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Annotated and updated checklist of marine crabs (Decapoda: Brachyura) of Mozambique supported by morphological and molecular data from shelf and slope species of the “MOZAMBIQUE” surveys

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Abstract

An updated checklist of Mozambican marine brachyuran crabs is generated based on an exhaustive revision of the existing literature, together with the additional records provided by the specimens collected throughout the three “MOZAMBIQUE” surveys carried out in Mozambican waters during three consecutive years (2007–2009) by the Instituto Español de Oceanografía, (Spanish Institute of Oceanography, IEO). A total of 269 species, grouped in 15 superfamilies, 26 families and 172 genera are reported in the checklist, and a detailed inventory is produced with the list and remarks about the brachyuran species collected. Thirty-nine crab species belonging to 19 families were identified based on morphological characteristics and/or genetic tools. DNA barcode sequences (16S rRNA and/or COI) were obtained for 37 species, including 16S and COI sequences that are new for 26 and 14 species, respectively. Colour photographs of fresh specimens illustrate the comments about most species, being the first time that the original colour pattern is described for some of them. New records in Mozambican waters are reported for the species *Paromolopsis boasi*, *Mursia aspera*, *Carcinoplax ischurodous*, *Tanaoa pustulosus*, *Euclosiana exquisita*, *Oxypleurodon difficilis*, *Naxioides robillardi*, *Samadinia galathea*, *Cyrtomaia gaillardi*, *Paramaja gibba*, *Pleistacantha ori*, *Parathranites granosus*, *Parathranites orientalis*, *Ovalipes iridescens* and *Charybdis smithii*, and second records for *Moloha alcocki*, *Samadinia pulchra* and *Charybdis africana*. In addition, *Raninoides crosnieri*, *S. galathea* and *P. ori* were collected for the first time after their descriptions. The female of *Samadinia galathea* is described for the first time, and a potential new species of *Mursia* is reported. Some records expand the known bathymetric range of certain species and/or their general distribution. New molecular and morphological data suggest the necessity of the revision of *P. boasi*, *R. crosnieri*, *C. africana* and the genera *Platymaia* and *Carcinoplax*. The variability and taxonomic validity of some morphological characters in brachyuran systematic is discussed.

Key words: Crustacea, Indian Ocean, new records, DNA barcoding, 16S rRNA, COI

Introduction

The coastline of Mozambique is characterized by a wide diversity of habitats which supports highly diverse ecosystems and endemism (Pereira *et al.* 2014). Mozambique is bounded by the Mozambique Channel and the West Indian Ocean (WIO) in the east. The productivity of the Mozambican sea waters is very much influenced by the peculiar geographic shape and location of the Mozambique Channel, which make it awfully specific in terms of ocean circulation and whose flow is dominated by a complex system of energetic and turbulent mesoscale eddies, approximately 100–300km across (Ternon *et al.* 2014). Mesoscale eddies continuously circulate throughout the channel, mostly southward along the Mozambican coast (Schouten *et al.* 2003), driving the productivity, distribution and abundance of phytoplankton and marine organism (Marsac *et al.* 2014). Thus, the Mozambique Channel is considered as one of the most turbulent areas in the world ocean involving a great diversity of marine species (Ternon *et al.* 2014).

The knowledge on decapods crustaceans in African waters and, more specifically, in the East African coast washed by the Indian Ocean, is quite limited. In general, the number of studies on decapod taxonomy carried out on both side of the Mozambique Channel, are much more abundant in Madagascar than in Mozambique (Castro 2012; Castro *et al.* 2013; Richer de Forges 2011). It is worth mentioning the number of new species described and/or revised from the decapod crustacean material collected during the deep-sea survey “MAINBAZA”, carried out in the Mozambique Channel in 2009 and deposited in the Muséum National d’Histoire Naturelle (Paris) (Ahyong 2014; Castro 2012, 2013; Komai & Chan 2010a,b).

In addition, there are several inventories of Decapoda in neighbouring areas of the WIO, some of them even including certain areas of Mozambique (Barnard 1950, 1955; Kensley 1977, 1980, 1981; Poupin 2008, 2010, 2016; Poupin *et al.* 2013; Stebbing 1910). The catalogue and checklist on decapods of Namibia, South Africa, and Mozambique (Emmerson 2016a, b, c) is the most updated work compiled so far.

The production of an updated checklist of Brachyura for Mozambique is especially interesting for this taxon, considering it is the most diverse infraorder within the Crustacea, with more than 7590 species worldwide (Davie & Ng 2021). In addition, some articles have been published on different genera and species from Mozambique (Ahyong 2014; Komai 2011), but any catalogue or inventory of all crab species that inhabit these waters has been produced so far (Martin 1992).

The aim of this study is to provide an updated checklist of the brachyuran crabs from the Mozambique waters, compiling all previous information, and updating the systematic considering all the last changes proposed. Besides, new data, including depth, coloration patterns, morphology and DNA barcodes from crabs collected by the “MOZAMBIQUE” surveys carried out by the IEO, are added.

Material and methods

The studied brachyuran specimens were collected during the ‘MOZAMBIQUE’ fishing surveys carried out by the IEO, in collaboration with the “Instituto Nacional de Investigação Pesqueira (IIP)” (National Institute of Fisheries Research) of Mozambique on board the Spanish R/V ‘Vizconde de Eza’, from middle March to middle April of three consecutive years (2007–2009). The working area included the shelf and slope of the Mozambique exclusive economic zone (EEZ), between 100–700m depth (see Figure 1). A total of 344 fishing hauls of a standard duration of 1 h were carried out in the three surveys by using a “Lofoten” bottom otter trawl, with 46 mm mesh size, covered with an internal 25mm mesh size cod-end. The crabs that are part of this work were collected in 83 of these hauls (see Table 1). Brachyuran specimens taken in each haul were sorted and identified to the lowest taxonomical level. Photographs of fresh specimens were taken on board. In order to check and complete the species identification, a number of specimens of all the species caught during the surveys were preserved (formalin and/or ethanol) and transported to the laboratory at the IEO in Cadiz (Spain), where they were exhaustively reviewed together with the corresponding pictures.

All specimens were sexed and measured (mm). For each specimen, two standard measures were taken: the maximum carapace width (CW), as the widest part of carapace including the lateral spines, and the maximum carapace length (CL), as length of the dorsal midline from the middle of the frontal region to the posterior margin of the carapace. These measurements are given following the format CW×CL (mm). Some alternative measures were taken when needed, i.e.: for specimens with prominent rostral spines susceptible to fracture, postrostral length (PRL) was measured instead CL; for specimens with great lateral spines (i.e: *Mursia africana*, *Mursia flamma* and *Mursia* sp.), CW was measured excluding the lateral spines. In those cases, the abbreviation of the measurement is specified.

Total genomic DNA of a sample of the specimens of all different species collected in the “MOZAMBIQUE” surveys was extracted from muscle tissue from one pereopod, eye, or female pleopod, following a modified Chelex 10% protocol by Estoup *et al.* (1996). Target mitochondrial DNA from the 16S rRNA and COI genes was amplified with polymerase chain reaction (PCR) using the following cycling conditions: 2 min at 95°C, 40 cycles of 20s at 95°C, 20s at 45–48°C, 45s (16S) or 47s (COI) at 72°C, and 5 min 72° C. Primers 1472 (5′- AGA TAG AAA CCA ACC TGG -3′) (Crandall & Fitzpatrick 1996) and 16L2 (5′-TGC CTG TTT ATC AAA AAC AT-3′) (Schubart *et al.* 2002) were used to amplify a maximum of 540 bp of 16S, while primers COH6 (5′- TAD ACT TCD GGR TGD CCA AAR AAY CA -3′) and COL6b (5′- ACA AAT CAT AAA GAT ATY GG -3′) (Schubart & Huber 2006) allowed amplification of a maximum of 670 bp of COI. PCR products were sent to Stab Vida company to be purified and then bidirectionally sequenced. Sequences were edited using the software Chromas version 2.6.4.

A BLAST (Basic Local Alignment Search Tool) on NCBI (National Center for Biotechnology Information) web facility on GenBank sequences database (<http://www.ncbi.nlm.nih.gov/genbank/>) was performed with the obtained final DNA sequences in order to get the best matches for species identification. The COI sequences were also searched in the official Barcode of Life database (BOLD) (http://v3.boldsystems.org/index.php/IDS_OpenIdEngine). Identifications were considered as positive when comparative sequences showed similarity values greater than 99%, with differences in 1–3 or 1–12 mutations in 16S or COI, respectively. All sequences obtained for both genes are deposited in Genbank (see Table 2).

The examined specimens and the DNA vouchers are deposited in the “Colección de Crustáceos Decápodos y Estomatópodos del Centro Oceanográfico de Cádiz- CCDE-IEOCD” from IEO (<https://www.gbif.es/coleccion-coleccion-de-crustaceos-decapodos-y-estomatopodos-del-centro-oceanografico-de-cadiz/>) (Muñoz, I. & García-Isarch, E. 2021).

For updating the checklist, the list of records from Mozambique included in the work of Emmerson (2016c) was used as a base. This was complemented with further information obtained through an extensive review of existing literature. All records in the study area were registered in a specific database containing all the information available from the consulted sources and the new records from the “MOZAMBIQUE” surveys. The species and higher taxa were listed following the classification in Davie *et al.* (2015a), updated in WoRMS (2021), and following recent changes posterior to Davie *et al.* (2015a) as indicated. Species were listed by alphabetic order within their respective family, with updated information on their depth range or habitat (estuarine, intertidal, and subtidal), when available. Species recorded from the “MOZAMBIQUE” surveys are indicated, being specified those that are new records in the area.

The following abbreviations, symbols and acronyms are used in this work (in alphabetic order):

TABLE 1. List of the trawl haul stations where the crabs of this study were collected from the “MOZAMBIQUE” surveys M07, M08 and M09, including date, depth and coordinates.

Survey	Station	Date	Depth (m)	Haul mean latitude	Haul mean longitude
M07	1	13/03/2007	449	26.201 S	33.202 E
M07	4	14/03/2007	620	26.781 S	33.148 E
M07	10	15/03/2007	382	25.593 S	34.972 E
M07	13	16/03/2007	620	23.835 S	35.832 E
M07	18	17/03/2007	530	21.923 S	35.718 E
M07	27	23/03/2007	425	20.631 S	35.895 E
M07	34	20/03/2007	627	18.433 S	37.467 E
M07	37	20/03/2007	243	18.283 S	37.45 E
M07	40	21/03/2007	190	17.453 S	38.578 E
M07	41	21/03/2007	445	17.556 S	38.463 E
M07	52	23/03/2007	556	18.951 S	37.203 E
M07	62	27/03/2007	174	22.227 S	35.607 E
M07	64	28/03/2007	138	22.363 S	35.600 E
M07	69	29/03/2007	366	22.880 S	35.817 E
M07	70	29/03/2007	519	22.737 S	35.868 E
M07	78	30/03/2007	300	23.408 S	35.788 E
M07	81	31/03/2007	548	24.298 S	35.677 E
M07	84	31/03/2007	129	24.475 S	35.443 E
M07	86	01/04/2007	558	24.410 S	35.640 E
M07	87	01/04/2007	620	24.458 S	35.635 E
M07	106	05/04/2007	259	25.203 S	34.195 E
M07	123	08/04/2007	184	25.675 S	33.163 E
M08	4	15/03/2008	643	22.87 S	35.933 E
M08	6	15/03/2008	428	23.002 S	35.855 E
M08	9	16/03/2008	541	21.168 S	35.723 E
M08	15	18/03/2008	283	18.103 S	37.575 E
M08	16	13/03/2008	235	18.300 S	37.442 E
M08	18	19/03/2008	217	17.440 S	38.607 E
M08	22	20/03/2008	618	18.687 S	37.348 E
M08	24	20/03/2008	402	19.015 S	37.135 E
M08	25	20/03/2008	265	19.207 S	36.990 E
M08	32	24/03/2008	458	22.452 S	35.798 E
M08	33	18/03/2008	530	22.585 S	35.852 E
M08	39	25/03/2008	631	23.100 S	35.942 E
M08	43	26/03/2008	375	23.557 S	35.813 E
M08	45	21/03/2008	658	23.732 S	35.873 E
M08	50	27/03/2008	623	24.420 S	35.652 E
M08	54	28/03/2008	211	24.193 S	35.603 E
M08	55	29/03/2008	411	24.618 S	35.538 E
M08	57	29/03/2008	366	24.687 S	35.501 E
M08	62	30/03/2008	467	25.065 S	35.346 E
M08	65	31/03/2008	546	25.398 S	35.175 E
M08	67	31/03/2008	378	25.603 S	34.962 E

.....continued on the next page

TABLE 1. (Continued)

Survey	Station	Date	Depth (m)	Haul mean latitude	Haul mean longitude
M08	68	31/03/2008	244	25.543 S	34.86 E
M08	69	31/03/2008	277	25.394 S	34.607 E
M08	71	01/04/2008	577	25.878 S	34.733 E
M08	74	01/04/2008	336	25.348 S	34.272 E
M08	75	02/04/2008	256	25.203 S	34.212 E
M08	76	02/04/2008	222	25.197 S	34.063 E
M08	77	02/04/2008	290	25.248 S	34.073 E
M08	78	02/04/2008	392	25.460 S	34.153 E
M08	81	03/04/2008	606	25.950 S	34.637 E
M08	104	07/04/2008	692	26.770 S	33.198 E
M08	107	08/01/2008	549	26.470 S	33.280 E
M09	4	13/03/2009	258	26.223 S	33.070 E
M09	5	14/03/2009	548	26.850 S	33.090 E
M09	8	14/03/2009	648	26.587 S	33.272 E
M09	9	14/03/2009	540	26.475 S	33.273 E
M09	10	15/03/2009	305	26.528 S	33.069 E
M09	14	15/03/2009	608	26.327 S	33.482 E
M09	17	16/03/2009	419	24.878 S	35.433 E
M09	19	16/03/2009	542	24.693 S	35.532 E
M09	27	17/03/2009	543	22.970 S	35.898 E
M09	31	18/03/2009	457	22.665 S	35.835 E
M09	32	18/03/2009	529	22.603 S	35.855 E
M09	33	18/03/2009	470	22.487 S	35.810 E
M09	34	19/03/2009	628	21.318 S	35.722 E
M09	44	21/03/2009	639	17.600 S	38.427 E
M09	45	21/03/2009	322	17.565 S	38.420 E
M09	46	21/03/2009	212	17.447 S	38.595 E
M09	51	24/03/2009	548	18.945 S	37.207 E
M09	54	24/03/2009	619	19.122 S	37.115 E
M09	56	26/03/2009	511	21.703 S	35.677 E
M09	58	26/03/2009	334	21.900 S	35.638 E
M09	60	27/03/2009	304	22.110 S	35.665 E
M09	63	27/03/2009	617	22.385 S	35.858 E
M09	65	28/03/2009	578	23.620 S	35.867 E
M09	67	28/03/2009	625	23.853 S	35.828 E
M09	81	31/03/2009	374	25.597 S	34.967 E
M09	83	31/03/2009	299	25.587 S	34.642 E
M09	84	31/03/2009	254	25.352 S	34.647 E
M09	92	02/04/2009	619	25.967 S	34.618 E
M09	107	05/04/2009	685	26.570 S	33.715 E

CCDE-IEOCD: Crustacean decapods and stomatopods Collection of the Cadiz Center of Oceanography (in Spanish: Colección de Crustáceos Decápodos y Estomatópodos del Centro Oceanográfico de Cádiz); **CL:** maximum carapace length; **CSIC:** Spanish National Research Council (in Spanish: Consejo Superior de Investigaciones Científicas); **CW:** maximum carapace width (including lateral spines); ♀: female; **G1:** first gonopod of male; **G2:**

second gonopod of male; **IEO**: Spanish Institute of Oceanography (in Spanish: Instituto Español de Oceanografía); **IIP**: National Institute of Fisheries Research of Mozambique (in Portuguese: Instituto Nacional de Investigação Pesqueira); **IP**: Indo-Pacific; **IWP**: Indo-West Pacific; ♂: male; **M07/M08/M09**: surveys MOZAMBIQUE0307, MOZAMBIQUE0308, MOZAMBIQUE0309, respectively; **MB-exp.**: Mainbaza expedition; **MNHN**: National Museum of Natural History, Paris (in French: Muséum National d'Histoire Naturelle); **ov.**: ovigerous; **pers. comm.**: personal communication; **PRL**: post-rostral length; **P2/P3/P4/P5**: second, third, fourth, and fifth pereopod, respectively; **Stn.**: Station; **WIO**: Western Indian Ocean.

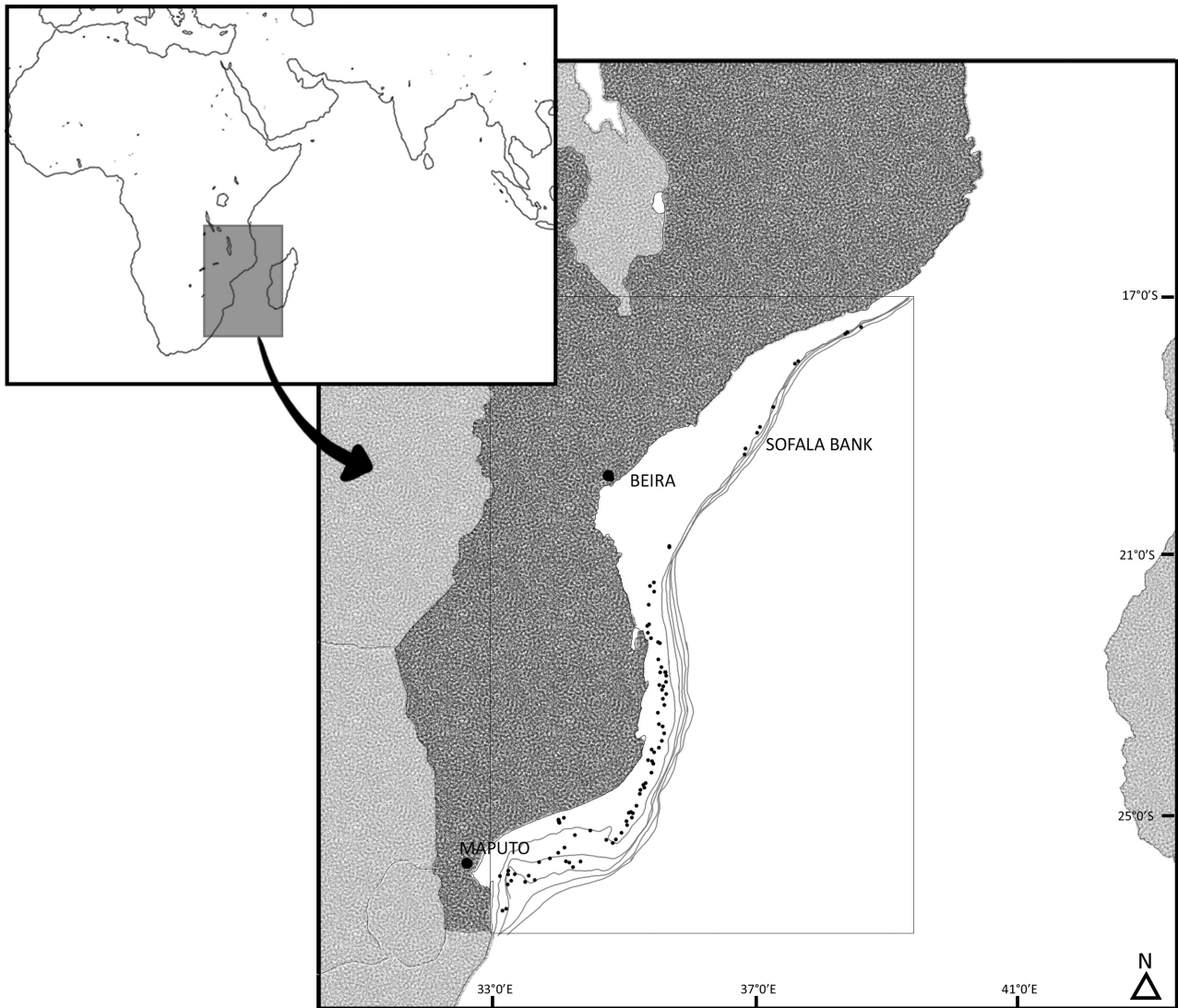


FIGURE 1. Study area with the location of the fishing stations (black dots) of the three “MOZAMBIQUE” surveys (2007–2009) reported in Table 1.

Results

A total of 176 specimens belonging to 39 brachyuran species were collected in the “MOZAMBIQUE” surveys. DNA barcodes (16S rRNA and/or COI) were successfully obtained for 83 specimens belonging to 37 species. An annotated list of all taxa collected in systematic order is provided in the following taxonomic account, including data of the material examined, systematic remarks, distribution, habitat, coloration, and DNA barcodes of each one.

Taxonomic account

Section PODOTREMATA Guinot, 1977

Superfamily HOMOLODROMIOIDEA Alcock, 1900

Family HOMOLODROMIIDAE Alcock, 1900

This family contains only two extant genera (*Homolodromia* A. Milne-Edwards and *Dicranodromia* A. Milne-Edwards) and 25 species (Davie *et al.* 2015a). Two single species are recorded in the Indian Ocean: *H. bouvieri* A. Milne-Edwards and *H. crosnieri* Guinot (Cleva *et al.* 2007; Guinot, 1995), being *H. bouvieri* the only species cited in Mozambican waters (Doflein 1904; Martin, 1992). According to the checklist by Emmerson (2016c), a different *Homolodromia* species has recently been found in waters of Mozambique (MB-exp) which seems to be different from those described so far. For this reason, we have considered to include this species as *Homolodromia* sp. in the checklist. Carrying behaviour is quite common in Homolodromiidae, generally bearing sponges (Guinot & Wicksten 2015).

Homolodromia A. Milne-Edwards, 1880

Homolodromia bouvieri Doflein, 1904

(Figure 2A)

Material examined. M08, Stn. 22, 618m, ♂ 29.6×25.5mm (IEO-CD-MZ08/1777), 16S (MZ424903), COI (MZ434752); M08, Stn. 39, 631m, ♂ 25×28.7mm (IEO-CD-MZ08/1908), 16S (MZ424904), COI (MZ434753); M08, Stn. 104, 692m, ♀ 29.9×34.8mm (IEO-CD-MZ08/1801), 16S (MZ424905), COI (MZ434754).

Habitat and distribution. Currently there are only 6 species within the genus *Homolodromia* (Davie *et al.* 2015a), being *H. bouvieri* the only one with representation in southern African waters (Kensley 1981; Martin 1992; Sasaki 2019), including Mozambique. General distribution of *H. bouvieri*: off Natal, 500–700m (Kensley 1977, 1981), Kenia (863m) and Mozambique (850–960m) (Doflein 1904; Martin 1992). Nevertheless, the species was not reported in Mozambican waters in the checklist by Emmerson (2016c).

Results and remarks. Our specimens agree well with the descriptions given by Doflein (1904), the redescription of the species from specimens from Mozambique made by Martin (1992), and the comparison with the new species described recently from the northern Indian Ocean, *H. rajeevani* Padate, Cubelio & Jayachandran and previously confused with *H. bouvieri* (Padate *et al.* 2020). Three specimens were collected during the M08, at depths between 618–692m. These records extend the bathymetric range of this species in Mozambique waters, from 850–960m to 618–960m, and also its geographical distribution, being the specimens reported southernmost Mozambique.

Colouration observed. The specimens had a homogeneous dark beige colour with a certain yellowish tone.

DNA barcodes. 16S and COI sequences were obtained for the three specimens. There are not sequences of these two genetic markers available for this genus on any public database. Therefore, these are the first 16S and COI barcodes for this species and genus. In the case of 16S each specimen showed a different haplotype differing in one mutation each, while only two haplotypes were observed for COI, differing from one another in one single mutation.

Superfamily HOMOLOIDEA De Haan, 1839 [in De Haan, 1833–1850]

Family HOMOLIDAE De Haan, 1839 [in De Haan, 1833–1850]

The homolids are also known as “carrier crabs” or “porter crabs” due to their behaviour of carrying things on them, mainly helped by the P5 that are modified for this (Miyake 1983; Guinot *et al.* 1995, 2013). The presence of fouling on their bodies is also quite common (Guinot & Wicksten 2015).



