

# Discovery of A New Mammal Species (Soricidae: Eulipotyphla) From Narcondam Volcanic Island, India

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## Research Article

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# Abstract

The present study discovered the existence of a new *Crocidura* species of shrew (Soricidae: Eulipotyphla) from Narcondam Island, India by using both morphological and molecular approaches. The new species, *Crocidura narcondamica* sp. nov. is medium-sized and has a distinct external morphology (darker-grey dense fur with a thick and darker tail) and craniodental (braincase is rounded and elevated with weak lambdoidal ridges) characters in comparison with other close congeners. This description illuminates the first discovery of soricid fauna (shrew) from this volcanic island and a total of 12 *Crocidura* species catalogued in the Indian checklist of mammals. The newly discovered species maintained sufficient genetic distances (12% to 16.6%) with other *Crocidura* species known from the Indian mainland, Andaman and Nicobar Archipelago, and Myanmar. Both Maximum-Likelihood and Bayesian phylogeny showed distinct clustering of all soricid species and exhibited congruence with the previous evolutionary hypothesis. The present phylogenetic analyses also furnished the oldest evolutionary lineages of this newly discovered species in comparison with other congeners, which assumed to be possible colonization of this species due to immature radiation in Narcondam Island.

## Introduction

Species in the genus *Crocidura* Wagler 1832 are commonly referred to as white-toothed shrews, which are inhabited in the sub-leaf stratum and burrow<sup>1</sup>. These insectivore mammals belong to the family Soricidae of order Eulipotyphla. It is a widespread and speciose genus occurring in Africa, Europe, South, and Southeast Asia<sup>2,3</sup>. These shrews are characterized by a small to the medium-sized body with usually short dense grey fur, first-unicuspid teeth is large as compared to others, protruding forward and hooked, small cusp present behind the main cusp, unpigmented teeth, and zygomatic arches are incomplete<sup>4</sup>. The genus *Crocidura* (three upper unicuspids) can be differentiated from the nearest genus *Suncus* (four upper unicuspids) through dental formula<sup>1</sup> (Supplementary Fig. S1). The genus *Crocidura* has currently recognized as the most diverse taxonomic group of shrews, with over 200 described species<sup>3,5</sup>. However, due to the secret behaviour and conserved external morphological characters, shrews are regarded as typically least studied mammalian fauna throughout their range distribution<sup>6,7</sup>. So far, 13 species of *Crocidura* are known from Indian mainland, Andaman and Nicobar (AN) Archipelago, and Myanmar (Supplementary Table S1). Although, these regions houses members of 10 genera (*Anourosorex*, *Blarinella*, *Chimarrogale*, *Crocidura*, *Episoriculus*, *Feroculus*, *Nectogale*, *Sorex*, *Soriculus*, and *Suncus*) under the family Soricidae<sup>3</sup>, the AN Archipelago is known to have only a single genus *Crocidura* with four species, namely Andaman shrew *C. andamanensis*, Andaman spiny shrew *C. hispida*, Jenkin's shrew *C. jenkinsi*, and Nicobar shrew *C. nicobarica*<sup>8</sup>.

The first record of the genus *Crocidura* from India was reported as *C. andamanensis* and *C. nicobarica* by Miller (1912)<sup>9</sup>, based upon a single specimen collected at South Andaman Island and Great Nicobar Island respectively. Subsequently, based upon a single specimen Thomas (1913)<sup>10</sup> described *C. hispida* from the northern middle Andaman Island and Chakraborty (1978)<sup>11</sup> described *C. jenkinsi* from Mt.

Harriet National Park, South Andaman Island<sup>2</sup>. In the last two decades between 2000 and 2020, a total of 24 species have been newly discovered throughout the world, of which 13 species were discovered from Indo-Malayan regions especially from the oceanic islands<sup>5,6,12-21</sup>. The molecular studies are also consecutively used to discriminate the shrew species, detect the cryptic diversity, phylogenetic evolution, biogeographic origin and radiation, and phylogeography<sup>22-42</sup>. On the contrary of Indian shrew, only a single study has been aimed to assess the genetic signature of two endemic species, *C. andamanensis* and *C. nicobarica* from AN Archipelago<sup>43</sup>. Therefore, understanding of the species diversity of these groups of islands remains incomplete. The present study is based on the assumption that a few hitherto unreported shrews exist beyond their prevailing biogeographic distribution in AN Archipelago, which warrants further investigation through integrative approaches. We performed both morphological and molecular assessment to confirm a new shrew species from the volcanic Narcondam Island in AN Archipelago, which is herein described as *Crocidura narcondamica* sp. nov. (Fig. 1). The newly discovered species is validated by morphometric comparison with thirteen other congeners distributed in AN Archipelago, mainland of India, and its close biogeographic realms Myanmar. We also performed a phylogenetic analysis with the publicly available genetic information of 21 sorcid species to corroborate the taxonomic identity and evolutionary relationship of this novel species.

## Materials And Methods

### Study Area

Narcondam Island (13.45°N 94.27°E; Fig. 2) is located about 130 km east of North Andaman, about 446 km of the west of Myanmar<sup>44-46</sup>. The island covers 6.8 km<sup>2</sup> areas and the highest peak (volcanic cone) is 710 m above sea level; however, the base lies approximately 1000 m beneath the sea<sup>44</sup>. This isolated island is part of a volcanic arc that continues northward from Sumatra to Myanmar<sup>47</sup>. The climatic condition of this small-wide conical island can be defined as a humid, tropical, and coastal climate. The island is densely vegetated, bounded by cliffs on the southern side and capped by three peaks. The forest types can broadly be categorized as three zones: wet evergreen on the slopes and highest zones of the volcano, moist deciduous or semi-evergreen at lower hills, and littoral forest along the coastline<sup>46</sup>.

