



## Molecular and morphological evaluation of the aphid genus *Hyalopterus* Koch (Insecta: Hemiptera: Aphididae), with a description of a new species

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### Abstract

Aphids in the genus *Hyalopterus* Koch (Hemiptera: Aphididae) are pests of stone fruit trees in the genus *Prunus* globally, causing damage directly through feeding as well as transmission of plant viruses. Despite their status as cosmopolitan pests, the genus is poorly understood, with current taxonomy recognizing two, likely paraphyletic, species: *Hyalopterus pruni* (Koch) and *Hyalopterus amygdali* (Blanchard). Here we present a systematic study of *Hyalopterus* using a molecular phylogeny derived from mitochondrial, endosymbiont, and nuclear DNA sequences (1,320 bp) and analysis of 16 morphometric characters. The data provides strong evidence for three species within *Hyalopterus*, which confirms previous analyses of host plant usage patterns and suggests the need for revision of this genus. We describe a new species *H. persikonus* Miller, Lozier & Footit n. sp., and present diagnostic identification keys for the genus.

**Key words:** Molecular, morphology, evaluation, *Hyalopterus*

### Introduction

Entomologists have long been aware of the problems involved in identifying and describing species of closely related, morphologically similar groups of insects (Walsh 1864; Brown 1959; Hebert *et al.* 2004). The lack of informative morphological characters in many groups has led to difficulties in delineating species and determining their evolutionary relationships using traditional criteria, and such taxa have become appropriately known as ‘cryptic species’ (Brown 1959; Bickford *et al.* 2007). Cryptic species are especially common among the phytophagous insects, and careful research over the last several decades has revealed many morphologically similar complexes of reproductively isolated and previously unrecognized species with unique ecological characteristics (*e.g.* Guttman *et al.* 1981; Diehl & Bush 1984; Feder *et al.* 1998; Dres & Mallet 2002).

Accurate taxonomy that includes phylogenetic relationships is important for testing hypotheses regarding ecological and evolutionary patterns (Futuyma 1991; Nosil & Mooers 2005), and is also highly relevant for applied scientists striving to detect as well as prevent biological invasions and manage insect pests (Miller & Rossman 1995; Gordh & Beardsley 1999; Hoelmer & Kirk 2005). Rapid and accurate identification of a novel pest species allows access to a much wider store of biological data, which may include information on ecology, potential regions of origin, and interacting natural enemies. All such knowledge can assist in determining the most appropriate management strategies for a given species, including the need for quarantine or the development of a biological control program. For example, cryptic pest species of similar morphology may be