FIGURE 2. A, *Homolodromia bouvieri*, ♀ IEO-CD-MZ08/1801; B, *Homola orientalis*, ♂ IEO-CD-MZ09/1806; C, *Homolochunia valdiviae*, ♀ IEO-CD-MZ09/1805; D, *Moloha alcocki*, ♀ IEO-CD-MZ09/1793; E, *Paromolopsis boasi*, ♀ IEO-CD-MOZ08/1827; F, *Latreilla metanessa*, ♀ IEO-CD-MZ09/1810; G, *Latreilla valida*, ♀ IEO-CD-MZ09/1779. Scale bars: 1cm.

According to Davie *et al.* (2015a), Homolidae includes 14 genera and 70 species, while only six genera and seven species have been cited in Mozambican waters (Barnard 1950; Guinot 1967a; Guinot & Richer de Forges 1995; Kensley 1981; Ng & Kumar 2015; Poupin 2018). Also, an *Homologenus* sp. was reported by Emmerson (2016c) based on a personal communication by Chan from the MB-exp.

Homola Leach, 1816

Homola orientalis Henderson, 1888

(Figure 2B)

Material examined. M07, Stn. 81, 548m, ♂ 22.7×32.6mm (IEO-CD-MZ07/1900), 16S (MZ424906); M08, Stn. 68, 244m, ♂ 24.2×31.4 mm (IEO-CD-MZ08/1821), COI (MZ434755); M09, Stn. 10, 305m, ♂ 43.8×53.7mm (IEO-CD-MZ09/1806), 16S (MZ424907), COI (MZ434756).

Habitat and distribution. The geographic distribution of *Homola orientalis* is the IWP from the East African coast, Gulf of Aden to Australia, Hawaiian Islands, Polynesia, New Zealand (Kensley 1981) and Korea (Lee *et al.* 2013). It is the most common homolid species inhabiting the upper bathyal zone of the whole IWP. Its known depth distribution range is 38–650m according to Guinot & Richer de Forges (1995) and 20–650m according to Emmerson (2016c). In Mozambican waters, it is reported at depths of 150–200m (Emmerson 2016c; Kensley 1981; Sasaki 2019).

Results and remarks. Three males were collected during M07, M08 and M09, from 244 to 548m depth, thus extending its bathymetric distribution in Mozambique to deeper waters (from 200 up to 548m). The specimens agree well with the description and figures in Guinot & Richer de Forges (1995). Some of them had epibionts, mostly barnacles.

Colouration observed. The specimens were orange, with small bright orange spots, especially abundant along the legs, where they form not very well-defined transverse bands. The fingers were black, except in their proximal portion.

DNA barcodes. The 16S sequences of the males IEO-CD-MZ09/1806 and IEO-CD-MZ07/1900 are 100% equals and fit 98.3% with an incomplete sequence of 406 bp (hypervariable parts deleted) of *H. orientalis* from Taiwan (?) (MSLKHC-Hoori, Genbank code KJ132562) included in the study by Tsang *et al.* (2014). The COI sequence of the specimens IEO-CD-MZ09/1806 and IEO-CD-MZ08/1821 (the same haplotype) differs 5.15% from the sequence of *H. orientalis* from China (?), a sequence included in an unverified complete mitochondrial sequence (KT182071) by Shi *et al.* (2016).

Homolochunia Doflein, 1904

Homolochunia valdiviae Doflein, 1904

(Figure 2C)

Material examined. M07, Stn. 18, 530m, ♀ ov 33.6×38.5mm (IEO-CD-MZ07/1914); M07, Stn. 38, 620m, ♀ 38×41.8mm; ♂ 65.4×80.7mm (IEO-CD-MZ07/1922); M08, Stn. 9, 541m, ♂ 32.2×37.7mm (IEO-CD-MZ09/1822); M08, Stn. 81, 606m, ♀ 21.6×27.2mm (IEO-CD-MZ08/1825); M09, Stn. 9, 540m, ♂ 31.8×38mm (IEO-CD-MZ08/1796), 16S (MZ424908), COI (MZ434757), M09, Stn. 54, 619m, ♀ ov 32×36.7mm (IEO-CD-MZ09/1805-1), 16S (MZ424909), COI (MZ434758); ♀ ov 31.2×35.7mm (IEO-CD-MZ09/1805-2), 16S (MZ424910), COI (MZ434759); M09, Stn. 63, 617m, ♂ 25.7×30.2mm (IEO-CD-MZ09/1804-1), 16S (MZ424911), COI (MZ434760); ♂ 31.5×37.9mm (IEO-CD-MZ09/1804-2), 16S (MZ424912), COI (MZ434761).

Habitat and distribution. The genus *Homolochunia* comprises four species which are found exclusively in the IWP, with *H. valdiviae* being the species with the widest distribution range. It is a benthic and tropical species (Palomares & Pauly 2020), inhabiting waters between 600 and 650m depth according to Kensley (1981), and between 395 and 1000m according to Poupin (2018). General distribution: IWP: Japan and Indonesia (Miyake 1983), India (Padate *et al.* 2020), Mozambique, Madagascar, New Caledonia, and Mayotte Island (Poupin 2010,

2018), off Natal (Kensley 1981) and Tanzania (Guinot 1967a).

Results and remarks. Our specimens agree well with the description and figures given by Guinot & Richer de Forges (1995). Ten specimens have been recorded, collected between March and April of M07, M08 and M09, at depths between 530 and 620m. These specimens did not carry anything in the P5, but they do have the entire carapace covered by soft fouling. In addition, some specimens had small sponges on the dorsal side of the P2-P4 merus.

Colouration observed. Variable. The specimens from 2007 were pinkish, not very striking, with the cephalothorax darker, possibly as a consequence of the fouling attached to their dense tomentum, while specimens from 2009 were of a quite homogeneous bright orange colour. The pseudorostral spines and the P1 and P5 legs ended in a whitish colour.

DNA barcodes. Sequences of 16S (the same haplotype) were obtained for five specimens (IEO-CD-MZ08/1796, 1804(2) and 1805(2)), being the firsts made available for this species. Five sequences of COI (628 to 636 bp) were obtained for the same five specimens and represent five haplotypes differentiated in one to three positions. The sequence of the male IEO-CD-MZ08/1796 fit 100% with a COI sequence of *H. valdiviae* (Bold MDECA043-10) collected in the MB-exp and deposited at the MNHN (MNHN_IU200810122).

***Moloha* Barnard, 1947**

***Moloha alcocki* (Stebbing, 1920)**

(Figure 2D)

Material examined. M09, Stn. 84, 254m, 2 ♂ 54.1×64.3mm; ♂ 54.4×65mm (IEO-CD-MZ09/1793), 16S (MZ424913).

Habitat and distribution. Seven species of *Moloha* are known in the IWP (Ng & Kumar 2015), of which only three are recorded in the WIO. *Moloha alcocki* inhabits the continental shelf off southern African waters from Namibia to Mozambique (Kensley 1980a, 1981) and Maldives (Gordon 1950). It has a wide depth range, between 80 and 800m, being reported at 312m in Mozambican waters (Kensley 1980a, 1981).

Results and remarks. The two female specimens agree well with the description and figures of Guinot & Richer de Forges (1995) and clearly differ from the close species *Moloha major* (Kubo), in the following features: non-cylindrical P2-P4, armed on the upper edge of 4-5 large inclined spines, and another strong distal one, and in the branchial areas of the carapace, near of the union with the cardiac areas, bearing numerous small spines.

The two specimens were collected in the same station, at 254m, in 2009. They were large and had barnacle epibionts on their carapace and legs. These specimens are the second record of the species in Mozambique and extend its minimum depth from 312 to 254m in Mozambican waters.

The variation of names (changes and synonyms) has made that even today there is a great confusion on the species nomenclature, being reported differently in some publications and online resources: as *Homola* (*Paromola*) *alcocki* (Stebbing, 1920), *Homola alcocki* (Stebbing 1920), *Latreillopsis alcocki* Stebbing, 1920, *Paromola alcocki* (Stebbing, 1920), *Thelxiope alcocki* (Stebbing, 1922) (WORMS 2021). Also, it appears indistinctly as *M. alcocki* and *Paromola alcocki* in GBIF.org (2021, unpublished record), or as *Maloha alcocki* in Emmerson (2016b).

Colouration observed. The specimens were bright orange, not uniform, but marble-like in appearance, with small lighter and darker orange patches, even red, both on the cephalothorax and on the ambulatory legs. The dactyls from P2 to P4 are darker, turning to reddish brown, without spots. The chelipeds' fingers were black. After preservation in ethanol, the specimenscarapaces turned to beige colour, the legs and chelipeds to very light brown and only the finger tips remain with their black original colour.

DNA barcodes. Only a 16S sequence (526 bp) was obtained from one of the ovigerous females. This sequence fits 99.43% (3 mutations) with the sequence of *Moloha major* (Kubo) (as *Moloha majora*) (KT182069), a complete mitochondrial genome by Shi *et al.* (2016).

Paromolopsis Wood-Mason in Wood-Mason & Alcock, 1891

Paromolopsis boasi Wood-Mason in Wood-Mason & Alcock, 1891

(Figures 2E, 3)

Material examined. M08, Stn. 39, 631m, ♀ov 39×43.6mm (IEO-CD-MZ08/1827), 16S (MZ424914), COI (MZ434762); M09, Stn. 65, 578m, ♂ 34×38.9mm (IEO-CD-MZ09/1762), 16S (MZ424915), COI (MZ434763).

Habitat and distribution. *Paromolopsis boasi* was the only species of the genus worldwide, until *Paromolopsis piersoni* (Schweitzer *et al.* 2004) was described from fossil records in Oregon (Pacific Northwest of North America). This species presents an IP distribution: Madagascar, Channel of Mozambique, Mayotte Island, La Reunion, Sri Lanka, Andaman Island, Laquedives Island, Indo-Malaysian Archipelago, New Caledonia, Queensland and Japan. It inhabits mud bottoms, from 284 to 1124m (most common between 400 and 700m) (Guinot & Richer de Forges 1995; Poupin 2010, 2018).

Results and remarks. This work provides the first record of *P. boasi* from Mozambique waters. Only two specimens of *P. boasi* were collected in M08 and M09, between 578–631m depth. Our specimens were identified using the descriptions given by Guinot & Richer de Forges (1995) and Schweitzer *et al.* (2004).

Guinot and Richer de Forges (1995) had already doubted about the validity of a single species from all the known localities of *P. boasi*, pointing out differences in the dorsal carapace ornamentation, variation in body tomentum and carapace proportions and different sizes of frontal spines. This fact was also raised by Padate *et al.* (2020), who found differences between Indian and Pacific specimens. Guinot and Richer de Forges (1995) already suggested the potential separation of *P. boasi* into at least two species. A review of this genus, including genetic analysis of *P. boasi* specimens from different areas is recommended to clarify this issue.

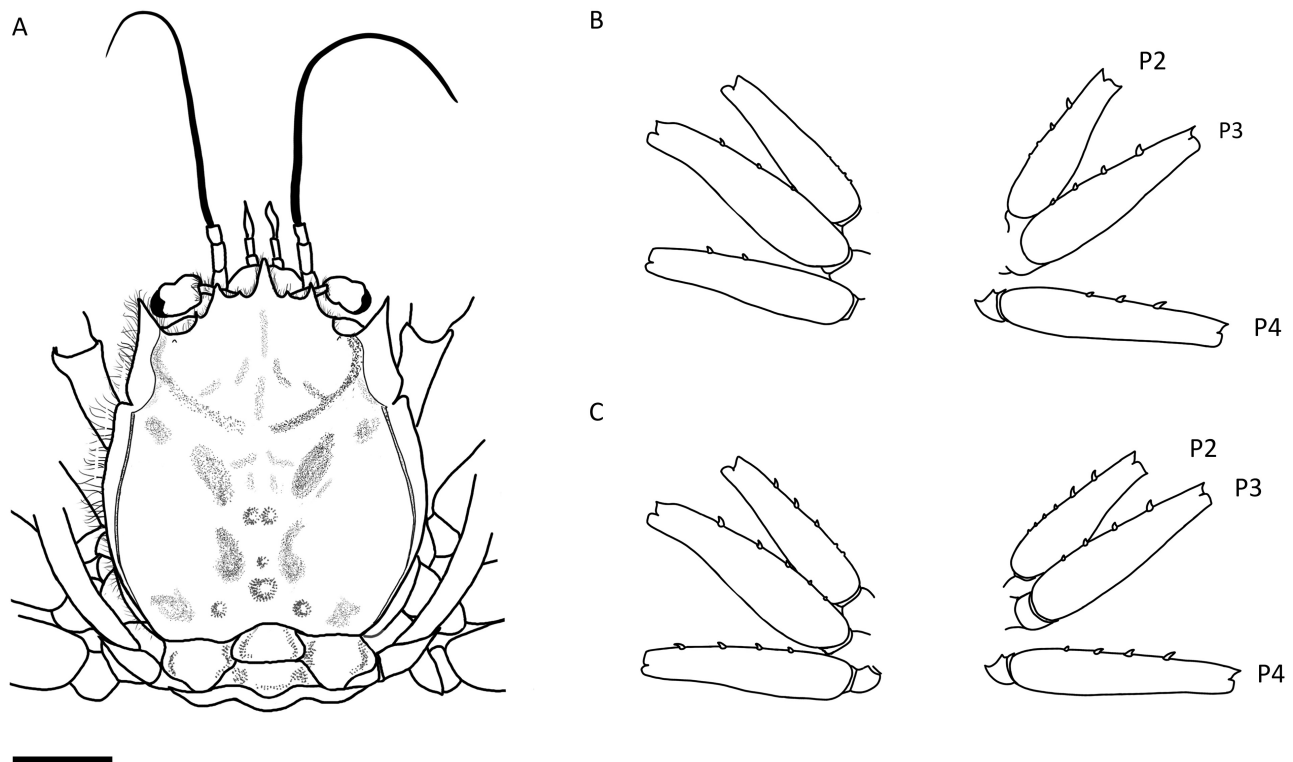


FIGURE 3. A, *Paromolopsis boasi* IEO-CD-MZ09/1762 ♂, dorsal view; B, *P. boasi* ♀ov IEO-CD-MZ08/1827 P2-P3-P4 left and right; C, *P. boasi* IEO-CD-MZ09/1762 ♂ P2-P3-P4 left and right. Scale bars: 1cm.

The most remarkable characteristics of these two specimens (see Figure 3) are: anterolateral spines acute but not sharpening towards the end; dorsal face of the carapace quite rough and grainy; merus length of P5 does not exceed the anterolateral spine; long setae on the edges of the carapace, as well as on the edges of the ambulatory legs; the top edge of P2-P4 merus armed with separated spines of different size, not uniform in number neither between different pereopods nor between specimens. The biggest specimen (IEO-CD-MZ08/1827) is an ovigerous female

that responds to the next pattern from the outside inward (see Figure 3B): right side, P2, two sharp, curved and well separated medium-size spines + two small blunt and less separated spines or tubercles, not clearly visible; P3, four well visible spines on merus, that decrease dorsally in size and space between them; P4, three well visible, pointed and curved spines, diminishing in size dorsally; left side, P2, small tubercles in the most proximal area; P3, three well visible and curved spines (two last broken); P4, two well visible and curved size-decreasing spines. The male (IEO-CD-MZ09/1762), responds to (see Figure 3C): right side, P2, two big, pointed and curved spines + four smaller spines, neither pointed nor curved, which decrease in size dorsally until being almost inconspicuous and adjacent; P3, four pointed and curved and dorsally size-diminishing; P4, four pointed and curved spines becoming much smaller towards the dorsal zone; left side, P2, three big, pointed and curved spines, being the two first specially big + two neither pointed nor curved small spines, almost inconspicuous; P3, five spines that decrease in size and space between them, the last neither pointed nor curved, P4, four pointed and curved spines, with dorsally diminishing size. All these characters are in line with the characteristics of the specimens cited in waters of the Indian Ocean (Guinto & Richer de Forges, 1995).

Colouration observed. Carapace was bright orange, with the most depressed areas of the gastric zones white. Meri of the ambulatory legs were also orange, slightly pinker in their proximal area; carpi are orange-pink; propodi are whitish with pink tones and the dactyli almost white.

DNA barcodes. 16S and COI sequences obtained for the two specimens are equal in 500 and 639 bp, respectively. The 16S sequence fits 100% with an incomplete sequence of *P. boasi* of 406 bp (hypervariable parts deleted) from Taiwan (?) (NTOU B00091, Genbank code KJ132606) included in the study by Tsang *et al.* (2014). The COI sequence is the first one available for this species.

Family LATREILLIIDAE Stimpson, 1858

According to Davie *et al.* (2015a), Latreillidae includes two genera, *Latreillia* P. Roux and *Eplumula* Williams, and seven species, three of them cited in Mozambican waters (*Latreillia metanesa* Williams, *Latreillia pennifera* Alcock and *Latreillia valida* De Haan) (Kensley 1981; Poupin 2010, 2018, Emmerson 2016b,c). Free living and mostly deep water species, individuals typically carry seaweeds, hydroids, gorgonians and/or corals on them (Davie *et al.* 2015b).

Latreillia P. Roux, 1830 [in P. Roux, 1828–1830]

Latreillia metanesa Williams, 1982

(Figure 2G)

Material examined. M09, Stn. 81, 374m, ♀ov 3.7×7.7mm (IEO-CD-MZ09/1810), 16S (MZ424916).

Habitat and distribution. IWP, from East Africa (Somalia, Kenya, Mozambique, Madagascar) to French Polynesia and the Hawaiian Islands at depths between 22 and 806m (Castro *et al.* 2003), with records in South China Sea, Taiwan, Philippines, Indonesia, Vanuatu, New Caledonia, and Japan (Sasaki 2019). In Mozambican waters, the species is recorded between 112 and 403m (Castro 2013). It inhabits bottoms of sand, foraminifera, coral and rock (Williams 1982).

Results and remarks. Only one specimen was studied, being an ovigerous female, collected in March 2009 (M09) at 374m depth. This specimen agrees well with the descriptions and figures in Castro *et al.* (2003). The specimen was collected badly damaged.

Colouration observed. The carapace was crossed longitudinally by orange and beige lines, which curve at the posterior edge of the carapace. The ambulatory legs, as well as the chelipeds, bear orange and beige transverse lines.

DNA barcodes. There are not sequences available for this species on any public database. Thus, the 16S sequence is the first one for this species and is close (98.49%), at intrageneric distance, to one sequence of *Latreillia valida* (MK204361).

Latreillia valida De Haan, 1839 [in De Haan, 1833–1850]

(Figure 2F)

Material examined. M09, Stn. 46, 212m, ♂ 11.2×18.5mm (IEO-CD-MZ09/1779-1), 16S (MZ424917), COI (MZ434764); ♀ ov 10.9×17.6mm (IEO-CD-MZ09/1779-2), 16S (MZ424918), COI (MZ434765).

Habitat and distribution. WIO, from South Africa and Madagascar, to Western Australia and Western Pacific Ocean, from Japan to as far east as Tonga. The depth range recorded for the species is 30–898m (Castro 2013), while in Mozambican waters is 112–898m according to Castro (2013) and 30–731m according to Emmerson (2016b,c).

Results and remarks. Two specimens, one male and one ovigerous female, were collected at the same station in March 2009 (M09), at 212m depth. These individuals were damaged, with some broken legs. Our specimens agree well with the descriptions and figures in Castro *et al.* (2003).

Colouration observed. The carapace was almost transparent, with certain orange tone, covered with longitudinal red lines and another wider and complete red line, which borders all its posterior edge. Transverse red bands were along the ambulatory legs, being not uniform and little marked.

DNA barcodes. 16S and COI sequences of both specimens are equal in 412 and 636 bp, respectively. 16S and COI sequences fit 99.28% (only differ in one mutation) and 99.69% (differing in two mutations), respectively, with the sequences of *L. valida* (MK204361), a mitochondrial complete genome obtained by Bao *et al.* (2019).

Superfamily RANINOIDEA De Haan, 1839 [in De Haan, 1833–1850]

There is some confusion regarding the taxonomic status of Superfamily Raninoidea. Some authors and web platforms consider it to comprise two families, Raninidae De Haan, and Lyreididae Guinot (Davie *et al.* 2015a), while others consider the Lyreididae as a subfamily, Lyreidinae, within the Raninidae as Ribes (1989), Emmerson (2016b,c), and WORMS (2021). In this work we have followed the more recent classification by Davie *et al.* (2015a), considering Raninidae and Lyreididae as two independent families.

Family LYREIDIDAE Guinot, 1993

According to Davie *et al.* (2015a), this family includes two genera (*Lyreidus* De Haan and *Lysirude* Goeke) and six species. These species, known as “frog crabs”, are mainly distributed in warm and tropical waters of the Atlantic and IWP (Poor 2004). Only *Lyreidus brevifrons* Sakai has been cited in Mozambique waters (Emmerson 2016b,c). A *Lyreidus* sp. was also reported for Mozambique by Emmerson in his checklist.

Lyreidus De Haan, 1841 [in De Haan, 1833–1850]

Lyreidus brevifrons Sakai, 1937

(Figure 4A)

Material examined. Stn. 40, 190m, ♂ 22.1×38.3mm; ♂ 25.2×44.9mm (IEO-CD-MZ07/1898); M07, Stn. 41, 44 m, ♂ 21.3×37.9mm (IEO-CD-MZ07/1906), M08, Stn. 6, 428m, ♂ 19.9×32.9mm (IEO-CD-MZ08/1798); M08, Stn. 32, 458m, ♂ 24.5×43.6mm (IEO-CD-MZ08/1770); M08, Stn. 33, 530m, ♂ 19.5×34.8mm (IEO-CD-MZ08/1782-1), 16S (MZ424919), COI (MZ434766), ♂ 17.8×30.5mm (IEO-CD-MZ08/1782-2), 16S (MZ424920), COI (MZ434767); M08, Stn. 78, 392m, ♂ 23.9×41.7mm (IEO-CD-MZ08/1771), 16S (MZ424921), COI (MZ434768).

Habitat and distribution. Species distributed throughout Japan, the South China Sea, west of the Philippines and Dar-es-Salaam, Tanzania (Sakai 1976), Madagascar, Reunion Island (Poupin 2010; Ribes 1989) and New Caledonia (Poupin 2010).

Results and remarks. Our specimens agree well with the descriptions and figures in Goeke (1985). Eight specimens were collected during March and April of M07, M08 and M09, at depths between 190 and 530m. These records confirm the presence of *L. brevifrons* in Mozambican waters, and extend its depth range to deeper waters up to 530m.



FIGURE 4. A, *Lyreidus brevifrons*, ♂ IEO-CD-MZ08/1771; B, *Raninoides crosnieri*, ♂ IEO-CD-MZ07/1910; C, *Calappa africana*, ♀ IEO-CD-MZ08/1815; D, *C. africana*, ♂ IEO-CD-MZ08/1797; E, *Mursia africana*, ♂, IEO-CD-MZ08/1797; F, *Mursia aspera*, ♂ IEO-CD-MZ07/1903 (preserved); G, *Mursia flamma*, ♀ IEO-CD-MZ07/1904; H, *Mursia* sp., ♂ IEO-CD-MZ09/1775. Scale bars: 1cm.

Colouration observed. Orange-brown, with the gastric and intestinal areas a little clearer, almost orange. Ambulatory legs were dorsally orange coloured, not homogeneous, with some clearest and pale patches, almost white. The ventral side of the specimens, legs and chelae were very pale, between rose and pale orange. Antennules and ocular peduncles were orange dark. A wide white line separates the gastric and branchial areas, and a big clear spot in both sides of the branchial area was observed in some individuals.

DNA barcodes. For 16S three equal sequences of 424, 500 and 507 bp were obtained, that fit 100% with a sequence of *L. brevifrons* from Taiwan (KM983394), a complete mitochondrial genome obtained by Shi *et al.* (2015). The three COI sequences represent two haplotypes, differing in two mutations, and fit 98.58 and 98.91% (nine and seven mutations), respectively with the COI sequence of the same specimen of *L. brevifrons* from Taiwan (KM983394).

Family RANINIDAE De Haan, 1839 [in De Haan, 1833–1850]

According to Davie *et al.* (2015a), this family includes ten genera and 40 species. Only the genera *Cosmonotus* (White), *Notopus* (De Haan), *Ranina* (Lamarck) and *Raninoides* (H. Milne Edwards) have been cited off Mozambique (Emmerson, 2016b,c).

***Raninoides* H. Milne Edwards, 1837**

***Raninoides crosnieri* Ribes, 1989**

(Figure 4B)

Material examined. M07, Stn. 40, 190m, ♂ 16.2×27.1mm (IEO-CD-MZ07/1910), 16S (MZ424922).

Habitat and distribution. The known distribution of *Raninoides crosnieri* is the type locality, Madagascar, at depths between 160 and 210m (Ribes 1989).