### Ethics statement, sampling, and morphological examination:

To conduct the field survey and sampling, prior permission was acquired from the office of the Principal Chief Conservator of Forests (Wildlife), Andaman and Nicobar Islands, Port Blair (Letter No CWLW/WL/24/339, dated 04 February 2020). The experimental protocols were approved by the Zoological Survey of India and were carried out in accordance with relevant guidelines in compliance with the ARRIVE 2.0. (<https://www.arriveguidelines.org>)<sup>48</sup>. Due to the secret behaviour of the animal, two individuals of this unique shrew species were captured from the same location (13° 27.290'N 94° 16.436'E) by the pitfall method. The external measurements were taken in the field include head and body length (HB), tail length (TL), ear length (E), and hindfoot length including claw (HF). The photographs of

whole-body specimens were taken by the fourth author in the field. The collected specimens were preserved in 70% molecular grade ethanol for further investigation. Skulls were extracted later, cleaned, and prepared after bringing back to the museum (Fig. 1a-e) and deposited in the National Zoological Collections (NZC-Mammal and Osteology section) of Zoological Survey of India (ZSI), Kolkata, India under the registration numbers 29313 and 29314. The nomenclature of external characters and craniodental follows Hutterer et al. (2018)<sup>20</sup>. Field methods followed as guidelines approved by the American Society of Mammalogists<sup>49</sup>. The craniodental measurements were taken by the first author with digital calipers accurate to the nearest 0.01 mm. The measurements include condylo-incisive length (CIL), braincase height (BH), rostrum width (RW), hard palatine length (PL), maxillary breadth (MB), least interorbital breadth (LIOB), braincase breadth (BB), upper toothrow length (UTR), maximum breadth across the outer anterobuccal margins of the parastyles of the second upper molars (M2-M2), length of the anterior tip of fourth premolar (P4) to posterior border of M3 (P4-M3), braincase length (BL), postglenoid width (PGL), the maximum length from the anterior face of the first upper incisor to the posterior margin of the third unicuspid (I-UN3), length of 1st upper incisor (in lateral view) from tip to upper margin of cingulum (LI1), mandibular toothrow length (MTR), length of mandible from the tip of incisor to the posterior edge of the condyle (ML), length of lower molar series (m1-m3), length of 1<sup>st</sup> lower incisor from tip to posterior margin of the cingulum (Li1), and height of the coronoid process (COR) (Table 1, Supplementary Table S2). Only adult specimens were included, as determined by fully erupted molars and fused basioccipital suture<sup>6,50</sup>. Photographs of cranial and dental were taken by a Nikon D7000 camera. The collected specimens of possible new species of shrews were compared with the morphometric data of other thirteen congeners reported from AN Archipelago, the mainland of India and Myanmar (Supplementary Table S2). The external and craniodental characters were also compared with the archival specimens of *C. attenuata* and *C. jenkinsi* available in NZC of ZSI, Kolkata (Fig. 3, Supplementary Figs. S2 and S3).

## Comparative materials

The museum specimens of *C. attenuata* and *C. jenkinsi* available in the NZC of ZSI, Kolkata were compared for morphology and craniodental based species identification of the newly collected shrew species (Figs. 1 and 3, Supplementary Figs. S2 and S3). The morphometric measurements of other known congeners distributed in AN Archipelago, the mainland of India and Myanmar were also acquired from published literatures<sup>6,9,51-53</sup> (Supplementary Table S2). The morphology and craniodental measurements along with other collateral information of the museum and other comparative species are given in Supplementary Table S2.

## DNA extraction, PCR amplification, and sequencing

The genomic DNA was extracted from both holotype and paratype specimens by standard phenol-chloroform isoamyl alcohol method<sup>54</sup>. The extracted DNA was visualized through 1% agarose gel electrophoresis. The published primer pair (mcb 398: 5'-TACCATGAGGACAAATATCATTCTG-3' and mcb 869: 5'-CCTCCTAGTTTGTAGGGATTGATCG-3')<sup>55</sup> was used to amplify the widely applied mitochondrial

Cytochrome b (mtCytb) gene segment for the identification of shrew species<sup>56,57</sup>. The 25 ml PCR mixture comprises 10 pmol of each primer, 20 ng of DNA template, 1X PCR buffer, 1.0–1.5mM of MgCl<sub>2</sub>, 0.25mM of each dNTPs, and 1 U of Platinum Taq DNA Polymerase High fidelity (Invitrogen, Life Science Technologies). The PCR reaction was performed in Veriti® Thermal Cycler (Applied Biosystems, Foster City, CA) with the published thermal profile. The PCR products were purified using a QIAquickR Gel extraction kit (Qiagen Inc., Germantown, MD) with standard protocol. The cycle sequencing was executed by using BigDye® Terminator ver. 3.1 Cycle Sequencing Kit (Applied Biosystems, Inc.) and 3.2 picomoles of each primer on Veriti® Thermal Cycler. The products were cleaned by BigDye X-terminator kit (Applied Biosystems Inc.) with standard protocol and subsequently bidirectional sequenced by the 48 capillary ABI 3730 Genetic Analyzer.

### Sequence quality control and dataset preparation

The study obtained both forward and reverse chromatograms from the holotype and paratype samples. The noisy parts of each chromatogram were trimmed at both end and quality value (>40) was used to screen for making the consensus sequences through SeqScanner Version 1.0 (Applied Biosystems Inc., CA, USA). The sequences were translated through online platform ORF finder (<http://www.ncbi.nlm.nih.gov/gorf/gorf.html>) to check the amino acid array for the vertebrate mitochondrial gene. The annotated sequences were contributed in the GenBank global database. A total of 49 mtCytb publicly available sequences of 21 species belonging to the Soricidae family including 16 sequences of eight *Crocidura* species were acquired from GenBank. Total 51 sequences were aligned by ClustalX software<sup>58</sup> to form a combined dataset (473 bp) for further genetic distance and phylogenetic analysis. The sequence (Accession no. MW114662) of *Parascaptor leucura* under the family Talpidae was used as an out-group in the present phylogenetic analyses.

