

Phylogenetic Review of American Genus *Macrocypraea* (*Mollusca, Caenogastropoda, Cypraeidae*) Based on Phenotypic Characters

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Abstract

All Recent species of the American genus *Macrocypraea* are analyzed phylogenetically based on phenotypic features. The database was inserted in a wider phylogeny on *Cypraeoidea* previously published. The result is (((*M. cervus* (*M. cervinetta* (*M. mammoth* *M. zebra*))) *Cypraea tigris*) remaining *Cypraeoidea*). The monophyly of the genus is supported by four synapomorphies, and the proximity with *C. tigris* (among the anatomically known species) is demonstrated. The result is compatible with the subgeneric division *Lorenzicypraea* for *M. cervus* and *Macrocypraea* s.s. for remaining species.

Keywords: Anatomy; Morphology; Taxonomy; Systematics; *Cypraeoidea*

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Introduction

The genus *Macrocypraea* [1] (*Caenogastropoda, Cypraeidae*) only occurs in America (**Figure 1**). In Tropical and Subtropical Pacific coast occurs *M. cervinetta* [2]. Its counterpart in Atlantic coast is *M. zebra* [3], in such synonym, *Cypraea exanthema* [4], is the type species of the genus. Other two species have their distribution more restrict: *M. cervus* [5], occurring in Gulf of Mexico, Florida and Cuba; and *M. mammoth* [6], endemic from Trindade, a Brazilian oceanic island located approximately in middle of South Atlantic (**Figure 1**). This set of four species are all Recent species of the genus, that have other five fossil species from Eocene to Pleistocene of Florida and Central America [7,8]. The genus is usually divided into two subgenera, including the monotypic *Lorenzicypraea* [7] for *M. cervus*.

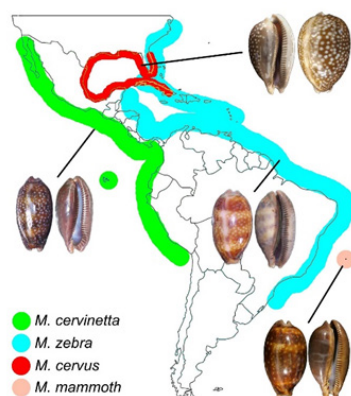


Figure 1: America map showing approximate distribution of the four species of *Macrocypraea* as indicated by the colors (the thickness of them is exaggerated), with examples of shells of each species from MZSP collection.c

All Recent species of *Macrocypraea* have their anatomical details known, mainly by two recent papers [6,9], making a complementary phylogenetic study possible. A phylogenetic analysis based on phenotypic features is a good base for analyzing the taxonomy of its species, to determine which genera are closer related to it, and can be also used on a comparative basis with molecular analyses [10,11]. As a phylogeny of the *Cypraeoidea* based on phenotype is available [9,12] the present paper has as objective to insert the surveyed data on four *Macrocypraea* species in that scenario [9] complementing that study, and saving long explanations on methodology in the present paper.

Materials and Methods

The list of material studied is already published and mostly consisted of fixed specimens deposited in museum' collections [6, 9, 12]. The anatomical features of the species can be obtained as follows: for *Macrocypraea zebra* and *M. cervinetta* : [9]; for *M. cervus* and *M. mammoth*: [6]. Details of the phylogenetic analysis are found in [6,12,13], in such same methodologies and algorithms are applied herein. The set of characters in Table 1 are particularly based only on [9], which is more focused to cypraeids and already have two of the species (*M. zebra* and *M. cervinetta*) included. Data on *M. rhinoceros* and *M. cervus* [6] were analyzed and inserted in the data-matrix by Simone (2004: 173) [9]. Two lines were added to that matrix in **Table 1** as well as two terminal taxa corresponding to both species. The new matrix was analyzed following the methods by [9]. The modified portion of that cladogram showing *Macrocypraea* and its sister-taxon, *Cypraea tigris* [3], is shown in **Figure 2**. The remaining cladogram is exactly the same as reported by [9] and is not illustrated.