Results and remarks. Only one specimen was recorded at 190m depth in M07. It is a male mostly agreeing with the description of *R. crosnieri* given by Ribes (1989), although not completely. There are characteristics that clearly distinguish it from *Raninoides personatus* Henderson, the other similar species of the Indian Ocean, and agree with the *R. crosnieri* description, such as: a sub-distal spine in the carpus of the chelipeds (although it is accompanied by a distal one) and the edge of the carpus rough; the upper edge of P4 somewhat concave; on the upper edge of P5 which there are indications that there was a spine in each, which are broken. However, the rostrum of this specimen (see Figure 5A) differs with that described by Ribes (1989) for *R. crosnieri* (see Figure 5B), and rather fits the description of the rostrum of *R. personatus* “rounded at its end” (see Figure 5C). Ribes (1989) considered the rostrum shape as one of the main differences separating *R. crosnieri* from *R. personatus*, and therefore this new evidence put under question the taxonomic validity of this feature.

This is the first record of *R. crosnieri* in Mozambique waters, and the second one of this species worldwide.

Colouration observed. The cephalothorax and pleon were orange-brown, with marble-like spots. The legs and chelipeds were light beige, with some not very well-defined faint brown-orange spots.

DNA barcodes. There are not sequences available for this species on any public database. The 526 bp sequence of 16S obtained for the specimen IEO-CD-MZ07/1910 is the first genetic marker for this species.

Section EUBRACHYURA Saint Laurent, 1980

Subsection HETEROTREMATA Guinot, 1977

Superfamily CALAPPOIDEA De Haan, 1833 [in De Haan, 1833–1850]

Family CALAPPIDAE De Haan, 1833 [in De Haan, 1833–1850]

According to Davie *et al.* (2015a), this family includes nine genera and 89 species. Only two of these genera have

been recorded in Mozambican waters, *Calappa* Weber and *Mursia* Desmarest (Emmerson 2016b,c; Lai & Ng 2006; Spiridonov & Apel 2007). Calappidae crabs are known as box-crabs and inhabit from shallow to deep waters, usually burying (Davie *et al.* 2015a).

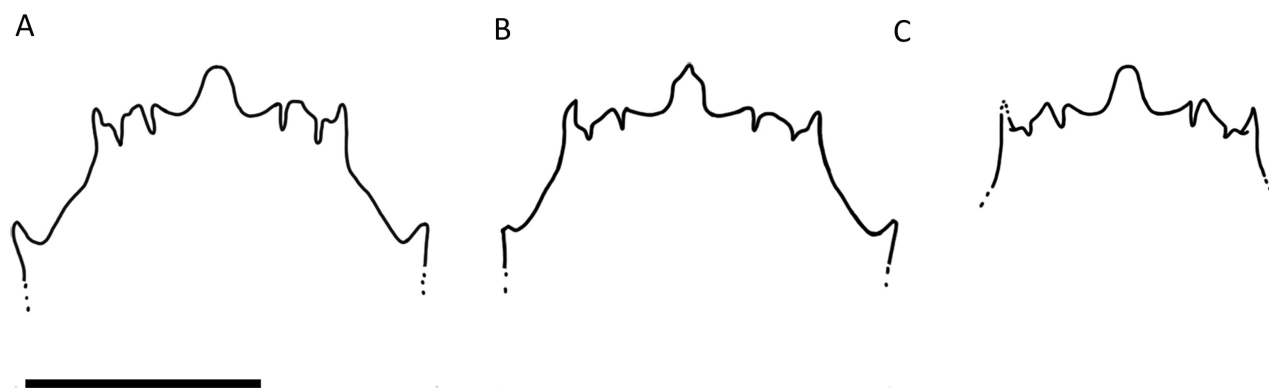


FIGURE 5. Rostrum. A, *Raninoides crosnieri* ♂ IEO-CD-MZ07/1910; B, *Raninoides crosnieri*; C, *Raninoides personatus*. B and C after Ribes (1989). Scale bars: 1cm.

Calappa Weber, 1795

Calappa africana J.C.Y. Lai & P.K.L. Ng, 2006

(Figure 4C, D)

Material examined. M07, Stn. 37, 243m, ♂ 88.8×65.1mm (IEO-CD-MZ07/1923); M08, Stn. 15, 283m, ♀ 88.8×64.4mm (IEO-CD-MZ08/1815), 16S (MZ424923), COI (MZ434769); M09, Stn. 4, 258m, ♀ 121.1×82.6mm (IEO-CD-MZ09/1791), 16S (MZ424924), COI (MZ434770).

Habitat and distribution. This species was confused for many years with *Calappa japonica* Ortmann, 1892, until it was described by Lai & Ng (2006) as a new species. Since then, *C. japonica* has been confined to the Pacific and *Calappa africana* to the Southeast African coast, South Africa, and Mozambique (58m) (Barnard 1950, 1955; Kensley 1981), Kenia and Somalia (type locality, 70–80m) (Lai & Ng 2006).

Results and remarks. To identify our specimens, we use the original description (Lai & Ng 2006) and a posterior revision of *C. africana* together with *C. japonica* and *C. exanthematosus* Alcock & Anderson made by Ng *et al.* (2011). The three studied individuals were collected in the three surveys (M07, M08 and M09) at depths of 243, 283 and 258m, respectively. These specimens were initially identified as *C. africana* as they had many diagnosis characters similar to those of the original descriptions by Lay & Ng (2006), although other characters did not totally agree with them. It is the case for the second male pleopods (G2) (see Figures 6A, B) which are more curved, distally crook-like, as described for *C. japonica* by Galil (1993) (see Figure 6D) than “G2 subequal in length to G1, slender, curved, distal tip rounded” as described by for *C. africana* Lay & Ng (2006) (see Figure 6C). Our records extend the depth range in Mozambican waters from 58 up to 283m.

Colouration observed. Lai & Ng (2006) described the colour of the freshly preserved paratype of *C. africana* as follow: “... the dorsal surface of the carapace is beige to light brown in colour, speckled with salmon pink to light red mottles”. Barnard (1950) also described the colours of preserved specimens of *C. japonica*, which today must be referred to *C. africana*: “As preserved, pale with salmon pink mottling around the pustules and on hinder half of the carapace”. The colour of our preserved specimens agrees well with those descriptions. Photographs taken from two fresh specimens show the following live coloration pattern: the dorsal carapace surface, as well as the outer part of the chelae varies from brown-red to yellow. The female captured in M08 (IEO-CD-MZ08/1815) was more yellowish, while the male from M07 (IEO-CD-MZ07/1923) was more reddish (see Figures 4C,D). In addition, the carapace has a dorsal pattern of large yellow spots surrounded by red, but without any reticulate pattern, which is typical of *C. japonica* (Ng *et al.* 2011). The spots on the upper half of the carapace were marked, even with volume (as tubercles), while the ones in the lower half were much less pronounced and fading.

DNA barcodes. 16S and COI were obtained for two specimens, IEO-CD-MZ08/1815 and IEO-CD-MZ09/1791.

The 16S sequences had no differences between them, and for COI two haplotypes differing only in one position were obtained. There are not sequences available for *C. africana* on any public database. However, the 16S sequences fit 99.44% (only differ in three positions) with an unpublished sequence of *C. japonica* (MG029426) obtained by Deepak *et al.* probably from an Indian specimen and fit 99.56% (only differ in two positions) with a shorter sequence (450 bp) of *C. japonica* from Japan obtained by Ewers-Saucedo *et al.* (2016). Respect to COI the two haplotypes differ in one or two mutations of another unpublished COI sequence (KT003706) of *Calappa* sp. (voucher CSP2) also obtained by Deepak *et al.* and probably also belonging to an Indian specimen. According to these data, probably the *Calappa* sp. is an individual of *C. africana*, a closer species to *C. japonica* as indicated by the low divergence in the 16S gene, and both species could be sympatric in Indian waters.

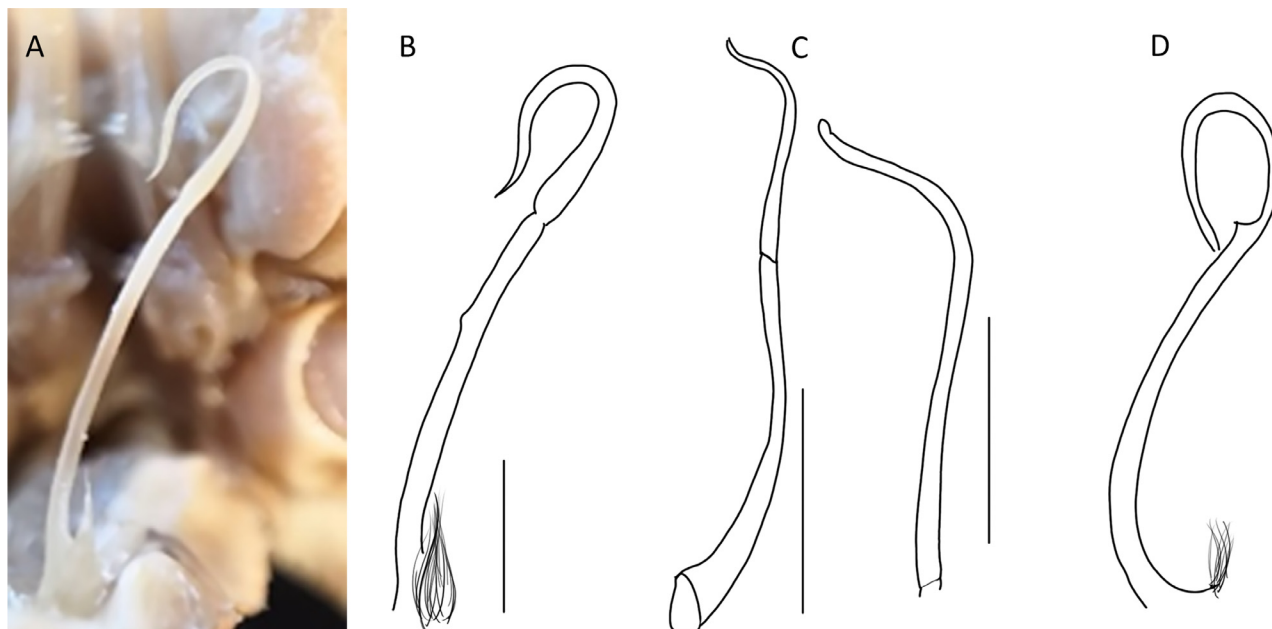


FIGURE 6. A and B, G2 *Calappa africana* IEO-CD-MZ07/1923; C, G2 *Calappa africana* (after Lay & Ng, 2006); D, G2 *Calappa japonica* (after Galil, 1993). Scale bars: 1mm.

Mursia Desmarest, 1823

Mursia africana Galil 1993

(Figure 4E)

Material examined. M07, Stn. 69, 366m, 51×39.1mm (CW without lateral spine) (IEO-CD-MZ07/1896), 16S (MZ424925), COI (MZ434771); M08, Stn. 54, 211m, ♂ 50.4×38.6mm (IEO-CD-MZ08/1797), 16S (MZ424926), COI (MZ434772).

Habitat and distribution. This is one of the three species of *Mursia* recorded in Southeast African waters (Emmerson 2016b,c; Spiridonov & Apel 2007). Its geographical distribution ranges from Kenya to Mozambique, at depths between 177–290m (Spiridonov & Apel 2007) and Thailand (Sasaki 2019). This distribution could be extended to Somalia if we consider a specimen deposited in the *Collection Crustacea SMF* (Senckenberg Institute, Germany), record published by GBIF.org (2021, unpublished record).

Results and remarks. These two specimens collected in M07 and M08, agree well with the description by Galil (1993). The specimens were caught at depths between 211 and 366m, this extending the depth range in Mozambique and worldwide, up to 366m.

Colouration observed. The carapace and chelae were orange brown with small red tubercles and to a lesser extent, with white tubercles, these mainly through the intestinal region. Bigger tubercles and the anterolateral edge of the carapace were red with white tips. Pereiopods were cream coloured ventrally, and light orange dorsally. After preservation, both in alcohol and formaldehyde, specimens keep the dorsum of carapace light brown, with the deeper areas between tubercles reddish and ambulatory legs in beige.

DNA barcodes. There are not available sequences for this species on any public database. The 16S sequences are equal for both specimens and there are two haplotypes for COI (differing in three mutations), and in both cases differ markedly from the other 16S and COI sequences of *Mursia* spp. in Genbank and BOLD.

Mursia aspera Alcock, 1899

(Figure 4F)

Material examined. M07, Stn. 70, 519m, ♀ 62.5×45.6mm (IEO-CD-MZ07/1903), 16S (MZ424926).

Habitat and distribution. *Mursia aspera* is distributed off Madagascar, the Seychelles, and Maldives (Galil 1993), between 150 and 384m depth and in Japan, at a depth range of 200–250m (Sakai 1965).

Results and remarks. Only one specimen was collected in M07, at 519m, off Inhambane. This specimen agrees well with the descriptions and figures of Galil (1993) and Spiridonov & Apel (2007). This is the first record of the species in Mozambican waters that also expands the maximum depth range of the species worldwide, from 384 to 519m.

Colouration observed. Pictures of fresh specimens are not available.

DNA barcodes. Only a 16S sequence (530 bp) was obtained, this being the first DNA sequence for the species, since there is not any other sequence on any public database.

Mursia flamma Galil, 1993

(Figure 7G)

Material examined. M07, Stn. 10, 382m, ♂ 63.3× 46.8mm (CW without lateral spine) (IEO-CD-MZ07/1904).

Habitat and distribution. *Mursia flamma* is distributed in the southwest of the WIO, between Kwazulu-Natal in South Africa, Mozambique and Madagascar (Emmerson 2016b,c; Galil 1993; Spiridonov & Apel 2007), between 210 and 520m depth (Emmerson 2016b,c).



FIGURE 7. *Mursia flamma*, ♂ IEO-CD-MZ07/1904: photography of merus of right cheliped showing four spines (red arrow indicates the position of the fourth spine). Scale bar: 1cm.

Results and remarks. One single male specimen was collected at 382m depth. For identification, the keys provided by Galil (2003) and Spiridonov & Apel (2007) were used.

This specimen does not completely conform to the original description of *M. flamma*. In addition, there are certain characters that do not match the posterior redescription made by Galil (2003). The median tooth of the rostrum of our specimen is not triangular, as described by Galil (2003), but rounded, as described in the review of

M. flamma made by Spiridonov & Apel (2007). Galil (2003) reported three spines on the merus of the chelipeds, but our specimen has four, one of them being minute. While Spiridonov & Apel (2007) described three spines, a minute fourth spine can be appreciated in the merus of the cheliped in some pictures of *M. flamma* of the MNHN, this suggesting that the number of spines on the merus of the cheliped could be three or four, the fourth being a tiny one (see Figure 7). Thus, the number of spines of the cheliped might not be a distinctive character for *M. flamma*.

Colouration observed. Our specimen was quite strong reddish-brown, with slightly lighter tubercles, the larger ones with whitish tips, as well as the spines on the posterior margin of the carapace. Chelipeds have the same colour as the carapace, and pereopods were lighter reddish tone with the proximal part of the merus and the dactyli whitish.

DNA barcodes. The specimen was preserved in formalin and therefore, it was not possible to get DNA sequences.

***Mursia* sp.**

(Figure 4H)

Material examined. MOZ09, Stn. 84, 254m, ♂ 19.4×15.8 mm (CW without lateral spine), 30.1mm (CW including lateral spines) (IEO-CD-MZ09/1775-1), 16S (MZ424928), COI (MZ434773); ♂ 13.9×15.5mm (CW without lateral spine), 19.8mm (CW including lateral spines) (IEO-CD-MZ09/1775-2), 16S (MZ424929), COI (MZ434774).

Results and remarks. Both male specimens were collected at the same station in 2009, at 254m depth, near the southern border of Mozambique. The specimens were small, maybe juveniles in which the typical characters of the adults are usually overdone, and consequently, they did not exactly fit to the original descriptions based on adults. In any case, the morphology did not allow to identify them as any of the species described and listed in the IP by Crosnier (1997a,b), Galil (1993, 2001), Galil & Takeda (2004), Spiridonov & Apel (2008) or Takeda & Galil (2005), or any other known species of *Mursia*.

Colouration observed. The carapace and chelipeds were orange-brown, with slightly lighter tubercles, the larger ones with a white top. The pereopods were light orange with whitish dactylus.

DNA barcodes. The two 16S sequences are equal and do not correspond with any other sequence on any public database. However, the two COI sequences represent two haplotypes that differ in two positions, and both differing in only one mutation respect to two equal COI sequences obtained of the same specimen MNHN_IU200810365 collected at 303m depth in the Mb-exp. The first sequence deposited in BOLD (MDECA061-10) was only attributed to *Mursia* sp. by Chan, but in the MNHN appears as *M. flamma*. The second sequence, deposited in Genbank (KU853991) and submitted by Ewers-Saucedo *et al.* (unpublished) was identified as *Mursia cristiata*. Clearly, the sequence KU853991 does not correspond to *M. cristiata*, since the 16S sequence of this species (KU206617) does not match with the 16S sequence of *Mursia* sp. Molecular as well as morphological data suggest that probably this specimen deposited at the MNHN (currently as *M. flamma*) and the two males collected in M09, belong to the same undescribed species of *Mursia*.

Superfamily CANCROIDEA Latreille, 1802

Family CANCRIDAE Latreille, 1802

According to Davie *et al.* (2015a) this family includes six genera and 33 species. Only the genus *Platepistoma* Rathbun has been recorded in Mozambican waters.

***Platepistoma* Rathbun, 1906**

***Platepistoma guezei* (Crosnier, 1976)**

(Figure 8A)

Material examined. M07, St. 18, 530m, ♀ 67.7×52.6mm (IEO-CD-MOZ07/279); M08, Stn. 4, 643m, ♀ 57.2×43.6mm

(IEO-CD-MZ08/1852-1), ♂ 71.7×43.6mm (IEO-CD-MZ08/1852-2), 16S (MZ424930), COI (MZ434775); M09, Stn. 9, 540m, ♀ ov 45.2×33.9mm (IEO-CD-MZ09/1765), 16S (MZ424931), COI (MZ434776); M09, Stn. 27, 543m, ♀ 61.8×46.2mm, ♂ 63.9×46.8mm, ♂ 68.3×52.2mm (IEO-CD-MZ09/1853), COI (MZ434777); M09, Stn. 56, 511m, ♂ juvenile, 12×9.4mm (IEO-CD-MZ09/1761).

Habitat and distribution. Known only from Reunion Island and Madagascar in the southwestern Indian Ocean. The reported bathymetric range is 350–720m (Davie 1991).

Results and remarks. The keys from Crosnier (1976), Davie (1991) and Davie & Ng (2012) were used to identify the seven specimens collected at depths between 511–643m in the three surveys. In all specimens, a combination of the features described by Crosnier (1976) for *P. guezei* and by Davie & Ng (2012) for *P. seani* were observed. Davie & Ng (2012) differentiated both species based in several characters like: setal coverage from dorsal carapace, carpus and chela; definition of carapace regions; spines of the carapace margins; number of horizontal rows of spines in claws; spines on the carpus of the claw or shape of the male telson. However, none of the seven specimens clearly matches with the complete description of any of both species, and finally we have opted for *P. guezei* considering that *P. seani* was described on the basis of one single individual, therefore not covering all the expected variability of the species as well as the features of the male.

Colouration observed. Specimens were covered by a dense brownish tomentum overall and have pink pereopods with white dactyls and their tips black. The fingers of the chelae were black.

DNA barcodes. Since there are not sequences available for this genus on any public database, the two equal 16S sequences of the specimens from MZ08 and MZ09 as well as the three COI sequences (three haplotypes), are the first DNA markers for this species as well as for the genus.

Superfamily ERIPHIOIDEA MacLeay, 1838

Family DAIROIDIDAE Števcíć, 2005

This family was described in 2005 by Števcíć only for the genus *Dairoides* Stebbing. Previously, these species were considered xanthid crabs (Barnard 1950; Kensley 1981), later parthenopids (Sakai, 1976), rather than Eriphiidae. In accordance with Davie *et al.* (2015a), this family includes only one genus and three species, *Dairoides kusei* (Sakai), *Dairoides margaritatus* Stebbing and *Dairoides seafdeci* Takeda & Ananpongsuk. *D. margaritatus* is the only species cited in the area (Barnard 1950; Guinot 1967a,b; Kensley 1981; Stebbing 1920).

Dairoides Stebbing, 1920

Dairoides margaritatus Stebbing, 1920

(Figure 8B)

Material examined. M07, Stn. 84, 129m, ♀ 39.7×26.1mm (IEO-CD-MZ07/1911), 16S (MZ424932), COI (MZ434778).

Habitat and distribution. It could be an endemism of southern Africa, distributed from KwaZulu-Natal to Mozambique (Stebbing 1920; Barnard 1950; Guinot 1967a,b; Kensley 1981; Emmerson 2016b,c) at depths between 20 to 180m (Kensley 1981).

Results and remarks. One female specimen of *Dairoides margaritatus* was collected in M07 at 129m. The keys by Guinot (1967b) were used for identification.

Colouration observed. Pictures of the fresh specimen are not available.

DNA barcodes. There are not 16S and COI sequences of this species on any public database, and therefore, these are the first ones. In Genbank there are only one 16S (HM637979) and one COI (HM638030) sequences available for *Dairoides kusei* based in one specimen (ULLZ 9183) from Hawaii obtained by Lai *et al.* (2014). The 16S sequence differs in three mutations (in 533 bp, 99.43% similarity) that could be in the intrageneric range, as well as in the case of the COI sequence varying in 58 positions (in 588 bp). The results (especially for COI sequence) of the BLAST and BOLD searches also suggest the affinity of *Dairoides* with Parthenopidae, as already pointed out by Lai *et al.* (2014).



FIGURE 8. A, *Platepistoma guezeti*, ♀ IEO-CD-MOZ07/279; B, *Dairoides margaritatus*, ♀ IEO-CD-MZ07/1911 (preserved); C, *Carcinoplax ischurodous*, ♂ IEO-CD-MZ08/1824; D, *Carcinoplax longimanus*, ♂ IEO-CD-MZ08/1787; E, *Carcinoplax longimanus*, ♀ IEO-CD-MZ08/1851; F, *Tanaoa pustulosus*, ♀ IEO-CD-MZ08/1776; G, *Euclosiana exquisita*, ♀ IEO-CD-MZ08/1757. Scale bars: 1cm.

Superfamily GONEPLACOIDEA MacLeay, 1838

Family GONEPLACIDAE MacLeay, 1838

This family has been extensively studied and consequently, has experienced many taxonomic changes in recent years (Castro 2007; Davie 2002; Karasawa & Kato 2003; Karasawa & Schweitzer 2006). According to Davie *et al.* (2015a) the family includes 20 genera and 90 species, most of them restricted to the IWP. Only two genera have been cited in Mozambican waters, *Carcinoplax* H. Milne-Edwards and *Psopheticus* Wood-Mason.

Carcinoplax H. Milne Edwards, 1852

Carcinoplax ischurodous (Stebbing, 1923)

(Figure 8C)

Material examined. M07, Stn. 13, 620m, ♂ 36.5×25mm (IEO-CD-MZ07/1918); M08, Stn. 39, 631m, ♂ 51.6×33mm, ♂ 54.4×33.7mm (IEO-CD-MZ08/1824), 16S (MZ424933), COI (MZ434779); M09, Stn. 14, 608m, ♂ 39.5×25.9mm (IEO-CD-MZ09/1768), 16S (MZ424934), COI (MZ434780).

Habitat and distribution. IWP, from South Africa (Barnard 1950) to the southwestern Pacific Ocean (Guinot & Richer de Forges 1980) at depths of 464–800m, being one of the few *Carcinoplax* species mainly distributed on the slope and not on the continental shelf (Castro 2007). The morphology of *C. ischurodous* differs considerably from the rest of its congeneric species, this suggesting the possibility of belonging to a different genus (Guinot 1989; Manning & Holthuis 1988).

Results and remarks. The three specimens, each one collected in one of the three surveys at depths between 608 and 631m, perfectly fit the descriptions and figures of Castro (2007). The species was reported in the latest checklist for the area (Emmerson 2016c), but only from records off South Africa. Thus, this is the first record of *C. ischurodous* in Mozambican waters. Anyway, we are aware from GBIF.org (2021, unpublished record) of the existence of conserved specimens of *C. ischurodous* housed on the MNHN from the MB-exp (2009) (unpublished).