### Genetic distance and phylogenetic analysis

The Kimura-2-parameter (K2P) genetic distance was calculated in MEGAX<sup>59</sup>. The most suitable model for the present dataset was estimated by using JModelTest v2 with the lowest BIC (Bayesian Information Criterion) score<sup>60</sup>. The maximum-Likelihood (ML) phylogenetic tree was constructed using the IQ-Tree web server (<http://iqtree.cibiv.univie.ac.at>) with GTR+G+I model and 1000 bootstrap support<sup>61</sup>. The Bayesian (BA) tree was constructed in Mr. Bayes 3.1.2 by selecting nst=6 for GTR+G+I model with one cold and three hot chains of metropolis-coupled Markov Chain Monte Carlo (MCMC), was run for 1,000,000 generations with 25% burn-in with trees saving at every 100 generations<sup>62</sup>. The MCMC analysis was used to generate the convergence metrics, until the standard deviation (SD) of split frequencies attained to 0.01 and the potential scale reduction factor (PSRF) for all parameters neared 1.0. The web-based iTOL tool (<https://itol.embl.de/>) was used for better illustration of the BA phylogenetic tree<sup>63</sup>.

## Results

*Crocidura narcondamica* sp. nov.

## Systematic Zoology

Class: Mammalia Linnaeus, 1758

Order: Eulipotyphla Waddell et al., 1999

Family: Soricidae G. Fischer, 1814

Subfamily: Crocidurinae Milne-Edwards, 1872

Genus: *Crocidura* Wagler 1832

**Etymology.** *narcondamica*: The new species is named of the type locality, Narcondam Island from where the type specimens were collected. The specific epithet is treated as a noun in apposition.

### Type specimens

Holotype. Adult female, ZSI 29313, collected at Narcondam Island (13° 27.290'N, 94° 16.436'E) Andaman and Nicobar Archipelago, in the Bay of Bengal, India (Fig. 2); 11 m elevation; collected by the fourth author, April 17, 2020, at 9.58 hrs. The specimen consists of a fluid-preserved skin and cleaned skull. Skull extracted by the first author. Paratype. Locality and collector as for holotype. Adult male, ZSI 29314. The specimen consists of a fluid-preserved skin and cleaned skull. Skull extracted by the first author.

### Diagnosis

The species is assigned to the genus *Crocidura* by having small body size and presence of three upper unicuspid. *C. narcondamica* sp. nov. (Fig. 1) differs from its congeners occurring in AN Archipelago, the mainland of India, and Myanmar as follows (Table 1, Supplementary Table S2): *C. narcondamica* sp. nov. possess darker-grey dense fur dorsally and a thick and darker tail (Fig. 1a), whereas the species known from the AN Archipelago possesses different dorsal pelage and tail; *C. jenkinsi* (Supplementary Fig. S3a) and *C. hispida* has spiny dorsal fur with slender tail, *C. andamanensis* has bluish-grey washed with brown and darker brown tail, *C. nicobarica* has bristly scooty brown dorsal fur with slender tail and *C. attenuata* has a soft brownish-grey dorsal fur with a slender tail<sup>2,51</sup> (Supplementary Fig. S2a).

With regard to the head and body (HB) length of *C. narcondamica* sp. nov. (holotype: 67 and paratype: 63 mm) is shorter than in *C. jenkinsi* (107 mm), *C. nicobarica* (120 mm), *C. hispida* (85 mm), *C. andamanensis* (114 mm), *C. fuliginosa* (range 72-100 mm) and *C. pullata* (73-89 mm). However, the head and body length of this new species was overlapped with rest of the congeners: *C. attenuata* (60-89 mm), *C. cranbrookii* (65-86 mm), *C. horsfieldii* (49-71 mm), *C. indochinensis* (53-71 mm), *C. pergrisea* (65-86 mm), *C. rapax* (56-70 mm) and *C. vorax* (54-90 mm). The tail length (TL) (58.5 and 55.6 mm) of *C. narcondamica* sp. nov. was significantly varied from all the comparative congeners except *C. attenuata* (Supplementary Table S2). Although the HB and TL of the newly discovered species were overlapped with

*C. attenuata*, the morphological characters are significantly different (soft brownish-grey dorsal pelage with a brownish slender tail; Supplementary Fig S2a).

The length of the hindfoot, relative to head and body length of *C. narcondamica* sp. nov. (holotype: 13.4 and paratype: 12.4 mm) also differs from two Indian species, *C. pullata* (14-16 mm) and *C. horsfieldii* (10-13 mm); two Myanmar species *C. cranbrooki* (14-16 mm) and *C. indochinensis* (10-13 mm), and two species *C. fuliginosa* (15-19 mm) and *C. rapax* (11-13 mm) sharing their range distribution in both India and Myanmar. However, the rest of the congeners known from the same biogeographic regions showed overlapped length of the hindfoot (Supplementary Table S2).

With regard to the craniodental characters, the newly discovered species were further examined and compared with the closest congener *C. attenuata* (Fig. 3, Supplementary Fig. S2). The braincase (BC) of *C. narcondamica* sp. nov. is rounded and elevated (Figs. 1b and 1d), with weak lambdoidal ridges (LR; Fig. 1b) than that of *C. attenuata* (slightly flattened with developed LR (Supplementary Figs. S2c and S2e). The foramen ovale (FO)-openings are more prominent than in *C. attenuata* (Fig. 3b). In *C. narcondamica* sp. nov., the condylobasal length (holotype: 19.6 and paratype: 18.9 mm), palatal length (7.4 and 7 mm), upper tooththrow (8.8 and 7.9 mm), maxillary tooththrow (7.7 and 7 mm) and mandible length (11.6 and 10.8 mm) which are significantly either higher or lower than other congeners (Supplementary Table S2). Significantly, with regard to the first unicuspid or incisor (I1) in *C. narcondamica* sp. nov. was less sharp and slightly protruded from rostrum than in *C. attenuata* (Figs. 1d and 3c).

