

Identification of new species of *Kalloconus* and *Africonus* (Gastropoda, Conidae) from the Cabo Verde Islands through mitochondrial genome comparison

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ABSTRACT

The new species *Kalloconus marimaris* sp. nov. and *Africonus angeluquei* sp. nov. are described from the material obtained during the MNCN sampling campaigns at the Cabo Verde Islands. The new species have been characterized by examination of their shell and radular teeth morphology and by the comparison of mitochondrial genomes obtained through next-generation DNA sequencing techniques. Phylogenetic analyses suggest that *K. marimaris* sp. nov., known from Sal Island, is a sister species to *Kalloconus ateralbus*, whereas *A. angeluquei* sp. nov. from Maio Island is a sister species to *Africonus josephinae* and *Africonus borgesii* from Boa Vista Island. The estimated genetic distances were consistent with the full species rank for the new taxa described herein.

INTRODUCTION

The Cabo Verde Archipelago is renowned for the high number of endemic cone snail species (Rolán 1990, Monteiro *et al.* 2004, Cunha *et al.* 2005, Duda & Rolán 2005, Peters *et al.* 2016). As a result of the systematic sampling of cone snail populations across the Cabo Verde archipelago, we have been able to reconstruct a statistically robust phylogeny based on almost complete mitochondrial genomes (consisting of 10,000 to 16,000 DNA base pairs) and using probabilistic methods that include most of currently accepted species. Mitochondrial genomes compare to partial gene sequences provide robust phylogenetic inferences with highly resolved trees below the family level (Abalde *et al.* 2017 and references therein). Based on the reconstructed phylogeny and on genetic distance comparisons, the taxonomic status of the analyzed cone species was revised: DNA sequence divergences below or above a given threshold allowed for postulating

synonyms or confirming valid species, respectively (Abalde *et al.* 2017). In this fashion, and regardless of the large amount of names introduced in recent years for different Cabo Verde cone snail populations, the number of valid species for the archipelago was reduced to about one half. Nevertheless, some cone populations, which showed sequence divergences above the threshold, did not correspond to any of the already named species. By following this criterion, the new species *Africonus freitasi* Tenorio, Afonso, Rolán, Pires, Vasconcelos, Abalde & Zardoya, 2017 was recently described based on two populations previously reported from São Vicente Island (Röckel *et al.* 1980, Rolán 2005). Similarly, we found several populations of *Kalloconus* from Sal Island, and of *Africonus* from Maio Island, which exhibited DNA sequence divergences consistent with the hypothesis of separate species, yet formally undescribed. Therefore, we hereby introduce these new species with the respective names *Kalloconus marimaris* sp. nov.

and *Africonus angeluquei* sp. nov. The morphological features of the shells of the new species are compared with those of their sister taxa in the phylogeny, namely *Kalloconus ateralbus* (Kiener, 1845) (Figure 1A) and *Africonus josephinae* (Rolán, 1980) (Figure 1C) plus *Africonus borgesii* (Trovão, 1979) (Figure 1D).

MATERIAL AND METHODS

Taxonomy follows Tucker & Tenorio (2009) with the updates and modifications based on Tucker & Tenorio (2013) and Abalde *et al.* (2017). The specimens studied were collected by snorkeling during campaigns carried out by the MNCN in the Cabo Verde Islands between 2013 and 2014, at depths between 1–3 m. Distribution maps were generated using GeoMapApp (<http://www.geomapapp.org>) using the global multi-resolution topography (GMRT) as default basemap.

We describe shell morphology using the terminology established in Röckel *et al.* (1995). For morphometric comparisons, adult shells

were measured using digital calipers, with measurements rounded to 0.1 millimeter. For comparison of shell morphometry, the analysis was performed using analysis of covariance (ANCOVA) for the corresponding morphometric trait, using species hypotheses as factor and aperture height (AH) as co-variate. Statistical tests were carried out using STATGRAPHICS CENTURION XVII, once all the measurement sets passed the normality tests.

We used the terminology for radular morphology of Tucker & Tenorio (2009), and the abbreviations in Kohn *et al.* (1999). The radular sac was dissected from the cone snail and soft parts were digested in concentrated aqueous potassium hydroxide for 24 hours. The resulting mixture was then placed in a Petri dish and examined with a binocular microscope. The entire radula was removed with fine tweezers and rinsed with distilled water, then mounted on a slide using Aquatex (Merck) Mounting Medium, and examined under a compound microscope. Photographs were obtained with a CCD camera attached to the microscope.