Colouration observed. Fresh specimens looked polished, with the carapace orange-brown with some white small spots, and the posterolateral margin lighter; the chelipeds were bright orange with some deep-orange patches on the merus; the fingers and the knob at the beginning of the fingers were bright white. The pereiopods were pale orange with unarmed and pinkish dactyls.

DNA barcodes. There are not sequences of this species on any public database. The two equal 16S sequences and the two COI sequences (two haplotypes) are the first ones for this species. The BLAST search results for 16S show a 94.01% similarity with *Goneplax rhomboides* (JN591655) (27 mutations, including two gaps), and 93.79% with *Carcinoplax surungensis* (FJ943433) (36 mutations, including five gaps), and a longer distance respect to *Carcinoplax longimanus* (this study), 45 mutations, including four gaps. All these evidences support the possibility that *C. ischurodous* could belong to a different genus closer to *Goneplax* than to *Carcinoplax*.

Carcinoplax longimanus (De Haan, 1833)

(Figure 8D,E)

Material examined. M07, Stn. 106, 259m, ♀ 54.3×43.9 (IEO-CD-MZ07/1919); M08, Stn. 68, 244m, ♂ 59.2×48mm; ♂ 58.5×46.5mm; ♂ 66×52.4mm; ♂ 55.2×44.1mm (IEO-CD-MZ08/1787); M08, Stn. 69, 277m, ♀ 44.2×36.6mm; ♂ 65.4×51.2mm; ♂ 67.5×52.6mm; ♂ 52×42mm; ♂ 49.2×49mm; ♂ 54.8×45.7mm; ♂ 50×41.1mm (IEO-CD-MZ08/1786); M08, Stn. 74, 336m, ♀ 52.4×41.2mm (IEO-CD-MZ08/1851), 16S (MZ424935), COI (MZ434781); M08, Stn. 75, 256m, ♀ 51.2×41.2mm, ♀ 50.6×40.9mm (IEO-CD-MZ08/1826); M09, Stn. 83, 299m, ♂ 62×47.7mm (IEO-CD-MZ09/1828); M09, Stn. 84, 254m, ♀ 51.2×41.4mm (IEO-CD-MZ09/1829-1), COI (MZ434782), ♂ 24.2×18.1mm, ♂ 50.66×40.2mm (IEO-CD-MZ09/1829-2), 16S (MZ424936), COI (MZ434783).

Habitat and distribution. Wide distribution from South and East Africa to the western Pacific Ocean (Korea and Japan to Indonesia) from 6 to 377m depth (Castro 2013). In waters of Mozambique, it was cited between

66–377m (Emmerson 2016c) and between 80 and 120m (Sasaki 2019). It is a very abundant species in a wide depth range and quite common in the bycatch of shrimp trawl fisheries (Oh *et al.* 2009; Sobrino *et al.* pers. comm.). They are benthic crabs, which inhabits mud or sand bottoms where they build burrows (Castro 2007; Hsueh & Hung 2009; Kensley 1981; Ng 1998).

Results and remarks. Our specimens agree well with the descriptions and figures by Castro (2007). We checked 19 specimens of *C. longimanus* collected in M07, M08 and M09 surveys, at depths between 244 and 336m.

There is great size-related morphometric variability in this species. The antero-lateral teeth are polished over time and become smaller in relation to the specimen size with growing, in a way that the carapace edge seems to be unarmed in the biggest individuals. Moreover, there is also a certain sexual dimorphism, as the females and juvenile males have short chelipeds, while the chelipeds are exceptionally long in adult males (see Figure 8D), the merus and propodus being almost three times longer than in juveniles and females while the carpus remains practically the same length (see Figure 8E). These features were also illustrated by Yamashita (1965), Guinot (1989) and Ikeda (1998).

Colouration observed. Specimens looked polished, the carapace being orange-brown, the chelipeds bright orange with the fingers, the spines and the knobs at the beginning of the propodus, bright white. The pereopods were orange with the junction between merus-carpus and carpus-propodus white. Dactyli were brown, partly due to their dense tomentum. After preservation in ethanol or formalin, females and juveniles acquire a uniform bone colour, while the carapace of big males turns to brown.

DNA barcode. The two 16S sequences obtained for specimens from M08 and M09 fit 100% with an incomplete sequence of *C. longimanus* of 406 bp (hypervariable parts deleted) from Taiwan (?) (NTOU B00091, Genbank code KJ132525) included in the study by Tsang *et al.* (2014). Respect to COI sequences, each specimen presents a different haplotype (differing in just one mutation). These sequences show a similarity between 98.89 and 99.21% with three unpublished (private) sequences of specimens of *Carcinoplax longimanus* (as *C. longimana*) from South Korea deposited in BOLD. However, they present a similarity of 84.4% with *C. ischurodous* (99 mutations) that underline the above-mentioned differences of this species with congeneric ones, supporting the possibility of a different genus for *C. ischurodous*.

Superfamily LEUCOSIOIDEA Samouelle, 1819

Family LEUCOSIIDAE Samouelle, 1819

Leucosiidae is one of the most extensive family of crabs. It comprises three subfamilies, Cryptocneminae Stimpson, Ebaliinae Stimpson, and Leucosiinae Samouelle, with a total of 71 genera and 488 species (Davie *et al.* 2015a). They have similar shapes, usually small with rounded carapace, hence they are known as nut or pebble crabs (Poore 2004; Ward & Rainer 1988). According to Emmerson (2016b,c), ten species of Leucosiidae belonging to the three subfamilies have been cited in Mozambique waters, most of them in intertidal or shallow waters. This group has been intensively studied in recent years, with the description of new genera and species, and replacement of several species (Galil 2003a,b,c, 2005,b, 2006a,b, 2009; Galil & Ng 2010).

Subfamily EBALIINAE Stimpson, 1871

Tanaoa Galil, 2003

Tanaoa pustulosus (Wood-Mason in Wood-Mason & Alcock, 1891) (Figure 8F)

Material examined. M07, Stn. 4, 620m, ♂ 26.2×26.6mm; ♂ 25.5×25.5mm (IEO-CD-MZ07/1901); M07, Stn. 13, 630m, ♀ 36.8×34.8mm (IEO-CD-MZ07/1913); M07, Stn. 40, 190m, ♀ ov. 39.4×39.6mm (IEO-CD-MZ07/1899); M07, Stn. 70, 519m, ♀ ov. 41.5×38.1mm (IEO-CD-MZ07/1894); M08, Stn. 4, 643m, ♂ 39.7×37.7mm (IEO-CD-MZ08/1778); M08, Stn. 6, 428m, ♂ 36.2×35.6mm; (IEO-CD-MZ08/1811); M08, Stn. 45, 658m, ♀ 33×33.8mm

(IEO-CD-MZ08/1917-1), 16S (MZ424937); ♂ 37.6×36.9mm (IEO-CD-MZ08/1917-2), 16S (MZ424938), COI (MZ434784); M08, Stn. 65, 546m, ♀ 37.5×38.7mm (IEO-CD-MZ08/1776); M09, Stn. 33, 470m, ♀ 36×34.8mm (IEO-CD-MZ09/1766); M09, Stn. 67, 625m, ♀ ov. 36×36.6mm (IEO-CD-MZ09/1799-1), 16S (MZ424939), COI (MZ434785); ♂ 36.4×36.6mm (IEO-CD-MZ09/1799-2), 16S (MZ424940), COI (MZ434786).

Habitat and distribution. *Tanaoa pustulosus* is distributed along the IP (Fiji, New Caledonia, New Zealand, Japan, Taiwan, Indonesia, Philippines, Andaman Sea, Seychelles, Comoro Islands, Madagascar, Reunion, Mozambique Channel and East Africa), at 85–977m depth (Galil 2003c).

Results and remarks. Our specimens agree well with the descriptions and illustrations included in the work of Galil (2003c), in which the genus *Randallia* Stimpson was redefined, and the new genus *Tanaoa* erected. Thirteen specimens of *T. pustulosus*, collected in the three surveys (M07, M08 and M09), at depths between 190 and 658m, were examined. These specimens are the first records of *T. pustulosus* in Mozambican waters. After our surveys, some specimens were collected in the MB-exp in 2009 (Chan & Ng, pers. comm. to Emmerson, 2016c).

Colouration observed. The dorsal surface of the carapace was orange, with red tubercles on the gastric area and whitish tubercles on the cardiac and intestinal areas. Legs were pale pinkish-white.

DNA barcodes. There are not 16S sequences available for this species in Genbank, and thus, the four sequences (two haplotypes, differing in one position) of the specimens from MZ08 and MZ09 are the first ones for this species. There is only one COI sequence deposited in BOLD (MDECA231-10), corresponding to a specimen of *T. pustulosus* collected in Mozambique, by the MB-exp in 2009 (date collection: 2009-04-09) deposited at the MNHN (MNHN-IU200812672). The COI sequences of three specimens from MZ08 and MZ09 represent three different haplotypes (varying in one-two positions), fitting 99% with the BOLD sequence (varying in three to five positions).

Subfamily LEUCOSIINAE Samouelle, 1819

Euclosiana Galil & Ng, 2010

Euclosiana exquisita (Galil, 2003)

(Figure 8G)

Material examined. M08, Stn. 18, 217m, ♀ 26.9×28.4mm (IEO-CD-MZ08/1757), 16S (MZ424941), COI (MZ434787).

Habitat and distribution. According to Galil (2003b), *Euclosiana exquisita* is known only from the type-location, Madagascar, at 185–314m depth.

Results and remarks. Only one female was collected in M08 at 217m depth. This specimen agrees well with the descriptions and figures by Galil (2003b). *E. exquisita* has not been reported in the area before and therefore our specimen is the first record of the species in Mozambican waters. After the MOZAMBIQUE surveys, some specimens were collected in the MB-exp in 2009 (MNHN Collection).

Colouration observed. Carapace and chelipeds were reddish brown, with three bright orange circles on each gastric region, being the median circle the largest. The anterior third of carapace is coarsely pitted. There were two very pale and poorly marked circles on the cardiac region, and a couple of faint lines on the middle of the intestinal region that remain after preservation, none of them described by Galil (2003b). The granules of the chelipeds were white, and the legs with orange and white bands. The ventral side was white. After preservation in ethanol, the carapace and chelipeds turned to brown, and the circles and legs to bone colour.

DNA barcodes. There are not 16S sequences available for this species in Genbank, being this the first one. There is only one COI sequence deposited in BOLD (MDECA222-10), corresponding to one specimen identified as *Leucosia* sp. by Chan, that was collected in Mozambique by the MB-exp in 2009 (date collection: 2009-04-09), and deposited at the MNHN (MNHN-IU200812661). The COI sequence of the female IEO-CD-MZ08/1757 fits 99.68% with the BOLD sequence (differing in two mutations). Therefore, the specimen MNHN-IU200812661 identified as *Leucosia* sp. must be considered to be *Euclosiana exquisita*.

In Genbank there are sequences of 16S and COI for *Euclosiana crosnieri*, *E. scitula*, and *E. unidentata*, deposited by Shi *et al.* (2020). The distances with *Euclosiana exquisita* are the expected for congeneric species: 16S (98%, five mutations) and COI (94%, 35 mutations). However, the high divergence of *E. crosnieri* and *E. scitula*

respect to *E. unidentata* (16S, 96.8%, 12 mutations - including three gaps - and COI, 87%, 86 mutations) suggests an intergeneric distance. It must be pointed out that *E. crosnieri* and *E. scitula* could be synonyms, as they present exactly the same 16S and COI sequences.

Superfamily MAJOIDEA Samouelle, 1819

Family EPIALTIDAE MacLeay, 1838

According to Davie *et al.* (2015a), this large family includes 89 genera and 452 species. Four subfamilies are recognized, Epialtinae MacLeay, Pisinae Dana, Pliosomatinae Števcíć, and Tychinae Dana (Ng *et al.* 2008). They inhabit shallow waters, even intertidal (Emmerson 2016b,c). All the subfamilies except Pliosomatinae are represented in the study area

Subfamily PISINAE Dana, 1851

Oxypleurodon Miers, 1885

Oxypleurodon difficilis (Guinot & Richer de Forges, 1985)

(Figures 9A, 10)

Material examined. M08, Stn. 55, 411m, ♂ 14×16.5mm (IEO-CD-MZ08/1774), 16S (MZ424942), COI (MZ434788); M08, Stn. 107, 549m, ♂ 21×28.2mm (IEO-CD-MZ08/1897-2); ♀ ov. 18.8×23.8mm (IEO-CD-MZ08/1897-1), 16S (MZ424943), COI (MZ434789); M09, Stn. 9, 540m, ♀ 18.1×27.3mm (IEO-CD-MZ09/1823-0a); ♀ 17.9×25.5mm (IEO-CD-MZ09/1823-0b); ♂ 21.5×30.1mm (IEO-CD-MZ09/1823-1), 16S (MZ424944), COI (MZ434790); ♀ ov. 22.2×29.3mm (IEO-CD-MZ09/1823-2), 16S (MZ424945), COI (MZ434791).

Habitat and distribution. Only one species of *Oxypleurodon* was previously reported in Mozambican waters, *Oxypleurodon holthuisi* (Richer de Forges, 2018) while *Oxypleurodon difficilis* (Richer de Forges, 1984) was recorded in nearby waters of Madagascar (Guinot & Richer de Forges 1986).

Results and remarks. Seven specimens were collected during the M08 and M09 surveys, at depths from 411 to 549m. The keys and descriptions consulted for their morphological revision were Lee *et al.* (2017), Guinot & Richer de Forges (1984), Richer de Forges (1995, 2010, 2018) and Richer de Forges & Ng (2013). These are the first records of this specie in Mozambique waters.

Following the key for *Oxypleurodon* of the IP (Guinot & Richer de Forges 1984), these seven specimens could be identified as *O. difficilis* but there are certain characters that are not coincident with the original description. Guinot & Richer de Forges (1984) described the intraspecific variability in the shape and size of the rostrum. According to them, juvenile males are similar to females in presenting a shorter and thicker rostrum than males. However, the adult males of *O. difficilis* IEO-CD-MZ08/1774 and IEO-CD-MZ08/1897 present short rostrum, and oppositely, the females IEO-CD-MZ09/1823-0a and IEO-CD-MZ09/1823-2 bear elongated rostrum. In some specimens, the rostra are straight and in others curved upwards. In relation to the size of the channels between dorsal plates, Guinot & Richer de Forges (1984) described wider channels in the juvenile males, but this is also a variable feature in our specimens. Therefore, more similar to *O. aurorae* respect to this character. In addition, Guinot & Richer de Forges (1984) described the cardiac plates of *O. difficilis* as: “always transversely oval-shaped”. However, our specimens show great variability in the shape of this plate, from laterally elongated (upward or downward) to inverted triangle-shaped (see Figure 10).

Colouration observed. The specimens had a salmon-pink carapace, rostrum dark orange and plates of the dorsal surface white; 4th-5th ambulatory legs white, and the chelipeds and 2nd and 3th legs salmon-pink, with propodus and dactyls clearly marked. Legs colour of *O. difficilis* described by Richer de Forges (2018) was merely white.

DNA barcodes. There are not 16S and COI sequences available for this species in Genbank or BOLD. The four equal sequences of 16S obtained for four specimens from MZ08 and MZ09 are the first ones for this species. There are two COI sequences deposited in BOLD (MDECA111-10 and MDECA112-10), corresponding to two

specimens of *O. stuckiae* collected in New Caledonia by Bouchet & Richer de Forges (date of collection: 1993-01-26), and deposited at the MNHN (MNHN-IU200812259 and MNHN-IU200812261). However, these sequences actually correspond to an unidentified *Heterocarpus* sp. according to the tree generated in BOLD and to the result of a BLAST search of these sequences in Genbank. The COI sequences obtained for four specimens of *O. difficilis* present only two haplotypes (differing in two positions). In a BLAST search, the maximum fit was 96% with the sequences of three *Plesionaka curvata*, and the rest of matches (<90 %) were with several majoid species. The sequences of *P. curvata* that were uploaded at Genbank (JX681746, JX681749, JX681750) by Zuccon *et al.* (2012) belong to specimens deposited in the MNHN (MNHN-IU200814409, MNHN-IU-2008-14410, MNHN-IU-2008-14412), which were also uploaded to BOLD (MDECA782-12, MDECA786-12, MDECA789-12), with other sequences of *P. curvata* that do belong to this species. Therefore, it seems that these three “strange sequences” of *P. curvata* could correspond to COI sequences of *O. stuckiae* since they fit 96% (22 mutations) with the sequences of *O. difficilis*, being in the expected range of intrageneric variability. Therefore, sequences of an unidentified *Heterocarpus* sp. were deposited instead of the sequences of *O. stuckiae* while the right sequences of *O. stuckiae* were deposited under the name of *Plesionaka curvata*.

***Naxioides* A. Milne-Edwards, 1865**

***Naxioides robillardi* (Miers, 1882)**

(Figure 9B)

Material examined. M07, Stn. 13, 620 m, ♀ 41.6×51.8mm (CW×PRL) (IEO-CD-MZ07/1892), 16S (MZ424946).

Habitat and distribution. *Naxioides robillardi* is distributed throughout the IWP: Gulf of Oman, East Africa (Kenya, Somalia), Madagascar, Reunion Island, Mauritius, Solomon, Indonesia, Hong Kong, Philippines, Australia, Japan (Poupin, 1995) and recently reported from Korea (Lee *et al.* 2020). It inhabits hard bottoms between 30 and 260m (Poupin 1995). *Naxioides hirtus* A. Milne-Edwards was the only species of *Naxioides* previously reported in Mozambican waters (Barnard 1950; Kensley 1981).

Remarks. The keys and descriptions used for the identification of this specimen were Griffin & Tranter (1986a), Miers (1886) and Poupin (1995). Poupin (1995) distinguished two forms of this species: *N. robillardi* forma *typica*, and *N. robillardi* forma *mammillata*, our specimen being coincident with the first. It should be noted that we collected one single female specimen in M07, at 620m depth. The absence of other specimens and the fact that the only one was lacking the chelipeds, made not possible to confirm all the characteristics used for distinguishing both forms. The present specimen is the first record of *N. robillardi* in Mozambican waters, extending the maximum depth reported for this species up to 620m.

Colouration observed. The carapace was beige and it is covered in short dense yellowish-brown pubescence, with purplish-red spines, similar to that described by Miers (1882). Ambulatory legs were purplish-red, with subtle light and dark bands, almost imperceptible. After preservation in formalin the specimen acquired a homogeneous bone colour, without traces of the purplish-red colour, contrary to the permanence of violet areas in merus and carpus of the ambulatory legs described by Poupin (1995) after preservation in ethanol.

DNA barcodes. There are not 16S sequences available for this species in Genbank, this being the first one. There are three equal COI sequences in Genbank (MT469872, MT469873, MT469874) obtained by Lee *et al.* (2020) from one specimen of *N. robillardi* from Korea. However, no COI sequence could be reared from the specimen IEO-CD-MZ07/1892 from MZ07 and therefore, comparison is not possible.

***Samadinia* Ng & Richer de Forges, 2013**

***Samadinia galathea* (Griffin & Tranter, 1986)**

(Figures 9C, 11)

Material examined. M09, Stn. 8, 648m, ♂ 15.5×16.7mm (IEO-CD-MZ09/1802-1), 16S (MZ424947), COI (MZ434792); ♀ ov. 9.5×11.5mm (IEO-CD-MZ09/1802-2), 16S (MZ424948), COI (MZ434792).

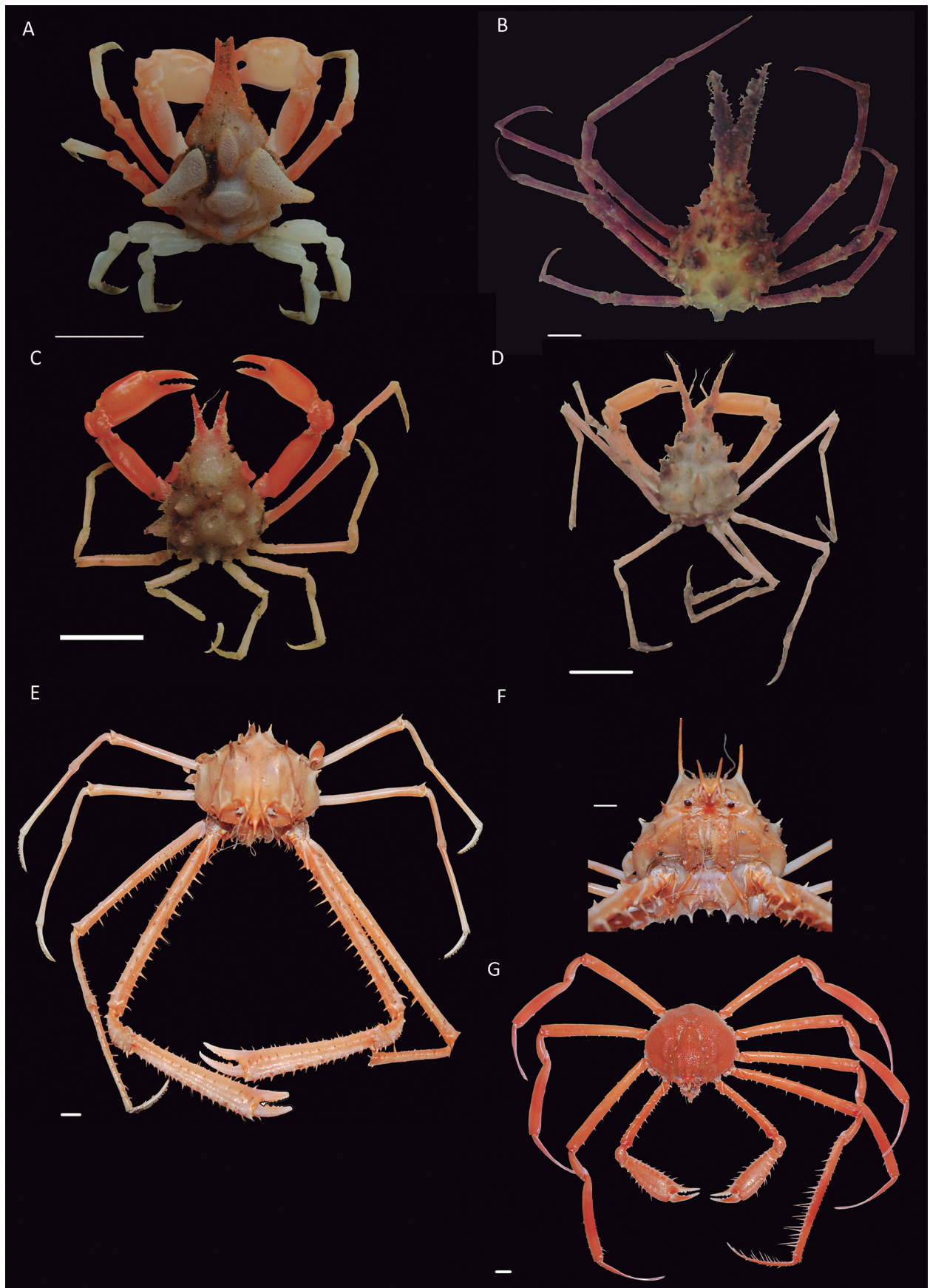


FIGURE 9. A, *Oxypleurodon difficilis*, ♂ IEO-CD-MZ08/1774; B, *Naxioides robillardi*, ♀ IEO-CD-MZ07/1892; C, *Samadinia galathea*, ♂ IEO-CD-MZ09/1802-1; D, *Samadinia pulchra*, ♂ IEO-CD-MZ07/1893; E,F, *Cyrtomaia gaillardi*, ♂ IEO-CD-MZ08/1788; G, *Platymaia alcocki*, ♂ IEO-CD-MZ08/1789. Scale bars: 1 cm.