## Description of the Holotype

The new species is a medium-sized white-toothed shrew under the genus *Crocidura*, with the head and body length of 67 and tail length of 58.5 mm. Its pelage is shorter with dense fur; darker-grey dorsally (Fig. 1a) and slight greyish ventrally. The snout is elongated with discernible vibrissae hairs dorsally and naked and pinkish ventrally. The eyes are small and compressed by the snout muscles. The external ears are small but well visible. The tail is thick and nearly naked with sparse bristle hairs on the proximal half. The tail length is shorter than head and body length. The tail pigmentation is darker to that of the dorsal pelage. The fore and hindfoot having five pale toes with transparent claws; plantar surfaces of feet are moderately pigmented; the upper side of the toes are having hairs. The cranial bones are thin and translucent; the braincase is rounded and slightly elevated with weak lambdoidal ridges in dorsal profile (Fig. 1b). The rostrum is angled downward and a slight depression is seen in the dorsal side of above the orbital region; the zygomatic arches are incomplete (Fig. 1b). The suture between the basioccipital and basisphenoid is fully fused (Fig. 1c). The mandible is slender, with a low mandibular ramus (Fig. 1e and 1f). The dentition is unpigmented, fully erupted; the total tooth is 28 (Fig. 1c and 1d). No significant morphological variations were observed between female (holotype) and male (paratype) specimens other than its external genital organs. There was little morphometric variation among individuals between the type series (Table 1).

**Distribution.** Presently known only from its type locality, Narcondam Island, Andaman and Nicobar Archipelago, in the Bay of Bengal, India.

**Habitat.** The new species was collected from a plantation and littoral forest along the coastline at 11 m elevation. No anthropogenic disturbances were observed in the habitat (Fig. 2).

### **Molecular identification and phylogenetic interpretation**

The partial mitochondrial mtCytb gene sequences (Accession Nos. MW417367 and MW417368) were generated from both holotype and paratype of the newly discovered shrew species and contributed to the global database (GenBank). The similarity search results in BLAST depicted 90% similarity with the publicly available sequence of *Crocidura* sp. collected from Xizang, China. However, the next closest results of the similarity search revealed 89.57% similarity with *Crocidura* sp. collected from Yunnan, China and *C. attenuata* (MK765768) collected from Jiangxi, China. The present dataset of 22 soricid species, including the newly described *C.narcondamica* sp. nov. showed an overall mean genetic distance of 23%. The highest mean genetic distance (31.7%) was observed between *Feroculus* and *Nectogale*, however the lowest (15.3%) was detected between *Crocidura* and *Chimarrogale* in the present dataset (Supplementary Table S3). The newly discovered species revealed sufficient mean genetic distances (12% to 16.6%) with other *Crocidura* species. Both ML and BA phylogenetic trees showed similar topologies and distinctly separated the newly described species (*C.narcondamica* sp. nov.) from other *Crocidura* congeners with high posterior probabilities and bootstrap supports (Fig. 4, Supplementary Fig. S4). The *Crocidura* congeners elucidate monophyletic clustering and clade separately as compared with other soricid genera.

## **Discussion**

Island ecosystems are believed to be a discrete biogeographic unit which are acted to be a significant model for evolutionary studies. The uneven distribution and ecology of any species induces diverse speciation/radiation in the island ecosystem<sup>64</sup>. In Miocene–Pliocene, the volcanic eruption produced many new islands and their sporadic land connections during Pleistocene, allows both geographic and temporal processes of species diversification in Southeast Asia<sup>30</sup>. The Indian plate separates from Africa-Madagascar- Seychelles and drifting towards Eurasian plate, which also allows multiple opportunities for animal dispersal and biological connection between the India mainland and Southeast Asian countries<sup>65</sup>. Due to the remoteness and inaccessibility throughout the year, the smaller islands of AN archipelago are meagrely explored in comparison with other larger islands.

The political boundary of India includes a number of islands in both Arabian Sea and Bay of Bengal. The islands of Arabian Sea are primarily built up by corals, whereas the Bay of Bengal islands are characterised by habitable submarine mountains<sup>44</sup>. The Narcondam Island is one of 836 groups of islands of the AN Archipelago, is a small dormant volcanic island with almost 80% forest cover<sup>44,66</sup> (Fig. 2). It is believed that the volcano was active during Holocene eruptions<sup>66,67</sup>. Owing as an isolated island,

the Narcondam Island might constitute an extraordinary bio-geography with its endemic flora and fauna. This island has been recognised by UNESCO as a World Heritage site due to its sensitive ecosystems and the occurrence of an endangered species, Narcondam hornbill (*Rhyticeros narcondami*). Further, this island has been also notified as Wildlife Sanctuary under the provisions of the Indian Wildlife (Protection) Act, 1972.

The unparalleled biogeography of oceanic islands provides a suitable habitat for many *Crocidura* species discovered in recent past. Therefore, the biogeographic history of this newly described species is important to discuss in terms of their population, evolution, and conservation. The genus *Crocidura* is morphologically distinct in comparison with other soricid genera distributed in India and Myanmar<sup>1,68</sup> (Supplementary Table S4). Most of the *Crocidura* species are morphologically very similar with *Suncus*, however can be distinguished by their number of unicuspid<sup>1,6</sup> (Supplementary Fig. S1). Apart from other morphology, the well visible external ears in *Crocidura* shrews are also indicating a tendency toward terrestrial lifestyle with subterranean habits<sup>20,69</sup>. The new species of *Crocidura* can be distinguished by morphology and molecular assessment from other congeners distributed in nearest biogeographic realms (Indian mainland and Myanmar).