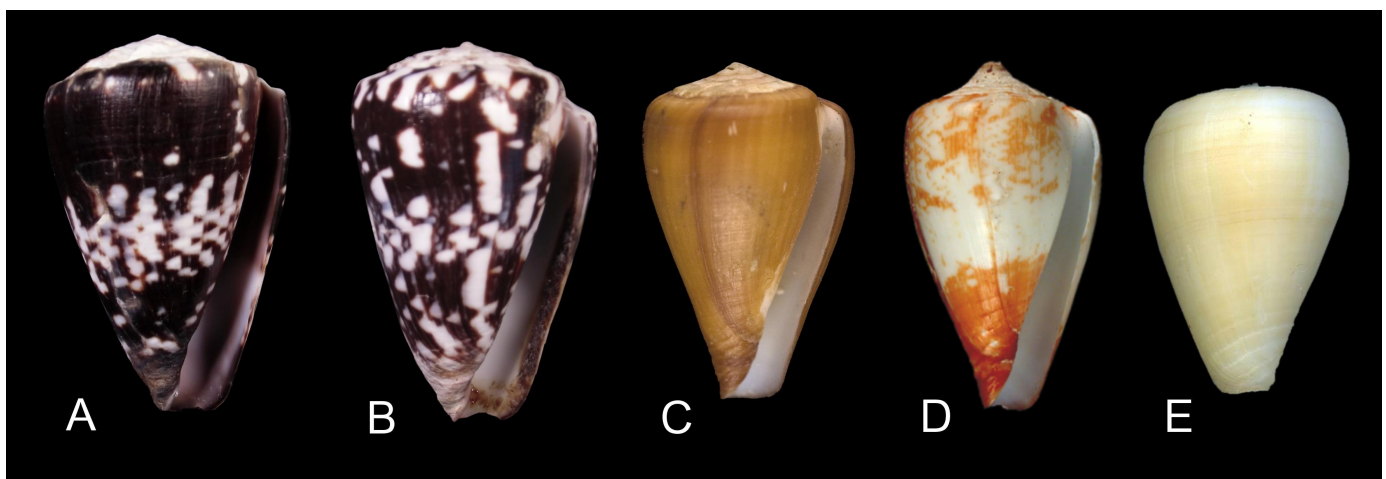


Figure 1. A) *Kalloconus ateralbus*, 42.3 mm, Calheta Funda, Sal Island, MNCN; B) *Kalloconus venulatus*, 50.7 mm, Morro de Areia, Boa Vista Island, MNCN; C) holotype of *Conus josephinae*, 25.8 mm, Sal-Rei, Boa Vista Island, MNCN; D) holotype of *Conus borgesii*, 26.1 mm, Baía das Gatas, Boa Vista Island, NHMUK; E) *Africonus josephinae* f. *guiandradoi*, mm, paratype 4, 24.3 mm, off NE Sal Rei, Baixa da Hortinha, Boa Vista Island, Paul Kersten coll., Hoornaar, The Netherlands.

DNA sequences are from Abalde *et al.* (2017). Nucleotide sequences of the 13 mitochondrial (“mt”) protein-coding and two rRNA genes were aligned independently using Translator X (Abascal *et al.* 2010) and MAFFT v7 (Kato & Standley 2013), respectively. All aligned genes were combined in a single dataset. Uncorrected *p* distances were estimated using MEGA (Kumar *et al.* 2016). Phylogenetic relationships were inferred using maximum likelihood (ML) and Bayesian inference (BI). For ML, we used RAxML v8.1.16 (Stamatakis 2006) with the rapid hill-climbing algorithm and 10,000 bootstrap pseudoreplicates (BP). For BI, we used MrBayes v3.1.2 (Ronquist & Huelsenbeck 2003), running 10 million generations, sampling every 1000 generations, and discarding the first 25% generations as burn-in. Best-fit partition schemes and substitution models were identified using PartitionFinder2 (Lanfear *et al.* 2017). Node support was estimated based on Bayesian posterior probabilities (BPP). The amphiatlantic *Chelyconus ermineus* was used as outgroup. *Lautoconus ventricosus* from Portugal, and *Kalloconus pulcher* from Senegal were included as representatives of the closest sister groups of Cabo Verde *Africonus* and *Kalloconus*, respectively.

Abbreviations

Museums and private collections

MNCN: Museo Nacional de Ciencias Naturales, Madrid, Spain.

MNHN: Muséum National d’Histoire Naturelle, Paris, France.

MHNS: Museo de Historia Natural de la Universidad de Santiago de Compostela, Spain.
NHMUK : Natural History Museum, London, UK.

UCV: reference collection of the University of Cabo Verde, Mindelo, Cabo Verde.

MJT: reference collection of Manuel J. Tenorio, Jerez, Spain.

CMLA: reference collection of Carlos M. L. Afonso, Algarve, Portugal.

Shell morphometry

S_L maximum shell length

MD maximum diameter

SH spire height

HMD height of maximum diameter

AH aperture height

RD relative diameter (= MD/AH)

RSH relative spire height (= SH/S_L)

PMD relative position of the maximum diameter (= HMD/AH)

Radular morphometry

B_L blade length

S_L/T_L shell length/radular tooth length

T_L/AP_L radular tooth size/anterior portion length

100B_L/AP_L 100 x blade length/anterior portion length

RESULTS

SYSTEMATICS

Family CONIDAE Fleming, 1822

Genus *Kalloconus* da Motta, 1991

Kalloconus marimaris sp. nov.

(Plate 1, Figures A–M)

Conus ateralbus – Monteiro *et al.* 2004: pl. 47, figs. 2, 5 & 7; pl. 48, figs. 1-7; pl. 49, figs. 1-6 (not *Conus ateralbus* Kiener, 1845).

Conus venulatus – Monteiro *et al.* 2004: pl. 52, figs. 1 & 3; Rolán 2005: pl. 49, figs. 744- 746 (not *Conus venulatus* Hwass in Bruguière, 1792).