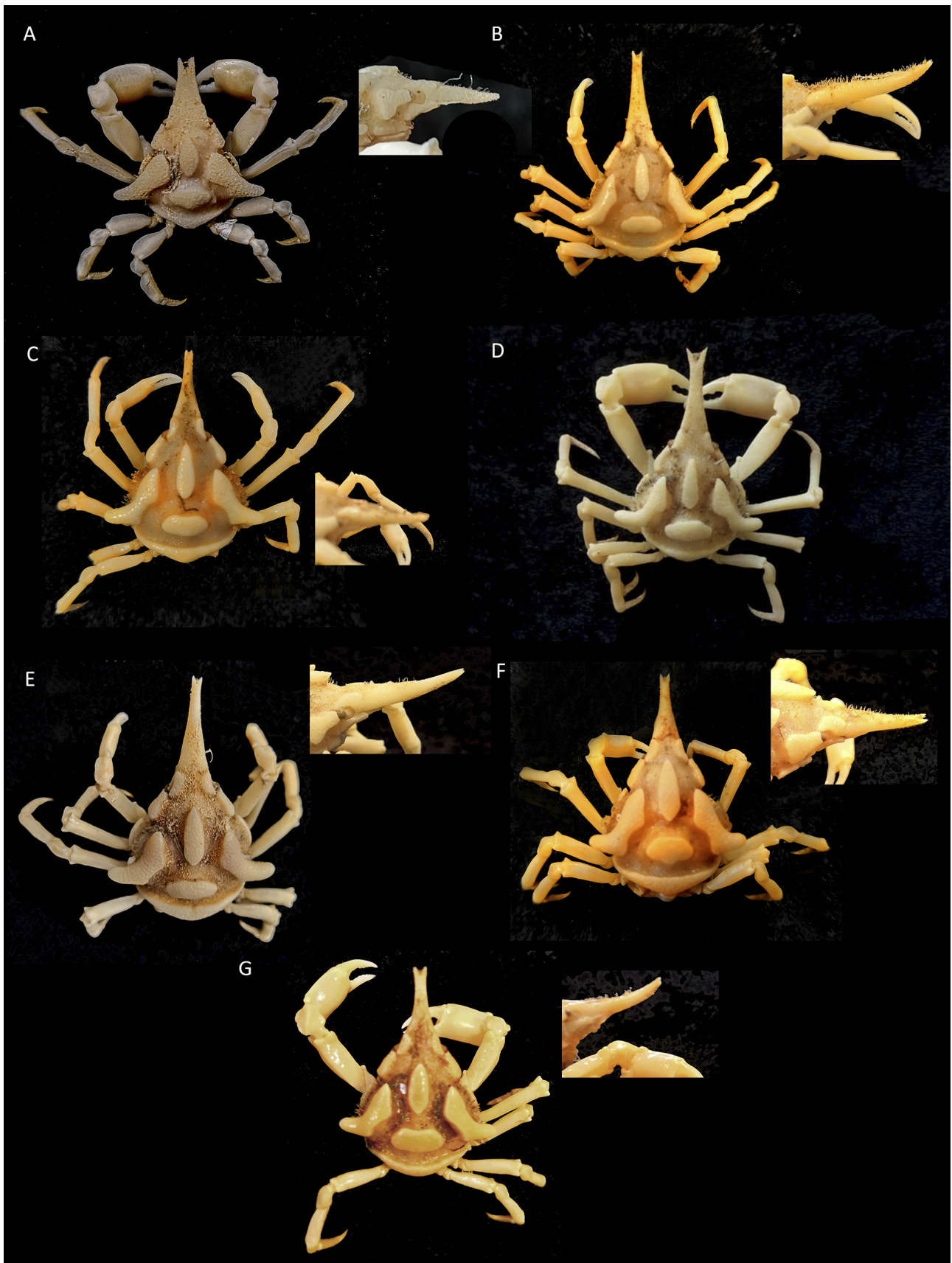


FIGURE 10. *Oxypleurodon difficilis*. A, ♂ IEO-CD-MZ08/1774; B, ♀ IEO-CD-MZ09/1823-0a; C, ♀ IEO-CD-MZ09/1823-0b; D, ♂ IEO-CD-MZ09/1823-1; E, ♀ IEO-CD-MZ09/1823-2; F, ♀ IEO-CD-MZ08/1897; G, ♂ IEO-CD-MZ08/1897.

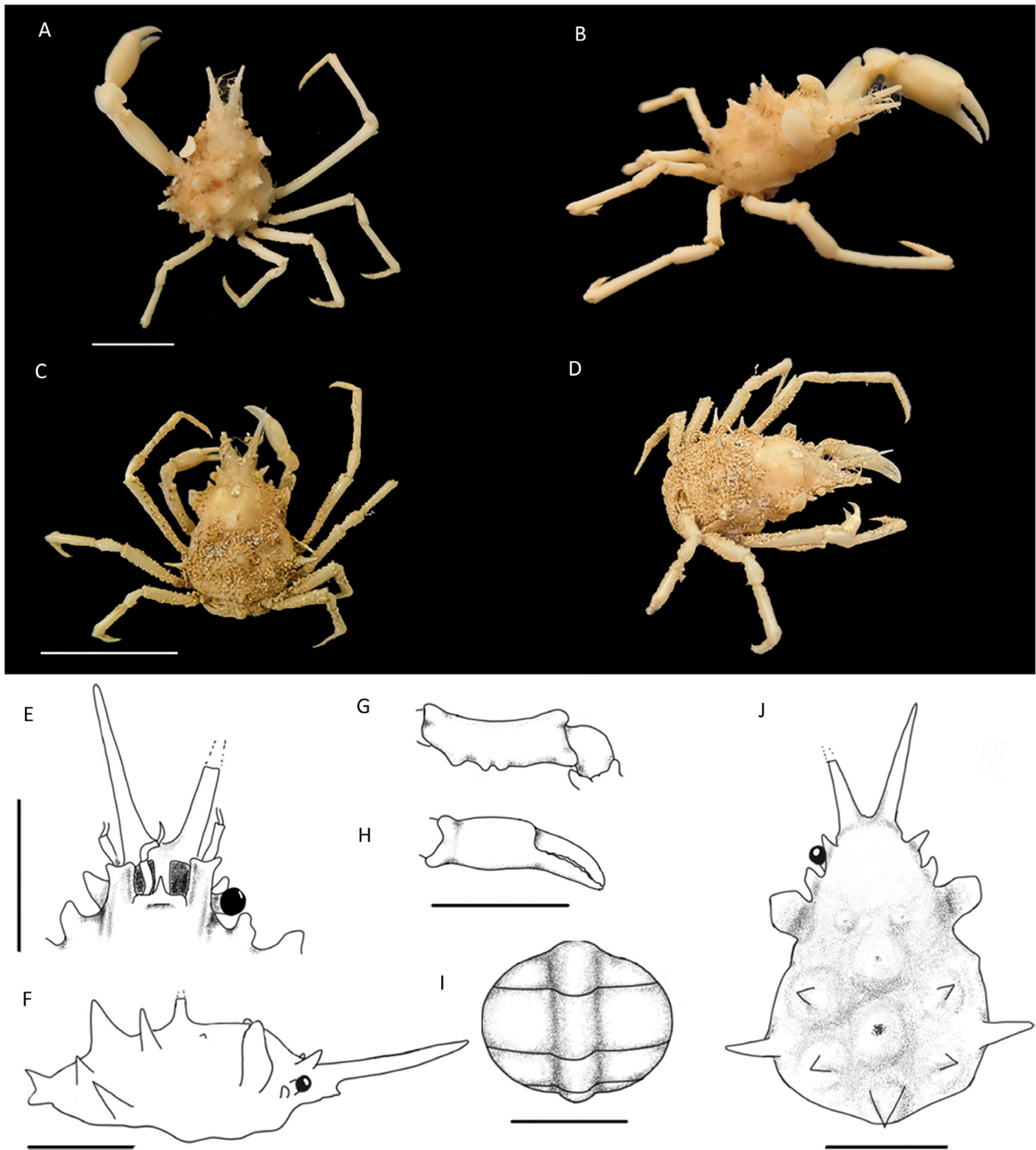


FIGURE 11. *Samadinia galathea*, A, B, ♂ IEO-CD-MZ09/1802-1; C, D, ♀ IEO-CD-MZ09/1802-2 (Scale bars: 1cm); E; *Samadinia galathea*, female, IEO-CD-MZ09/1902-2, ventral view of orbits; F, carapace, lateral view; G, right cheliped, merus and carpus; H, right chela; I, pleon; J, carapace, dorsal view (Scale bars: 0.5cm).

Habitat and distribution. *Samadinia galathea* was described by Griffin & Tranter (1986) as *Rochinia galathea*, from a male collected off Natal (South Africa) in 1951. This was the only existing record and thus, its distribution was limited to the topotypical locality, off Natal between 535 and 610m depth (Griffin & Tranter 1986).

Results and remarks. Our specimens agree well with the descriptions and figures of Griffin & Tranter (1986) and Richer de Forges & Ng (2013). Two individuals, one male and one ovigerous female were collected at the same station at 648m, in March 2009 (MZ09). This is the first record of *S. galathea* in waters of Mozambique, the second record worldwide and it extends the maximum depth reported for this species up to the 648m. In addition, it is the

first time that a female of this species is recorded, allowing the description of the female morphology, that differs somewhat to the described morphology of males. In the female, the mesogastric region is very inflated, “hump”-type, and the hepatic lobes are flattened and directed upwards (see Figure 11) while they curve backwards in the case of the male. The female was ovigerous, indicating that March was within the spawning season of this species in the area.

Colouration observed. The carapace was white, with some pinkish areas. The hepatic lobes and intestinal area were dark orange, the chelipeds orange and the ambulatory legs white with pinkish merus.

DNA barcodes. There are not 16S sequences available for this species or close relatives in Genbank. These equal 16S sequences of the male and female specimens are the first ones and confirm that the two specimens, despite their clear morphological differences, belong to the same species. There is one COI sequence deposited in BOLD (MDECA051-10), corresponding to one specimen identified by Chan as *Rochinia* sp., collected in Mozambique by the MB-exp in 2009 (date collection: 2009-04-09) and deposited at the MNHN (MNHN_IU200810334), that fits 100% with the two equal COI sequences of the male and female of *S. galathea*. There is also a second COI sequence deposited in BOLD (MDECA724-10) corresponding to one specimen identified by Chan as Epialtidae sp. and collected in Madagascar, that fits 99.39% (four mutations) with *S. galathea*, this being the distance expected at intraspecific level in a COI sequence. Therefore, both specimens, *Rochinia* sp. and Epialtidae sp., would correspond to *S. galathea*.

***Samadinia pulchra* (Miers, 1885)**

(Figures 9D, 12)

Material examined. M07, Stn. 34, 627m, ♂ 17×16.6mm; ♂ 11.5×17.5mm (broken lateral spines) (IEO-CD-MZ07/1893); M08, Stn. 22, 618m, ♀ 17.8×17.8mm; ♀ 13.9×14.9mm; ♀ 14.1×14.6mm (IEO-CD-MZ08/1819-1), 16S (MZ424949), COI (MZ434794); ♂ 10×11.9mm (IEO-CD-MZ08/1819-2), 16S (MZ424950), COI (MZ434795); M09, Stn. 31, 457m, ♀ 17.2×17.8mm (IEO-CD-MZ09/1817); M09, Stn. 34, 628m, ♀ 13.8×15.9mm (IEO-CD-MZ09/1758); M09, Stn. 51, 548m, ♀ 12.8×14mm (IEO-CD-MZ09/1818); M09, Stn. 53, 619m, ♂ 14×13.9mm (IEO-CD-MZ09/1783), 16S (MZ424951), COI (MZ434796).

Habitat and distribution. IWP from east Africa to Philippines and Japan (Griffin & Tranter 1986). It was recorded in waters of Mozambique by Richer de Forges & Ng (2013) at 355–636m depth.

Results and remarks. The specimens examined conform to the description made by Griffin & Tranter (1986). The ten specimens studied were collected during M07, M08 and M09, between 457 and 628m depth. This is the second published record of *Samadinia pulchra* off Mozambique, although according to the collection date, our specimens from 2007 and 2008 surveys represent the firsts collected in these waters. The species was reported as *Rochinia pulchra* by Richer de Forges & Ng (2013) from the MB-exp in 2009. The specimens reviewed here differ in the length and morphology of the rostrum, as it was already observed by Richer de Forges & Ng (2013). There are specimens with the rostral spines very curved downwards, while others have them almost straight. The same occurs with the opening angle between both rostral spines, exceptionally long and outwards curved in some specimens. Apart from the shape differences observed in the rostrum, we have also found differences between the lengths of the pseudo-thorn spines of the studied individuals (see Figure 12).

Colouration observed. The body was whitish, with orange carapace spines, rostral spines and chelipeds and pink ambulatory legs.

DNA barcodes. There are not 16S sequences available for this species or close relatives in Genbank. These equal three 16S sequences of the two males and one female are the first ones and differ in 13 mutations from the 16S sequences of *S. galathea* (97.5% similarity), in the expected interspecific range. The three specimens present the same COI haplotype, that fit 100% with one COI sequence deposited in BOLD (MDECA049-10), corresponding to a specimen identified by Chan as *Rochinia* sp., collected in Mozambique by the MB-exp in 2009 (date collection: 2009-04-09) and deposited at the MNHN (MNHN_IU200810330). According to these new data, this record must be attributed to *S. pulchra*.

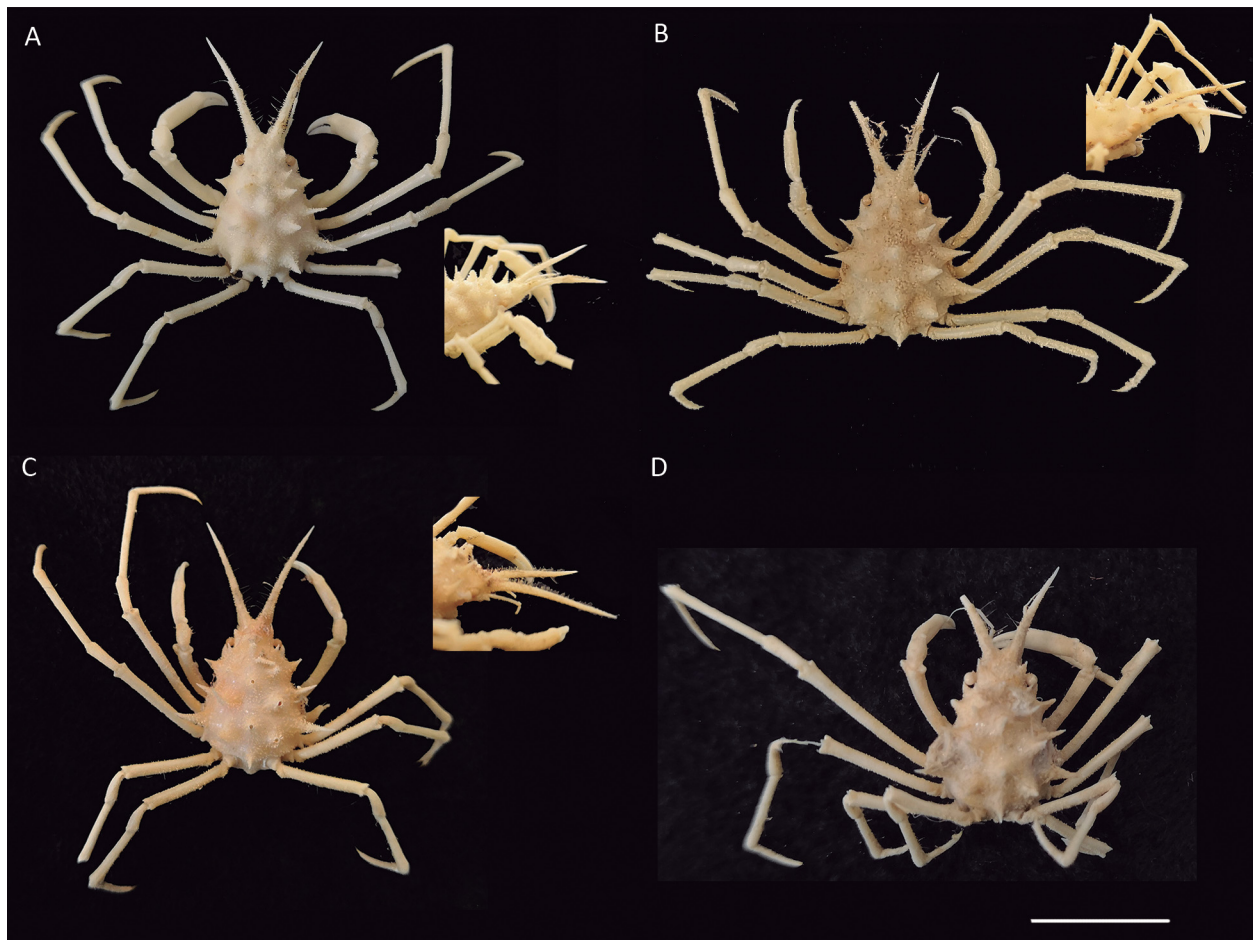


FIGURE 12. *Samadinia pulchra*. A, ♂ IEO-CD-MZ09/1783; B, ♀ IEO-CD-MZ09/1819-1a; C, ♀ IEO-CD-MZ09/1819-1b; D, ♂ IEO-CD-MOZ09/1819-2. Scale bars: 1cm.

Family INACHIDAE MacLeay, 1838

This family includes three subfamilies: Eucinetopinae Števc̆ić, Inachinae MacLeay and Podochelinae Neumann, 35 genera and 192 species (Davie *et al.* 2015a). Between the Inachinae, up to 17 species have been cited in Mozambique in the checklist of Emmerson (2016b,c).

Subfamily INACHINAE MacLeay, 1838

Cyrtomaia Miers, 1886

Cyrtomaia gaillardi Guinot & Richer de Forges, 1982

(Figures 9E,F)

Material examined. M07, Stn. 52, 556m, ♀ 67.5×60mm (CW×PRL) (IEO-CD-MZ07/1925); M08, Stn. 39, 631m, ♂ 62×59.9mm (IEO-CD-MZ08/1788); M09, Stn. 27, 543m, ♂ 66×64.5mm (IEO-CD-MZ09/1807); M09, Stn. 32, 529m, ♂ 63×57.3mm (IEO-CD-MZ09/1808), 16S (MZ424952).

Habitat and distribution. This species is distributed in Madagascar, Nicobar Island and Indonesia (Guinot & Richer de Forges 1982a).

Results and remarks. The specimens were identified following the key of Guinot & Richer de Forges (1982a,b, 1984, 1986). Four specimens of *Cyrtomaia gaillardi* were studied, that had been collected during the three surveys

(M07, M08 and M09), at depths between 529 and 631m. Although this species was recorded off Madagascar (Guinot & Richer de Forges 1982a), it is not registered in any checklist of the area (WIO) (Barnard, 1950; Emmerson 2016b,c; Kensley 1981; Poupin 2010, 2018), being *C. murrayi* Miers the only species of this genus cited in the area. Therefore, these specimens are the first record of *C. gaillardi* in Mozambique waters. Subsequently, in April 2009, one specimen was collected during the MB-exp (GBIF.org 2021, unpublished record).

Colouration observed. Specimens were light orange, with whitish finger tips, dactylus and proximal region of the merus.

DNA barcodes. There are not 16S sequences available for this genus in Genbank, except for a short sequence of 164 bp of *Cyrtomaia owstoni* deposited by Komai *et al.* (2019) that fits 100% with the 16S sequence (552 bp) of *C. gaillardi*. Considering the short length of the sequence and the low number of mutations expected at congeneric level nothing could be concluded. According to Guinot & Richer de Forges (1982a), *C. owstoni* has long branchial spines, these being the longest of the dorsal side of carapace, while protogastric spines are the longest in *C. gaillardi*. These clear morphological features make it difficult to confuse both species. Unfortunately, not COI sequence was obtained, although in any case there is not any COI sequence available in Genbank or BOLD for comparison.

Platymaia Miers, 1885

Platymaia alcocki Rathbun, 1918

(Figure 9G)

Material examined. M07, Stn. 1, 449m, ♀ 53.8×53.9mm; ♂ 68.2×68.2mm (IEO-CD-MZ07/1920), 16S (MZ424953), COI (MZ434797); M08, Stn. 68, 244m, ♂ (IEO-CD-MZ08/1789); M09, Stn. 19, 542m, ♂ 84.2×73.5mm (IEO-CD-MZ09/1854-2), 16S (MZ424954), COI (MZ434798).

Habitat and distribution. This species has an IP distribution, Andaman Sea, Great Nicobar, East African coast (Griffin & Trander 1986), East China Sea and Hong Kong (Sasaki 2019) and has been cited by Emmerson (2016c) in Mozambican waters, between 210–655m.

Results and remarks. The four studied specimens of *Platymaia alcocki* were collected in M07 and M09, at depths between 449 and 542m. The specimens were identified following Guinot & Richer de Forges (1986) and Griffin & Tranter (1986a,b). Although *P. alcocki* and *P. wyvillethomsoni* Miers were confused in the past, some features described mainly by Griffin & Tranter (1986a) allowed us to confirm the identification of our specimens as *P. alcocki*, among them: similar length of the interantennular spines in relation to the rostral spines; rostral spines curved inward; margins of the supraorbital eave gently tuberculated in males and sharply tuberculated and swollen in females; gastric regions strongly elevated and protogastric ridges tuberculated without spines; and apex of the tip of the first pleopod of the male curved up.

Colouration observed. Colour of carapace and legs bright orange, with some white parts as tips of quelipeds, dactyli and spines, basi-ischium and deeper areas of carapace.

DNA barcodes: There are not 16S sequences available for this species in Genbank. There is only a short (400 bp) and incomplete 16S sequence of *Platymaia remifera*, deposited in Genbank by Tsang *et al.* (2014) that probably correspond with the version of the sequence after alignment and removal of hypervariable positions, for example after application of GBLOCKS. Therefore, it is not possible a real comparison without the complete sequence. There is a COI sequence (MDECA062-10) in BOLD, corresponding to a specimen identified by Chan as *Platymaia* sp. that was collected in Mozambique by the MB-exp in 2009 (date collection: 2009-04-09) and deposited at the MNHN (MNHN_IU200810370). However, the COI haplotype of the two specimens of *P. alcocki* present a similarity of 83.5% respect to that of *Platymaia* sp., representing distances expected at intergeneric level.

Platymaia turbynei Stebbing, 1902

(Figure 13A)

Material examined. M07, Stn. 4, 620m, ♂ 38.8×48.4mm (IEO-CD-MZ07/1924); M08, Stn. 22, 618m, ♂ juvenile 8.3×8.7mm (IEO-CD-MZ08/1780-1), COI (MZ434799); ♂ juvenile 8.9×8.1mm (IEO-CD-MZ08/1780-2), COI

(MZ434800); 9.3×9.1mm (IEO-CD-MZ08/1780-3) 16S (MZ424955), COI (MZ434801); M09, Stn. 19, 542m, ♂ 24.2×39.8mm (IEO-CD-MZ09/1854-1); M09, Stn. 92, 619m, ♂ 25.3×42mm (IEO-CD-MZ09/1795).

Habitat and distribution. *Platymaia turbynei* is distributed along the east coast of South Africa, from Natal to southern Mozambique Channel, Madagascar, and Reunion Island (Griffin & Tranter 1986), between 200 and 880m (according to Kensley 1981) or 996m (according to Emmerson 2016c) in Mozambican waters.

Results and remarks. The six specimens were collected between March and April of M07, M08 and M09, at depths of 542–620m. Their morphological characters are in agreement with the descriptions included in the revision of some majoid crabs of IWP made by Griffin & Tranter (1986).

Colouration observed. Fresh specimens showed reddish carapace and salmon-colour legs. The spines are darker.

DNA barcodes. As already commented above for the 16S sequence of *P. alcocki*, there are not 16S sequences available for this species on any public database. There is only a short (400 bp) and incomplete 16S sequence of *Platymaia remifera*, deposited in Genbank by Tsang *et al.* (2014). Therefore, it is not possible a real comparison without the complete sequence, but the 15 mutations found in the 400 bp suggest a distance that fits well at intrageneric level. When comparing with the 16S sequence of *P. alcocki*, the similarity found of 91% could be considered in the limit between intra or intergeneric distance. This distance increased when comparing the COI sequences, with a similarity of 83%, that also supports a divergence at intergeneric level. There is a COI sequence (MDECA062-10) in BOLD that corresponds to one specimen identified by Chan as *Platymaia* sp. which was collected in Mozambique by the MB-exp in 2009 (date collection: 2009-04-09) and deposited at the MNHN (MNHN_IU200810370). This COI sequence fits 99.67 and 99.02% (one and seven mutations, respectively) with the two COI haplotypes obtained for *P. turbynei*, and for this reason it must be attributed to this species.

Family MAJIDAE Samouelle, 1819

According to Davie *et al.* (2015a) this family includes 31 genera and 126 species. This author divides the family in three subfamilies, Eurynolambrinae Števcíć, Majinae Samouelle and Planoterginae Števcíć. Only the subfamily Majinae is known to be present in Mozambican waters.

