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Authors: Narayanan, Surya, Poorna Bhat, Hulegaru Nagaraja, Paran, Dhanu, Das, Sandeep, and Aravind, Neelavar Ananthram

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Truly Absent or Sampling Gaps? Insights on the Potential Distribution of *Duttaphrynus hololius* (Günther, 1876) from Peninsular India

SURYA NARAYANAN¹, HULEGARU NAGARAJA POORNA BHAT¹,
DHANU PARAN², SANDEEP DAS^{3,4}, AND NEELAVAR ANANTHRAM ARAVIND^{1,5,*}

¹SMS Foundation Centre for Biodiversity and Conservation, Ashoka Trust for Research in Ecology and the Environment (ATREE), Royal Enclave, Srirampura, Bangalore, Karnataka 560064, INDIA

²Kaleeswari mill street, Vettaikaranputhur, Pollachi, Tamil Nadu 642129, INDIA

³Department of Zoology, St. Joseph's College, Irinjalakuda, Thrissur, Kerala 680121, INDIA

⁴Forest Ecology and Biodiversity Conservation Division, Kerala Forest Research Institute, Peechi, Kerala 680653, INDIA

⁵Yenepoya Research Centre, Yenepoya (Deemed to be University), University road, Derlakatte, Mangalore 575018, INDIA

Abstract: *Duttaphrynus hololius* is an uncommon species of toad presumably endemic to peninsular India. Since the original description, no records originated from the type locality “Malabar” or the Western Ghats. At the same time, several authors reported it from the other parts of peninsular India and the Eastern Ghats. This led to confusion and made previous workers question the true origin of the type locality of *D. hololius*. Some works also predict the distribution of this species based on niche modelling techniques. This work provides new records from the Western Ghats and vicinity for the first time after its description with new molecular data. We also discuss pre-colonial and colonial “Malabar” and predict the suitable range of *D. hololius* under different climatic scenarios based on the further analysis carried out herein using the species distribution modelling approach.

Key words: *Duttaphrynus hololius*; Malabar; DNA; Niche modelling; Western Ghats

INTRODUCTION

Duttaphrynus hololius (Günther, 1876) is one of the more studied toad species originally described from “Malabar” in the Western

Ghats based on a single specimen housed in the collections of the Natural History Museum, London (previously British Museum of Natural History [BMNH]). Günther's description of *Bufo hololius* (= *Duttaphrynus hololius*) was based on a single specimen from the collections of Richard Henry Beddome, which he possibly had sourced from Malabar. Shortly after the description, Beddome (1880) listed *D.*

* Corresponding author.

E-mail address: aravind@atree.org

hololius in his checklist of the amphibians of the “Nilagiri district”, thereby reaffirming its presence in the region. Unfortunately, this work largely was ignored, and very few works pertaining to *D. hololius* cited this record (Srinivasulu et al., 2013; Ganesh et al., 2020). In addition, several different assumptions were made about its type locality and actual distribution in the Western Ghats (Ganesh et al., 2013, 2020).

After a long gap since the initial description (Günther, 1876), many authors reported *D. hololius* from several parts of peninsular India, mainly from the India peninsula including the Eastern Ghats (Satyamurthi, 1967; Pillai and Ravichandran, 1991; Daniels, 1992; Chandramouli et al., 2011; Adimallaiah et al., 2012; Kalaimani et al., 2012; Srinivasulu et al., 2013; Ganesh et al., 2018). Apart from the new locality reports, studies also concentrated on natural history, breeding and larval development (Chandramouli et al., 2011; Ganesh et al., 2013; Chandramouli and Kalaimani, 2014; Ganesh et al., 2020). However, no studies reported this species from the Western Ghats, which prompted previous workers to question the validity of the type locality and its distribution in the Western Ghats (Srinivasulu et al., 2013; Ganesh et al., 2020). Additionally, Srinivasulu et al. (2013) and Ganesh et al. (2020) predicted the distributional range of *D. hololius* using species niche modelling techniques. They concluded that the Western Ghats are an unsuitable range, further adding to the confusion concerning distribution.

Identifying new areas of species’ distribution based on field studies and ecological niche modeling will help prioritise areas for conservation and simultaneously increase our knowledge of species’ ecological niche (Urbina-Cardona and Flores-Villela, 2010; Kumar et al., 2014; Joshi et al., 2017; Ishihama et al., 2019). Ecological niche modelling (ENM) or species distribution modelling correlates species distribution data with environmental information to predict the potential distribution of species in space and time. ENM is widely used in ecology, biogeography, invasive species

niche utilization, and taxonomy, identifying the suitable niche for further surveys or reintroduction, and prioritisation of conservation strategies (Kumar et al., 2014; Sarma et al., 2015; Joshi et al., 2017).

During our recent fieldwork in the periphery of Anamalai Tiger Reserve in the Western Ghats, we found habitats that are similar to that reported for the *Duttaphrynus hololius* (Chandramouli et al., 2011; Srinivasulu et al., 2013; Ganesh et al., 2018, 2020). Here we report the first observations of *D. hololius* from the Western Ghats and vicinity since its original description in 1876 (Günther, 1876). We also discuss the possible distribution based on ENM analysis for current and future scenarios, along with discussion about its type-locality, Malabar. Additionally, we provide new DNA sequence data for the population of *Duttaphrynus hololius* from the Western Ghats.

