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**Systematics of the Australian Longicorn Beetle Genus
Uracanthus Hope 1833 (Coleoptera: Cerambycidae:
Cerambycinae: Uracanthini)**

**A thesis presented in partial fulfillment of
the requirements for the degree of
Doctor of Philosophy
in
Plant Science (Entomology)
at**



**Institute of Natural Resources
Massey University
Palmerston North
New Zealand**

Duangrat Thongphak

2007

CANDIDATE'S DECLARATION

I hereby declare that the dissertation, submitted in partial fulfilment of the requirements for the degree of Doctor of Philosophy and entitled "Systematics of the Australian Longicorn Beetle Genus *Uracanthus* Hope 1833 (Coleoptera: Cerambycidae: Cerambycinae: Uracanthini)", is my own work and that the thesis material has not been used in part or in whole for any other qualification.



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14 March 2007

SUPERVISOR'S DECLARATION

This is to certify that the research carried out in the Doctoral thesis entitled “Systematics of the Australian Longicorn Beetle Genus *Uracanthus* Hope 1833 (Coleoptera: Cerambycidae: Cerambycinae: Uracanthini)” was done by Duangrat Thongphak in the Institute of Natural Resources at Massey University, Palmerston North, New Zealand. The thesis material has not been used in part or in whole for any other qualification, and I confirm that the candidate has pursued the course of study in accordance with the requirements of the Massey University regulations.



Professor Qiao Wang

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14 March 2007

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This is to certify that the research carried out in the Doctoral thesis entitled “Systematics of the Australian Longicorn Beetle Genus *Uracanthus* Hope 1833 (Coleoptera: Cerambycidae: Cerambycinae: Uracanthini)” in the Institute of Natural Resources at Massey University, New Zealand:

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- (iv) has complied with all the ethical and genetic policies applicable to this study.



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ABSTRACT

Uracanthus is a large group of longicorn beetles in the Australian Region. The larvae of this genus are borers of at least 31 genera of trees and parasitic plants, including some economically important crops such as citrus, litchi, peach, plum, and apricot. Several species are important pests of orchards. Adults visit flowers of various tree species and are attracted to the light. In this thesis, I undertook a thorough taxonomic revision, analysed the phylogeny using morphological and molecular characters, and appraised biogeographic distribution of the genus.

In the taxonomic revision, I redefine the scope of the genus, describe and illustrate new and previously known species, and provide a key to all species. The revised Australian *Uracanthus* includes 39 species, eight of which are established as new to science: *U. pseudogigas* sp. nov., *U. maculatus* sp. nov., *U. griseus* sp. nov., *U. bicoloratus* sp. nov., *U. perthensis* sp. nov., *U. punctulatus* sp. nov., *U. quadristriolatus* sp. nov., and *U. bistrisolatus* sp. nov. Six new synonyms are proposed (senior synonyms last): *U. multilineatus* McKeown with *U. ventralis* Lea, *U. dentiapicalis* McKeown with *U. parvus* Lea, *U. marginellus* Hope and *U. inermis* Lea (not Aurivillius) with *U. bivittatus* Newman, *U. fuscostriatus* McKeown with *U. lateroalbus* Lea, and *U. daviumbus* Gressitt with *U. longicornis* Lea. Dorsal views of all species are presented as photographs, terminalia of both sexes illustrated, and distributions mapped. Brief comments are also given on the biology of this genus.

In the full morphological phylogenetic analyses of all 39 species, I use 55 informative characters and cladistic method to test the monophylies of *Uracanthus* and its species groups. My results show that the monophylies of the genus and seven species groups are confirmed. However, several species groups still need additional steps to become monophyletic and are currently considered paraphyletic. In the molecular phylogenetic studies, due to the situations beyond my control (difficulties of extracting DNA from some old species and prohibitions of extracting DNA from type specimens), I analyse only 21 species. I extract and amplify the cytochrome oxidase I (COI) region of the

mtDNA from 21 species and perform a phylogenetic analysis using molecular characters. To make the molecular phylogeny comparable to the morphological phylogeny, I also cladistically analyse the phylogeny of these 21 species using morphological and combined morphological-molecular characters. A comparison of trees obtained from morphological, mtDNA and combined data shows that the relationships of several closely related taxa remain constant, for example, the sister relationships of *U. gigas* + *pseudogigas*, *U. insignis* + *punctulatus*, and *U. acutus* + *loranthi*. However, the placement of *U. insignis* and *U. punctulatus* on the phylogenetic trees varies from the most basal in the full morphological analysis to the highly derived in the combined and molecular analyses. Considering the amount of available data is more limited in the molecular analysis than in the morphological analysis, the molecular phylogeny presented in this study should be interpreted with caution.

The *Uracanthus* fauna can be divided into five subregions: the Kosciuskan, Western and Eyrean in southern and central Australia, and the Torresian and Timorian in northern Australia. The fauna are richest with highest endemism in the Kosciuskan and Western. The Kosciuskan and Western are similar in faunal composition and closely related; the Eyrean has probably acted as a faunal exchange transit area between the Kosciuskan and Western, and the two northern Australian subregions have no endemic species. When the areas of endemism of each species are attached to the phylogenetic tree generated from the full morphological analysis, a clear picture of the distribution patterns of species groups in relation to phylogeny is obtained. It is suggested that the speciation and species radiation of *Uracanthus* may have occurred first in the Kosciuskan, then in the Western, and finally in the Eyrean, Torresian, and Timorian.

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