

DNA barcoding reveals the occurrence of cryptic species in host-associated population of *Conogethes punctiferalis* (Lepidoptera: Crambidae)

P. R. Shashank · A. K. Chakravarthy ·
B. R. Raju · K. R. M. Bhanu

Received: 18 November 2013 / Accepted: 26 January 2014
© The Japanese Society of Applied Entomology and Zoology 2014

Abstract *Conogethes punctiferalis* (Guénee) is a critical pest that commonly infests castor (*Ricinus communis* Linnaeus) and cardamom (*Elettaria cardamomum* Maton) in India. The moths of both castor and cardamom appear to be similar in wing pattern and color. However, the results of behavioral studies elicited a doubt that there may be differences in terms of host specialization. In the present study, we conducted morphological studies and DNA barcode analyses using cytochrome oxidase I gene, which unraveled the mystery of *C. punctiferalis* breeding on castor and cardamom. The differences in male aedeagus and female bursae were prominent, yet, not sufficient enough to say that they are different species. The results showed high haplotype diversity (0.817 ± 0.073) and nucleotide diversity (0.0285 ± 0.002) in *C. punctiferalis*. In addition, topologies of neighbor-joining trees indicate that *Conogethes* sp. breeding on castor belongs to *C. punctiferalis* while those on cardamom are of a separate clade. Further genetic analysis revealed significant genetic

differentiations among the two sampled populations, reflecting limited gene flow. Neutrality tests and mismatch distributions showed population expansion in *C. punctiferalis*, while the results of an analysis of molecular variance (AMOVA) indicated the existence of significant genetic variation among the examined host races. Conclusively, analysis using mitochondrial DNA showed an amount of genetic divergence between the two host-associated populations compatible with cryptic species rather than host races.

Keywords *Conogethes* · Barcoding · Castor · Cardamom · Cryptic species

Introduction

The accurate identification of insect species is one of the important aspects in entomological science. In most groups, traditional taxonomic research is based on morphological characters. It is not impossible to identify cryptic and polymorphic species through morphological taxonomy. However, there are some difficulties that depend on experts. For this purpose, molecular methods have been found valuable in discriminating cryptic species of insects (Jackson and Resh 1998; Pilgrim et al. 2002). Cryptic species are defined as two or more distinct species classified as a single nominal species because they are morphologically indistinguishable (Bickford et al. 2007). One of the mechanisms thought to promote speciation in phytophagous insects is shifts to new hosts that lead to the establishment of new species via an intermediate step of host-race formation (Bush 1969; Dres and Mallet 2002). The occurrence of insect host races exhibit recently

Electronic supplementary material The online version of this article (doi:10.1007/s13355-014-0248-0) contains supplementary material, which is available to authorized users.

P. R. Shashank (✉) · A. K. Chakravarthy
Department of Agricultural Entomology, Gandhi Krishi Vigyan Kendra, University of Agricultural Sciences, Bangalore 560065, India
e-mail: spathour@gmail.com

B. R. Raju
Department of Crop Physiology, Gandhi Krishi Vigyan Kendra, University of Agricultural Sciences, Bangalore 560065, India

K. R. M. Bhanu
A Division of Pest Control (India) Pvt. Ltd., Bio-Control Research Laboratories, 36/2, Sriramanahalli. Nr. Rajankunte, Doddballapur Road, Bangalore 561 203, India