

## **TAXONOMIC STUDY OF MICRO-MOLLUSCS: A CASE STUDY USING THE CONDYLOCARDIIDAE**

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### **ABSTRACT**

Several taxa of small and taxonomically difficult bivalve families are currently being revised. This paper discusses the characters of the condylocardiids, superfamily Carditoidea, to highlight the methods and infrastructures used in the Australian Museum to revise this group. The revision includes the use of the database program Platypus to catalog the taxa and develop a bibliography. To examine characters, many of which are hardly visible under the stereomicroscope, Scanning Electron Microscopes (SEM) are used. This technique is essential to observe the fine detail of the hinge teeth, prodissoconchs and other microscopic sculptures that are necessary for separating many of the taxa. After an evaluation of the characters present in the taxon, a character matrix is set up in the program DELTA, which is later used to generate a description of each taxon and interactive keys or standard keys. Once all the material has been identified to species it is entered into the main database in the mollusc collection. From this database, distribution maps are generated. Geographic Information System (GIS) programs can then be used to evaluate the probability that the area of distribution actually does represent the species distribution by evaluating background sampling intensity.

### **INTRODUCTION**

This paper deals with the problems of revising micro-molluscs, and the techniques available to facilitate their study. It also re-

views the two subfamilies, Condylocardiinae and Cuninae.

Micro-molluscs make up the majority of molluscan diversity but are much more poorly known than larger species. This is in part because of their greater diversity, but more importantly because they are usually not collected and incorporated in accessible research collections. However, their collection requires few special techniques, and no special resources other than time taken for sorting and identification.

Only a few malacological collections in the world have significant collections of micro-molluscs. In the study described below we are using the research collection in the Australian Museum, Sydney (AM), to investigate the taxonomy of several groups of small bivalves. This collection contains a large number of micro-molluscs collected over the past 120 years, which were collected by writers such as John Brazier, Charles Hedley, Tom Iredale, etc. Charles Hedley made a significant contribution to the number of lots in the collection as well as describing 12 new species and one new genus from Australia between 1902 and 1909.

Private collections, especially those of Jacques Voorwinde and Charles Laseron have also contributed substantially to the available material. Iredale (1936) named five new genera and four new species of Australian condylocardiids, all from New South Wales and Tasmania.

Charles Laseron, an amateur malacologist associated with the Australian Museum, described 17 new species and five new genera

in a review of the New South Wales species, Laseron (1953).

Outside the AM, Ralph Tate associated with the South Australian Museum, Melbourne (SAM) described three new species (from 1887 to 1889) and three with William May (from 1900 to 1901).

Bernard Cotton at the South Australian Museum (SAM), described nine new species and two new genera (1930, 1931). He also described one species with Frank Godfrey (Cotton & Godfrey 1938).

A few other authors also contributed to the knowledge of condylocardiids in Australia, *viz.*, Verco (1908) described five new species, Gatliff & Gabriel (1912) and Tenison-Woods (1877) both described one new species.

The material available in the AM has greatly expanded since the 60's, through collection efforts focusing especially on micro-molluscs. These include collecting in deep water and many previously poorly collected locations around Australia. None of the species so far described are from Western Australia and northern Australia. The available material for this study comprises approximately 5000 lots from all states and territories.

#### PART 1: GETTING STARTED

The present material is the result not only of collecting, but also a huge sorting effort. The Australian Museum has highly competent volunteers who pick mollusc specimens from samples and sort the separated material into species so it can be incorporated in the collection. People without any special knowledge of molluscs can undertake this part. These samples are labelled and sorted to family so they can be lodged in the collection. This stage requires the involvement of someone with skill in identifying molluscs, at least to family level. Errors in identification at this stage can mean that material is effectually lost to revisors of groups for years, as the material in some families may not be resorted until a revisor of those groups

is involved. Bearing this in mind, a competent researcher might also check the material in families, which resemble the taxon of interest.

In this case, carditids, crassatellids and astartids are somewhat similar in hinge characters are generally much larger.

For the initial species-level sort, it is useful to ignore described taxa while sorting because species concepts are likely to change and new taxa will probably be found. Consistency of sorting is enhanced if the distribution of the taxa being sorted is taken into consideration. If a taxon has two or more disjunct areas of distribution this may point towards species complexes.