Type material: Holotype and 14 paratypes. The holotype is deposited in the Museo Nacional de Ciencias Naturales, Madrid, Spain, under the number MNCN 15.05/79664, *see* Table 1 for details. Additional uncataloged paratypes are in the reference collection of MJT.

Type	Institution	Dimensions (mm)	Locality
Holotype	MNCN 15.05/79664	38.6 x 23.9	Serra Negra, Sal Island, Cabo Verde Islands, 16°38'16.5"N, 22°53'56"W, 1-3 m.
Paratype 1	MNCN 15.05/79666	37.2 x 23.1	same data as the holotype
Paratype 2	MNCN 15.05/79671	29.7 x 19.6	same data as the holotype
Paratype 3	MNHN-IM-2014-6899	30.9 x 17.6	same data as the holotype
Paratype 4	MNCN 15.05/79668	31.7 x 21.6	same data as the holotype
Paratype 5	MNCN 15.05/79674	28.3 x 17.3	same data as the holotype
Paratype 6	MNCN 15.05/79676	27.3 x 17.6	same data as the holotype
Paratype 7	MNCN 15.05/79680	40.1 x 27.4	Rabo de Junco, Sal Island, Cabo Verde Islands, 16°41'44"N, 22°58'35"W, 1-3 m.
Paratype 8	MNCN 15.05/79684	39.8 x 27.6	same data as paratype 7
Paratype 9	MNCN 15.05/79689	36.6 x 22.9	same data as paratype 7
Paratype 10	MNCN 15.05/79699	40.9 x 24.2	Murdeira, Sal Island, Cabo Verde Islands, 16°40'43"N, 22°56'10"W, 1-3 m.
Paratype 11	MNCN 15.05/79688	41.5 x 27.1	same data as paratype 7
Paratype 12	MHNS 100636	36.2 x 22.6	same data as paratype 7
Paratype 13	UCV 2018/00005	33.9 x 21.9	same data as paratype 7
Paratype 14	CMLA	40.3 x 24.9	same data as paratype 7

Table 1. Detailed listing of type specimens.

Material examined: A total of 49 specimens from separate populations to the east (Serra Negra) and west (Rabo de Junco and Murdeira) coasts of Sal Island, Cabo Verde archipelago have been studied. Most specimens are deposited at the MNCN collection.

Type locality: Serra Negra, Sal Island, Cabo Verde archipelago, 16°38'16.5"N, 22°53'56"W, 1–3 m.

Distribution and habitat: The species is endemic to Sal Island, Cabo Verde archipelago, where it has been collected in the east (Serra Negra) and west (Murdeira to Rabo de Junco) coasts of the island in shallow water (from a few centimeters down to 5 m) (Figure 2). The populations from both sides of the island are isolated from each other, and exhibit subtle morphological differences in shell pattern. The species lives half-buried in sand among rocks (Figure 3).

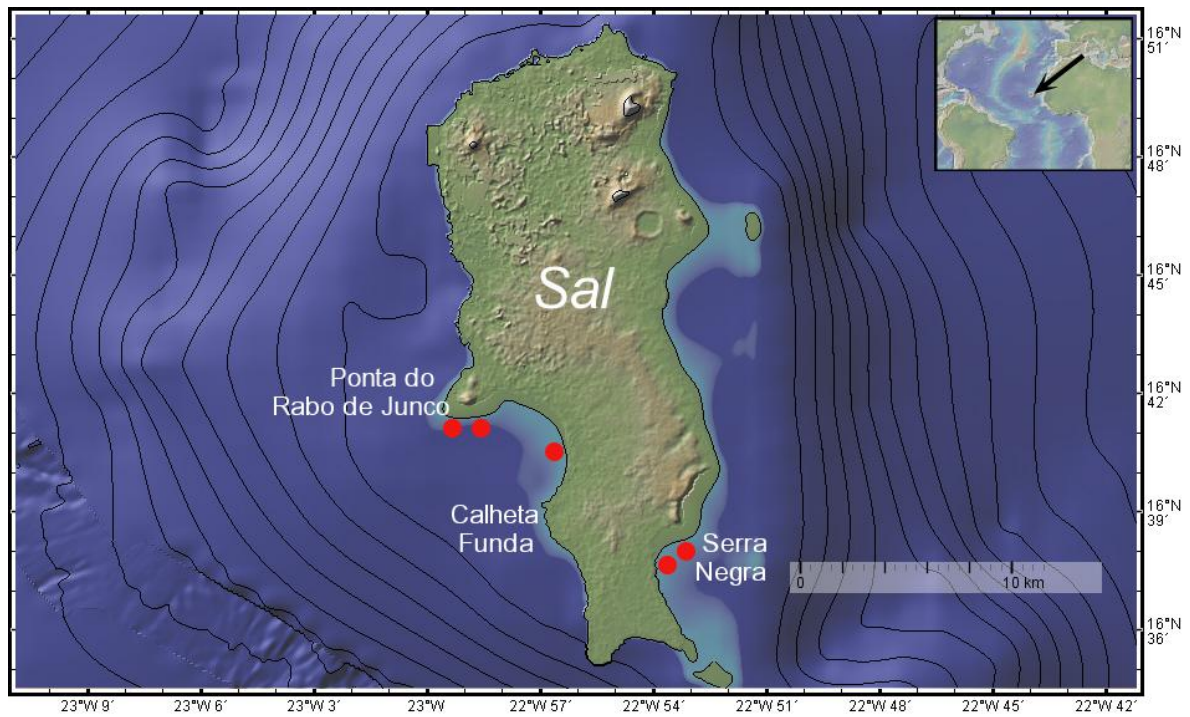


Figure 2. Distribution map for *Kolloconus marimaris* (red circles). Symbols indicate the points where the species has been sampled. The bathymetric levels are represented by curved lines.