MATERIALS AND METHODS

Study region

The fieldwork was conducted in the forest areas, villages and farmlands that had rocky outcrops in Pollachi, Tamil Nadu along the eastern slopes of the Western Ghats and the rocky areas in the adjoining Palakkad district, Kerala lying in the Palghat gap. SN and DP conducted fieldwork in Kaliyapuram (10° 31' 51.96" N, 76° 55' 31.44" E; 328 m above sea level [asl]), Chemmanampathy (10° 34' 3.01" N, 76° 51' 40.43" E; 421 m asl), Sethumadai (10° 30' 31.68" N, 76° 51' 45.49" E; 392 m asl), Aliyar (10° 29' 25.08" N, 76° 56' 58.18" E; 307 m asl), and villages in Pollachi Town, Tamil Nadu, between 22–28 July 2020. All the sampling sites in Tamil Nadu fall within the drier rain shadow region of the Western Ghats. Most of the hillocks sampled were situated amidst coconut plantations and forest areas dominated by thorny scrub jungle.

Distribution data

Species occurrence data for *Duttaphrynus hololius* were downloaded from different sources like Citizen Science Portals (CSP); India

TABLE 1. List of GenBank sequences used for the molecular analysis in this study. *indicates the sample from the present study.

Species	Voucher code	12S+tVal+16S	Locality
<i>Duttaphrynus atukoralei</i>	VUB 0101	FJ882835	Sri Lanka
<i>Duttaphrynus brevirostris</i>	SDB 4714	FJ882786	Not Available
<i>Duttaphrynus crocus</i>	CAS 220193	FJ882789	Myanmar
<i>Duttaphrynus dhufarensis</i>	CAS 227584	FJ882837	Oman
<i>Duttaphrynus himalayanus</i>	KIZ 08305	MW111525	Himalayas
<i>Duttaphrynus hololius</i>	SDB 4240	FJ882781	Vellore, Tamil Nadu, India
<i>Duttaphrynus hololius</i> *	BNHS 6138	ON974999	Kaliyapuram, Tamil Nadu, India
<i>Duttaphrynus melanostictus</i>		KJ697684	India
<i>Duttaphrynus parietalis</i>	SDB 10100	FJ882784	Not Available
<i>Duttaphrynus scaber</i>	SDB 532	FJ882785	India
<i>Duttaphrynus stomaticus</i>	CAS 232071	KJ532264	Not Available
<i>Duttaphrynus stuarti</i>	KIZ 014053	MW133341	China
<i>Beduka koynayensis</i>	SDB 2004 012	FJ882782	The Western Ghats, India

Biodiversity Portal (Vattakaven et al., 2016), GBIF (GBIF, 2021) and HerpMapper (HerpMapper, 2021), published literature (see Appendix), and supplemented with the locations reported in this study. Identifications of all the records from the CSP were confirmed by comparing the available photographs with the literature (original description; Günther, 1876) and by comparing the images of type specimens provided in Srinivasulu et al. (2013). A total of 37 distribution points were collated from the sources mentioned above. To avoid overfitting the model, we have removed all variables closer to each other <5 km randomly using spThin package in R (Aiello-Lammens et al., 2015). The thinning approach helps to reduce spatial sampling biases. Finally, we used only 27 records for the niche modelling. The nomenclature of the toad used in this work follows Dubois et al. (2021). The Museum abbreviations used in the study are as follows: CAS: California Academy of Sciences, USA; KIZ: Kunming Institute of Zoology, China; VUB: Vrije Universiteit Brussel, Belgium; SDB: Sathyabama Das Biju [personal voucher], BNHS: Bombay Natural History Society, India.

Molecular analysis

Genomic DNA was extracted from toe-clip samples stored in absolute ethanol at -20°C , using the DNeasy (QiagenTM®) blood and tissue kit. We generated DNA sequence data for one sample (BNHS 6138) of *Duttaphrynus hololius* from Kaliyapuram, Tamil Nadu, India. We amplified a single large fragment covering the mitochondrial 12S, complete tDNA-Valine (*t-Val*) and a partial fragment of 16S rRNA gene (1082 base pairs) using the existing primers (LX12SN1(f) and LX16S1R(r) (Zhang et al., 2017). PCR amplifications were carried out in a S1000TM Thermal Cycler (Bio-Rad, USA). Amplified PCR products were run on a 2% agarose gel and viewed with an Essential V4 (UVITEC Cambridge, UK) gel documentation system. PCR products were Sanger sequenced in both directions at Barcode Bio-Sciences (Bangalore, India). Sequences were aligned using ClustalW implemented in MEGA 7 (Higgins et al., 1994; Tamura et al., 2011). The newly generated sequence was aligned with 11 *Duttaphrynus* spp. and one *Beduka koynayensis* (used as outgroup) was downloaded from the Genbank (Table 1). Uncorrected pairwise genetic distances were calculated using MEGA 7.