A rough sketch or photograph of each recognised taxon may also be useful, as memorising many taxa can be difficult. Small sketches, Polaroids, or digital images normally suffice. For further species-level resolution it is often necessary to use a scanning electron microscope (SEM). At the AM we use a computer controlled SEM (LEO). The computer is used to display the picture of the shell, capture the image to file or printer, manipulate the picture for sharpness, contrast, etc. A joystick is used to control the position of the stub in the horizontal plane, while another joystick controls the tilt from 0-180° and the 360° rotation.

The SEM is easily operated and is very good for "browsing" through multiple specimens mounted on a stub. Although some characters like shell colour and transparency are lost in the SEM, microscopic sculptural and shape detail is gained, and this is often where the characters distinguishing taxa are found.

#### *The choice of characters*

Selecting characters to separate species is one of the most important tasks. The characters should be as inclusive as possible, that is, they should include all accessible characters that may serve to separate the taxa. Ideally the characters should also be homologous, *i.e.* "derived from the same (or a corre-

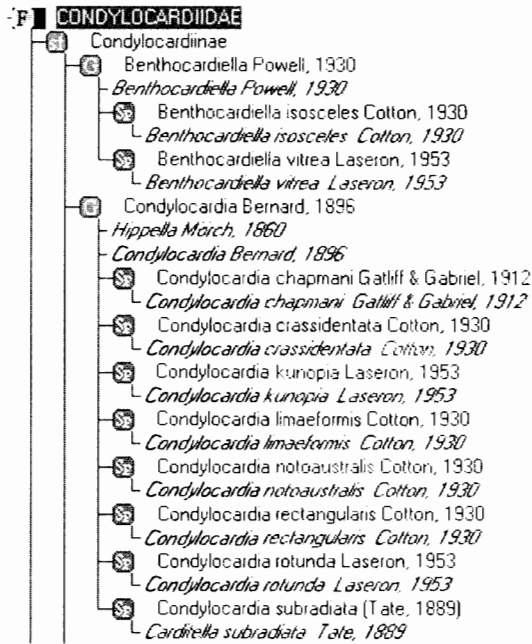


Figure 1. Taxonomic interface in Platypus, showing a part of the family Condyllocardiidae. The names to the right of the ranks (F (family), Sf (subfamily), G (genus), and Sp (species)) are the valid names. The name(s) listed below the valid name is the available name(s).

sponding) feature of their nearest common ancestor" (Mayr & Ashlock 1991).

This criterion is sometimes difficult to apply, for example, in distinguishing characters and states of the hinge teeth in bivalves. The notion of "number of cardinal teeth" in heterodonts is not precise enough for a proper description as the cardinals are derived from various juvenile teeth. While it is meaningless to compare hinge teeth derived from different ancestral features, in practice recognising those differences can be difficult.

In the present study the work of Bernard and Munier-Chalmas (*sensu* Moore 1969, p. N53) has been used as the guideline for the choice of hinge teeth characters.

Knowledge of the spectrum of shapes, ornamentation, hinge configurations, etc., is necessary before selecting the characters, although modification of these characters is possible retrospectively, allowing some re-

finement.

Various measurements of shell dimensions should also be taken, as some species may be readily distinguished by size and shape parameters.

It is well known that there is substantial convergence in the shell morphology of molluscs, and a thorough knowledge of the anatomy of the species groups under revision would benefit the revision. However, in many cases, including the present example, this is not possible because the available material mainly consists of dried, empty shells, and only very local taxa may be used as "archetypes" of the genus groups.

#### Applying names

The next step is to pair the published knowledge of the group with what you have discovered in your initial species-level sort. This phase in the study of the condyllocardiids showed that there had been repetitive description of the same taxa, in some cases, probably resulting from a lack of adequate illustrations of the described species types and phenotypic variation. The importance of adequate illustrations and descriptions of the species is highlighted at this stage, as well as the need for adequate knowledge of the published literature within the group.

The information needed for this phase is the original literature containing the descriptions and illustrations of described taxa, and if possible the type material. The types are normally obtained from various museums and universities around the world. In the case of the condyllocardiids, and unusually for Australian taxa, only very few types had to be borrowed from overseas institutions.