Figure 3. *Kolloconus marimaris* sp. nov. alive in natural habitat, Rabo de Junco, Sal Island (photo credit: Carlos M. L. Afonso).

Etymology: Named after Maria del Mar Albarrán, sister-in-law of the first author, who recently and prematurely passed away. Known as Marimar by family and friends, she was a beloved wife and mother, with devotion for the sea and especially for the beautiful beaches of the Atlantic coast of her native province of Cadiz.

Description of the shell: Morphometric parameters: $S_L = 25-45$ mm; mean $S_L = 35.5$ mm; $RD = 0.70-0.79$; $RSH = 0.09-0.21$; $PMD = 0.81-0.89$.

Shell moderately small to medium-sized. Profile broadly and ventricosely conical to broadly conical. Protoconch paucispiral, white at the nucleus with yellowish early whorls. Early postnuclear whorls and late teleoconch whorls smooth. Spire of moderate height, most often heavily eroded, of straight or slightly sigmoid profile. Teleoconch whorls flat or slightly concave. Cords are absent. Shoulder subangulate to angulate. Last whorl sides straight or slightly convex. Aperture narrow, white, and of uniform width. Pattern of the last whorl very variable. Most often chestnut brown with small triangular white markings, but there are also specimens orange or pinkish-white in color. White triangular markings arranged in one broad spiral band in the center of the last whorl, flanked above and below by spiral areas showing little or no pattern. Other two spiral bands of white triangular markings are often present near the shoulder and the base respectively, although these are not as dense as the central band, and might be even absent in some specimens. Thin, equally-spaced spiral lines of a darker shade of the ground color (brown or orange) may be present, specially in specimens from western coast populations. Spire pattern consisting of alternating white and ground color (brown or orange) irregular blotches. In general, there is a large variability

in color and pattern (*see* Plate 1). Periostracum yellow, thin and translucent. Operculum small and rounded.

Living animal and radula: The animal is light purplish with areas of a darker purple color, specifically the tip of the siphon. 30 to 38 teeth in radular sac. Radular tooth (Figure 4A, B) of the vermivorous type, of medium relative size ($S_L/T_L = 45-54$), with a short barb, not very marked. Waist not very well marked but evident. Anterior and posterior sections are essentially equal in length ($T_L/AP_L = 1.9-2.0$). Blade rounded, covering most of the anterior section ($100B_L/AP_L = 65\%$ to 80%). Serration with 20 - 31 denticles arranged in one row, becoming two rows below. The serration ends in a small terminating cusp. The denticles are rather coarse in the apical portion, becoming small and even obsolete in the lower third. Base rather broad, with a small spur.

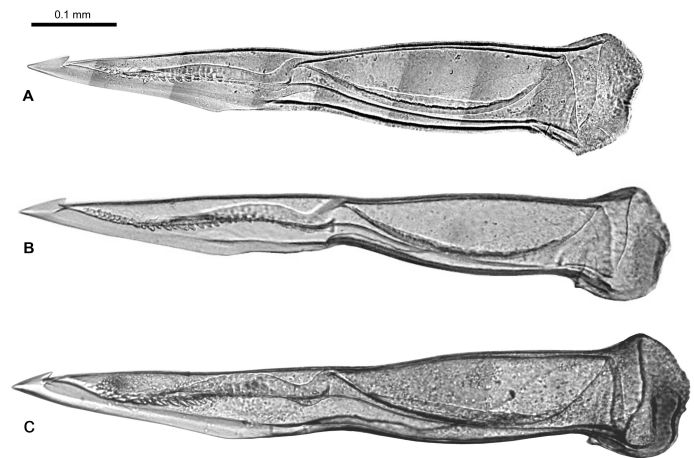


Figure 4. Radular teeth of: A) *K. marimaris* sp. nov., Serra Negra, Sal Island, S_L 33.1 mm; B) *K. marimaris* sp. nov., Rabo de Junco, Sal Island, S_L 38.0 mm; C) *K. ateralbus*, Calheta Funda, Sal Island, S_L 39.5 mm.

DIFFERENTIAL DIAGNOSIS

Kalloconus marimaris sp. nov. is similar to *K. ateralbus* (Kiener, 1845) (Figure 1A), and it has been previously figured in the literature as the latter species. Indeed, both species are very similar in shape, size, and morphology of the radular teeth (Figure 4). The slight differences in the morphometric parameters of shell and radula are not statistically significant. However, the two species are molecularly distinct. This was already suggested by phylogenetic studies on population genetics of the species in the *Kalloconus venulatus* (Hwass in Bruguière, 1792) group based on partial gene sequences (Cunha *et al.* 2008), and the splitting at the species level is hereby confirmed by analyzing mt genomes. In a well-resolved and highly supported phylogenetic tree (Figure 5), both species are recovered as sister taxa, separated by an uncorrected *p* distance of ca. 1.1 %. Specimens from the populations of Serra Negra and Rabo de Junco appear clustered together (*p* distances <0.1%), as sister group to *K. ateralbus*. The most evident morphological features for the separation of *K. marimaris* sp. nov. and *K. ateralbus* are related to shell background color and pattern, as well as to the color of the aperture. Thus, the background color of *K. ateralbus* is black, with a pattern of white triangular markings most often arranged as a midbody broad spiral band. There is some variability in the extent of the distribution of the white triangular markings in the body whorl, but the background color is constant. In the case of *K. marimaris* sp. nov., the background color is variable, ranging from dark brown to orange, yellow or even milky white. The aperture in *K. marimaris* sp. nov. is white, but purplish in the case of *K. ateralbus*. The two species have separate areas of distribution. *K. ateralbus*

