



# Morphological and genetic variation of the pine shoot tunnel beetle *Placusa pinearum* (Staphylinidae) in China

J.-Y. Gao<sup>1</sup>, B.-Z. Ji<sup>1</sup> and S.-W. Liu<sup>2</sup>

<sup>1</sup>College of Forest Resources and Environment, Nanjing Forestry University, Nanjing, China

<sup>2</sup>Management Office of Dr. Sun Yat-sen's Mausoleum, Nanjing, China

Corresponding author: B.-Z. Ji

E-mail: jbz9885@njfu.edu.cn

Genet. Mol. Res. 12 (2): 2086-2101 (2013)

Received December 18, 2012

Accepted May 25, 2013

Published June 21, 2013

DOI <http://dx.doi.org/10.4238/2013.June.21.4>

**ABSTRACT.** *Placusa pinearum*, a newly described beetle species found living in pine shoot tunnels bored by the pine tip moth, *Dioryctria rubella* (Pyralidae), has potential as a vector to transport biological agents for controlling this moth pest of pine trees because of the high degree of niche overlap (co-occurrence) between them. In order to help determine the suitability of potential biological control vectors, it is useful to obtain knowledge concerning the intraspecific variation of the vector. We examined *P. pinearum* collected from 14 different geographical populations in China using morphological and molecular markers. An UPGMA dendrogram based on morphological characters showed divergence of populations of *P. pinearum* in a comparison of beetles from southwestern and 3 other geographic regions (central, northwestern, and eastern regions). We also compared 965-nucleotide sequences of the mitochondrial cytochrome oxidase subunit I gene from 56 individuals; 19 haplotypes were identified based on 28 polymorphic sites in this region. A Bayesian phylogenetic tree showed significant genetic divergence among the different populations in eastern China. In addition, absence of shared haplotypes, coupled with high pairwise  $F_{ST}$  values, demonstrated

significant genetic divergence between the populations from the southwest and the other 4 main geographical regions (eastern, southern, central, and northwestern regions). Generally, we found the morphological divergence to be congruent with genetic divergence in these *P. pinearum* populations. This information should be useful for selection of suitable source materials in the species gene pool for future biological control programs.

**Key words:** *Placusa pinearum*; Morphological variation; COI; Genetic structure; Intraspecific divergence; Biological control