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A review of the family Clenchiellidae (Mollusca: Caenogastropoda: Truncatelloidea)

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Abstract

The truncatelloidean family Clenchiellidae, previously treated as a tribe or subfamily of Hydrobiidae, is diagnosed as a distinct family including *Clenchiella* and three new genera, *Coliracemata*, *Colenuda* and *Coleglabra*. The family is characterised by the discoidal shell with spiral keels or cords, and a wide umbilicus. All species are found in mangrove swamps or adjacent habitats in tropical estuaries, with the exception of one riverine and one lacustrine species. *Clenchiella* includes the type species, *C. victoriae* Abbott, from the Philippines, the widespread *C. minutissima* (Wattebled) (= *C. papuensis* Benthem Jutting) from Vietnam, Singapore, Thailand, Papua New Guinea and tropical Australia, and three new species, *C. bicingulata* **n. sp.** from Singapore and Thailand, *C. varicosa* **n. sp.** from Hong Kong and Taiwan, and *C. iriomotensis* **n. sp.** from Okinawa, Japan. *Coliracemata* **n. gen.** includes *C. mortoni* **n. sp.** (type of the genus) from Hong Kong, *C. katurana* **n. sp.** from Okinawa, *C. clarkae* **n. sp.** from northeastern Australia, and tentatively *C. microscopica* (Nevill) and

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C. innocens (Preston) from India. *Colenuda* **n. gen.** consists of a single species, *C. kessneri* **n. sp.**, from Northern Territory, Australia. *Coleglabra* **n. gen.** includes *C. nordaustralis* **n. sp.** (type of the genus) from Northern Territory and *C. sentaniensis* (Benthem Jutting) from a freshwater lake in Irian Jaya. Anatomical characters are described for nine of the twelve species. The Clenchiellidae is shown to be more closely related to Calopiidae, Tornidae, and Iravadiidae, than to Hydrobiidae.

Key words: *Clenchiella*, *Coliracemata*, *Colenuda*, *Coleglabra*, taxonomy, anatomy, phylogeny, mangrove, estuary, Indo-Pacific, Iravadiidae, Calopiidae

Introduction

Small gastropods associated with tropical estuaries are very diverse (*e.g.,* Brandt 1974) and poorly known taxonomically. Several groups of the superfamily Truncatelloidea (previously part of the Rissooidea, see Criscione & Ponder 2013) are commonly found in such habitats—some of the more diverse being Stenothyridae, Assimineidae and Iravadiidae. Although a range of studies in the last decade has elucidated these truncatelloidean families (Fukuda & Ponder 2003, 2004, 2005, 2006; Criscione & Ponder 2013; Golding 2014a, b), one small group has all but escaped attention in the literature, namely species included in a group represented by the genus *Clenchiella.*

Clenchiella was introduced by Abbott (1948) for a new Philippine species, *C. victoriae*. Abbott did not associate any other taxa with the genus in the 1948 paper but he tentatively assigned *Valvata* (?) *microscopica* Nevill, 1877 shortly afterwards (Abbott 1949). Since then, relatively few references to the genus have appeared in the literature.

When Abbott (1948) introduced *Clenchiella* he included it in the subfamily Amnicolinae, in the "Amnicolidae (=Hydrobiidae) with some hesitation." He noted that the shell and operculum were "strikingly similar to members of the Valvatidae but the animal excludes it from that group." Taylor (1966) introduced the tribe Clenchiellini within Hydrobiidae, subfamily Cochliopinae. Subsequently the *Clenchiella* group has been treated as a subfamily of Hydrobiidae (Starobogatov 1970, Ponder & Warén 1988, Kabat & Hershler 1993, Bouchet & Rocroi 2005) or as a distinct family in the 'Tateoidea' (Ioganzen & Starobogatov 1982). Taylor (1975) incorrectly used the generic name for some lower Tertiary fossils from the USA (see below) but otherwise the only use of the name appears to be confined to the Indo-West Pacific.

In this paper we review the status of *Clenchiella* and related taxa, and review the taxonomy of the species based on the material available to us.

Material and methods

Material was collected in mangroves, or in closely associated habitats. Specimens were washed or picked from the surface of leaves and other objects lying in surface water on mud. External features of living specimens were examined (for the species from Hong Kong, Singapore and Queensland by W.F.P.; species from Darwin and Japan by H.F.). Specimens were relaxed overnight using menthol crystals and fixed in approximately 10% neutral formalin.

Anatomical investigation was undertaken using a Leica stereoscopic microscope with a drawing apparatus. Specimens were dissected after the shell was removed by dissolving in dilute hydrochloric acid.

Specimens were prepared for examination with a scanning electron microscope (SEM) using standard methods (see Geiger *et al.* 2007 for details).

For molecular analysis, entire animals were processed using a DNeasy kit (Qiagen, Inc., Hilden, Germany) and QiaCube® robot to extract genomic DNA. The mitochondrial gene COI was utilised in this study, mainly to assess the validity of the taxon *Clenchiella minutissima* (Wattebled, 1884). COI primers used were LCO1490 (GGTCAACAAATCATAAAGATATTGG) for the forward direction and HCO2198 (TAAACTTCAGGGTGACC AAAAAATCA) for the reverse direction (Folmer *et al.* 1994).

Biogeography of *Clenchiella minutissima*

Clenchiella minutissima is by far the most recorded clenchiellid species, and appears to have a widespread distribution throughout the Indo-Pacific (Fig. 14). Among the Australian individuals sequenced (four from Qld, one from NT, one from WA), there is negligible branch length throughout the east coast localities, with identical sequences obtained for three of the four Queensland individuals. The Darwin sequence differs marginally from those from Queensland, while the Port Hedland sequence exhibits the highest divergence within the *minutissima* clade. These preliminary results suggest that the highest degree of gene flow occurs along the Queensland coast, possibly attributed to the continuity of suitable habitat, in which the planktotrophic larvae of *Cl. minutissima* (as indicated by the protoconch) may be readily dispersed between estuarine systems. Conversely, as the Darwin locality is roughly equidistant to the WA and Queensland localities respectively, the greater sequence divergence and thus comparatively reduced gene flow between WA and NT are possibly due to the discontinuity of mangrove habitats along sections of the WA coast, notably along the Eighty Mile Beach situated between Broome and Port Hedland. However, based on the similarity in shell characters as well as the moderate topology and sequence divergence indicated by the molecular analysis, the conservative approach herein is to view these populations as conspecific.

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