Subfamily MAJINAE Samouelle, 1819

Paramaja Kubo, 1936

Paramaja gibba (Alcock, 1895)

(Figure 13B)

Material examined. M07, Stn. 37, 243m, ♀ ov. 50.2×58.4mm (IEO-CD-MZ07/1916); M07, Stn. 78, 300m, ♂ 50.2×59.6mm (IEO-CD-MZ07/1912); M08, Stn. 25, 265m, ♂ 46.8×53.4mm (IEO-CD-MZ08/1781), 16S (MZ424956), COI (MZ434802); M08, Stn. 67, 378m, ♀ 49.1×52mm (IEO-CD-MZ08/1820), 16S (MZ424957), COI (MZ434803); M09, Stn. 60, 304m, ♂ 61.4×69mm (IEO-CD-MZ09/1800), 16S (MZ424958), COI (MZ434804).

Habitat and distribution. Majidae is constantly under review. In 2015, Ng and Richer de Forges described seven new genera to separate the species that were included within *Maja* Lamarck, 1801 until that moment. In this study *Maja gibba* was replaced in *Paramaja*, a genus described by Kubo in 1936. *Paramaja gibba* is close to *Paramaja kominatoensis* Kubo, a commonly mistaken and misidentified species. *Paramaja gibba* is distributed from the IWP, Madagascar (Mozambique Channel), India, Thailand to Western Australia (Ng & Richer de Forges 2015), and Japan (Sakai 1976), at 230–600m depth.

Results and remarks. These specimens agree well with the descriptions and figures of Ng & Richer de Forges (2015): “*in adults, pseudorostral horns dorso-ventrally flattened; carapace dorsal surface relatively less swollen, with numerous small and large distinct tubercles and granules which are never swollen*”. The five studied specimens were collected during the M07, M08 and M09 surveys, at depths from 243 to 378m. These are the first record of *P. gibba* off Mozambique. Subsequently, in April 2009, two specimens were collected during the MB-exp (GBIF.org 2021, unpublished record).



FIGURE 13. A, *Platymaia turbynei*, ♂ IEO-CD-MZ07/1924; B, *Paramaja gibba*, ♀ IEO-CD-MZ08/1820; C, *Sakaija africana* ♀ IEO-CD-MZ08/1784; D, *Pleistacantha ori*, ♀ IEO-CD-MZ08/12545; E, *Parathranites ori*, ♀ IEO-CD-MZ08/1767; F, *Paratranites granosus*, ♀ IEO-CD-Mz08/1785; G, *Parathranites orientalis*, ♀ IEO-CD-MZ07/1909 (preserved). Scale bars: 1cm.

Colouration observed. The specimens were bright orange with darker sunken areas and clearest lateral areas; legs were bone-colour although they seem to be brown due to fouling attached to them, as they were very hairy. Chelipeds were pale orange, with white finger tips. After preservation, both in ethanol and formalin, carapace and chelipeds turned to pale bone colour, while legs keep the brown-like colour due to the fouling.

DNA barcodes. There are not 16S and COI sequences available for this species on any public database. The three sequences obtained for 16S represent three different haplotypes, differing in one and two mutations, and they are the first 16S sequences for this species. One of these haplotypes belonging to the female IEO-CD-MZ09/1820 matches 100% with a 16S sequence (GQ153568) of *P. kominatoensis* (as *Maja kominatoensis*), obtained by Sotelo *et al.* (2009) from one specimen from Philippines. Similarly, in the case of COI, the three specimens present three different haplotypes, two of them differ only in one position, and another one that vary in three and four mutations. The COI sequence of the male IEO-CD-MZ09/1800 also matches 100% with two sequences (MG029415, KX757758) of two specimens of *P. kominatoensis* (as *Maja kominatoensis*) from India uploaded to Genbank by Deepak *et al.* (unpublished), and 99% with the COI sequence (GQ153558) of *P. kominatoensis* (as *Maja kominatoensis*) from Philippines (Sotelo *et al.* 2009). These data from 16S and COI barcodes put into question the validity of both species as separate taxa and support the suggestion by Griffin & Tranter (1986) that they may be synonymous. Therefore, a review of these two species (*P. gibba* and *P. kominatoensis*), including more specimens and more molecular data (also nuclear genes), is needed to clarify their taxonomic relationships and distributions.

***Sakaija* Ng & Richer de Forges, 2015**

***Sakaija africana* (Griffin & Tranter, 1986)**

(Figure 13C)

Material examined. M08, Stn. 18, 217m, ♀ 18.8×24.6mm (CW×PRL) (IEO-CD-MZ08/1784), 16S (MZ424959), COI (MZ434805).

Habitat and distribution. *Sakaija* is a new genus described by Ng & Richer de Forges in 2015, that previously belonged to *Maja*. This species seems common in the Mozambique Channel at depths around 300m (Ng & Richer de Forges 2015). It was recorded between 244–301m in Mozambican waters (Emmerson 2016c).

Results and remarks. Our specimen agrees well with the descriptions and figures of Griffin & Tranter (1986) and Ng & Richer de Forges (2015). Only one specimen was revised, that had been collected at 217m in MZ08. This record extends the minimum depth from 244 to 217m.

Colouration observed. The carapace was bright orange with red tubercles on it, except on its posterior edge, where the tubercles are white. The postorbital and intestinal spines had white tips and the pseudorostral spines were red. Legs were whitish, with a wide orange transversal band on the carpus. After preservation, all the specimens turned to bone colour with orangish merus and carpus.

DNA barcodes. There are not 16S and COI sequences available for this genus and species on any public database. Therefore, these are the first 16S and COI sequences obtained for this genus and species. The BLAST and BOLD searches do not match with any sequence >95% of similarity.

Family OREGONIIDAE Garth, 1958

The classification made by Davie *et al.* (2015a) was followed. Davie's and WoRMS (2021) classification agree with Marco-Herrero *et al.* (2013), that based on the molecular and larval morphology evidence, proposed the removal of *Ergasticus* A. Milne-Edwards, and related genera (*Bothromaia* A.B. Williams & Moffitt, *Parapleisticantha* Yokoya, *Pleistacantha* Miers and *Pleisticanthoides* Yokoya) from Inachidae MacLeay and their placement within the Oregoniidae as a separate subfamily, Pleistacanthinae Števčić. Oregoniidae, with this new composition, includes nine genera and 34 species. Only the genus *Pleistacantha* was cited in Mozambique waters. However, some authors still include the genus *Pleistacantha* within Inachidae (Emmerson 2016c).

Pleistacantha Miers, 1879

Pleistacantha ori Ah Yong & P.K.L. Ng, 2007

(Figures 13D,E)

Material examined. M07, Stn. 10, 382m, ♂ 33.2×44.9mm (CW×PRL) (IEO-CD-MZ07/1895); M08, Stn. 24, 402m, ♀ 17.1×25mm (IEO-CD-MZ08/1760), 16S (MZ424960), COI (MZ434806); M08, Stn. 50, 623m, ♀ 17.6×23.5mm (IEO-CD-MZ08/1905-1), 16S (MZ424961), COI (MZ434807); ♀ 17.9×23.8mm (IEO-CD-MZ08/1905-2), 16S (MZ424962), COI (MZ434808); M08, Stn. 57, 366m, ♀ ov. 86.6×108.5mm (IEO-CD-MZ08/2545); M08, Stn. 62, 467m, ♀ 19.5×27.6mm (IEO-CD-MZ08/1767), 16S (MZ424963), COI (MZ434809); M09, Stn. 4, 258m, ♀ 82.1×102.3mm (IEO-CD-MZ09/1857); M09, Stn. 27, 543m, ♂ 15.9×23.4mm (IEO-CD-MZ09/1769); M09, Stn. 31, 457m, ♂ 10.4×15.4mm (IEO-CD-MZ09/1764); M09, Stn. 60, 304m, ♂ 73×91.5mm (IEO-CD-MZ09/1856), 16S (MZ424964); M09, Stn. 63, 617m, ♀ 16.5×23.5mm (IEO-CD-MZ09/1759), 16S (MZ424965), COI (MZ434810).

Habitat and distribution. *Pleistacantha ori* had been misidentified and confused with *Pleistacantha moseleyi* (Miers) for many years, until it was described by Ah Yong & Ng (2007) as a new species. It is presently known from off the Natal coast, South Africa, and Madagascar, between 238 and 480m depth (Ah Yong & Ng 2007). It was cited by Emmerson (2016c) in waters of Mozambique.

Results and remarks. Several different keys and descriptions were used to identify our specimens: Ah Yong & Ng (2007), Griffin (1974), Griffin & Tranter (1986) and Ng *et al.* (2017). This was due to the difficult identification of this species because the different sizes of the studied specimens, the common morphological variability between adults and juveniles and the high variability in the size and morphology of the spines found between specimens. Genetic was used to confirm that the smallest specimens analysed belong to the same species than the adults. Eleven specimens, collected between 2007 and 2009, at depths between 258 and 623m, were studied. Our records extend the depth range from 480 to 623m for this species in its complete geographical distribution.

Colouration observed. Our specimens had white carapace, being dark orange in the most prominent zones of the branchial, gastric and cardiac regions. The pseudo-spines were orange, with white tips. The pleon was basically white. The ambulatory legs were whitish orange with long longitudinal spots on merus and carpus, while dactyli looks brown due to the dense tomentum and fouling on them. Smallest individuals had orange carapace with fewer white areas, white legs with many orange transverse stripes and white dactylus, with no fouling on them.

DNA barcodes. There are not 16S and COI sequences available for this species on any public database. Therefore, these are the firsts 16S and COI sequences obtained for this species. The six sequences obtained for 16S belong to a unique haplotype. The BLAST search matches 96.5% (intra-generic distance) with *Pleistacantha kannu* (MH384947) from India, submitted by Ravichandran *et al.* (unpublished), the only species of this genus with a valid sequence in Genbank. There is a sequence of *Pleistacantha sanctijohannis* (LC430736) deposited by Komai *et al.* (2019), but it is noticeably short s (only 164 bp) and does not allow any accurate comparison. Respect to COI, the five sequences obtained for *P. ori* represent four different haplotypes (differing in one, two and five positions), and the only COI sequence of the genus in Genbank, *Pleistacantha kannu* (MH425628) from India, does not match, and look like a bacterial sequence.

Superfamily PORTUNOIDEA Rafinesque, 1815

According partially to WoRMS (2021) and following the last and more recent review by Spiridonov (2020), this superfamily comprises four families, Brusiniidae Števcíć, Carcinidae MacLeay, Geryonidae Colosi, and Portunidae Rafinesque. Some taxa previously included in Portunoidea like families Polybiidae Ortmann, Thiidae Dana, or Ovalipidae Spiridonov, Neretina & Schepetov, are now placed as subfamilies Polibiinae and Thiinae (in Family Carcinidae) and Ovalipiinae (in Family Geryonidae).

Family CARCINIDAE MacLeay 1838

Subfamily PARATHRANITIINAE Spiridonov, 2020

This is a new subfamily established by Spiridonov (2020) including only the genus *Parathranites* Miers. It was placed in the family Carcinidae based on morphological and molecular evidences gathered in recent studies, especially that by Evans (2018).

***Parathranites* Miers, 1886**

***Parathranites granosus* Crosnier, 2002**

(Figure 13F)

Material examined. M08, Stn. 25, 265m, ♀ 20.9×15.2mm (IEO-CD-MZ08/1785), 16S (MZ424966), COI (MZ434811).

Habitat and distribution. Philippines, Indonesia, Admiralty Islands, at a depth range of 107–274m (Crosnier 2002).

Results and remarks. Only one female specimen was collected in M08 at 265m depth. This specimen agrees well with the descriptions and figures in Crosnier (2002). This is the first record of *P. granosus* off Mozambique.

Colouration observed. No pictures are available.

DNA barcodes. There is only a short (400 bp) and incomplete 16S sequence for this genus in Genbank belonging to *P. orientalis* (Miers) deposited by Tsang *et al.* (2014). This corresponds probably to the version of the sequence after alignment and removal of hypervariable positions, for example after application of GBlocks, as mentioned above for other species in the same work. Although a robust comparison is not possible without the complete 16S sequence, the 11 mutations found in the 400 bp in relation to the 511 bp of the 16S sequence of the female IEO-CD-MZ08/1785 suggest a distance that fits well at interspecific level. There are not COI sequences of this species on any public database, but the BOLD search shows 88.61 to 95.16% of similarity with other species of this genus as *P. tuberosus* Crosnier, *P. intermedius* Crosnier, and *P. orientalis*.

***Parathranites orientalis* (Miers, 1886)**

(Figure 13G, preserved)

Material examined. M07, Stn. 62, 174m, ♂ 25.5×17mm; ♀ 31.1×21, ♀ 24,1×16.9mm (IEO-CD-MZ07/1909).

Habitat and distribution. Japan, China, Philippines, Indonesia, east coast of Australia, New Caledonia, Vanuatu, Fiji, Tonga and Futuna in a depth range of 80–405m, Madagascar at 235–455m depth, and east coast of South Africa.

Results and remarks. These two specimens were collected in M07, at the same station at 174m depth. They agree well with the description and figures in Crosnier (2002), being the first record of *P. orientalis* off Mozambique.

Colouration observed. The carapace was bright orange, with some more reddish areas and white anterolateral sides. The legs were bright orange with narrow white bands in the proximal zones of merus and carpus and in the proximal and distal areas of propodus. Dactyli of P5 were transparent.

DNA barcodes. The specimen was preserved in formalin and therefore, it was not possible to get DNA sequences.

Family GERYONIDAE Colosi, 1923

According to Davie *et al.* (2015a) this family comprises five genera and 39 species. Geryonidae includes some species of high commercial interest, such as the pink Geryon *Chaceon macphersoni* Manning & Holthuis, 1988 (Doherty 2015; Groenevel *et al.* 2013).

Subfamily GERYONINAE Colosi, 1923

Chaceon Manning & Holthuis, 1989

Chaceon macphersoni Manning & Holthuis, 1988

(Figure 14A)

Material examined. M07, Stn. 86, 558m, ♀ 46.9×37mm (IEO-CD-MZ07/1907); M08, Stn. 45, 658m, ♀ 78×66.5mm, ♀ 75.2×61.9mm (IEO-CD-MZ08/1792), ♂ 62.8×51.4mm (IEO-CD-MZ08/1792-1), 16S (MZ424967), COI (MZ434812); M09, Stn. 5, 548m, ♀ 93.1×78.2mm (IEO-CD-MZ09/1814), COI (MZ434813); M09, Stn. 44, 639m, ♀ 135.9×111.6mm (IEO-CD-MZ09/1858), 16S (MZ424968), COI (MZ434814); M09, Stn. 107, 685m, ♀ 47×33.1mm (IEO-CD-MZ09/1812), 16S (MZ424969), COI (MZ434815).

Habitat and distribution. *Chaceon macphersoni* occurs at depths between 293 and 900m (Emmerson 2016c) and up to 1025m (Groenevel *et al.* 2013), in the WIO, off Mozambique, southern Madagascar and eastern South Africa, and extends westwards up to Cape Columbine along the Atlantic coast of South Africa (Groenevel *et al.* 2013; Emmerson 2016c). Catches of *C. macphersoni* made off eastern South Africa and Mozambique were attributed to *Chaceon quinquegens* (Smith) (as *Geryon quinquegens*) up to 1989, when the family Geryonidae was revised, the new genus *Chaceon* erected, and *C. macphersoni* was described (Manning & Holthuis 1988, 1989). This species constitutes an important retained by-catch in multispecies crustacean trawl fisheries and deep-water trap fisheries for spiny lobsters off southern Mozambique (Paula & Silva 1985).

Results and remarks. Our specimens agree well with the descriptions and figures of Manning & Holthuis (1989). Seven specimens were collected during the three surveys (M07, M08 and M09) between 548 and 685m depth.

Colouration observed. The carapace was dorsally yellowish, splashed of small white spots around the branchial and protogastric areas, and with white edges. Chelipeds were pinkish, almost white, and the legs have light pink merus and carpus, and maroon propodus and dactylus.

DNA barcodes. The 16S sequences of three specimens represent two haplotypes (differing in two positions). There are not 16S sequences of this species in Genbank, being these the first ones for this species. The closer matches are with *Chaceon maritae* (LN809920) obtained by Hernández *et al.* (2019) and with *C. granulatus* (FM208775) deposited in Genbank by Schubart & Reuschel (2009), varying in six and nine mutations, respectively. Respect to COI, the four sequences obtained for *C. macphersoni* represent four different haplotypes (differing in two-three positions), that fit 99.2–99.68% of similarity with four sequences of *C. macphersoni* from South Africa available in BOLD as “private”, and therefore with no access to the sequences and no more data available for comparison.

Subfamily OVALIPIINAE Spiridonov, Neretina & Schepetov, 2014

The subfamily Ovalipiinae was described as family Ovalipidae by Spiridonov *et al.* (2014). However, Spiridonov (2020), in agreement with the suggestion by Evans (2018) based on his molecular phylogenetic reconstruction, accepted the closer relationships of *Ovalipes* with geryonids and consequently moved this group as a subfamily of the Geryonidae with only one genus. They are pelagic species known as swimming crabs (Kensley 1981).

Ovalipes Rathbun, 1898

Ovalipes iridescens (Miers, 1885)

(Figure 14B)

Material examined. M07, Stn. 1, 449m, ♂ 83.3×67.8mm (IEO-CD-MZ07/1921); M08, Stn. 43, 375m, ♀ 84.3×68.8mm; ♀ 65.5×55.5mm; ♂ 105.1×82.2mm (IEO-CD-MZ08/1790); M09, Stn. 17, 419m, ♂ 94.1×75mm (IEO-CD-MZ09/1809), COI (MZ434816).



FIGURE 14. A, *Chaceon macphersoni*, ♀ IEO-CD-MZ09/1812; B, *Ovalipes iridescens*, ♀ IEO-CD-MZ07/1921. C, *Scylla serrata*, ♀ IEO-CD-MZ08/2238 (preserved); D, *Charybdis africana*, ♂ IEO-CD-MZ08/1813; E, *Charybdis feriata*, ♂ IEO-CD-MZ07/1902 (preserved); F, *Charybdis smithii*, ♂ IEO-CD-MZ08/1813; G, *Monodaeus tuberculidens*, ♂ IEO-CD-MZ07/1803. Scale bars: 1cm.

Habitat and distribution. This species is distributed in the IP: Indonesia, Australia, Japan, and South Africa (Stephenson & Rees 1968), Mozambique (Kensley 1981) and New Caledonia (Poupin 2010), mainly at deep waters (Stephenson & Rees 1968), between 80 and 400m (Emmerson 2016c).

Results and remarks. *Ovalipes iridescens* specimens were revised following the descriptions of Stephenson & Rees (1968). These specimens were collected between 375 and 449m depth, in the central and southern areas off Mozambique, during the three surveys (M07, M08, M09), and these records extend the maximum depth from 400 up to 449m.

Colouration observed. The specimen was bright orange colour with certain iridescence and with some whitish areas in the posterior half of the carapace. The cardiac, branchial, and gastric regions of the carapace were dark orange, with two lighter oval spots on both sides of the cardiac region. The hepatic area was whitish, with a row of highly accentuated crescent-shaped white dots. Chelipeds were orange, with a large iridescent stain on the merus and white fingers. Ambulatory legs had whitish merus, orange carpus and propodus and orange-brown dactylus. The ventral area of the individual was white. After preservation, in both ethanol and formalin, the specimen turned bone-coloured, keeping the iridescence on certain areas of the carapace and merus.

DNA barcodes. There is a COI sequence for *O. iridescens* in BOLD (MDECA151-10) from a specimen collected in Indonesia (MNHN IU-200812533) (date of collection: 1991-19-21) identified by Moosa, that only fits 93.57% (39 mutations) with the COI sequence of the specimen IEO-CD-MZ09/1809. However, there is one sequence in BOLD of *Ovalipes* sp. (MDECA064-10), corresponding to one specimen identified by Chan, that was collected in Mozambique during the MB-exp in 2009 (date collection: 2009-04-09) and deposited at the MNHN (MNHN IU200810370). This sequence fits 97.85% (13 mutations) with ours, being in the limit between inter or intraspecific variability.

Family PORTUNIDAE Rafinesque, 1815

Portunidae is a large family comprising seven subfamilies and 36 genera according to the recent update by Spirodonov (2020). It has been relatively well studied in recent years, based both on morphological analysis and molecular phylogenies (De Grave *et al.* 2009; Evans 2018, Karasawa *et al.* 2008; Mantelatto *et al.* 2018; Schubart & Reuschel 2009; Schweitzer *et al.* 2010; Spiridonov *et al.* 2014) and consequently subject of many recent changes. According to Emmerson (2016c), only two subfamilies occur in Mozambique, Portuninae Rafinesque and Thalamitinae Paulson, because he considered *Scylla* not in the new subfamily Necronectinae Glaessner but in Portuninae.

Subfamily NECRONECTINAE Glaessner, 1928

Scylla De Haan, 1833 [in De Haan, 1833-1850]

Scylla serrata (Forskål, 1775)

(Figure 14C, preserved)

Material examined. M08, Stn. 16, 235 m, ♀ 142.1× 95.6mm (IEO-CD-MZ08/2238), 16S (MZ4249709), COI (MZ434817).

Habitat and distribution. *Scylla serrata* is a common species in the IP, included in all the IWP checklists (Crosnier 1962; Kensley 1981; Poupin 2010, 2018; Emmerson 2016c). It is distributed along the coasts of East South Africa (South Africa, Mozambique, Somalia, Madagascar), Australia and Japan (Crosnier, 1962). According to Keenan *et al.* (1998), *S. serrata* is the most widespread species within the genus. It is a coastal species, even intertidal (Stephenson 1972), which uses estuaries and mangroves as nurseries, as it is the case of the Saco mangrove creek, on Inhaca Island (South Mozambique) (Paula *et al.* 2004). Although the species is associated with mangroves that are flooded with ocean water during most of the year, it can also tolerate reduced salinities (Keenan *et al.* 1998).

Results and remarks. The unique specimen was determined using the key and illustrations of Crosnier (1962) and Apel & Spiridonov (1998). It is a large individual collected in M08 at 235m depth. Poupin (2010) and Emmerson

(2016c) reported this species in brackish waters of intertidal areas. Therefore, this new record extends the bathymetric range of *S. serrata* to deep waters up to 235m. The specimen was collected in front of the Quelimane estuary in Mozambique, which might be a nursery area for this species, while adults might migrate towards deeper waters.

Colouration observed. Photographs of the live specimen are not available.

DNA barcodes. The 16S sequence of the specimen IEO-CD-MOZ08/2238 fits 100% with several sequences of *Scylla serrata* deposited in Genbank. According with a BOLD search, the COI sequence presents the same haplotype (HVDBC124-12) of a specimen (HVDBC_KZN_310) from Mapelane (South Africa) collected by Greenfield (BOLD) and deposited at the University of Johannesburg, and also fits 100% with a sequence (SBBM039-13) from a specimen collected in Transkei (South Africa) and identified by Mostert. It presents a minimum of one mutation with respect to the rest of COI haplotypes that are available in Genbank and BOLD for *S. serrata*.

Subfamily THALAMITINAE Paulson, 1875

Charybdis De Haan, 1833 [in De Haan, 1833–1850]

Charybdis (Gonioneptunus) africana Shen, 1935

(Figure 14D)

Material examined. M07, Stn. 123, 184m, ♂ 84.4×57.5mm (IEO-CD-MZ07/1915); M08, Stn. 77, 290m, ♂ 24.3×16.7mm, ♂ 23.4×15.9mm (IEO-CD-MZ08/1813-1), 16S (MZ424971), COI (MZ434818), ♂ 24.1×17.1mm; ♂ 21×14.5mm, ♂ 24.3×16.7mm, ♂ 27×18.9mm (IEO-CD-MZ08/1813-2), 16S (MZ424972), COI (MZ434819); M09, Stn. 45, 322m, ♂ 41.2×29mm (IEO-CD-MZ09/1816), 16S (MZ424973), COI (MZ434820).

Habitat and distribution. *Charybdis (Gonioneptunus) africana* occurs between 48 and 126m, off South Africa (Barnard 1950; Shen 1935) and Mozambique (Kensley 1981).

Results and remarks. These specimens were identified at genus level following Crosnier (1962), at subgenus level following Leene (1938) and at species level following Shen (1935) and Barnard (1950). A total of eight individuals were collected during the three surveys (M07, M08 and M09), at depths between 184 and 322m. This is the second record in Mozambican waters, which expands the species depth range from 126 up to 322m. *Charybdis africana* and *Charybdis bimaculata* have been considered synonyms (Sakai 1939), although WoRMS currently considers them as valid species. The similarity between the characters used by Shen (1935) and Barnard (1950) to separate both species might have justified that they were considered synonyms by Sakai (1939). However, Shen (1935) established differences in the relationship CW/CL, this being 1.46 for *C. africana* and 1.55 for *C. bimaculata*. Considering this as a distinctive character for both species, our specimens with CW/CL ratios between 1.42–1.47 are closer to *C. africana*. The tip shape of G1 could be a distinctive character between the species, only described so far for *C. bimaculata* (Leene 1938) but not for *C. africana*. The G1 shapes of the specimens (all males) are similar to those described for *C. bimaculata*, although their tips are more elongated and pointed (see Figure 15B).

