

## Methods

### Taxonomic Procedures

The initial list of NG Xyleborini was constructed from the Catalog of Scolytidae and Platypodidae (Wood and Bright 1992; Bright and Skidmore 1997, 2002) and augmented by species from a personal collection, museum collections worldwide, and reports in original literature. It was not possible to cover all species that were historically reported from New Guinea. In some instances, specimens of the reported species were not located in any museum (see the end of this volume for listing). Another common reason was that it was impossible to validate many of the published doubtful records of species from New Guinea. Wood and Bright (1992) list several species from New Guinea, records of which could not be verified either in museum collections or in literature. Material was considered insufficient for study if either the female type or a series of non-type females identified by at least two experts were not available.

The generic classification followed in this work is that of Wood (1989), augmented in Wood and Bright (1992), and in supplements (Wood and Bright 1992; Bright and Skidmore 1997, 2002), and recently modified by Hulcr et al. (2007a) and Hulcr and Cognato (2010a).

In individual treatments of genera and species, we list changes and alternative names published after Wood and Bright (1992). For full taxonomic history of each entity, see Wood and Bright (1992) and Bright and Skidmore (1997, 2002). For genera, see Alonso-Zarazaga and Lyal (2009).

All genus-level groups in this work are designated as monophyletic, with the single exception of the Xyleborini, *incertae sedis*. All species in this group were originally designated as *Xyleborus*, but they differ significantly from each other; the group is clearly polyphyletic. They are left in *Xyleborus* until further data and phylogenetic analyses suggest otherwise.

### Species Delimitation

In our species delimitation, we first distinguished informative co-varying characters from highly homoplastic characters (Hulcr et al. 2007a; phylogenetic analyses in Hulcr and Cognato 2010a), and subsequently identified groups of individuals sharing the informative characters that can thus be diagnosed as