seems restricted to the SW of Sal Island, in the Bays of Algodoeiro and Calheta Funda. The northern range of its distribution has a contact zone with that of *K. marimaris* sp. nov. in Murdeira Bay. The shell morphology of certain morphs of the molecularly distinct species *K. venulatus* (Figure 1B) (*p* distance 2.4 %) may appear very similar to that of *K. marimaris* sp. nov. Both species share the white-colored aperture, and a high variability in shell color and pattern. However, all the populations of *K. venulatus* are distributed throughout the islands of Boa Vista and Maio, being absent from Sal Island.

Genus *Africonus* Petuch, 1973

Africonus angeluquei sp. nov.
(Plate 2, Figures A–M)

Conus sp. – Röckel *et al.* 1980: p. 141, fig. 123; pl. 2, 2nd row, figs. c, d.

Conus josephinae – Monteiro *et al.* 2004: pl. 110, figs. 1-6 (not *C. josephinae* Rolán, 1980).

Type material: Holotype and 14 paratypes. The holotype is deposited in the Museo Nacional de Ciencias Naturales, Madrid, Spain, under the number MNCN 15.05/78710. *See* Table 2 for details. Additional uncataloged paratypes are in the reference collection of MJT.

Material examined: More than 50 specimens from several locations in Maio Island, Cabo Verde archipelago, have been studied. These specimens are deposited in the MNCN, MJT and CMLA collections.

Type locality: Lage Branca, Baía do Galeao, Maio Island, Cabo Verde archipelago, 15°18'32"N, 23°8'18"W, 1-3.