Keeping track of all the references with the exact page, plate, figure location, as well as all the appropriate type information is tedious. To aid this process, and to present a way of validating the taxonomic decisions being made, the taxonomic database program Platypus can be consulted at :

(<http://www.environment.gov.au/abrs/>

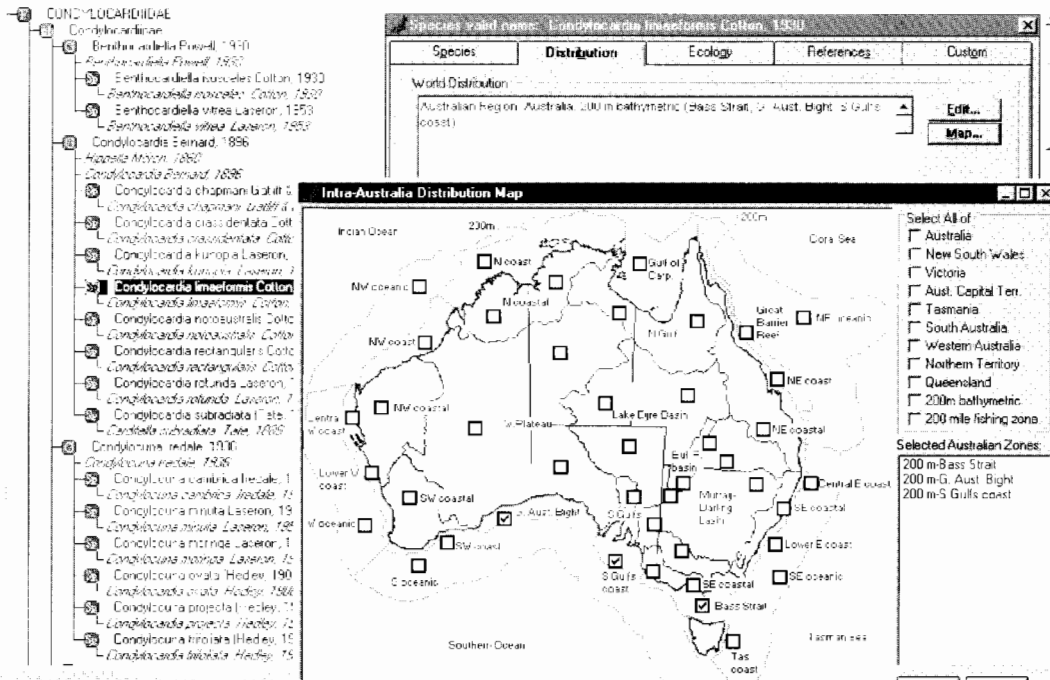


Figure 2. The species valid name information of *Condylocardia limaeformis* is opened by double clicking the valid name to the right side of the rank icon. The element contains information on common name, distribution, ecology, and general references. The distribution chart has been opened to show how the distribution area is compiled.

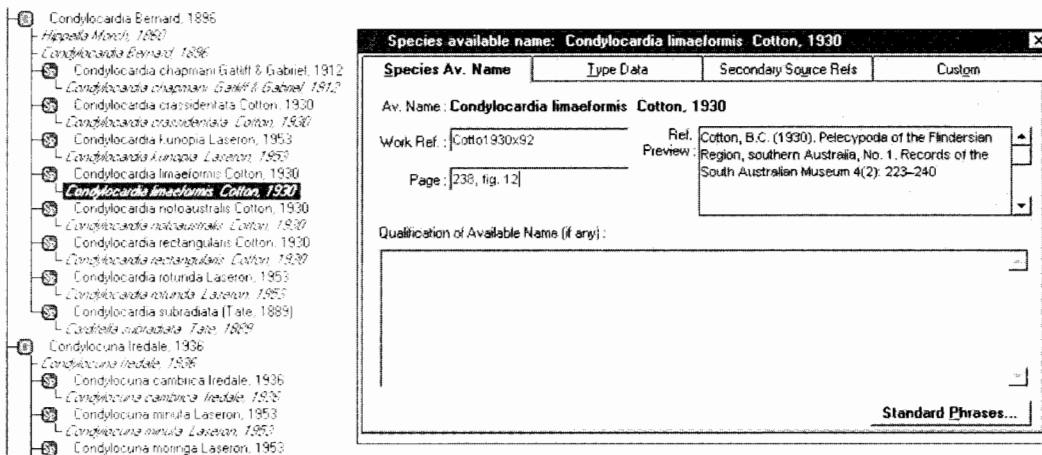


Figure 3. The species available name elements contain data regarding the original reference, type data, and source for the compilation.

platypus.html). It was developed by Australian Biological Resources Study (ABRS) in Canberra. The interface (Fig. 1) is easily un-

derstandable and separated into valid name element, which contains data regarding common name, distribution (Fig. 2), ecology and