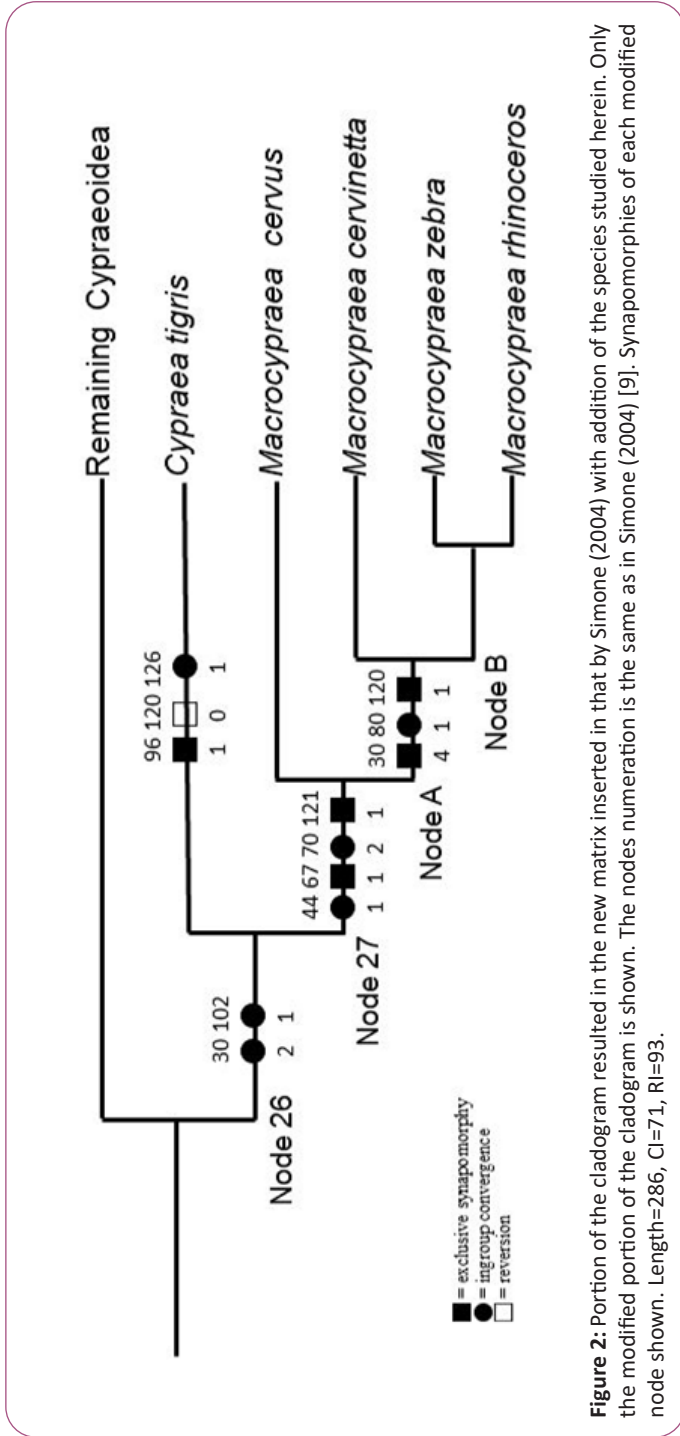


Figure 2: Portion of the cladogram resulted in the new matrix inserted in that by Simone (2004) with addition of the species studied herein. Only the modified portion of the cladogram is shown. The nodes numeration is the same as in Simone (2004) [9]. Synapomorphies of each modified node shown. Length=286, CI=71, RI=93.

Taxon\ character	1	2	3	4	5	6	7	8	9	10	11	12	13
12345	67890	12345	67890	12345	67890	12345	67890	12345	67890	12345	67890	12345	67890
M. zebra	11210	11010	00111	12100	01011	11014	00101	21211	00111	11121	11111	11012	11000
M. cervinetta	11210	11010	00111	12100	01011	11014	00101	21211	00111	11121	11111	11012	11000
M. rhinoceros	11210	11010	00111	12100	01011	11014	20101	21211	00111	11121	11111	11012	11000
M. cervus	11210	11010	00111	12100	01011	11014	00101	21211	00111	11121	11111	11012	11000

Table 1: Matrix of characters added to the matrix by Simone (2004) [9].

Results and Discussion

Using only the characters listed by [9], *Macrocypraea cervus* resulted as sister species to the species in the *Macrocypraea* branch (**Figure 2**) Node 27. The remaining three species resulted in a trichotomy (Node A). An additional analysis was performed with the addition of three characters, as follows: A) Anterior shell projection more elongated: exclusive to *M. zebra* and *M. rhinoceros*; B) Ocellated spots at lateral region of the shell: also exclusive to *M. zebra* and *M. rhinoceros*; C) Pallial papillae with base narrower than their middle region, with tip bearing 1-4 small projections: exclusive to *M. zebra* and *M. rhinoceros*. The addition of these 3 characters resulted in a different topology lacking polytomies: *M. zebra* and *M. rhinoceros* ended up in a same branch (**Figure 2**). Node B supported by the three above mentioned characters (A-C). In this case, the new cladogram in Figure 2 has length=86, CI=71, RI=93.

As reported above, the morphology-based phylogeny by [9] already contained *M. zebra* and *M. cervinetta*. The data on *M. cervus* and *M. mammoth*, joined to additional data on both anterior species, are in [6]. The presently obtained complementary cladogram (**Figure 2**). Reinforces the monophyly of *Macrocypraea* (Node 27). The node 27 is supported by four synapomorphies (character states as follows): 1) osphradium separated from posterior region of the gill (44/1); 2) pair of odontophore muscles mc comprising two bundles (67/1); 3) pair of m 11 with insertion surrounding ventral region of radular sac base (70/2); 4) bursa copulatrix located at middle level of pallial oviduct. In the topology presented herein, the first branch of *Macrocypraea* is *M. cervus*, separated from the other three species by three synapomorphies (Node A): 1) pallial papillae stubby, broad, with narrow base (30/4); 2) odontophore pair m7 originating at anterior border of ventral m4 branch (80/1); 3) bursa copulatrix U-shaped, bearing inner folds (120/1). The separation of *M. cervus* reinforces its separation in the subgenus *Lorenzicypraea* [7], in such it is type and single species. The remaining three species (Node A) represents the subgenus *Macrocypraea* s.s.

With the inclusion of the three extra characters discussed above, *M. zebra* and *M. rhinoceros* resulted in a proper node (**Figure 2**) Node B. Otherwise; both species resulted in a trichotomy with *M. cervinetta*. Moreover, *Cypraea tigris*, the type species of the genus (and, consequently, of the family and superfamily), resulted as the sister taxon to *Macrocypraea* s.s. node, a branch supported by two synapomorphies (Node 26): 1) Pallial papillae simple and long (30/2).

2) Presence of several transverse septa in the anterior duct of the digestive gland (102/1).

Conclusion

In some point of view, the subgenus *Lorenzicypraea* is valid and could be elevated to generic rank, a possibility that can be stressed in future wider revision. A different result, with *M. zebra* closer to *M. cervus*, rather than to *M. cervinetta*, was obtained in a molecular study. This competitor result must be analysed further deeper in future papers.

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