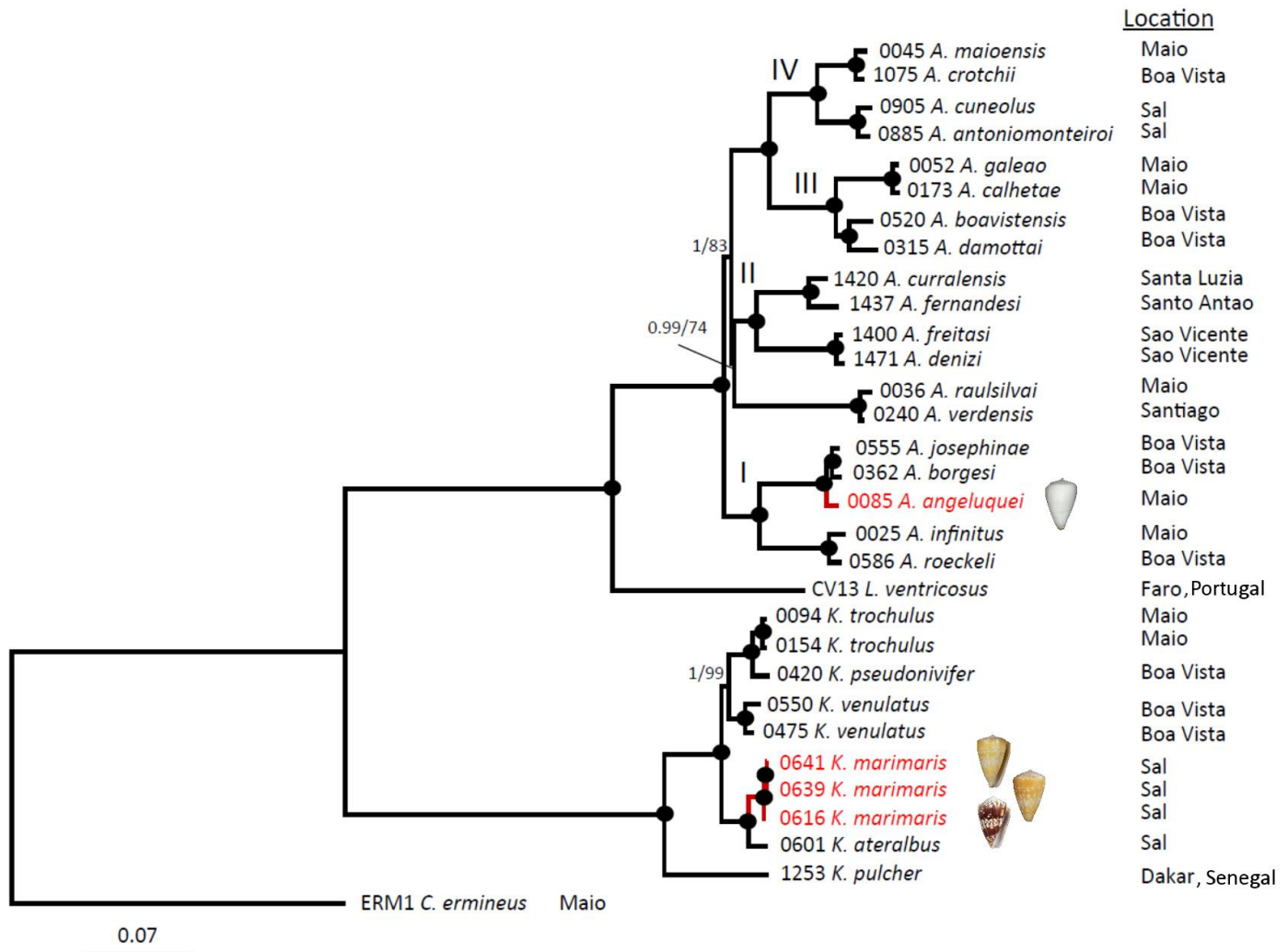


Figure 5. Phylogeny of cones endemic to Cabo Verde archipelago based on almost complete mitochondrial genomes (concatenated protein coding plus rRNA genes analyzed at the nucleotide level). Numbering of specimens follows Abalde *et al.* 2017. Their geographical distribution is indicated. Ventral images of the shell of the new species are provided. Numbers at nodes are statistical support values for BI (Bayesian posterior probabilities, BPP)/ ML (bootstrap proportions, BP). A black dot indicates maximal support (BPP 1/ BP 100%). Scale bar indicates substitutions/site. Four major lineages (I-IV) are recovered within *Africonus* as in Abalde *et al.* 2017. GenBank accession nos. are provided in Abalde *et al.* (2017) except for MH243427 and MH243428 corresponding to individuals 0639 and 0641, respectively.

Type	Institution	Dimensions (mm)	Locality
Holotype	MNCN 15.05/78710	30.0 x 19.0	Lage Branca, Baia do Galeao, Maio Island, Cabo Verde Islands, 15°18'32"N, 23°8'18"W, 1-3 m.
Paratype 1	MNCN 15.05/78708	21.7 x 13.2	same data as the holotype
Paratype 2	MNCN 15.05/78707	18.8 x 12.2	same data as the holotype
Paratype 3	MNHN-IM-2014-6900	24.8 x 15.8	same data as the holotype
Paratype 4	MNCN 15.05/78709	28.4 x 17.6	same data as the holotype
Paratype 5	MNCN 15.05/78713	21.3 x 13.2	same data as the holotype
Paratype 6	MNCN 15.05/78712	21.7 x 13.1	same data as the holotype
Paratype 7	MNCN 15.05/78804	37.8 x 24.0	Praia Real, Maio Island, Cabo Verde Islands, 15°19'45"N, 23°10'39"W, 1-3 m.
Paratype 8	MNCN 15.05/78802	34.0 x 20.7	same data as paratype 7
Paratype 9	MNCN 15.05/78807	30.0 x 20.0	same data as paratype 7
Paratype 10	MNCN 15.05/78714	20.4 x 11.8	same data as the holotype
Paratype 11	MNCN 15.05/78646	24.3 x 14.8	Baía do Pau Seco, Maio Island, Cabo Verde Islands, 15°15'26"N, 23°13'16"W, 1-3 m.
Paratype 12	MHNS 100637	18.1 x 11.3	same data as the holotype
Paratype 13	UCV 2018/00006	18.8 x 12.0	same data as the holotype
Paratype 14	CMLA	25.2 x 15.2	same data as paratype 7

Table 2. Detailed listing of type specimens.

Distribution and habitat: The species has been collected in the west coast (Baia do Pau Seco) and the north coast (Porto Cais, Praia Real and Baia do Galeao) of Maio Island, Cabo Verde archipelago (Figure 6). It has been found under rocks on sand, in 2 to 5 m depth.

Etymology: Named after Dr. Angel Luque del Villar, Associate Professor of Zoology at the Universidad Autónoma de Madrid. Dr. Luque del Villar is a specialist in taxonomy,

systematics, ecology and biogeography of marine gastropods. He also works in various marine benthic communities and in the conservation of marine species and habitats.

Description of the shell: Morphometric parameters: $S_L = 18-34$ mm; mean $S_L = 26.8$ mm; $RD = 0.69-0.79$; $RSH = 0.08-0.16$; $PMD = 0.80-0.87$.