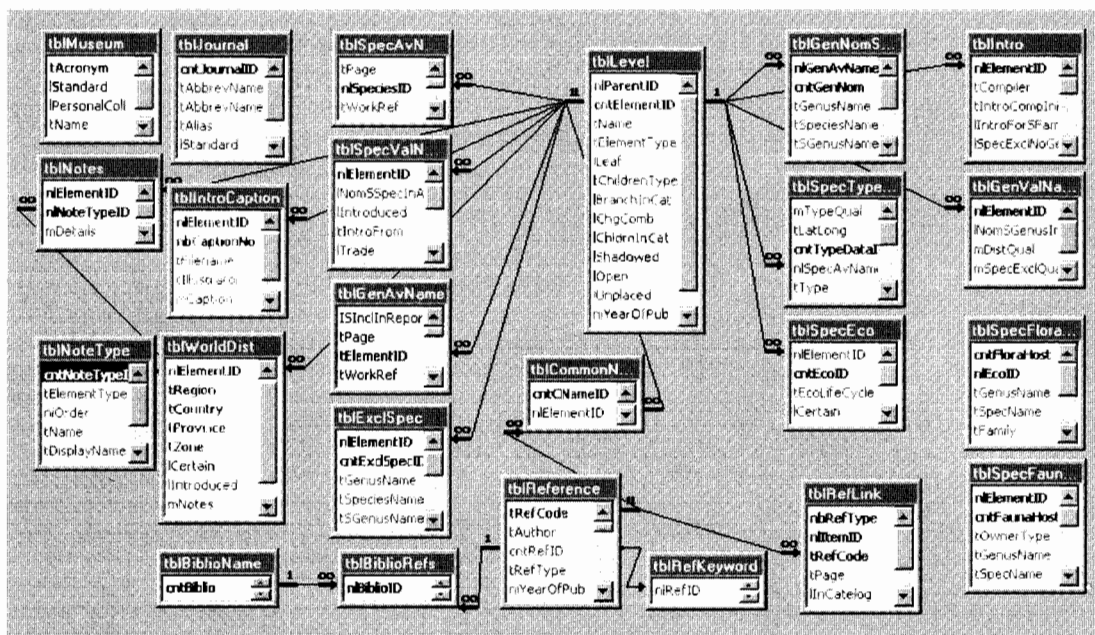


Figure 4. The modules of Platypus are based on interlinked Microsoft Access and lookup tables.

synonymy references as well as general references. The available name element contains the core data for the taxa, like original reference (Fig. 3), type data, and source of references. “Drag ‘n drop” technology makes it easy to move around available names and their related data (original reference, type data, etc) as the revision is undertaken. The modular layout (Fig. 4) of the programme assures that data attached to a Valid and Available Name always follows it wherever it is being moved.

Clickable distribution maps and pick-lists for ecological parameters make data consistent. Built into the interfaces are queries in the relational database that produce reports e.g. as a Checklist or a Catalogue. Other user reports may be designed by the user using “Queries” and “Report” in the relational database, which is Microsoft Access based.

#### *Describing taxa*

The examination and documentation of the taxa being investigated has also been made

easier, especially with the use of digital imaging. The advantage of using digital imaging is the low cost with respect to consumables, and the drawbacks are the initial costs and the limits to resolution. However, considerable advances and cost reductions in this technology are likely to occur in the near future.

Once the images have been captured, examination can be done directly on a computer monitor or on hard prints. Images may be further analysed by using e.g. measuring programmes such as NIH-Image or Image/J (<http://rsb.info.nih.gov/nih-image/>).

The Delta software (overview and links at <http://biodiversity.uno.edu/delta/>) may be used to create character matrices from which descriptions and keys can be generated, as well as distance matrices and data suitable for phylogenetic analysis. As the various taxa are examined they are scored according to the states recognised in the character list. Once scored, descriptions can be generated automatically once the required param-