Phylogenetic analysis was carried out using

the CIPRES Science Gateway v3.3 (Miller et al., 2010). Maximum Likelihood (ML) analysis was carried out in RaxML version 1.8 (Stamatakis, 2006), implementing the GTR+I+G model of sequence evolution. Support for internal branches in the ML tree was quantified using a thorough bootstrap (1000 replicates). *Beduka koynayensis* was used to root the tree.

Bioclimatic data and ecological niche modelling

Nineteen bioclimatic variables with a spatial resolution of 30 arc seconds (approximately 1 km²) for the current climate were downloaded from WorldClim Database version 2 (Hijmans et al., 2005; Fick and Hijmans, 2017). For future scenarios, i.e., 2070 (average for 2061–2080), we used Intergovernmental Panel on Climate Change (IPCC) data in its fifth Assessment Report (AR5) (Moss et al., 2010) for two different future greenhouse scenarios, i.e., Representative Concentration Pathway (RCP's) 2.6 and 8.5 (Bernie, 2010). The RCPs are representations of possible changes in future anthropogenic greenhouse emissions. For example, RCP 2.6 assumes that GHG emissions peak between 2010–2020, whereas RCP 8.5 assumes that emissions continue to rise throughout the 21st century. For future climatic modelling, we used HadGem general circulation model, which is one of the highly used GCM for climate change studies (Sarma et al., 2015). The Bioclimatic variables and Altitude used had a spatial resolution of 1 km², i.e., 30 arc seconds.

The potential geographic distribution of *Duttaphrynus hololius* was modelled using the Maximum entropy algorithm model (MaxEnt) version 3.4.1k (Phillips et al., 2006) for the current climate scenario and projected for two future climate change scenarios. MaxEnt approximations are based on the probable occurrence of species records finding the maximum entropy distribution with high extrapolative accuracy (Soucy et al., 2018; Zhang et al., 2018; Raman et al., 2020). To avoid model complexity and multi-collinearity, only seven variables (Table 2) were retained for further

analysis based on their low degree of correlation between themselves (Pearson's coefficient value of $|r| \leq 0.7$). Among the distribution records of *D. hololius*, 25% were randomly selected as test data, and the remaining 75% were used for model training. We used the default feature in MaxEnt to run the model. The area under the receiving operator curve (AUC) is threshold-independent and widely used to evaluate the predicted accuracy of the model performance (Phillips et al., 2006). The model performance was classified as poor (0.5–0.6), fair (0.6–0.7), good (0.7–0.8), very good (0.8–0.9), or excellent (0.9–1), and higher AUC values indicate better model performance (Swets, 1988). The predictive performance of the model was evaluated using True Skill Statistics (TSS) as it is the independence of prevalence, the ratio of presence to pseudo absence data in the presence-absence predictions (Allouche et al., 2006). TSS accounts for both sensitivity and specificity, and its value ranges from –1 to +1, where +1 indicates perfect agreement and scores ranging from 0.7 to 0.9 specify fair to good model performance (Allouche et al., 2006; Li et al., 2016; Shrestha et al., 2018). Partial AUC was calculated using ntBox (Osorio-Olvera et al., 2020). The jackknife results and response curves were used to evaluate the importance of each variable to the distribution of *D. hololius* (Elith et al., 2011). MaxEnt output map was converted into binary 'presence-absence' map in ArcGIS 10.5.1 using ten percentile training presence clog log value to define a suitable and unsuitable area for species. This threshold selects the value above which 90% of the training locations are correctly classified and is one of the most common thresholds used in MaxEnt habitat suitability models (Young et al., 2011; Zarzo-Arias et al., 2019). All GIS analysis was performed in QGIS Ver 3.18 (QGIS Development Team, 2017).

The distribution range for *D. hololius* across Peninsular India was calculated using Extent of Occurrence (EOO) and Area of Occupancy (AOO) methods as described and used in IUCN's Red List assessments (IUCN, 2001).

TABLE 2. Predictor variables used in the modelling and their percentage of contribution.

Code	Variables	% Contribution
Bio1	Annual Mean Temperature	6.9
Bio2	Mean Diurnal Range (Mean of monthly (max temp–min temp))	2.2
Bio3	Isothermality (BIO2/BIO7) (*100)	44.6
Bio12	Annual Precipitation	7.8
Bio14	Precipitation of Driest Month	5.1
Bio15	Precipitation Seasonality (Coefficient of Variation)	29.1
Bio19	Precipitation of Coldest Quarter	4.4

We used GeoCAT, a web-based Geospatial Conservation Assessment Tool, to calculate EOO and AOO. Both EOO and AOO were used to assess restricted-range species under criterion B of IUCN's Red List (Willis et al., 2003). EOO was calculated by constructing the minimum convex hull around known occurrence points of *D. hololius* and AOO as the number of grids occupied by points multiplied by 4 km² in GEOCAT (See Willis et al., 2003; Bachman et al., 2011). A grid size of 2 km x 2 km was used as recommended by IUCN for conservation assessment (IUCN, 2001). We calculated EOO using minimum presence area after converting the map derived from the niche model to a binary map using a 10% training threshold presence (Joshi et al., 2017).