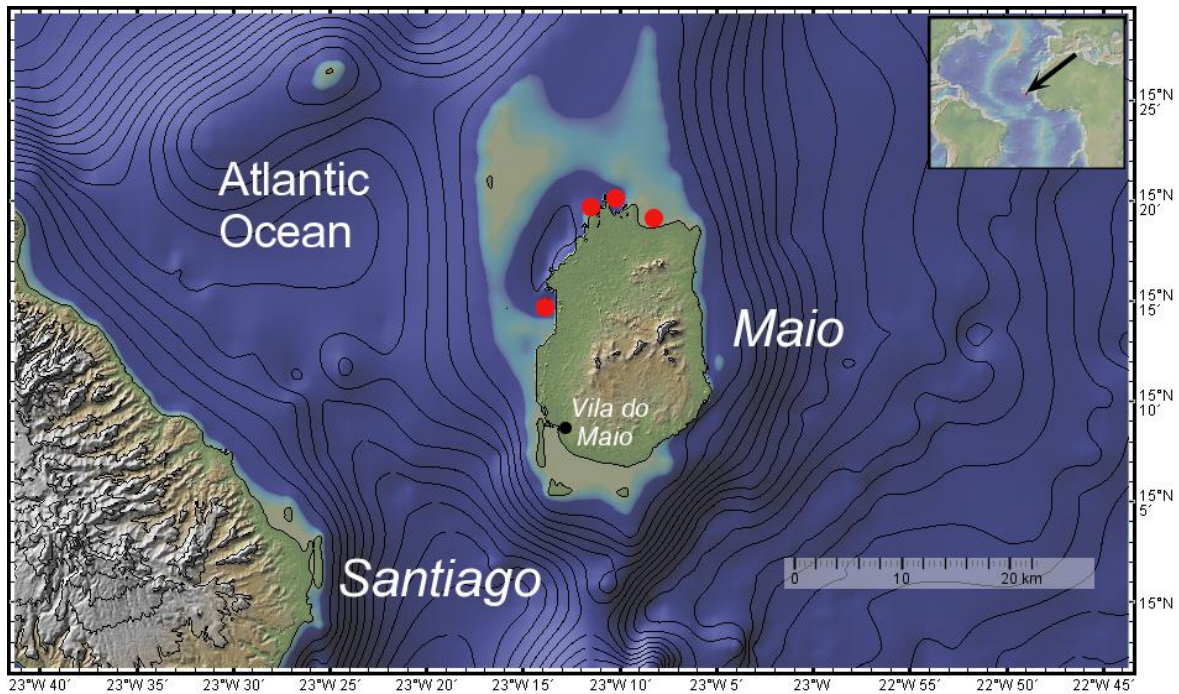


Figure 6. Distribution map for *Africonus angeluquei* (red circles). Symbols indicate the points where the species has been sampled. The bathymetric levels are represented by curved lines.



Figure 7. *A. angeluquei* sp. nov. alive in artificial conditions (photo credit: Carlos M. L. Afonso).

Shell moderately small, broadly and ventricosely conical in shape. Spire is low to moderate and concave in profile. Reddish brown protoconch (when not eroded), paucispiral of 1.25 whorls. Teleoconch sutural ramp flat or slightly convex, with 3-4 cords clearly visible on the early whorls, becoming obsolete in later whorls. Shoulder subangulated to rounded. Aperture white. Shell essentially patternless, of uniform color, which ranges most often from pure white to yellow, and less frequently from light brown to chestnut brown. Some specimens display fine spiral lines in variable number of a darker or lighter color than the background. Occasionally, a change in the color may occur during the growth of the shell, resulting in a bi-colored shell. Periostracum yellow, thin and translucent.

Living animal and radula: The animal has a uniform very dark red color, almost black in appearance (Figure 7). 36 to 38 teeth in radular sac. The radular tooth (Figure 8A) is of the vermivorous type, very broad, and of medium to large relative size ($S_L/T_L = 36-42$). Apical barb small but clearly marked. The anterior portion is shorter than the posterior portion ($T_L/AP_L = 2.2-2.3$). Blade rounded, covering most of the anterior portion ($100B_L/AP_L = 75\%$ to 80%). Serration with 20 to 32 small denticles arranged in two rows, becoming three rows towards the base. Terminating cusp sharp and prominent. Basal spur present.

DIFFERENTIAL DIAGNOSIS

A. angeluquei sp. nov. has been previously identified as the Maio population of the taxon *Africonus josephinae* (Rolán, 1980) (Figure. 1C). Indeed, both species exhibit almost identical shell and radular morphologies (Figure. 8A,B). However, the phylogenetic analysis (Figure 5) shows that the genetic distance between *A. angeluquei* sp. nov. from Maio and

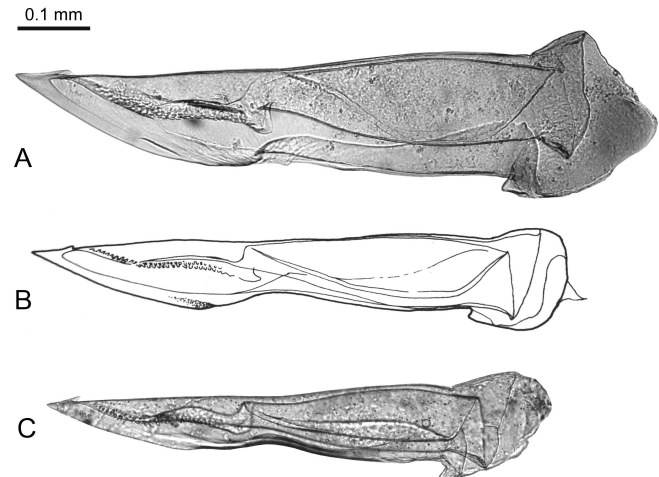


Figure 8. Radular teeth of : A) *A. angeluquei* sp. nov., Praia Real, Maio, S_L 33.0 mm; B) *A. josephinae*, Sal-Rei, Boa Vista, S_L 32.0 mm (drawing by Dr. Emilio Rolán); C) *A. borgesii*, Derrubado, Boa Vista, S_L 23.4 mm.