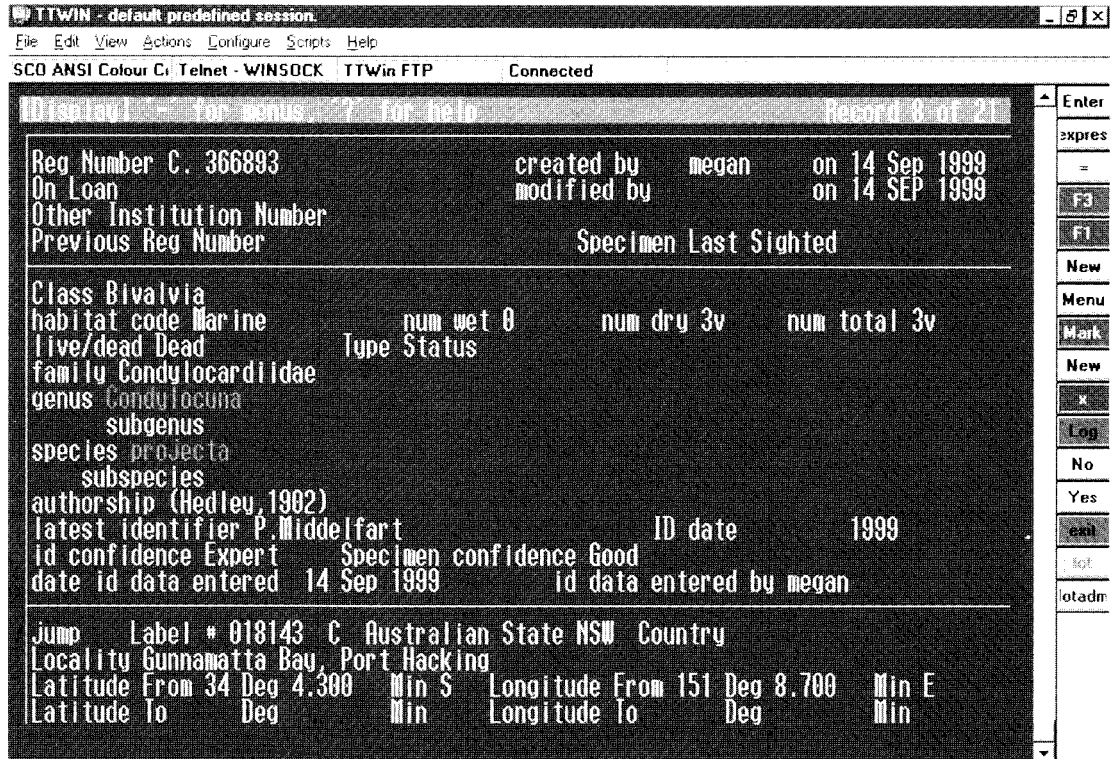


Figure 5. The information of lot C.366893 in TextPress in The Australian Museum collection database.

eters have been set out.

The core data for any revision is the referral to the material examined, be that the type or other specimens. In most collections specimen lots are given a unique number. In the Australian Museum Malacological Collection the number C. 366893 is for the taxon *Condyllocuna projecta* (Hedley, 1902) (Fig. 5). The prefix C. stands for Conchology. The database holds the locality details for each collection event as a label number, in the present case #018143 representing Gunnamatta Bay, Port Hacking, NSW, and including time of collection event.

As the revision paper is progressing the distribution details, either as text or maps (Fig. 6) may be generated directly from the collection database by querying and outputting the data as text or as latitude and longitude data on a map. The AM database also allows the addition of data relat-

ing to borrowed or otherwise examined lots from other institutions so that all these data may be viewed together. The distribution output may be further analysed to identify "outliers" (see Fig. 6), which need further checking.

## PART 2: OVERVIEW OF THE CHARACTERS OF THE CONDYLOCARDIINAE AND CUNINAE

### CONDYLOCARDIIDAE CONDYLOCARDIINAE

#### *Condylocardia* Bernard, 1896

The type species of *Condylocardia*, is *Condylocardia santi-pauli* Munier-Chalmas in Bernard, 1896a (= *Condylocardia pauliana* Bernard, 1896b (nomen emend.)). This species is very closely related to *Condylocardia crassica* Bernard, 1896, whose

