Characterization and identification of *Acerophagus papayae* Noyes and Schauf (Hymenoptera: Encyrtidae), an introduced parasitoid of papaya mealybug, *Paracoccus marginatus* Williams and Granara de Willink through DNA barcode

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INTRODUCTION

India is the leader in papaya (*Carica papaya* L.) production contributing to approximately 50% of the world production of 6 million tonnes of fruits cultivated in 8000 ha in various states of the country (Shylesha et al., 2010). The invasive papaya mealybug (PMB), *Paracoccus marginatus* Williams and Granara de Willink has caused havoc in agricultural and horticultural crops ever since its first report from Coimbatore during 2008. The insect has assumed the status of a major pest and caused severe damage to economically important crops and huge losses in Tamil Nadu, Karnataka, certain parts of Andhra Pradesh, Kerala and Maharashtra. It is polyphagous infesting more than 60 species of economically important host plants including papaya, hibiscus, cotton, tomato, brinjal, tapioca, silk cotton, mulberry, jatropha, pigeon pea, teak, *Parthenium hysterophorus* and several other plants (Tanwar et al., 2010). *Acerophagus papayae* Noyes and Schaufl (Encyrtidae) (Plate 1) is one of the efficient parasitoids for the suppression of papaya mealybug in its native range (Muniappan, 2006; Amarasekare et al., 2009). It was imported from Puerto Rico in 2010 through USDA–APHIS and cultures are maintained on *P. marginatus* infested papaya seedlings in the quarantine laboratory of NBAII, Bangalore. Subsequently, natural occurrence of the parasitoid was observed in significant numbers during surveys for natural enemies of papaya mealybug in papaya fields at Pune (Pokharkar et al., 2010). These parasitoids were identified as *A. papayae* using morphology based taxonomy at NBAII. However, a study was undertaken for DNA barcoding of *A. papayae* in order to supplement and confirm that the introduced and Pune populations belonged to the same species.
Fig. 1. PCR amplification of COI region of *A. papayae* (M: 50bp Ladder, Lane 1: *A. papayae* (673bp) USA, Lane 2: *A. papayae* Pune (~670bp))

Plate 1. *Acerophagus papayae*, an important parasitoid of papaya mealybug

Fig. 2. Pair-wise alignment of *A. papayae* (US & Pune) using DNASTAR

Fig. 3. DNA Barcode ID of *A. papayae* (USA): ACERO001-10
RESULTS AND DISCUSSION

CO1 (674bp) region of *A. papayae* from USA and Pune were visualized on 1.8% gel (Fig. 1) with a low range ladder (Fermentas Mass Ruler 1000bp). The PCR products were purified with MinElute PCR purification kit (Qiagen). The PCR product was sequenced using an ABI prism 310 DNA sequencer by Big Dye Terminator kit (Qiagen). The PCR product was sequenced using an ABI prism 310 DNA sequencer by Big Dye Terminator (Fermentas Mass Ruler 1000bp). The PCR product was sequenced using an ABI prism 310 DNA sequencer by Big Dye Terminator (Fermentas Mass Ruler 1000bp).

The sequence length of 673 bp along with specimen information, taxonomical and collection details were submitted to BOLD, Canada (Barcode of Life Data Systems) and DNA barcode was generated (www.boldsystems.org) (Fig. 2) with the published sequence in NCBI of *A. papayae* (USA) by BLAST analysis tool and the similarity was found to be 98%. The study revealed that the *A. papayae* populations from Pune and USA are one and the same. The barcode developed for *A. papayae* is a diagnostic tool for the identification of the parasitoid. The CO1 gene has proved to be suitable for species identification in a large range of animal taxa, including butterflies and moths (Hebert et al., 2004; Burns et al., 2008), spiders (Greenstone et al., 2005), mosquitoes (Kumar et al., 2007) and wasps (Smith et al., 2008). It appears that *A. papayae* might have got introduced fortuitously into India along with papaya mealybug from Sri Lanka.

REFERENCES