RESULTS

Field observations and ecology

Across all the sampling sites, we found live individuals of *Duttaphrynus hololius* only from the hillock in Kaliyapuram, Pollachi. Apart from this, we found one road-killed individual of *D. hololius* from the Palghat gap and one individual from Chinnar Wildlife Sanctuary in Kerala. Detailed summary of observations and sites are given below.

a) A total of 26 individuals of *D. hololius* were observed between 22 July 2020 and 28 July 2020 from a rocky hillock in Kaliyapuram, Pollachi, Tamil Nadu (10° 31' 51.96" N, 76° 55' 31.44" E; 328 m asl) during 1900–2200 h. Four juveniles were also found during the same period. However, no tadpoles or

breeding pools were found. All the individuals were observed on the surface of the rocks, and upon approaching, many individuals were seen to move fast and hide under the rock crevices. This is one of the many hillocks in this region, surrounded mainly by coconut plantations in the vicinity of Anamalai Tiger Reserve (Fig. 1A–C).

b) We found one adult road-killed *D. hololius* on 10 August 2020 in Walayar, Palakkad district, Kerala (10° 48' 25.58" N, 76° 48' 13.248" E; 159 m asl) at 1300 h. This locality lies in the Palghat gap and is closer to the southern edge of the central Western Ghats. Numerous rocky outcrops and small hillocks are found in this region connecting the Western Ghats and are comprised of the thorny scrub forest to dry deciduous forest.

c) We observed one adult, *D. hololius*, on 17 March 2021 on a rocky patch amidst thorny scrub forests of the Pambar area in the rain shadow region of Chinnar Wildlife Sanctuary Idukki district, Kerala (10° 20' 44.07" N, 77° 13' 53.00" E; 471 m asl) at 1130 h. Also, some unconfirmed sightings and road-kill of the species were reported from the Karimutty area of Chinnar WLS in 2015 and 2016, which probably could be the first sightings from Kerala but requires confirmation through new surveys from this region. Based on the currently available data, the Extent of Occurrence (EOO) and Area of Occupancy (AOO) are 313,582.57 km² and 120.0 km², respectively (Table 3).

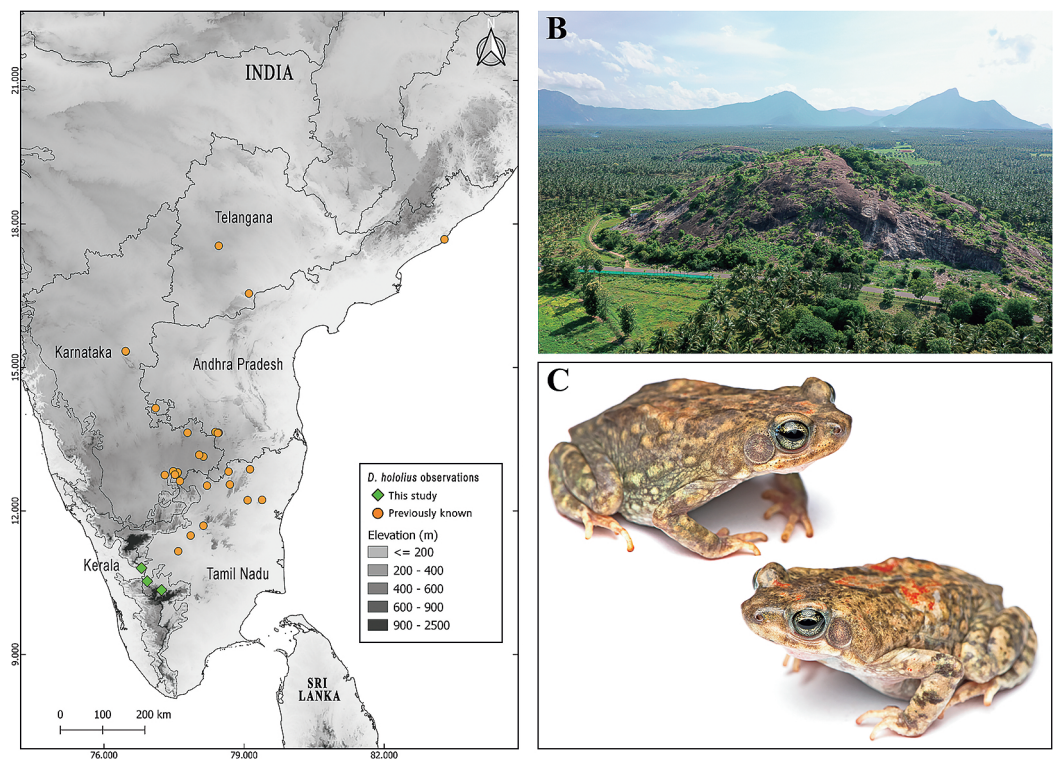


FIG. 1. A) Currently known distribution of *Duttaphrynus hololius* in Peninsular India, B) habitat of *D. hololius* in Kaliyapuram, Pollachi, Tamil Nadu, and C) *D. hololius* in life from Kaliyapuram, Pollachi, Tamil Nadu.

TABLE 3. Summary of model performance for *Duttaphrynus hololius*.

