Accepted Manuscript

Increasing the utility of barcode databases through high-throughput sequencing of amplicons from dried museum specimens, an example on parasitic Hymenoptera (Braconidae)

Julien Haran, Gérard Delvare, Jean-François Vayssieres, Laure Benoit, Perrine Cruaud, Jean-Yves Rasplus, Astrid Cruaud

PII: S1049-9644(18)30209-3

DOI: https://doi.org/10.1016/j.biocontrol.2018.04.001

Reference: YBCON 3746

To appear in: Biological Control

Received Date: 11 December 2017 Revised Date: 15 March 2018 Accepted Date: 5 April 2018



Please cite this article as: Haran, J., Delvare, G., Vayssieres, J-F., Benoit, L., Cruaud, P., Rasplus, J-Y., Cruaud, A., Increasing the utility of barcode databases through high-throughput sequencing of amplicons from dried museum specimens, an example on parasitic Hymenoptera (Braconidae), *Biological Control* (2018), doi: https://doi.org/10.1016/j.biocontrol.2018.04.001

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

ACCEPTED MANUSCRIPT

Increasing the utility of barcode databases through highthroughput sequencing of amplicons from dried museum specimens, an example on parasitic Hymenoptera (Braconidae)

Julien HARAN^{1*}, Gérard DELVARE¹, Jean-François VAYSSIERES², Laure BENOIT¹, Perrine CRUAUD³, Jean-Yves RASPLUS³, Astrid CRUAUD³.

Abstract

Parasitic hymenoptera are natural enemies of a wide range of crop pests. However, the complex taxonomy of this group and the scarcity of taxonomic expertise make difficult the accurate identification of species, which limits their use in biological control programs. In this study, we explored the potential of a two-step PCR approach combined with Illumina sequencing to recover mitochondrial protein coding genes (*COI* and *Cytb*) from dry specimens from a reference collection, whose DNA was extracted non-destructively. We studied 18 species of afrotropical Braconidae (Microgastrinae, Opiinae and Braconinae) collected 10 to 35 years ago. Depending on the target region, sequences were obtained from 61 to 90 % of the specimens. The full barcode was reconstructed in ca 90% of the species. A customized analysis pipeline allowed us to manage the high rate of contamination and to identify co-amplified sequences of hosts of parasitoids. As a result, in a single analysis, we were able to 1) generate new barcodes for poorly known species, 2) obtain a preliminary overview of intra specific variability, 3) generate a few data on host-parasitoid associations based on remains of hosts in adult wasps. This cost-effective approach should allow to improve the quality of reference molecular databases by capitalizing on museum specimens identified by expert taxonomists, in order to set up more efficient biological control programs.

Key words:

Braconidae, biological control, gut content, dry insect collections, sub-Saharan Africa

1. Introduction

Biological control of insect pests of crops by predators and parasitoids is a major component of the development of a sustainable agriculture worldwide (Cock et al., 2016). Among biological control agents, parasitic hymenoptera occupy a key position when it comes to setting up new pest management strategies (Wharton & Gilstrap 1983, Wong et al. 1992, Cross et al. 2001, Vayssières et

¹ CBGP, Cirad, Montpellier SupAgro, INRA, IRD, Univ. Montpellier, Montpellier, France

² UR Hortsys, Cirad, C.I. de Baillarguet, Montpellier, France

³ CBGP, INRA, Cirad, IRD, Montpellier SupAgro, Univ. Montpellier, Montpellier, France

^{*}corresponding author, julien.haran@cirad.fr

Download English Version:

https://daneshyari.com/en/article/8877623

Download Persian Version:

https://daneshyari.com/article/8877623

<u>Daneshyari.com</u>