Considering the molecular-based species identification, the newly discovered species is genetically distinct from other congeners. The previous studies evidenced that, the mtCytb gene is effectively used to discriminate the shrew species and detect cryptic diversity from different geographical regions<sup>41,42,56,57</sup>. The genetic assessment of *Crocidura* species also facilitates to describe the immature radiation and diversification in Southeast Asian countries<sup>30</sup>. The estimated K2P genetic distance, ML and BA phylogenies clearly discriminate all the studied soricid species with sufficient genetic distances and distinct clustering. The newly discovered species *C.narcondamica* sp. nov. maintain close genetic distance (12%) with *C. rapax* (distributed in China, India, Myanmar, and Taiwan) in comparison with other AN archipelago species, *C. andamanensis* with 16.6% and *C. nicobarica* with 15.1%. The genetic closeness with the long distance relatives from the type locality (Narcondam Island) to other geographical regions allows us to corroborate the previous evolutionary hypothesis on radiation and diversification<sup>28,30,42</sup>. The present molecular analysis of this newly discovered soricid mammal suggested possible colonization in Narcondam Island; which might derive by the volcanic uplift and sea level oscillations. In addition, the present topologies along with their ancestral positions elucidate that the newly discovered species might evolve earlier than other *Crocidura* congeners. Hence, we recommend to generate more molecular data of this group of mammals from different geographical regions to clarify their in-depth phylogenetic relationship, dating estimation, and biogeographical history in Indo-Malayan realm.

So far, the Narcondam Island is popularly known by the occurrence of the endemic Narcondam hornbill. The population and ecological study of animals of this island was restricted only on this bird. Later on, the researchers sought to focus a faunal expedition and recorded 17 fishes, eight reptiles, 28 birds, two mammals (Chinese Forest Rat, *Rattus andamanensis* and Island Flying Fox, *Pteropus hypomelanus*), 13

spiders, eight butterflies, and two sea cucumbers from this isolated island<sup>46</sup>. However, the diversity of mammalian fauna is very sparse in the Narcondam Island; especially there is no data was reported on soricid fauna (shrew). The discovery of *C. jenkinsi* from South Andaman Island by Chakraborty (1978)<sup>11</sup> has yet been considered as the latest discovery of *Crocidura* species from India. With this new description of Narcondam white-toothed shrew, *C.narcondamica* sp. nov., altogether twelve species of *Crocidura* are now known from India including AN Archipelago; viz., *C. andamanensis*, *C. attenuata*, *C. fuliginosa*, *C. hispida*, *C. horsfieldii*, *C. jenkinsi*, *C. nicobarica*, *C. pergrisea*, *C. pullata*, *C. rapax*, and *C. vorax*. Among the Indian *Crocidura* shrews, four species known from AN Archipelago has been categorized as threatened by the IUCN Red List of Threatened Species (2020-3) due to their remarkable endemism<sup>70</sup>. The habitat loss due to selective logging, anthropogenic activities, and natural disasters has been identified as the major threats for this group of animals in AN Archipelago<sup>71,72</sup>. As the Narcondam Island is uninhabited, the new species *C. narcondamica* sp. nov. survive with unusual adaptations and may not face these anthropogenic disturbances. It is reported that the water monitor (*Varanus salvator*) was plentiful in Narcondam Island<sup>46</sup>. Hence, the water monitor and raptors may be assumed to be potential natural predators to this species. Further studies on the taxonomy, ecology, and distribution of the new species will help to understand the present status of this species.

## Declarations

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### Competing interests

The authors declare that they have no competing interests.

### Author Contributions

Conceptualization: MK, SK; Data curation: GG; Formal analysis: MK, SK; Funding acquisition: CS, KC; Investigation: MK, SK, CV; Methodology: MK, SK, GG; Project administration: CS, KC; Resources: CS, KC; Software: MK, SK; Validation: MK, SK; Visualization: CS, CV, KC; Writing – original draft: MK, SK; Writing – review & editing: MK, SK, KC.

### Data Availability Statement

The following information was supplied regarding the accessibility of DNA sequences: The generated partial fragment of mitochondrial Cytochrome b gene sequences are deposited in GenBank of NCBI under accession number MW417367 and MW417368.