Model	Area-Current	Area-RCP 2.6	Area-RCP 8.6
EOO based on GeoCat	313,582.57		
AOO based on GeoCat	120		
EOO based on ENM	522,858.00	253,815.00	56,589.00

Description of the voucher specimen BNHS 6138

Medium-sized (SVL 46 mm), head wider (18.4 mm) than long (12.6 mm); snout truncate and depressed with sharp canthus rostralis (Fig. 2). Absence of cranial crests except for indistinct labial crest; very distinct and circular

tympanum in the horizontal distance slightly larger (4.4 mm) than the size of the eye (3.8 mm). Flattened parotoid glands. Dorsal skin without any warts at the head region with comparatively smooth and round warts throughout the posterior region. Pineal ocellus absent. Ventrums similar to dorsum in having smooth skin anteriorly and granular posteriorly. The first finger has a slightly enlarged disc. Fingers not webbed, toes basally webbed. Sub-articular tubercles and palmar tubercles present.

Molecular identification

Bocxlaer et al. (2009) published the first DNA sequence for the *D. hololius* from Vellore, Tamil Nadu (S. D. Biju, personal communication). In our phylogeny, based on the 12S+t-Val+16S fragment (1082 bp), *D. hololius* from Kaliyapuram, Tamil Nadu nests well

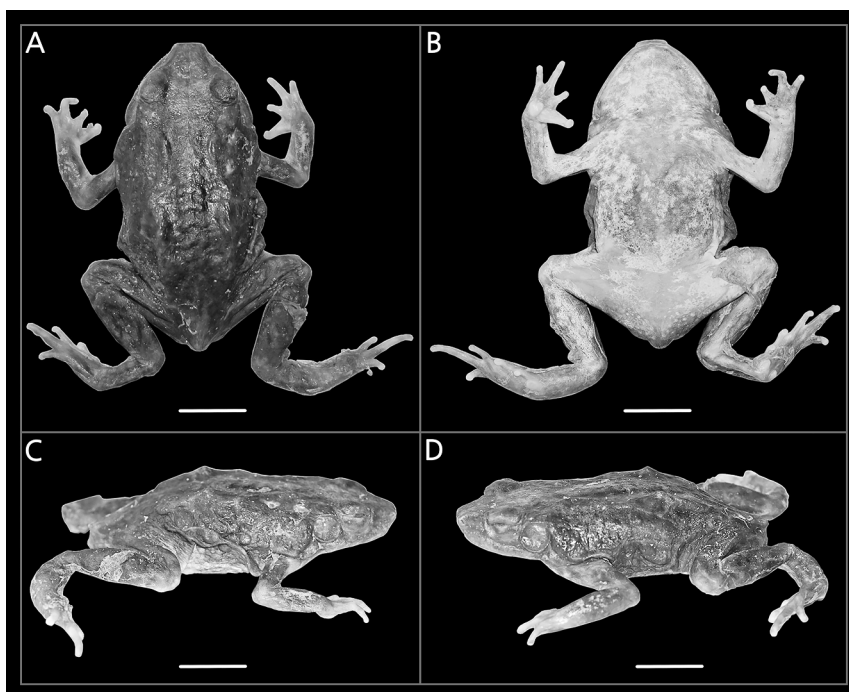


FIG. 2. Dorsal (A), Ventral (B) and Lateral (C and D) aspects of the voucher specimen (BNHS 6138) collected from Kaliyapuram, Pollachi, Tamil Nadu.

within the clade containing the other *Duttaphrynus* species and is nested together with the *D. hololius* from Vellore (Fig. 3). The uncorrected pairwise genetic distance between the two *D. hololius* samples varied with only 0.2%, despite the distance between the two locations and the habitat specificity. To date, all records pertaining to *D. hololius* originated from outside the Western Ghats, and the only available molecular data for this species are based on a non-topotypic material. Therefore, our data from the Western Ghats serve as critical in authenticating the true status of all previous records referred to as *D. hololius*.

Model performance and Potential distribution

The MaxEnt model prediction had high AUC (0.956) and pAUC (0.968) values for both training and test, and the true skill statistics value (TSS) was 0.826 (Table 4), indicating good model performance. From the Jackknife analysis, only Isothermality (Bio3),

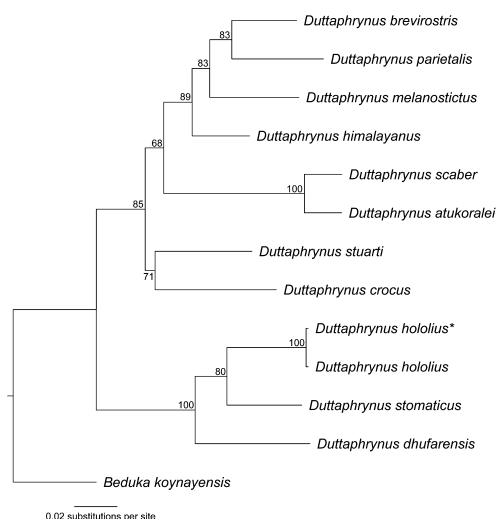


FIG. 3. Maximum Likelihood tree showing the relationships of the newly sequenced sample of *Duttaphrynus hololius* (marked with *) from the Western Ghats with the sample from Eastern Ghats and with other congeners. Numbers at internal branches are ML bootstrap support values.