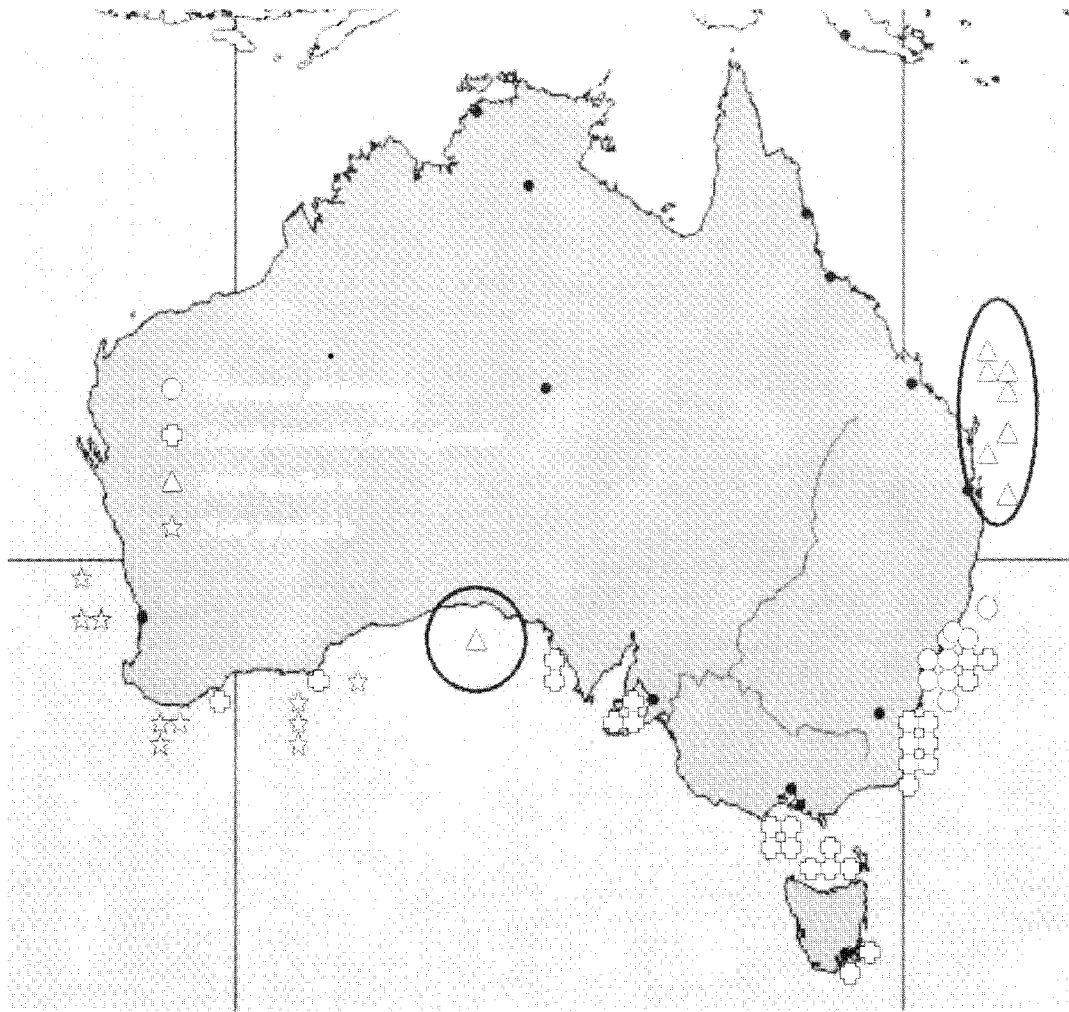


Figure 6. A plot of the distribution data of 4 species of condylocardiids in Australia. The encircled data point shows an "outlier" of *n. sp. a.*

original description includes an illustration of the ontogeny of the hinge teeth (Fig. 3 in Bernard, 1896, reproduced here as Fig. 7). From this hinge description the following characteristics are drawn.

The main characteristics of this group are small size (1 to approximately 10mm), equilateral to slightly opisthogyrous, equivalve, with concentric ribs and/or a radiating pattern of surface sculpture. The prodissoconch is large and conspicuous, indicating direct development. There is generally a sharp discontinuity between the prodissoconch and

the dissoconch. The hinge plate is narrow and the hinge teeth of the right valve consist of an anterior lateral tooth no.1 (LA 1), a cardinal tooth no. 3 subdivided into an anterior (CA3a) and a posterior (CA3b) part, a posterior cardinal no.3 (CP3), and a posterior lateral no. 3 (LP3). The left valve has an anterior lateral no. 2 (LA2), an anterior cardinal no. 2 (CA2), a posterior cardinal no. 2 (CP2) and a posterior lateral no. 2 (LP2) (see Fig. 7).

