



Tomicus armandii Li & Zhang (Curculionidae, Scolytinae), a new pine shoot borer from China

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Abstract

We describe a new species of forest bark beetle, *Tomicus armandii* Li & Zhang, collected from *Pinus armandii* in Yunnan, China. We used the D2 fragment of 28S rDNA to improve the taxonomy of *Tomicus*. The new species can easily be distinguished from the other *Tomicus* species using the following two morphological characters: punctures of interstria 2 on declivity appearing evenly biseriata or triseriata; erect interstitial setae on the declivity short, about 0.5× as long as distance between striae. The genetic distances of 28S rDNA measured between *T. armandii* and other species of *Tomicus* are similar to the distances between other *Tomicus* species, and these are much higher than intraspecific distances. The phylogenetic analysis of 28S rDNA agrees with the groupings obtained from morphological identification. DNA analysis has commonly been used in *Tomicus* taxonomy and is helpful for resolving taxon identification problems.

Key words: *Pinus armandii*, *Tomicus*, morphological characters, 28S rDNA

Introduction

The bark beetle genus *Tomicus* Latreille comprises seven species that are distributed throughout pine forests of Europe and Asia (Ye, 1991; Ye and Lieutier, 1997; Sun *et al.*, 2005; Kirkendall *et al.*, 2008). Six of these occur in China, including *T. puellus* (Reitter), *T. pilifer* (Spessivtsev), *T. brevipilosus* (Eggers), *T. piniperda* (L.), *T. minor* (Hartig), and *T. yunnanensis* (Kirkendall & Faccoli). These species use the phloem of the trunks as a source of nutrients during larval development, and have an obligate maturation feeding in the shoots as young adults. This leads to the rapid decline of the tree and may even kill it. Before 1999, outbreaks decimated over 200,000 ha of pine forest in Yunnan (Ye & Ding, 1999). Since then, intense research has been conducted into the biology, ecology, and control of these beetles (Ye, 1991, 1994; Ye & Li, 1995; Chen *et al.*, 2001; Ye & Zhao, 1995; Ye & Lieutier, 1997; Ye & Ding, 1999; Långström *et al.*, 2002; Lieutier *et al.*, 2003). Nevertheless, additional systematic research is necessary to extend our knowledge of the diversity of the Chinese species. Incorrect assumptions about species identification can lead to the application of incorrect control measures and, consequently, to a considerable waste of resources (Kirkendall *et al.*, 2008).

China has large regions of conifer habitat extending over mountain ranges. *Tomicus* species diversity in China is likely to be higher than is currently recognized. A lack of local scolytid taxonomic expertise and the absence of an appropriate method of identification have probably contributed to the underestimation of *Tomicus* diversity in China. For example, until several years ago, *Tomicus* populations in Yunnan were long assumed to be *T. piniperda* although they had a quite different ecology and behavior from that described for *T. piniperda* and they were more aggressive than that described for European populations of *T. piniperda* (Ye & Lieutier, 1997; Långström *et al.*, 2002; Lieutier *et al.*, 2003). In 2004, Duan *et al.* concluded that Yunnan populations comprise *T. brevipilosus* and a new, undescribed species because the genetic distances measured