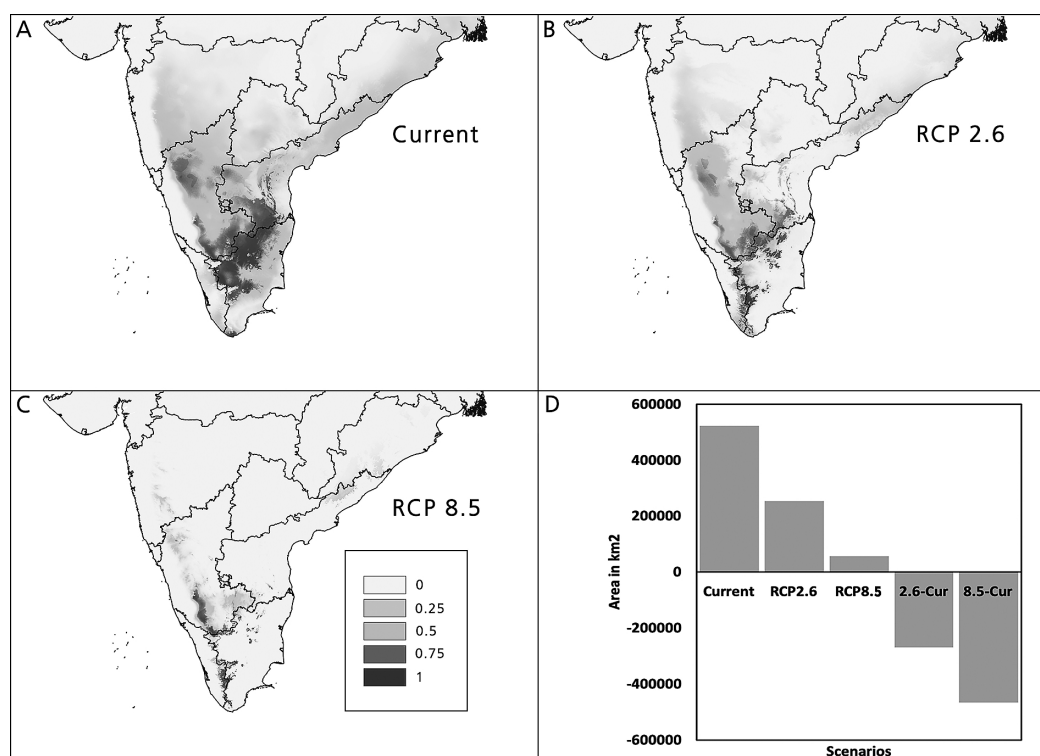


FIG. 4. Potential distribution of *Duttaphrynus hololius* under a) current b) RCP 2.6 and c) RCP 8.5. Changes in the area under different climate scenarios are provided in the inset figure (d).

TABLE 4. Extent of Occurrence (EOO) and Area of Occupancy (AOO) for *Duttaphrynus hololius* under different climate scenarios.

Stats	Values
AUC	0.956
pAUC	0.968
True Skill Statistics (TSS)	0.826
Kappa	0.777

Precipitation Seasonality (Bio15) and Annual Precipitation (Bio12) represented the top three variables with 44.6%, 29.1% and 7.8%, respectively (Table 2), contributing 81.5% to the model.

Results from the ENM analysis for current climate condition show a more robust and broader prediction for a larger area in the drier parts of north-western, central and north-

eastern Tamil Nadu, south-eastern Karnataka, southwestern Andhra Pradesh and more importantly, in the eastern slopes of the Western Ghats, extending partly into Kerala along the Palghat gap and Maharashtra (Fig. 4A).

Results from the climate change modelling for two scenarios (RCP 2.6 and RCP 8.5) show a steep and significant decline in the suitable range of *D. hololius*. According to the prediction, the suitable area under the RCP 2.6 drastically decreases to 253,815 km² from the current 522,858 km² and further decreases to 56,589 km² under the RCP 8.5, resulting in a tune of 51% and 89%, respectively from the present scenario (Fig. 4C–D). The suitable regions predicted under the RCP 2.6 are the drier regions in the northern Tamil Nadu, south-western Karnataka and south-eastern Andhra Pradesh, where the Eastern Ghats are scattered and most of the current records origi-

nate. The model also suggests the eastern slopes of the Western Ghats as a significantly suitable range, especially within Tamil Nadu (Fig. 4B). Furthermore, the predictions under RCP 8.5 show only the southern and central Western Ghats as significantly suitable regions and scattered regions in northern Tamil Nadu and south Karnataka (Fig. 4C).

DISCUSSION

Solving the “Malabar” issue

In this work, we report the first confirmed sightings based on photographs and/or vouchers of *D. hololius* from the Western Ghats since its first description by Günther in 1876. As mentioned earlier, to the best of our knowledge, Beddome (1880) is the first to list *D. hololius* in his checklist with “Western slopes of the Nilgiris” as the distribution. Both the western and southern limits of Nilgiris were reportedly bordered by the Malabar region (Grigg, 1880). The Western and Southern slopes by this implication are today’s Nilambur, Mallapuram, Palakkad Districts and Attapadi Hills in the state of Kerala, Southern India. Furthermore, one of the three records reported herein originates from Walayar, in Palakkad District, which is previously known to be a part of Malabar in present-day Kerala (see below).