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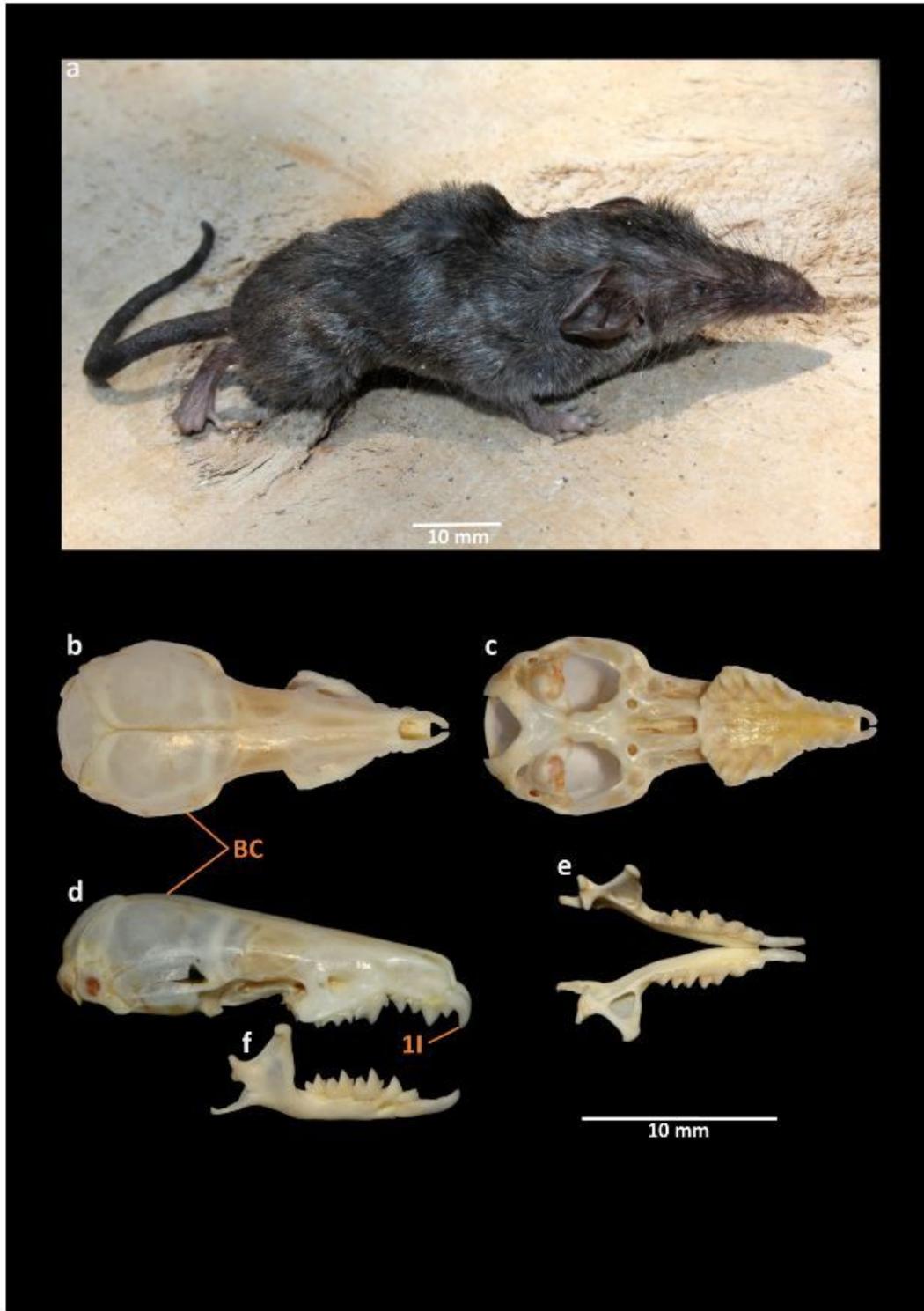
# Tables

Table 1

External and craniodental measurements of the examined specimens of *C. narcondamica* (holotype and paratype) from Narcondam Island, India. For trait abbreviations (columns) see Material and Methods. All measurements are in millimetres (n = 1).

| <b>Variable</b> | <b><i>C. narcondamica</i><br/>(Holotype, ZSI 29313)</b> | <b><i>C. narcondamica</i><br/>(Paratype, ZSI 29314)</b> |
|-----------------|---------------------------------------------------------|---------------------------------------------------------|
| HB              | 67                                                      | 63                                                      |
| TL              | 58.5                                                    | 55.6                                                    |
| E               | 6.4                                                     | 6                                                       |
| HF              | 13.4                                                    | 12.4                                                    |
| CIL             | 19.6                                                    | 18.9                                                    |
| BH              | 4.4                                                     | 4                                                       |
| RW              | 1.9                                                     | 1.7                                                     |
| PL              | 7.4                                                     | 7                                                       |
| MB              | 5.8                                                     | 5.1                                                     |
| LIOB            | 3                                                       | 2.8                                                     |
| BB              | 8.7                                                     | 8                                                       |
| UTR             | 8.8                                                     | 7.9                                                     |
| M2-M2           | 5.4                                                     | 5                                                       |
| P4-M3           | 4.9                                                     | 4.2                                                     |
| BL              | 7.3                                                     | 6.8                                                     |
| PGL             | 5.7                                                     | 5.2                                                     |
| I-UN3           | 3.9                                                     | 3.7                                                     |
| LI1             | 2                                                       | 2                                                       |
| MTR             | 7.7                                                     | 7                                                       |
| ML              | 11.6                                                    | 10.8                                                    |
| m1-m3           | 3.5                                                     | 3                                                       |
| Li1             | 3.2                                                     | 3                                                       |
| COR             | 4.5                                                     | 4.1                                                     |