Colouration observed. The common name of *C. bimaculata*, “two-spot swimming crab”, makes reference to the two spots located on the mesobranchial region of the carapace. No information on the presence or absence of these spots on *C. africana* is available. These eight specimens also had two spots, although they were not as remarkable as observed in the images available of *C. bimaculata*. Our specimens showed a white spot on the cardiac region of the carapace, which was also observed in the images of *C. bimaculata*, although in this case they were much more elongated, even reaching the edge of the carapace. General colouration was also different as *C. bimaculata* is brown and beige colour, marble-like, while our specimens had a reddish-brown carapace with red granules. Legs and chelae were beige, with very scattered red granules, with bigger size and presence on the chelae. Dactyli were yellowish dorsally and white ventrally.

DNA barcodes. The three 16S sequences present only one haplotype that fits 99.22–99.41% (three–four mutations) with four sequences of *C. bimaculata* from Taiwan (KX060391), South Korea (MG787408, NC_037695), and Vanuatu (KT365596), deposited at Genbank by Negri *et al.* (2018), Liu *et al.* (2018), Kim *et al.* (2018) and Evans (2018), respectively. The three different haplotypes found for COI sequences, differ in 11–12 mutations respect to several COI sequences of *C. bimaculata* (similarity ranging from 97.47 to 98.25%). As occurs for *Ovalipes iridescens*, these values fall just in the limit between inter or intraspecific variability.

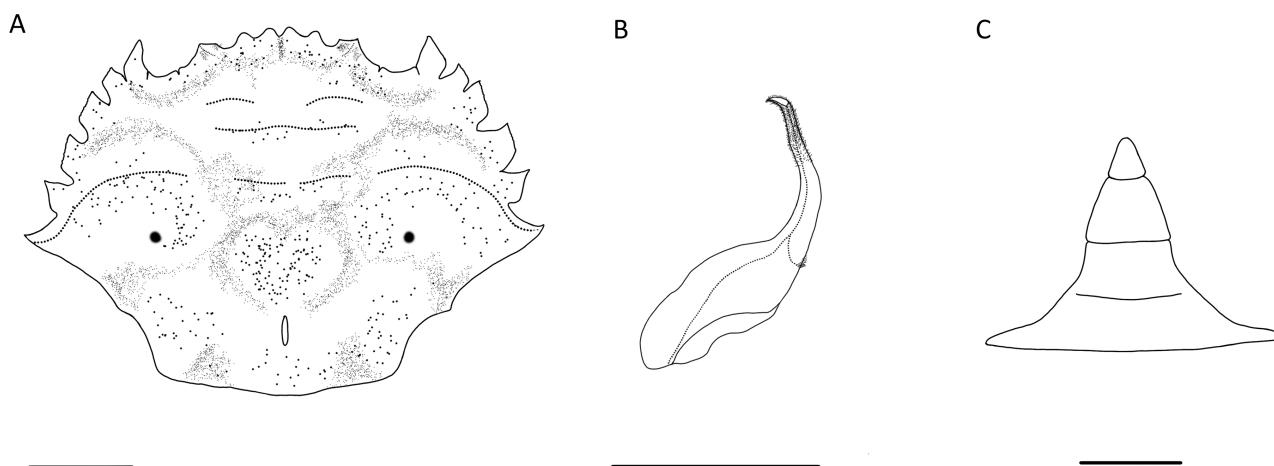


FIGURE 15. *Charybdis africana* ♂ IEO-CD-MZ08/1813-2. A, Carapace; B, G1; C, Telson. Scale bar: 1cm.

Charybdis (Charybdis) feriata (Linnaeus, 1758)

(Figure 14E, preserved)

Material examined. M07, Stn. 74, 138m, ♂ 26×16.8mm (IEO-CD-MZ07/1902), COI (MZ434821).

Habitat and distribution. Widely distributed in the IWP from South and East Africa through the Gulf of Oman, the Arabian Gulf, Pakistan, India, Sri Lanka to Indonesia, Singapore, Australia, Vietnam, China, and Japan (Apel & Spiridonov 1998). Crosnier (1962) described the distribution of the synonym species *Charybdis cruciate* (Herbst) in shallow waters of South Africa, Australia, and Japan, at 5-15m (rarely 30m). Not being recorded in Mozambique since the fifties of last century (Barnard 1950), it has been recently reported by personal observations of IIP-Mozambique.

Results and remarks. The single specimen agrees well with the description and figures in Crosnier (1962) and Apel & Spiridonov (1998). It was collected in March 2007 (M07) at 138m depth, increasing the previously reported bathymetric distribution of the species.

Colouration observed. No pictures of the fresh specimen are available.

DNA barcodes. Only the COI sequence could be obtained from this specimen, which represents a new haplotype for this species. The closer haplotype is a COI sequence of a specimen from Australia (MN184690), with differences in two positions (99.68% similarity), ranging between 98.65 to 97.30% of similarity (seven to 14 mutations) with respect to the rest of 60 haplotypes for this species in Genbank.

Charybdis (Gonihellenus) smithii MacLeay, 1838

(Figures 14F, 16)

Material examined. M08, Stn. 76, 222m, ♂ 64×44.6mm (IEO-CD-MZ08/1794-1), 16S (MZ424974), COI (MZ434822); ♂ 58×40.7mm (IEO-CD-MZ08/1794-2), 16S (MZ424975), COI (MZ434822).

Habitat and distribution. *Charybdis smithii* is a semi-pelagic species that spends a considerable part of its life in the water column (Turkay & Spiridonov 2006), extending its pelagic habitat from the mixed layer to upper mesopelagic waters (Romanov *et al.* 2009) at depths between 60 and 450m. It is distributed along the western and northern Indian Ocean, from off South Africa, Madagascar, Somalia, Seychelles, Maldives, Saya de Malha, Gulf of Aden, Red Sea, Bay of Bengal (Apel & Spiridonov 1998; Turkey & Spiridonov 2006), although most of the crabs are found in the western basin of the Indian Ocean (Romanov *et al.* 2008). *C. smithii* is common in the pelagic provinces of the western Indian Ocean, where they are driven to, by the wind monsoon regime. Based on the nutritive value determined for this species, Kumar *et al.* (2019) raised the possibility of its potential exploitation as a commercial resource.

Results and remarks. These two male specimens agree well with the descriptions and figures in Apel &

Spiridonov (1998) and Turkey & Spiridonov (2006). They were collected during the 2008 survey at 222m depth. This is the first record of *C. smithii* off Mozambique. Ng & Takeda (1999) reported that two closely allied species, *C. smithii* and *Charybdis omanensis*, differ in many morphometric and gonopodal characters. Turkey & Spiridonov (2006) reviewed the deep-water species belonging to *Charybdis* subgenus *Goniohellenus*, and described a new subspecies, *C. (G.) omanensis septentrionalis* Turkey & Spiridonov, 2006 restricted to the central and southern Red Sea and further extended to the Arabian Sea and India (Josileen *et al.* 2018). The diagnostic characters used for the identification of our specimens as *C. smithii* instead the subspecies *C. omanensis septentrionalis*, based on Turkey & Spiridonov (2006) are: posterolateral angles of the carapace nearly rounded instead almost forming a right-angle, as described for *C. omanensis septentrionalis* (see Figure 16A); the carapace not densely pilose and without the frontal patches of granules neither protogastrics areas with short bands of three–four lines of granules described for *C. omanensis septentrionalis*; tips of G1 of the two males are not twisted downwards as they are for *C. omanensis septentrionalis* (Apel & Spiridonov 1998) (see Figures 16B,C).

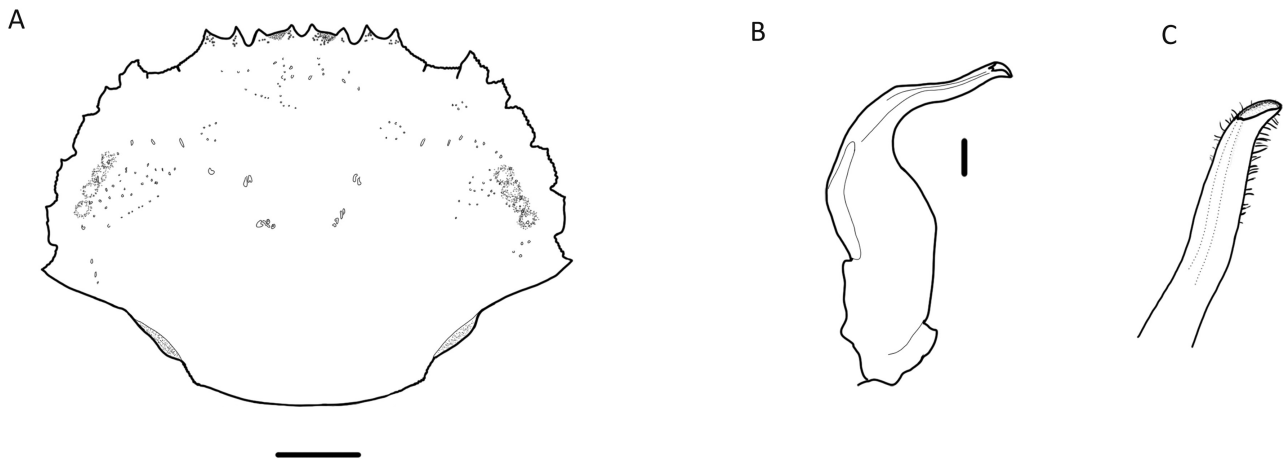


FIGURE 16. *Charybdis smithii* ♂, IEO-CD-MZ08/1794-1. A, Carapace (Scale bar: 1cm); B,C, G1 (Scale bars: 1mm).

Colouration observed. Both male specimens were reddish, with smooth carapace without granular patches, as described by Turkey & Spiridonov (2006). The tubercles on the chelipeds were dark red. Some irregular white spots were bordering the upper zone of the epibranchial region, with the shape of a semicircle. This colour pattern was not described by Apel & Spiridonov (1998) or Turkey & Spiridonov (2006). The finger tips were deep brown. After preservation in ethanol, the specimens turned to beige with some pinkish patches, the finger tips remaining brown.

DNA barcodes. The 16S and the COI sequences of the two specimens present the same haplotypes that fits 100% with the 16S and COI sequences of *C. smithii* (KX060404, KX060191) from the same specimen (MNH-B27685) from Oman (Negri *et al.* 2018). However, also de COI sequences fit 100% with the three sequences of *C. omanensis septentrionalis* (KY651228-KY651230) uploaded to Genbank by Josileen *et al.* (unpublished).

Superfamily XANTHOIDEA Guinot, 1967

Family XANTHIDAE MacLeay, 1838

The Xanthidae is a broad family, which according to Davie *et al.* (2015c), includes 129 genera and 629 species. Thirty of these genera are present in waters of Southern Africa (Serène 1984; Ng *et al.* 2008; Poupin 2010). The majority of xanthid species inhabit intertidal areas (Guinot & Macpherson 1988) and only two species have been cited by Emmerson (2016c) in waters deeper than 100m, *Actaea savignii* (H. Milne Edwards) and *Gaillardius rueppelli* (Krauss).

Subfamily Euxanthinae Alcock, 1898

Monodaeus Guinot, 1967

Monodaeus tuberculidens (Rathbun, 1911)

(Figure 14G)

Material examined. M07, Stn. 27, 425m, ♂ 12.2×8.9mm (IEO-CD-MZ07/1803); M09, Stn. 84, 254m, ♂ 13.6×9.3mm (IEO-CD-MZ09/1763), 16S (MZ424976), COI (MZ434824).

Habitat and distribution. Its distribution includes Reunion Island, the great bank Saya de Malha, South Africa and Angola, at 210 m (Guinot & Macpherson 1988), Mayotte Island (Poupin 2010, 2018), Mozambique (Emmerson 2016c) and Australia (GBIF.org 2021, unpublished record).

Results and remarks. The descriptions of Guinot & Macpherson (1988) and Serène (1984) were followed to identify the two male specimens. In one of the specimens (IEO-CD-MZ09/1763) the spines on merus and carpus of P2–P5 are not sharp. Both of them were collected in March (MZ07 and MZ09), at depths between 254 and 425m, and thus, these records extend the maximum depth of the species to 425m.

Colouration observed. The carapace was orange with white edges and some small red and white tubercles. Chelae were orange with red tubercle tips, white palm and brown fingers. Meri of chelipeds had orange and white bands and carpi and dactyli were orange with red tubercles.

DNA barcodes. The 16S sequence fits 100% with that of *Monodaeus tuberculidens* (HM798515) obtained by Lai *et al.* (2011). However, it differs in only 1 mutation to two sequences of *Monodaeus couchii* (AM076771 and HM798510) by Reuschel & Schubart (2006) and Lai *et al.* (2011). The COI sequence is also close to one of *M. tuberculidens* (HM751031), from the same specimen, also obtained by Lai *et al.* (2011), fitting 99.66% (two mutations). Similarly to 16S, in this case there are other 20 sequences of *M. couchii* presenting close haplotypes that vary in a range of five to eight mutations (98.66 to 99.21%). Therefore, *M. tuberculidens* and *M. couchii* are closer species that need to be further studied to clarify their relationship.

Discussion

This is the first checklist of marine brachyuran crabs exclusively for Mozambique, in which a total of 269 species, grouped in 15 superfamilies, 26 families and 172 genera are listed. Previous existing documents containing any checklist of Mozambican Brachyura are available as part of more general works, both in terms of geographical and taxonomical coverage, as it is the case for the *Catalogue and checklist on decapods of Namibia, South Africa and Mozambique* by Emmerson (2016a, b, c) or oppositely, they are focused on specific genera and/or species or on other decapod groups from Mozambique (Ahyong 2014; Komai 2011).

DNA barcodes, 16S rRNA and/or COI, were obtained for the vast majority of species studied from specimens collected during the “MOZAMBIQUE” surveys, between 2007 and 2009. The only exceptions were two species collected in the MZ07 survey and initially preserved in formalin, this making amplification of DNA not possible although 16S or COI or both markers (in three species), could be obtained in other eight species of the same survey and also initially preserved in formalin. When specimens had been fixed in formalin, the extractions were made using parts suspected to be less affected by the formalin preservation as eyes, gills, and other internal tissues, although this did not work in all specimens or for all genes.

DNA sequences were obtained for 83 specimens of 37 species (see Table 2). 16S sequences were obtained for 35 species (74 specimens, 42 haplotypes), and for 27 of them these are new sequences. COI sequences were obtained for a smaller number of species, 30 (73 specimens, 59 haplotypes), and 14 are new sequences. Both markers were obtained for 28 species, and in 14 of them both are new sequences. The sequences of 16S and COI genes are the first ones in the case of the genera *Platepistoma* and *Sakaija*.

DNA barcodes only allowed confirmation of identification for 11 species, all of them with COI (and six of them also with 16S): *Homola orientalis*, *Homolochunia valdiviae*, *Latreillia valida*, *Lyreidus brevifrons*, *Carcinoplax longimanus*, *Tanaoa pustulosus*, *Chaceon macphersoni*, *Scylla serrata*, *Charybdis feriata*, *C. smithii* and *Monodaeus tuberculidens*. This underlines the gap in barcodes studies of African brachyuran crabs. In five cases, COI sequences

have allowed identification of specimens previously collected by the Mainbaza 2009 expedition that are deposited in the MNHN of Paris as “sp.” (*Euclrosiana exquisita*, *Samadinia galathea*, *S. pulchra*, *Platymaia turbynei* and *Ovalipes iridescens*). In addition, COI sequences have pointed out the need of reviewing potential erroneous identifications of species in sequences deposited in Genbank (*Mursia flamma*, *Charybdis omanensis septentrionalis*, *Oxypleurodon stuckiae*) and revealed a possible new species (*Mursia* sp.).

The combination of molecular techniques (DNA barcodes) and morphological analyses of the brachyuran specimens allows accurate and reliable identification of certain species as well as highlighting taxonomical issues at specific or generic level, when studying the species of a given area. This kind of studies where morphological and molecular techniques are used in combination have been successfully applied to crustaceans in similar integrative works in other areas of the world (i.e.: Mantelatto *et al.* 2020 and Varela *et al.* 2021). These types of approaches provide baselines for future studies in these areas and not only taxonomical or phylogenetical ones (i.e.: Lunina *et al.* 2018; Van Der Wal *et al.* 2019), but ecological/populational or for detection of exotic species too.

In the present contribution, based on specimens collected during the “MOZAMBIQUE” surveys, the following 15 species represent new records of brachyuran species for Mozambique: *Paromolopsis boasi*, *Mursia aspera*, *Carcinoplax ischurodous*, *T. pustulosus*, *E. exquisita*, *Oxypleurodon difficilis*, *Naxioides robillardi*, *S. galathea*, *Cyrtomaia gaillardi*, *Paramaja gibba*, *Pleistacantha ori*, *Parathranites granosus*, *P. orientalis*, *O. iridescens* and *C. smithii*. This work also includes the second records of *Moloha alcocki*, *S. pulchra* and *Charybdis africana* in Mozambique as well as second records of *Raninoides crosnieri*, *S. galathea* and *P. ori* worldwide.

A remarkable finding is the collection and description for the first time of one female specimen of *Samadinia galathea*. This happened seventy years after the collection of a single male in South Africa in 1951, later described by Griffin & Tranter (1986) as a new species, *Rochinia galathea*. This female description evidences the sexual dimorphism in this species.

Some records extend the known bathymetric range for certain species in Mozambican waters: *Homolodromia bouvieri*, *H. orientalis*, *L. brevifrons*, *Calappa africana*, *Mursia africana*, *M. aspera*, *M. tuberculidens*, *Sakaija africana*, *O. iridescens*, *Scylla serrata* and *Ch. africana*, or even worldwide as it is the case for *M. africana*, *M. aspera* and *N. robillardi*.

During the present morphological revision some species and/or genera with characters that difficult a clear taxonomic assignation have been found, they requiring a more in-depth further review. In fact, the taxonomic value of certain morphological characters for congeneric species discrimination have shown to be not useful since they are shared by different species. This is especially problematic in features with diagnostic value to define taxa. This is the case for some morphological characters used to distinguish *R. crosnieri* from *Raninoides personatus* (rostral shape, following Ribes 1989) or *Calappa africana* from *C. japonica* (shape of G2, following Ah Yong & Ng 2006). In addition, some distinctive characters of certain species may not be valid for identification and consequently, a review of their use is recommended, as it was made for *M. flamma* by Galil (2003) and Spiridonov & Apel (2007) (median tooth of the rostrum, number of spines in merus of chelipeds), *O. difficilis* by Guinot & Richer de Forges (1984) (rostral shape, size of the channels between dorsal plates, shape of cardiac plate) and *P. boasi* by Guinot and Richer de Forges (1995) and Padate *et al.* (2020) (number of spines in merus).

A detailed revision of the taxonomic status of some genera is also recommended. Molecular and morphological analyses suggest a remarkable divergence at intrageneric level in *Carcinoplax*, *Platymaia* and *Platepistoma*. Probably new genera might be erected to reflex the correct systematic relationship between some species. For example, genetic data show that specimens morphologically identified as *Carcinoplax ischurodous* are closer to *Goneplax rhomboides* than to other *Carcinoplax* species.

In the case of *C. africana*, *Paramaja gibba* and *Monodaeus tuberculidens*, both morphology and molecular data suggest the necessity of new studies with more samples from different localities, including other congeneric species and using other genetic markers, to clarify the systematic position of these species.

The systematics of the checklist list have been updated taken into account the most recent changes. New taxa, as the subfamilies Gelasiminae Miers, Pinnixinae Števíć or Necronectinae Glaessner have been added, and new arrangements considered, like Ovalipidae Spiridonov, Neretina & Schepetov moved to Geryonidae Colosi as the subfamily Ovalipiinae Spiridonov, Neretina & Schepetov. Several species have been replaced in different genera (as *Eucrate creanata* (De Haan), *Raoulia piroculata* (Rathbun), *Thalamita helleri* Hoffmann, *Forestiana granulata* (Krauss), *Parasesarma guttatum* (A Milne-Edwards), *Danielella edwardsii* (MacLeay), *Chaenostoma sinuspersici* (Naderloo & Türkay), *Macrophthalmus (Mareotis) depressus* Ruppell, *Cranuca inversa* (Hoffmann),

Pinnixa penultipedalis Stimpson, and *Afropinnotheres dofleini* Lenz in Lenz & Strunck, and in other families, as *Pleistacantha* previously in Inachidae MacLeay and now in Oregoniidae Garth or *Parathranites*, previously in Polybidae and now in the subfamily Parathranitiinae Spiridonov, and even superfamilies as *R. piroculata* (Rathbun) now in Goneplacoidea MacLeay, and before in Pilumnoidea Samouelle. Several species synonyms have also been updated, as *Planes minutus* (Linnaeus).

TABLE 2. Updated checklist of marine brachyuran crabs from Mozambican waters, generated after review of the 153 references compiled, including: habitat (E: estuarine, Sp; supratidal, I: intertidal, Sb: subtidal, Sh; shelf, Sl: slope), new record for the area (NR), species recorded in this study “*”, and GenBank accession codes of the 16S rRNA and COI sequences obtained in this study, in bold new contributions.