The term Malabar was used for numerous floral and faunal collections made during the colonial era, often without precise locality information, and the extent of this region remains unclear. The pre-colonial part “Malabar,” in general, represented the areas with hills or on the hillside, and this name was widely used to describe the whole of what is now known as “Kerala” starting from Kannur to the Kollam without a clear demographic boundary (see map in Churchill [1703]). This name was also applied to the West Coast in the southern end, south of Kannur. However, subsequent to the last Anglo-Mysore war (1798–1799) and the formation of the Madras presidency, the Malabar district was formed. This originally encompassed nine larger taluks of then Chirakkal, Kottayam, Kurumbranad, Cali-

cut, Wynand, Ernad, Walavanad, Ponnani and Palghat and was annexed under the greater Madras presidency (Logan, 1887; Innes, 1908) lying between South Canara district (present day Dakshina Kannada) in the north-west, bordered by the cochin state in the south-west, Coorg and Mysore plateau in the northeast, and by Coimbatore District in the south-east (see map in Francis [1807]). This constitutes what is now known as Kannur, Calicut, Mallapuram, and Wayanad, part of the Thrissur and Palakkad districts of Kerala.

The potential distribution

Apart from the new records from the eastern slopes of the Western Ghats, our ENM analysis (current scenario) and the field observations suggest that *D. hololius* is widely distributed in Peninsular India, contrary to the predictions of the previous studies (Srinivasulu et al., 2013; Ganesh et al., 2020). In contrast, Srinivasulu et al. (2013) predicted a high probability (0.9–1.0) for most parts of the central and south-eastern Tamil Nadu and Nellore region in Andhra Pradesh, while Ganesh et al. (2020) predicted a high probability only for a smaller region covering the Vellore and Tiruvannamalai regions of Tamil Nadu. These incongruences between our findings and the previous works are probably because of the additional distribution points used in our study and/or over-parameterisation of the model. Earlier studies (Srinivasulu et al., 2013; Ganesh et al., 2020) used all 19 bioclimatic layers to model small data sets, which invariably influence the model outcome. As mentioned above, our future climate analysis also shows that, with a steep decline in the suitable range, the southern and parts of the Western Ghats might act as a climate refugia for the *D. hololius* under the RCP 8.5 for 2070. The climate change analysis from the past studies for the Peninsular Indian region shows that increase in drought (Rehana and Naidu, 2021) and extreme rainfall events clubbed with warmer winter months (Jayasankar et al., 2021). Insofar as amphibians are ectothermic animals with an amphibious life cycle, events like erratic rainfall,

warmer winter months, and increased temperature will only increase the species' vulnerability (Cushman, 2006; Buckley and Jetz, 2007), which is overwhelmed by human-induced land-use changes, especially in this case.

Conservation

At present, based on the available information, *D. hololius* is under Data Deficient category (Biju et al., 2004). Currently, *D. hololius* is known only from a very few protected areas (Biligiri Rangaswamy Temple Tiger Reserve, and Bannerghatta National Park in Karnataka and Chinnar Wildlife Sanctuary in Kerala). Also, a significant range of *D. hololius* lies outside the Protected Area network, which are highly human-dominated landscapes making it vulnerable for anthropogenic activities. Within the widely known and predicted range, such rocky habitat is heavily scattered and significantly lesser. Furthermore, it is pertinent to mention that these habitats undergo severe threats from anthropogenic pressure, mainly from a large number of small-scale mining and quarrying activities. These drier regions are often neglected in the conservation arena. They are even classified as "Wastelands" by the government in many parts and are not included in any conservation management plan. It is estimated that 5,924 illegal mines are operated in Kerala alone (Sajeev and Alex, 2017), but such statistics are not available for other states. However, within Tamil Nadu, regions highly suitable, as per the ENM like Salem, Madurai, and Krishnagiri, are the hotspots of mining activities. The current Extent of Occurrence (EOO) and Area of Occupancy (AOO) are relatively low and they are likely to further decrease under the climate change scenario. Given these considerations, as well as the threats from development activities, the future of this species looks grim. Based on EOO, AOO, habitat specialization of the species, and threats, we recommend this species to be considered Vulnerable. Given the results from this study, it is urgent for a strong conservation action plan to be developed.

CONCLUSION

Based on the findings and the discussions provided herein, we reject the previous notions that the type locality of *D. hololius* "Malabar" is an error and show its presence in the Western Ghats, at least in the drier eastern slopes. The long-believed notion that *D. hololius* is absent from the Western Ghats is perhaps because of the lack of intensive surveys in the drier regions of the Ghats. Therefore, we recommend more extensive sampling based on the ENM results in the drier and eastern slopes of the Western Ghats, where the ideal rocky outcrops are present to determine the actual distribution status of *D. hololius*. This is further warranted by our findings that the Western Ghats might serve as a crucial refugium for *D. hololius* under rapidly changing climatic conditions. In such cases, regional surveys and explorations by citizen scientists might help to explore a wider region in a short period of time. Also, a solid conservation action plan needs to be devised for the long-term survival of this habitat specialist and evolutionarily distinct species of Peninsular India.