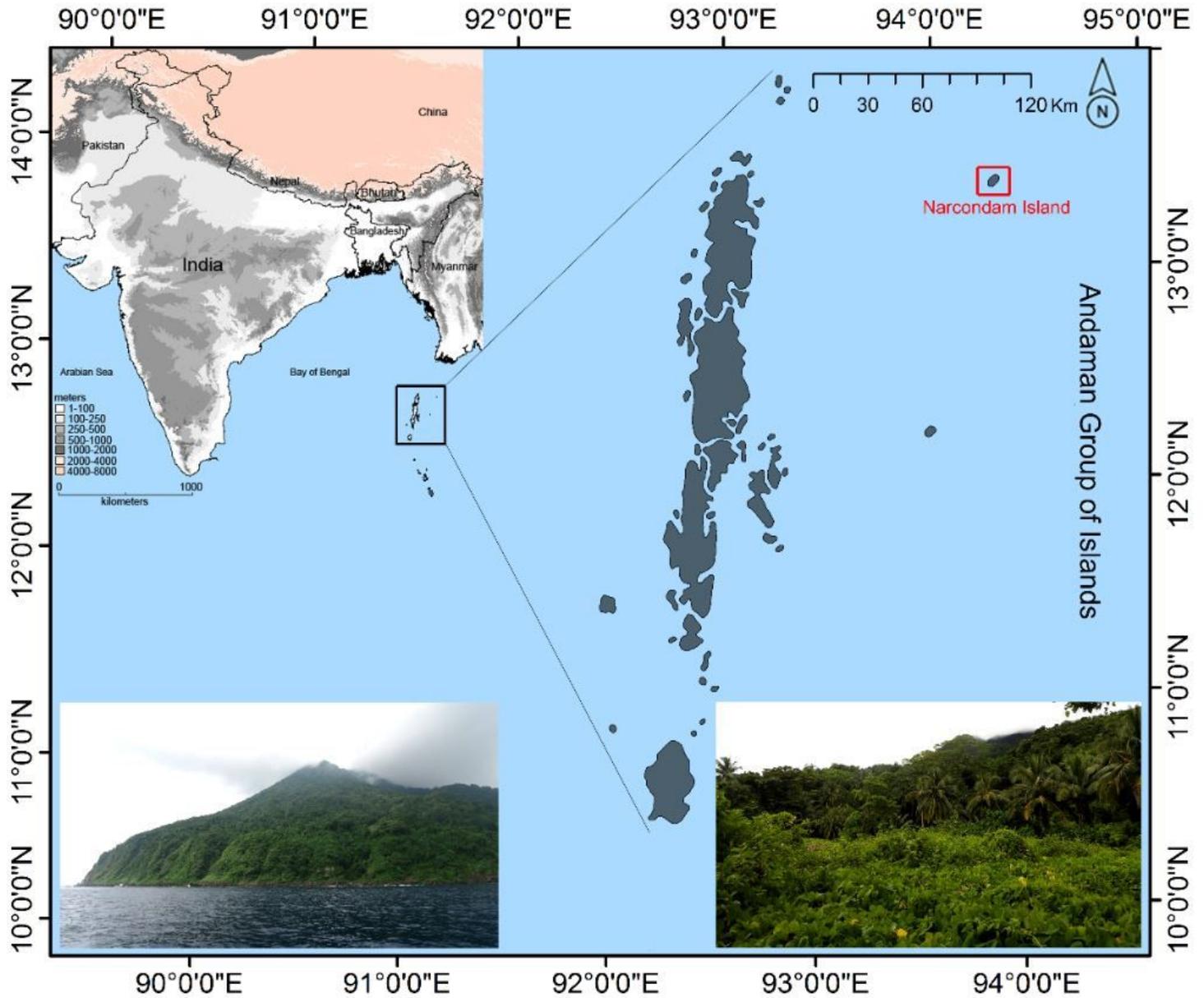
# Figures



**Figure 1**

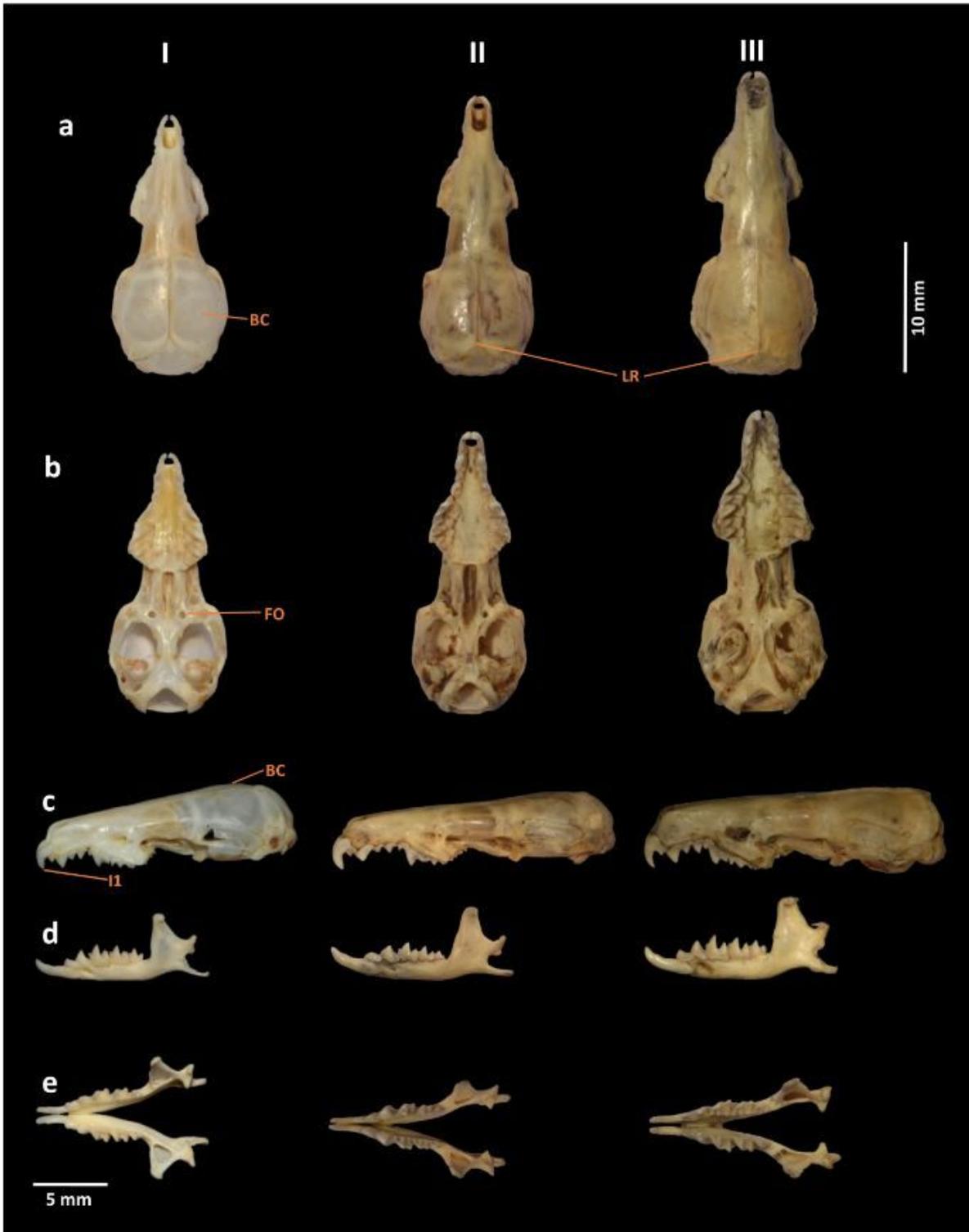
*Crocidura narcondamica* sp. nov. (holotype ZSI-29313, female). (a) Dorso-lateral view of female (adult live). Views of the cranium (b) dorsal, (c) ventral, and (d) lateral. Views of the mandible (e) lateral and (f)

occlusal. (BC= Braincase; I1- First incisor/first unicuspid). The photographs were captured by Nikon D7000 camera and edited manually in Adobe Photoshop CS 8.0.