Taxa / Species	Habitat	16S	COI
Podotremata Guinot, 1977			
Cyclodorippoidea Ortmann, 1892			
Cyclodorippidae Ortmann, 1892			
Cyclodorippinae Ortmann, 1892			
<i>Tymolus globosus</i> Spiridonov & Türkay	Sh-Sl		
Dromioidea De Haan, 1833 [in De Haan, 1833–1850]			
Dromiidae De Haan, 1833 [in De Haan, 1833–1850]			
Dromiinae De Haan, 1833 [in De Haan, 1833–1850]			
<i>Asciophilus caphyraeformis</i> Richters	I		
<i>Conchoecetes artificiosus</i> (Fabricius)	Sh		
<i>Cryptodromia bullifera</i> (Alcock)	I		
<i>Cryptodromia fallax</i> (Latreille in Milbert)	I		
<i>Lauridromia intermedia</i> (Laurie)	Sh		
<i>Lewindromia unidentata</i> (Rüppell)	Sb		
<i>Metadromia wilsoni</i> (Fulton & Grant)	Sh		
<i>Tumidodromia dormia</i> (Linnaeus)	Sh		
Homolodromioidea Alcock, 1900			
Homolodromiidae Alcock, 1900			
* <i>Homolodromia bouvieri</i> Doflein (NR)	Sl	MZ424903– MZ424905	MZ434752– MZ434754
Homoloidea De Haan, 1839 [in De Haan, 1833–1850]			
Homolidae De Haan, 1839 [in De Haan, 1833–1850]			
* <i>Homola orientalis</i> Henderson	Sh-Sl	MZ424906– MZ424907	MZ434755– MZ434756
<i>Homolochunia kullar</i> Griffin & Brown	Sl		
* <i>Homolochunia valdiviae</i> Doflein	Sl	MZ424908– MZ424911	MZ434757– MZ434761
<i>Homologenus</i> sp.	?		
<i>Lamoha murotoensis</i> (T. Sakai)	Sh-Sl		
<i>Latreillopsis tetraspinosa</i> Dai & Chen	Sh		
* <i>Moloha alcocki</i> (Stebbing)	Sh-Sl	MZ424913	
<i>Moloha alisae</i> Guinot & Richer de Forges	Sl		
* <i>Paromolopsis boasi</i> Wood-Mason in Wood-Mason & Alcock (NR)	Sl	MZ424914– MZ424915	MZ434762– MZ434763
Latreillidae Stimpson, 1858			
<i>Eplumula phalangium</i> (De Haan)	Sh-Sl		
* <i>Latreillia metanesa</i> Williams	Sh-Sl	MZ424916	
<i>Latreillia pennifera</i> Alcock	Sh		

.....continued on the next page

TABLE 2. (Continued)

Taxa / Species	Habitat	16S	COI
* <i>Latreillia valida</i> De Haan	Sh-Sl	MZ424917– MZ424918	MZ434764– MZ434765
Raninoidea De Haan, 1839 [in De Haan, 1833–1850]			
Lyreididae Guinot, 1993			
* <i>Lyreidus brevifrons</i> Sakai	Sh-Sl	MZ424919– MZ424921	MZ434766– MZ434768
<i>Lyreidus</i> sp.	?		
Raninidae De Haan, 1839 [in De Haan, 1833–1850]			
Notopodinae Serène & Umali, 1972			
<i>Cosmonotus grayi</i> Adams & White	Sh-Sl		
<i>Notopus dorsipes</i> (Linnaeus)	I-Sh		
Ranininae De Haan, 1839			
<i>Ranina ranina</i> (Linnaeus)	Sb-Sh		
Raninoidinae Lörenthey & Beurlen, 1929			
* <i>Raninoides crosnieri</i> Ribes (NR)	Sh	MZ424922	
Eubrachyura de Saint Laurent, 1980			
Heterotremata Guinot, 1977			
Aethroidea Dana, 1851			
Aethridae Dana, 1851			
<i>Aethra scruposa</i> (Linnaeus)	Sh		
<i>Aethra seychellensis</i> Takeda	Sh		
Calappoidea De Haan, 1833 [in De Haan, 1833–1850]			
Calappidae De Haan, 1833 [in De Haan, 1833–1850]			
* <i>Calappa africana</i> J.C.Y. Lai & P.K.L. Ng	Sh	MZ424923– MZ424924	MZ434769– MZ434770
<i>Calappa gallus</i> (Herbst)	Sh		
<i>Calappa guerini</i> Brito Capello	Sh		
<i>Calappa hepatica</i> (Linnaeus)	I-Sb		
<i>Calappa japonica</i> Ortmann	Sh-Sl		
<i>Calappa pustulosa</i> Alcock	Sh-Sl		
<i>Calappa woodmasoni</i> Alcock	Sl		
* <i>Mursia africana</i> Galil	Sl	MZ424925– MZ424926	MZ434771– MZ434772
* <i>Mursia aspera</i> Alcock (NR)	Sh-Sl	MZ424926	
* <i>Mursia flamma</i> Galil	Sl		
* <i>Mursia</i> sp.	Sl	MZ424928– MZ424929	MZ434773– MZ434774
Matutidae De Haan, 1835			
<i>Ashtoret lunaris</i> (Forskål)	Sb-E		
Cancroidea Latreille, 1802			
Cancridae Latreille, 1802			
* <i>Platepistoma guezei</i> (Crosnier) (NR)	Sl	MZ424930– MZ424931	MZ434775– MZ434777
Carpilioidea Ortmann, 1893			
Carpiliidae Ortmann, 1893			
<i>Carpilius convexus</i> (Forskål)	Sb-Sh		
Corystoidea Samouelle, 1819			

.....continued on the next page

TABLE 2. (Continued)

Taxa / Species	Habitat	16S	COI
Corystidae Samouelle, 1819			
<i>Gomeza bicornis</i> Gray	Sb		
Dorippoidea MacLeay, 1838			
Dorippidae MacLeay, 1838			
<i>Dorippe frascone</i> (Herbst)	Sb		
<i>Dorippe quadridens</i> (Fabricius)	Sb-Sl		
<i>Medorippe lanata</i> (Linnaeus)	Sb-Sl		
Ethusidae Guinot, 1977			
<i>Ethusina challengerii</i> (Miers)	Sl		
<i>Ethusina somalica</i> (Doflein)	Sl		
Eriphioidea MacLeay, 1838			
Dairoididae Števcíć, 2005			
<i>Dairoides kusei</i> (Sakai)	Sh		
* <i>Dairoides margaritatus</i> Stebbing	Sh	MZ424932	MZ434778
Eriphiidae MacLeay, 1838			
<i>Eriphia scabricula</i> Dana	I		
<i>Eriphia sebana</i> (Shaw & Nodder)	I		
<i>Eriphia smithii</i> MacLeay	I		
Menippidae Ortman, 1893			
<i>Menippe rumphii</i> (Fabricius)	I		
<i>Myomenippe fornasinii</i> (Bianconi)	I-Sb		
<i>Sphaerozius nitidus</i> Stimpson	I		
Oziidae Dana, 1851			
<i>Epixanthus dentatus</i> (White)	I		
<i>Epixanthus frontalis</i> (H. Milne Edwards)	I		
<i>Lydia annulipes</i> (H. Milne Edwards)	I		
Chasmocarcinidae Serène, 1964			
Chasmocarcininae Serène, 1964			
<i>Camatopsis rubida</i> Alcock & Anderson	Sh-Sl		
Euryplacidae Stimpson, 1871			
<i>Eucrate crenata</i> (De Haan)	48 m		
Goneplacoidea MacLeay, 1838			
Acidopsidae Števcíć, 2005			
Raouliinae Števcíć, 2005			
<i>Raoulia piroculata</i> (Rathbun)	I		
Goneplacidae MacLeay, 1838			
* <i>Carcinoplax ischurodous</i> (Stebbing) (NR)	Sl	MZ424933– MZ424934	MZ434779– MZ434780
* <i>Carcinoplax longimanus</i> (De Haan)	Sh-Sl	MZ424935– MZ424936	MZ434781– MZ434783
<i>Psopheticus crosnieri</i> Guinot	Sl		
<i>Psopheticus stridulans</i> Wood-Mason	Sl		
Hymenosomatoidea MacLeay, 1838			
Hymenosomatidae MacLeay, 1838			
<i>Elamena mathoei</i> (Desmarest)	I-E		
Leucosioidea Samouelle, 1819			
Leucosiidae Samouelle, 1819			

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TABLE 2. (Continued)

Taxa / Species	Habitat	16S	COI
Cryptocneminae Stimpson, 1907			
<i>Cryptocnemus holdsworthi</i> Miers	I		
<i>Leucisca squalina</i> MacLeay	I		
Ebaliinae Stimpson, 1871			
<i>Arcania septemspinosa</i> (Fabricius)	Sh		
<i>Ebalia agglomus</i> Barnard	I		
<i>Heteronucia angulata</i> Barnard	I		
<i>Myra subgranulata</i> Kossmann	I-Sb-E		
<i>Nucia speciosa</i> Dana			
<i>Ryphila cancellus</i> (Herbst)	I		
* <i>Tanaoa pustulosus</i> (Wood-Mason in Wood-Mason & Alcock)	Sh-Sl	MZ424937– MZ424939	MZ434784– MZ434786
Leucosiinae Samouelle, 1819			
* <i>Euclosiana exquisita</i> (Galil) (NR)	Sh-Sl	MZ424941	MZ434787
<i>Soceulia marmorea</i> (Bell)	Sl		
Majoidea Samouelle, 1819			
Epialtidae MacLeay, 1838			
Epialtinae MacLeay, 1838			
<i>Acanthonyx quadridentatus</i> Krauss	I-Sb		
<i>Acanthonyx scutellatus</i> MacLeay	I-Sb		
<i>Acanthonyx undulatus</i> (Barnard)	I		
<i>Huenia heraldica</i> (De Haan)	I-Sh		
<i>Menaethiops delagoae</i> Barnard	I-Sb		
<i>Menaethiops fascicularis</i> (Krauss)	I-Sb		
<i>Menaethiops natalensis</i> Barnard	I-Sb		
<i>Menaethius monoceros</i> (Latreille)	I-Sb		
Pisinae Dana, 1851			
<i>Doclea muricata</i> (Herbst)	Sh		
<i>Hyastenus diacanthus</i> (De Haan)	Sh		
<i>Hyastenus spinosus</i> A. Milne-Edwards	I-Sh		
<i>Hyastenus uncifer</i> Calman	Sb-Sl		
* <i>Oxypleurodon difficilis</i> (Guinot & Richer de Forges) (NR)	Sl	MZ424942– MZ424945	MZ434788– MZ434791
<i>Naxioides hirtus</i> A. Milne-Edwards	I-E		
* <i>Naxioides robillardi</i> (Miers) (NR)	Sb-Sh-Sl	MZ424946	
* <i>Samadinia galathea</i> Griffin & Tranter (NR)	Sl	MZ424947– MZ424948	MZ434792– MZ434793
* <i>Samadinia pulchra</i> (Miers) (NR)	Sl	MZ424949– MZ424951	MZ434794– MZ434796
Tychinae Dana, 1851			
<i>Stilbognathus cervicornis</i> (Herbst)	Sh		
Inachidae MacLeay, 1838			
Inachinae MacLeay, 1838			
<i>Achaeus barnardi</i> Griffin	Sh		
<i>Achaeus curvirostris</i> (A. Milne-Edwards)	Sb-Sh		
<i>Achaeus lacertosus</i> Stimpson	I-Sh		
<i>Achaeus spinosissimus</i> Griffin	Sh		

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TABLE 2. (Continued)

Taxa / Species	Habitat	16S	COI
<i>Camposcia retusa</i> (Latreille)	Sb		
<i>Chorinachus dolichorhynchus</i> (Alcock & Anderson)	Sh-Sl		
* <i>Cyrtomaia gaillardi</i> Guinot & Richer de Forges (NR)	Sl	MZ424952	
<i>Cyrtomaia murrayi</i> Miers	Sh-Sl		
<i>Inachus dorsettensis</i> (Pennant)	Sh-Sl		
<i>Inachus guentheri</i> (Miers)	Sh-Sl		
<i>Macropodia formosa</i> Rathbun	I-Sh		
<i>Oncinopus neptunus</i> Adams & White	Sb-Sl		
<i>Paratymolus barnardi</i> Loh & P.K.L. Ng	I-E		
* <i>Platymaia alcocki</i> Rathbun	Sl	MZ424953– MZ424954	MZ434797– MZ434798
* <i>Platymaia turbynei</i> Stebbing	Sl	MZ424955	MZ434799– MZ434801
<i>Sunipea indicus</i> (Alcock)	Sh - Sl		
Majidae Samouelle, 1819			
Majinae Samouelle, 1819			
<i>Entomonys spinosus</i> Miers	Sh - Sl		
<i>Majella brevipes</i> Ortmann	Sh - Sl		
* <i>Paramaja gibba</i> (Alcock)	Sh - Sl	MZ424956– MZ424958	MZ434802– MZ434804
<i>Prismatopus longispinus</i> (De Haan)	Sb		
<i>Prismatopus tosaensis</i> (T. Sakai)	Sh		
* <i>Sakaija africana</i> (Griffin & Tranter)	Sh-Sl	MZ424959	MZ434805
<i>Schizophrys aspera</i> (H. Milne Edwards)	Sb-Sh		
<i>Cyphocarcinus capreolus</i> (Paulson)	I		
<i>Micippa philyra</i> (Herbst)	Sb-Sh		
<i>Micippa thalia</i> (Herbst)	Sb-Sh-E		
Oregoniidae Garth, 1958			
* <i>Pleistacantha ori</i> Ahyong & P.K.L. Ng	Sl	MZ424960– MZ424965	MZ434806– MZ434810
<i>Pleistacantha oryx</i> Ortmann	Sh-Sl		
Palicoidea Bouvier, 1898			
Palicidae Bouvier, 1898			
<i>Pseudopalicus sexlobatus</i> (Kensley)	Sh		
Parthenopoidea MacLeay, 1838			
Parthenopidae MacLeay, 1838			
Daldorfiinae P.K.L. Ng & Rodríguez, 1986			
<i>Daldorfia horrida</i> (Linnaeus)	Sh		
Parthenopinae MacLeay, 1838			
<i>Enoplolambrus carenatus</i> (H. Milne Edwards)	Sb-Sh		
Pilumnoidea Samouelle, 1819			
Pilumnidae Samouelle, 1819			
Eumedoninae Dana, 1852			
<i>Eumedonus niger</i> H. Milne Edwards	Sb		
<i>Gonatonotus granulosus</i> (MacGilchrist)	I-Sb		
Pilumninae Samouelle, 1819			
<i>Actumnus setifer</i> (De Haan)	I-Sh		

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TABLE 2. (Continued)

Taxa / Species	Habitat	16S	COI
<i>Benthopanope indica</i> (de Man)	I		
<i>Eurycarcinus natalensis</i> (Krauss)	I		
<i>Heteropilumnus trichophoroides</i> (de Man)	Sb		
<i>Pilumnus dofleini</i> Blass	I-Sh		
<i>Pilumnus longicornis</i> Hilgendorf	Sh		
<i>Pilumnus vespertilio</i> (Fabricius)	I-Sb		
<i>Serenepilumnus pisifer</i> (MacLeay)	Sh		
Xenophthalmodinae Števcíć, 2005			
<i>Xenophthalmodes brachyphallus</i> Barnard	I		
<i>Xenophthalmodes moebii</i> Richters	I		
Portunoidea Rafinesque, 1815			
Carcinidae MacLeay 1838			
Parathranitiinae Spiridonov, 2020			
* <i>Parathranites granosus</i> Crosnier (NR)	Sh-Sl	MZ424966	MZ434811
* <i>Parathranites orientalis</i> (Miers) (NR)	Sh-Sl		
Geryonidae Colosi, 1923			
Geryoninae Colosi, 1923			
* <i>Chaceon machpersoni</i> Manning & Holthuis	Sl	MZ424967– MZ424969	MZ434812– MZ434815
Ovalipidae Spiridonov, Neretina & Schepetov, 2014			
* <i>Ovalipes iridescens</i> (Miers)	Sh-Sl		MZ434816
Portunidae Rafinesque, 1815			
Necronectinae Glaessner, 1928			
* <i>Scylla serrata</i> (Forskål)	Sh-Sl	MZ424970	MZ434817
Portuninae Rafinesque, 1815			
<i>Monomia argentata</i> (A Milne Edwards)	Sh		
<i>Portunus sanguinolentus</i> (Herbst)	Sh		
<i>Portunus segnis</i> (Forskål)	Sh		
<i>Portunus hastatooides</i> Fabricius	I-Sb		
Thalamitinae Paulson, 1875			
* <i>Charybdis (Gonionephtunus) africana</i> Shen	Sh-Sl	MZ424971– MZ424973	MZ434818– MZ434820
<i>Charybdis (Charybdis) annulata</i> (Fabricius)	I-Sb		
* <i>Charybdis (Charybdis) feriata</i> (Linnaeus)	Sb-Sh		MZ434821
<i>Charybdis (Charybdis) hellerii</i> (A. Milne-Edwards)	Sh		
<i>Charybdis (Charybdis) natator</i> (Herbst)	I-Sh		
<i>Charybdis (Charybdis) orientalis</i> Dana	Sh		
* <i>Charybdis (Goniohellenus) smithii</i> MacLeay (NR)	P	MZ424974– MZ424975	MZ434822– MZ434823
<i>Charybdis (Charybdis) variegata</i> (Fabricius)	Sh		
<i>Lissocarcinus laevis</i> Miers	Sb-Sh		
<i>Lissocarcinus orbicularis</i> Dana	Sb		
<i>Thalamita admete</i> (Herbst)	I-Sh		
<i>Thalamita bouvieri</i> Nobili	Sh		
<i>Thalamita crenata</i> Rüppell	I-E		
<i>Thalamita danae</i> Stimpson	I-Sh		
<i>Thalamita delagoae</i> Barnard	I		

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TABLE 2. (Continued)

Taxa / Species	Habitat	16S	COI
<i>Thalamita helleri</i> Hoffmann	I		
<i>Thalamita integra integra</i> Dana	I-Sb		
<i>Thalamita picta</i> Stimpson	I-Sb		
<i>Thalamita prymna</i> (Herbst)	I-Sb		
<i>Thalamita sima</i> H. Milne Edwards	I-Sb-Sh		
<i>Thalamita woodmasoni</i> Alcock	I-Sh		
Pseudozioidea Alcock, 1898			
Pseudoziidae Alcock, 1898			
<i>Pseudozius caystrus</i> (Adams & White)	I		
Trapezioidea Miers, 1886			
Tetraliidae Castro, Ng & Ahyong, 2004			
<i>Tetralia rubridactyla</i> Garth	Sb		
<i>Tetraloides nigrifrons</i> (Dana)	Sb		
Trapeziidae Miers, 1886			
Quadrellinae Števc̃ić, 2005			
<i>Quadrella boopsis</i> Alcock	I-Sh		
<i>Quadrella coronata</i> Dana	I-Sh		
<i>Quadrella maculosa</i> Alcock	Sh		
Trapeziinae Miers, 1886			
<i>Trapezia bidentata</i> (Forskål)	Sb		
<i>Trapezia cymodoce</i> (Herbst)	Sb		
<i>Trapezia digitalis</i> Latreille	Sb		
<i>Trapezia guttata</i> Rüppell	Sb		
<i>Trapezia lutea</i> Castro	Sb		
<i>Trapezia richtersi</i> Galil & Lewinsohn	Sb		
<i>Trapezia rufopunctata</i> (Herbst)	Sb		
Xanthoidea Guinot, 1967			
Xanthidae MacLeay, 1838			
Actaeinae Alcock, 1898			
<i>Actaea polyacantha</i> (Heller)	I		
<i>Actaea savignii</i> (H. Milne Edwards)	Sh		
<i>Actaeodes hirsutissimus</i> (Rüppell)	I		
<i>Actaeodes tomentosus</i> (H. Milne Edwards)	I		
<i>Forestiana granulata</i> (Krauss)	I		
<i>Gaillardiiellus rueppelli</i> (Krauss)	I-Sh		
<i>Psaumis cavipes</i> (Dana)	I-Sb		
<i>Pseudoliomera speciosa</i> (Dana)	I-Sb		
Chlorodiellinae P.K.L. Ng & Holthuis, 2007			
<i>Chlorodiella laevissima</i> (Dana)	I-Sb		
<i>Chlorodiella nigra</i> (Forskål)	I-Sb		
<i>Cyclodius obscurus</i> (Hombron & Jacquinet)	Sb		
<i>Cyclodius unguulatus</i> (H. Milne Edwards)	I		
<i>Pilodius areolatus</i> (H. Milne Edwards)	I-Sb		
<i>Pilodius pilumnoides</i> (White)	I-Sb		
Cymoinae Alcock, 1898			
<i>Cymo andreossyi</i> (Audouin)	Sb		

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TABLE 2. (Continued)

Taxa / Species	Habitat	16S	COI
Etisinae Ortmann, 1893			
<i>Etisus electra</i> (Herbst)	Sb		
<i>Etisus laevimanus</i> Randall	I		
Euxanthinae Alcock, 1898			
<i>Hypocolpus diverticulatus</i> (Strahl)	I		
* <i>Monodaeus tuberculidens</i> (Rathbun)	I-SI	MZ424976	MZ434824
Kraussiinae Ng, 1993			
<i>Kraussia rugulosa</i> (Krauss)	I-Sb		
Liomerinae Sakai, 1976			
<i>Liomera bella</i> (Dana)	I		
<i>Liomera cinctimanus</i> (White)	I		
<i>Liomera monticulosa</i> (A. Milne-Edwards)	I		
Polydectinae Dana, 1851			
<i>Lybia leptochelis</i> (Zehntner)	Sh		
<i>Lybia tessellata</i> (Latreille in Milbert)	Sb		
Xanthinae MacLeay, 1838			
<i>Lachnopus subacutus</i> (Stimpson)	Sb		
<i>Leptodius exaratus</i> (H. Milne Edwards)	Sb		
<i>Leptodius gracilis</i> (Dana)	I		
<i>Leptodius sanguineus</i> (H. Milne Edwards)	I-Sb		
<i>Macromedaeus voeltzkowii</i> (Lenz)	I		
<i>Neoxanthias impressus</i> (Latreille in Milbert)	I-Sb		
<i>Xanthias lamarckii</i> (H. Milne Edwards)	I-Sb		
<i>Xanthias punctatus</i> (H. Milne Edwards)	I-Sb		
Zosiminae Alcock, 1898			
<i>Atergatis ocyroe</i> (Herbst)	I		
<i>Atergatis roseus</i> (Rüppell)	I		
<i>Atergatis obesa</i> (A. Milne-Edwards)	I		
<i>Atergatis signata</i> (Adams & White)	I-Sb		
<i>Lophozymus dodone</i> (Herbst)	Sb		
<i>Zozymodes cavipes</i> (Dana)	I		
<i>Zozymodes xanthoides</i> (Krauss)	I		
Thoracotremata Guinot, 1977			
Cryptochiroidea Paulson, 1875			
Cryptochiridae Paulson, 1875			
<i>Hapalocarcinus marsupialis</i> Stimpson	Sb		
Grapsoidae MacLeay, 1838			
Grapsidae MacLeay, 1838			
<i>Grapsus fourmanoiri</i> Crosnier	I		
<i>Grapsus tenuicrustatus</i> (Herbst)	I		
<i>Metopograpsus messor</i> (Forskål)	I		
<i>Metopograpsus thukuhar</i> (Owen)	I		
<i>Pachygrapsus minutus</i> A. Milne-Edwards	I		
<i>Pachygrapsus plicatus</i> (H. Milne Edwards)	I		
<i>Planes marinus</i> Rathbun	P		
<i>Planes minutus</i> (Linnaeus)	P		

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TABLE 2. (Continued)

Taxa / Species	Habitat	16S	COI
Perenidae Števcíć, 2005			
<i>Percnon planissimum</i> (Herbst)	Sb		
Plagusidae Dana, 1851			
<i>Plagusia depressa</i> (Fabricius)	I-Sb		
Sesarmidae Dana, 1851			
<i>Chiromantes eulimene</i> (de Man in Weber)	I		
<i>Chiromantes ortmanni</i> (Crosnier)	I		
<i>Neosarmatium africanum</i> Ragonieri, Fratini & Schubarth	I		
<i>Parasesarma catenatum</i> (Ortmann)	I		
<i>Parasesarma leptosoma</i> (Hilgendorf)	Sp		
<i>Parasesarma plicatum</i> (Latreille)	I		
<i>Parasesarma guttatum</i> (A. Milne-Edwards)	I		
<i>Sarmatium crassum</i> Dana	I		
<i>Selatium elongatum</i> (A. Milne-Edwards)	I-Sp		
<i>Sesarmoides longipes</i> (Krauss)	I		
Varunidae H. Milne Edwards, 1853			
Varuninae H. Milne Edwards, 1853			
<i>Pseudograpsus elongatus</i> (A. Milne-Edwards)	I		
<i>Varuna litterata</i> (Fabricius)	I-E		
Ocypodoidea Rafinesque, 1815			
Camptandriidae Stimpson, 1858			
<i>Danielella edwardsii</i> (MacLeay)	I		
<i>Paratyloidiplax blephariskios</i> (Stebbing)	I		
Dotillidae Stimpson, 1858			
<i>Dotilla fenestrata</i> Hilgendorf	I		
<i>Lazarocleistostoma dentatum</i> (Tesch)	I		
Macrophthalmidae Števcíć, 2005			
Ylyograpsinae Števcíć, 2005			
<i>Ilyograpsus rhizophorae</i> Barnard	I		
Macrophthalminae Dana, 1851			
<i>Chaenostoma sinuspersici</i> (Naderloo & Türkay)	I		
<i>Macrophthalmus (Macrophthalmus) grandidieri</i> A. Milne-Edwards	I		
<i>Macrophthalmus (Mareotis) depressus</i> Rüppell	I		
<i>Venitus latreillei</i> (Desmarest)	I		
Ocypodidae Rafinesque, 1815			
Gelasiminae Miers, 1886			
<i>Austruca annulipes</i> (H. Milne Edwards)	I		
<i>Cranuca inversa</i> (Hoffmann)	I		
<i>Gelasimus hesperiae</i> (Crane)	I		
<i>Paraleptuca chlorophthalmus</i> (H. Milne Edwards)	I		
<i>Tubuca urvillei</i> (H. Milne Edwards)	I		
Ocypodinae Rafinesque, 1815			
<i>Ocypode ceratophthalmus</i> (Pallas)	Sp		
<i>Ocypode cordimana</i> Latreille	Sp		
<i>Ocypode madagascariensis</i> Crosnier	Sp		

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TABLE 2. (Continued)

Taxa / Species	Habitat	16S	COI
<i>Ocypode ryderi</i> Kingsley	Sp		
Pinnotheroidea De Haan, 1833			
Pinnotheridae De Haan, 1833 [in De Haan, 1833-1850]			
Pinnixinae Števc̆ić, 2005			
<i>Pinnixa penultipedalis</i> Stimpson	I		
Pinnotheridae De Haan, 1833 [in De Haan, 1833-1850]			
<i>Afropinnotheres dofleini</i> Lenz in Lenz & Strunck	Sb-Sh		
<i>Pinnotheres globosus</i> Hombron & Jacquinot	Sb		
<i>Pinnotheres</i> sp.	I-Sb		
<i>Xanthasia murigera</i> White	Sb		

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