The ligament is always internal and usually slightly posterior in location, but some-

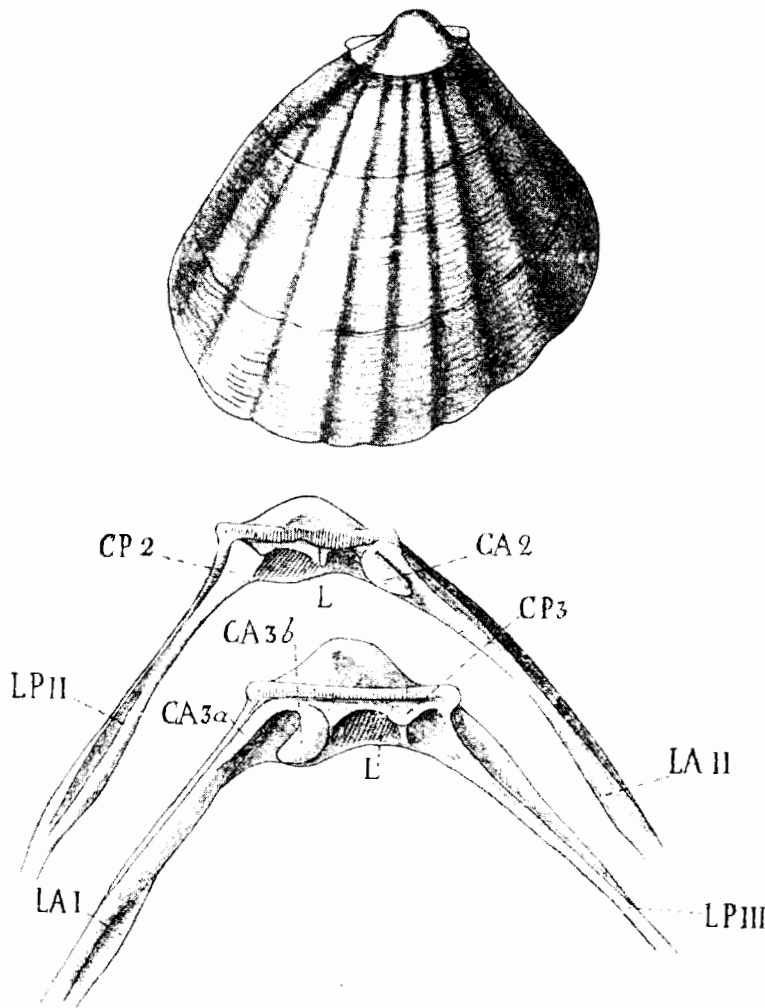


Figure 7. *Condylocardia crassicosta* Bernard, 1896, showing external aspect and the hinge teeth characteristic of *Condylocardia*. For explanation of abbreviations see text.

times central. There are 31 available species and ten available genus level names currently recognised in the Condylardiinae in Australia. The taxonomic revision currently being undertaken will see this number reduced to 20 species and eight valid genus names, of which six species and two genera are new.

#### CUNINAE

*Cuna* Hedley, 1902

The genus *Cuna* Hedley, 1902, was originally included in the Crassatellidae by Hedley,

while Laseron (1953) believed that this genus could be a close relative of the Carditidae. Chavan (in Moore, 1969) erected a new subfamily, the Cuninae, in the Condylardiidae. The last treatment of the group, *viz.* Chavan's has been followed here, although it must be stressed that the higher classification is in need of reassessment.

The type species of *Cuna* is *Cuna concentrica* Hedley, 1902 (Fig. 8). The main characteristics are small size (1-2 mm), equilateral or slightly opistogyrous, and equivalve. The surface pattern is concentric, some species with radiating ribs. Prodissoconch smaller than in *Condylocar-*