**Figure 2**

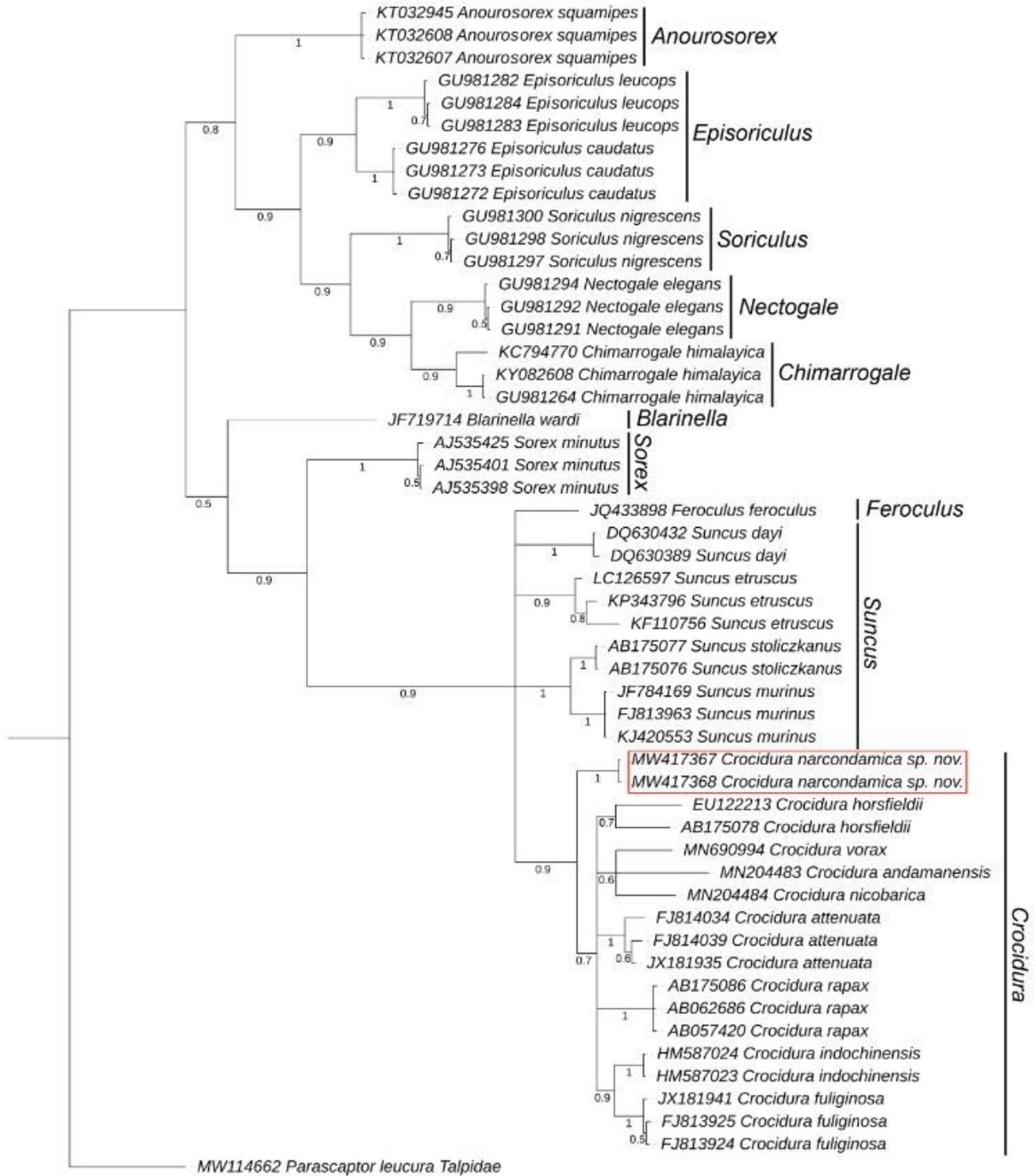
Map showing the Narcondam Island in the Andaman and Nicobar Archipelago, India along with the habitat of new species was encountered. Map prepared using QGIS 2.6.1 (<http://www.qgis.org>) and edited manually in Adobe Photoshop CS 8.0. Note: The designations employed and the presentation of the material on this map do not imply the expression of any opinion whatsoever on the part of Research Square concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. This map has been provided by the authors.



**Figure 3**

Cranium and mandible of (I) *C. narcondamica* sp. nov. (holotype, ZSI-28000) (II) *C. attenuata* (ZSI-16129) and (III) *C. jenkinsi* (ZSI-19860). From top to bottom, views are (a) dorsal, (b) ventral, (c) lateral views of the cranium, and (d) lateral and (e) occlusal views of the mandible. Distinct morphological features are labelled as BC= Brain case, LR= lambdoidal ridge, FO= Foramen ovale, and I1- First incisor/first unicuspid.

The photographs were captured by Nikon D7000 camera and edited manually in Adobe Photoshop CS 8.0.



**Figure 4**

The Bayesian phylogenetic analysis of mitochondrial Cytb gene depicted distinct clustering of *C. narcondamica* sp. nov. in comparison with other soricid species distributed in AN Archipelago, mainland of India, and Myanmar. The posterior probability supports were noted with each node. The GenBank

accession numbers, species name, and respective genera were marked as per clade pattern. The distinct clade of the newly discovered species was marked by red colour box. The figure prepared in web-based iTOL tool (<https://itol.embl.de/>) and edited manually in Adobe Photoshop CS 8.0.

## Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- [SupplementaryInformation.docx](#)