



Morphological and molecular characterization of a new species of *Diabrotica* (Coleoptera, Chrysomelidae, Galerucinae)

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Abstract

The new species *Diabrotica wartensis* Cabrera & Sosa-Gómez was found feeding on roots and leaves of sunflower and soybean in the north of the state of Paraná. A set of characters of diagnostic value: mouthparts, hind wing venation, binding patch, metendosternite, and details of male and female genitalia previously overlooked in the genus was provided. In addition to the morphological characterization, the molecular analyses of the COI mitochondrial gene and the ITS-1 rDNA nuclear region were included. The analysis of the ITS-1 nuclear region alone suggests proximity of *D. wartensis* to the *Diabrotica fucata* group, whereas molecular evidence based on combined analysis of COI and ITS-1 region suggest that this new species is distantly related to the Diabroticina with known sequences deposited in the GenBank.

Key words: *Diabrotica wartensis*, Chrysomelidae, Galerucinae, Brazil, systematics, molecular techniques

Introduction

Diabrotica Chevrolat is the largest group in the subtribe Diabroticina (Galerucinae: Luperini) represented by 338 species widely distributed in the Americas. This genus was divided into three species groups (Smith & Lawrence 1967): *D.* group *fucata*, *D.* group *virgifera*, and *D.* group *signifera*, the two former contain the greatest number of pest species. Little is known of the *signifera* group, with only eleven non pestiferous species.

Members of this genus are of great economic interest as it includes some of the most important row crop and vegetable pests. Adults damage foliage, fruit or flowers while larvae tunnel and feed on roots causing grain losses by reducing both plant stand and vigor. Considering species differ in their biology and insecticide susceptibilities, the early accurate identification of both adults and larvae of rootworms is important in order to define control measures.

Furthermore, it is often difficult to identify adults because of the high degree of morphological similarity (particularly color pattern) within species, whereas little is known about immature stages among which differences among species are less conspicuous. More recently, the use of molecular technology such as allozyme analysis, and mtDNA analysis allowed to access to other sources of characters useful for diagnostic and phylogenetic analysis of *Diabrotica* species (Krysan *et al.* 1989; Clark *et al.* 2001*a,b*). Studies on mtDNA sequences are important tools for species-level identification. Among the mitochondrial genes, the cytochrome oxidase subunit 1 (COI) is currently used as the standard barcode region for several Insecta species, including *Diabrotica* genus (Biodiversity Institute of Ontario 2006). The use of the COI has proved to be very