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APPENDIX

List of locations used in the present study.

No.	Locality	Source	Latitude	Longitude
1	Horsley Hills, Andhra Pradesh	Satyamurthi (1967)	13° 39' 0.040"	78° 22' 59.844"
3	Nagarjuna Sagar Tiger Reserve, Andhra Pradesh	Pillai and Ravichandran (1991)	16° 32' 50.744"	79° 6' 11.376"
4	Devarbetta, Hosur Forest Division, Tamil Nadu	Chandramouli et al. (2011)	12° 37' 28.945"	77° 37' 34.140"
5	Thommaguddai, Ambur Range, Tirupattur Forest Division, Tamil Nadu	Kalaimani et al. (2012)	12° 49' 21.976"	78° 40' 0.084"
6	Caves of Kundu Reddiyur, Alangayam Range, Tirupattur Forest Division, Tamil Nadu	Kalaimani et al. (2012)	12° 33' 12.553"	78° 41' 42.972"
7	Rajagiri Hill, Gingee, Tamil Nadu	Kalaimani et al. (2012)	12° 13' 52.298"	79° 23' 4.416"
8	Telangana State Forest Academy, Andhra Pradesh	Ganesh et al. (2020)	17° 32' 38.411"	78° 27' 26.532"
9	Hampi hillocks, Karnataka	Ganesh et al. (2020)	15° 19' 55.200"	76° 28' 1.200"
10	Rishi Valley School, Karnataka	Ganesh et al. (2020)	13° 37' 58.800"	78° 27' 28.800"
11	Vishakapatnam, Andhra Pradesh	Srinivasulu et al. (2013)	17° 40' 47.215"	83° 17' 22.848"
12	Bannerghatta, Karnataka	Daniels (1992)	12° 46' 55.074"	77° 33' 59.472"
13	Kaliyapuram, Pollachi, Tamil Nadu	This study	10° 31' 52.007"	76° 55' 31.656"
14	Walayar, Kerala	This study	10° 48' 25.589"	76° 48' 13.248"
15	Chinnar, Kerala	This study	10° 20' 44.070"	77° 13' 53.004"
16	Chennimalai, Tamil Nadu	Ganesh et al. (2018)	11° 9' 26.312"	77° 35' 22.128"
17	Sankagiri, Tamil Nadu	Ganesh et al. (2019)	11° 29' 10.216"	77° 51' 19.152"
18	Salem, Tamil Nadu	iNaturalist	11° 41' 30.718"	78° 7' 43.932"
19	Bannergatta, Karnataka	iNaturalist	12° 48' 18.886"	77° 34' 43.608"
20	Group of Monuments At Hampi, Hospet, Karnataka	iNaturalist	15° 20' 33.250"	76° 27' 43.380"
22	Unnamed Road, Hallimala, Karnataka	iNaturalist	12° 45' 7.494"	77° 18' 4.860"
23	Rishi Valley, Andhra Pradesh	iNaturalist	13° 38' 10.795"	78° 27' 13.932"
24	Bagayam, Vellore, Tamil Nadu	iNaturalist	12° 52' 18.507"	79° 7' 35.868"
25	Bagayam, Vellore, Tamil Nadu	iNaturalist	12° 52' 18.507"	79° 7' 35.868"
26	Andrahalli Betta, Karnataka	iNaturalist	13° 10' 26.520"	78° 2' 21.984"
28	Kolar, Karnataka	iNaturalist	13° 8' 10.371"	78° 7' 44.760"
29	Thettu, Andhra Pradesh	India Biodiversity Portal	13° 37' 42.240"	78° 26' 10.68"
30	Varlakonda, Karnataka	India Biodiversity Portal	13° 38' 8.160"	77° 47' 18.6"
31	Krishnagiri, Tamil Nadu	India Biodiversity Portal	12° 31' 46.560"	78° 12' 23.040"

APPENDIX

(continued)

No.	Locality	Source	Latitude	Longitude
32	Thiruvannamalai, Tamil Nadu	India Biodiversity Portal	12° 13' 31.080"	79° 4' 28.920"
33	Bannerughatta, Bengaluru, Karnataka	India Biodiversity Portal	12° 48' 18.720"	77° 34' 43.680"
34	Bangalore Urban, Karnataka	Herpmapper	12° 49' 49.979"	77° 28' 46.956"
35	Tumkur, Karnataka	Herpmapper	14° 8' 54.702"	77° 6' 23.508"
36	Bangalore Urban, Karnataka	Herpmapper	12° 45' 29.722"	77° 31' 4.512"
37	Bangalore Urban, Karnataka	Herpmapper	12° 45' 25.809"	77° 31' 3.432"
38	Bangalore Urban, Karnataka	Herpmapper	12° 45' 29.490"	77° 31' 12.396"
39	Kolar, Karnataka	Herpmapper	13° 10' 23.433"	78° 2' 16.260"