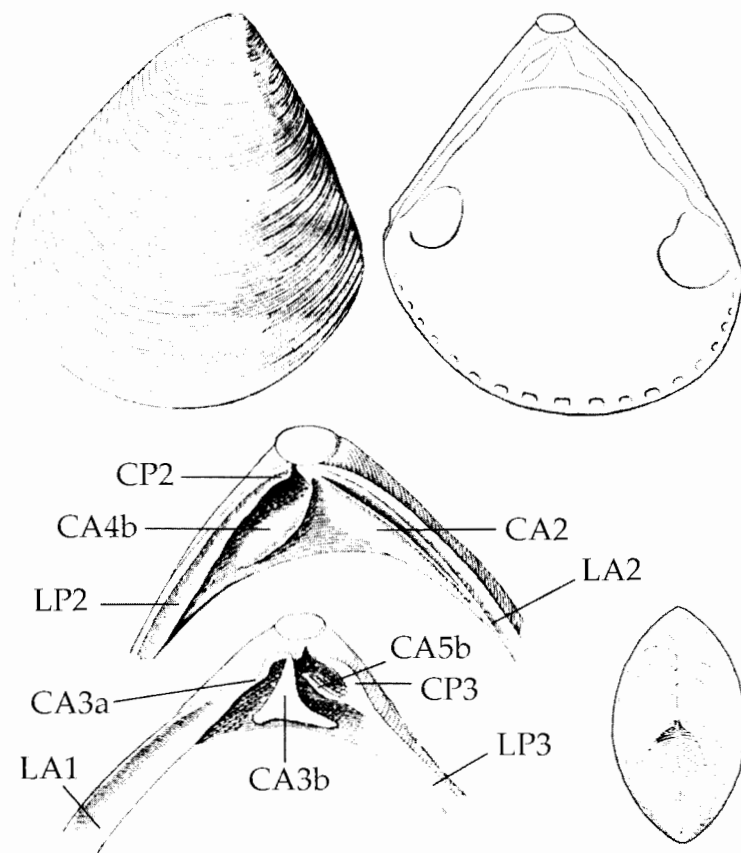


Figure 8.  
*Cuna concentrica* Hedley, 1902,  
showing the hinge teeth characteristics of  
*Cuna*.

*dia*, but as with that genus indicative of direct development (*viz.*, no distinction between prodissoconch I and II). There is a sharp discontinuity between the prodissoconch and the dissoconch. The hinge plate is quite wide, the hinge teeth of the right valve consisting of an anterior lateral no.1 (LA1), followed by a cardinal 3 which is split into a small anterior part (CA3a) and a very large triangular CA3b; followed by an anterior cardinal 5 (CA5b), and a very thin posterior cardinal 3 (CP3) and a posterior lateral 3 (LP3). The left valve hinge consists of an anterior lateral 2 (LA2), an anterior cardinal 2 (CA2), followed by an anterior cardinal 4 (CA4b), a posterior cardinal 2 (CP2), and a lateral posterior 2 (LP2). There are 17 available species and seven available genus level names currently recognised in the

Cuninae in Australia. The taxonomic revision currently being undertaken will see this number increased to approximately 38 species and eight genus valid names, of which 18 species and two genera are new.

#### DISCUSSION

The basic features that separate the Cuninae and Condylardiinae are (1) the size and microsculpture of the prodissoconch and (2) the size and shape of CA3; the occasional possession of CA5 in Cuninae. Most other features are shared. There are several cases where taxa cannot be readily included in either subfamily using the external features, although a decision can be made using hinge characters.

In this paper I have outlined the methods which may be used in the revision of small

molluscs, and for that matter, molluscs in general. There are many ways and opinions as to which are the best methods. Some workers prefer traditional methods using only a stereo microscope, paper, pen, and ink. These methods alone are now unsuitable for the adequate study of most groups of micro-molluscs. With the application of more modern and sophisticated methods enabling greater resolution and enhanced efficiency, we may begin to uncover the real diversity in the micro-molluscan world.

In this paper I have just touched on some of the methods that may be applied in modern taxonomic revisions. I have not touched the world of anatomy, ecology, biochemistry, molecular biology, genetics, and the fossil record as that would be way beyond the scope of this paper and impractical for major taxonomic revisions. However, these disciplines are being used to discuss and understand evolutionary processes, phylogenetic relationships and other aspects central to our overall understanding of species and speciation.

It is the hope that this overview will benefit the systematic work undertaken under the auspices of Tropical Marine Mollusc Programme, and encourage joint ventures between smaller and larger institutions to describe the marine molluscan diversity of SE Asia and Australia.

In Australia the fauna and flora are currently being catalogued and published in the traditional hard print format. These data are also now available as free interactive read-only expandable hierarchies at the Australian Biodiversity Information Facility (ABIF). For the hard and interactive catalogues, Platypus is being used as the data base tool. Many databases and checklists of marine molluscs are still being compiled but a few have been completed and may be viewed at <http://www.environment.gov.au/abrs/work/zoocat/>

These catalogues and checklists are being compiled by a large group of malacologists. Larger projects like major taxonomic revisions,

zoological catalogues and checklists involve collaboration, and it is the hope of the Australian Museum, that scientists from organisations like TMMP will visit the museum and work with the mollusc material in the museum, and enhance our knowledge of molluscs in SE Asia and Australia.

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