A. josephinae from Boa Vista (uncorrected p distance of 0.8 %) is consistent with the separation at the species level. Furthermore, the taxon *Africonus borgesii* (Trovão, 1979) (Figure 1D, Figure 8C), also known from Boa Vista Island, appears closer to *A. josephinae* (uncorrected p distance of 0.5 %) than *A. angeluquei* sp. nov. The observed differences between *A. angeluquei* sp. nov. and *A. josephinae* in shell and radular morphometric parameters are not statistically significant. In any case, the shell of *A. josephinae* is more pyriform than that of *A. angeluquei* sp. nov., with a more rounded shoulder. The shell of *A. angeluquei* sp. nov. is usually more conical, with straight sides and shoulder often subangulated. Apart from the different area of geographical distribution, both species differ in the ground color of the shell. The shell of *A. angeluquei* sp. nov. is most often white or yellow (Plate 2A-L), although brown and pinkish specimens are also known (Plate 2M). In the case of *A. josephinae*, the situation is reversed, as the most typical specimens are

brown, and yellow specimens are less frequent but not unknown. The recently named species *Africonus guiandradoi* Cossignani & Fiadeiro, 2017 (Figure 1E) from NE Sal Rei, Boa Vista Island, actually applies to such yellow specimens of *A. josephinae*, in this case with some fine brown spiral lines present. Hence, *A. guiandradoi* must be considered a synonym (color form) of *A. josephinae*. The occasional presence of fine dark brown spiral lines is a feature also observed in some specimens of *A. angeluquei* sp. nov. (Plate 2L), as it is the change of coloration of the shell as the species grows (Plate 2K). These features must be considered elements of the variability of the species, and lack any taxonomic value.

DISCUSSION

The taxonomy of cone snails has relied mostly on shell form and coloration (Tucker and Tenorio, 2009). The comparison of these phenotypic features is generally useful when there are conspicuous differences among taxa but shell has been shown to be highly homoplasious in some instances and subjected to diverse evolutionary forces that may confound taxonomic identification (Abalde *et al.* 2017). In some cases, differences in shell coloration and banding patterns among individuals may only reflect phenotypic plasticity and local adaptation (and not true species differences) and on the contrary, in other cases, shells having only subtle differences in coloration and banding patterns may result from convergence and cover cryptic species. To distinguish these problems, the use of robust molecular phylogenies is very helpful. The great diversification of cone snails in the Cabo Verde archipelago, which hosts 10% of cone species diversity worldwide, has attracted the attention of taxonomists, evolutionary biologists, and amateurs alike (Rolán 1990, Monteiro *et al.* 2004, Cunha *et al.* 2005, Duda

& Rolán 2005, Peters *et al.* 2016). To further understand how the extraordinary diversity of cone snails was originated and is maintained in these islands, a first crucial step was revising the taxonomic status of all described species under the light of a robust phylogeny, which was reconstructed based on mitochondrial genomes (Abalde *et al.* 2017). This phylogeny was useful in validating some species, uncovering synonyms, and in some few instances discovering cryptic species. Here, we described two cases belonging to the genera *Kalloconus* and *Africonus*, respectively. Each case represents a striking example of cones with similar morphology, but important mitochondrial sequence divergence, and found in different islands: *A. angeluquei* sp. nov. and *A. josephinae* are in Maio and Boa Vista, respectively whereas *K. marimaris* sp. nov. and *K. venulatus* are in Sal versus Maio and Boa Vista, respectively. Thus far, almost all species within *Africonus* are endemic to an island, which would be in agreement with the species status of *A. angeluquei* sp. nov. (another case of morphological convergence over islands is the recently described *A. freitasi* from São Vicente Island, which is very similar to *Africonus miruchae* from Sal Island; Tenorio *et al.* 2017). Additionally, in both cases, the closest sister group is not the species with the convergent phenotype but a different one: *A. josephinae* is closer to *A. borgesii* than *A. angeluquei* sp. nov., and *K. ateralbus* is closer to *K. marimaris* sp. nov. than *K. venulatus*. Therefore, the two newly described species are best identified with molecular techniques and by their geographic distribution rather than by their subtle shell differences, what should be considered for conservation purposes (Peters *et al.* 2016).

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Plate 1. *Kolloconus marimaris* sp. nov. **A-B.** Holotype, 38.6 mm; **C.** Paratype 1, 37.2 mm; **D.** Paratype 2, 29.7 mm; **E.** Paratype 3, 30.9 mm; **F.** Paratype 4, 31.7 mm; **G.** Paratype 5, 28.3 mm; **H.** Paratype 6, 27.3 mm; **I.** Paratype 7, 40.1 mm; **J.** Paratype 8, 39.8 mm; **K.** Paratype 9, 36.6; **L.** Paratype 10, 40.9 mm; **M.** Paratype 11, 41.5 mm.



Plate 2. *Africonus angeluquei* sp. nov. A-B. Holotype, 30.0 mm; C. Paratype 1, 21.7 mm; D. Paratype 2, 18.8 mm; E. Paratype 3, 24.8 mm; F. Paratype 4, 28.4 mm; G. Paratype 5, 21.3 mm; H. Paratype 6, 21.7 mm; I. Paratype 7, 37.8 mm; J. Paratype 8, 34.0 mm; K. Paratype 9, 30.0; L. Paratype 10, 20.4 mm; M. Paratype 11, 24.3 mm.