 bootstrap replicates performed to assess branch support. The sequences were compared to the closest available reference sequences in the NCBI nucleotide collection in GenBank (<http://blast.ncbi.nlm.nih.gov/Blast>). To root the phylogenetic tree, the sequence of *Diachasmimorpha longicaudata* Ashmead (Hymenoptera: Braconidae) was used as the out-group.

Results

A total number of 4500 pupae of *C. capitata* was collected from both infested fruits and pupae that dropped into the soil. The 10 *Pachycrepoideus vindemmiae* Rondani (Hymenoptera: Pteromalidae) emerged from pupae (Fig. 1). Morphological taxonomic identification results were consistent with molecular findings.

The universal primer set used in this study (LC01490 and HCO2198) targets the mitochondrial COI gene. It yielded efficient amplification in the parasitoid strain of *C. capitata*. The mean size of the amplified fragment was 630bp. The nucleotide sequences are available in GenBank under the accession number OM956372.

For the COI sequences, used the Maximum Likelihood model Tamura-3-parameter tree. Tree topology showed *P. vindemmiae* was highly distanced from *D. longicaudata* and other *P. vindemmiae* strains (Fig. 2).

Discussion

This study has examined to the presence of *C. capitata* parasitoids in Turkey (Adana). Our finding represents the first record in the Turkey of *P. vindemmiae* as a parasitoid of *C. capitata*. Kaçar (2020) indicated that *P. vindemmiae* attacks the pupae of *Drosophila suzukii* (Matsumura, 1931) (Diptera: Drosophilidae) and can effectively parasitize in the laboratory. Our study, *P. vindemmiae* ADN-01 was on a different branch from a clone from Turkey, Düzce (MK813907). *P. vindemmiae* individuals from *D. suzukii* and *C. capitata* were clearly discriminated by nucleotide sequences of COI with high bootstrap values.

Previously, *Spalangia cameroni* Perkins Rondani (Hymenoptera: Pteromalidae) and *P.vindemmiae* had been found as native pupal parasitoids of the medfly in Spain (Falco et al., 2006). Harbi et al. (2015) was

detected that *P. vindemmiae* parasitizing pupae of *C. capitata* in Tunus. *P. vindemmiae* is known to attack pupae of *Bactrocera dorsalis* (Hendel) (Diptera: Tephritidae) (Wang & Messing, 2004; Zhao et al., 2013).

Declarations

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Authors' contributions

GT, AT and SS conceived and designed the study and collected the data. GT and AT wrote the initial draft and analyzed the data, and all authors edited and contributed to subsequent drafts.

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Conflict of interest The authors declare that there are no interests to declare.

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.

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Figures



Figure 1

Pachycrepoideus vindemmiae

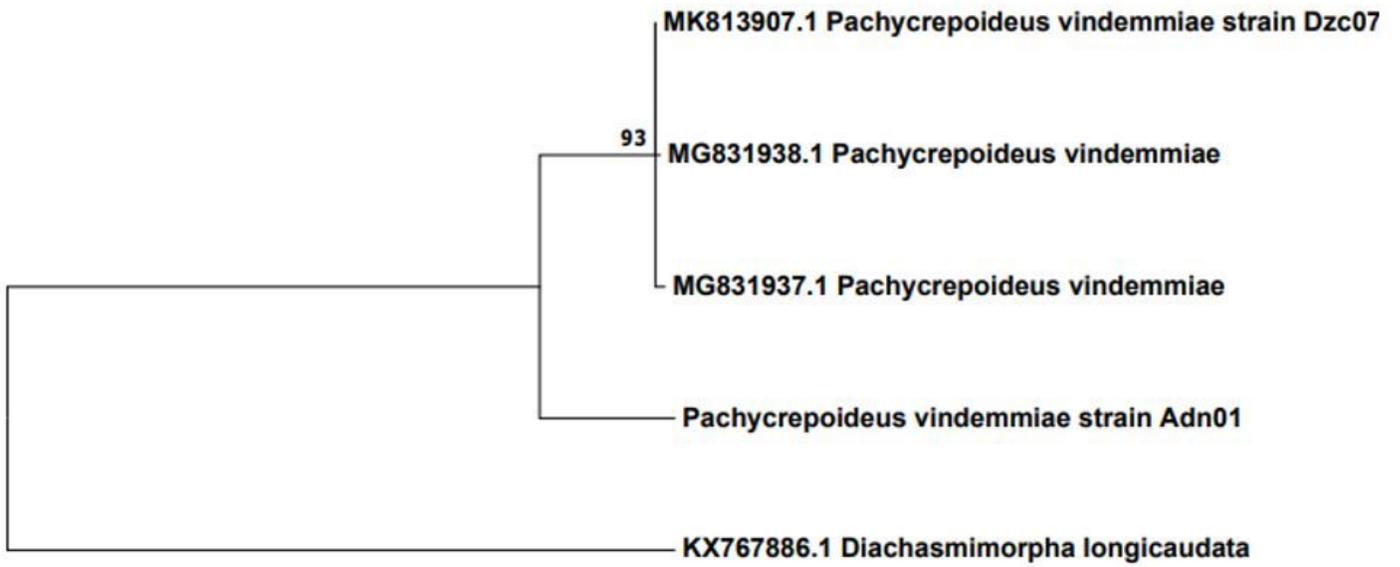


Figure 2

Phylogeny of the *Pachycrepoideus vindemmiae* associated with *Diachasmimorpha longicaudata* based on the COI locus (the out-group). The bootstrap values (percentage, based on 1000 replicates) are shown on the branches.