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## A NEW MONTANE-DWELLING SPECIES OF *Japalura* GRAY, 1853 (SQUAMATA: AGAMIDAE) FROM ARUNACHAL PRADESH, INDIA

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### Abstract

The montane agamid lizard *Japalura austeniana* (Annandale, 1908), is rare and is distributed across parts of the eastern Himalayas of India and China. Support from molecular and morphological data provides evidence for the existence of a species complex in the populations referred to that binomen, and we here describe a morphologically cryptic allied new species. Evidence from molecular data suggests the presence of additional undescribed species across the distribution of that species complex. Elevation might be the restricting factor for gene flow explaining most of the diversification of that montane species complex across the Himalayas.

**Keywords:** Agamidae, biodiversity hotspot, biogeography, conservation, Himalayas, systematics

### Introduction

The Agamid genus *Japalura* Gray, 1853, as defined by Smith (1935), is composed of a morphologically heterogeneous radiation of lizards. They have been recently split into several genera (Mahony 2009, Manthey 2010, Wang *et al.* 2019a) due to their paraphyletic nature (Wang *et al.* 2019a). Several species of the subfamily Draconinae show a high degree of morphological

divergence, which has led to erroneous generic allocations (Deepak *et al.* 2015, Pal *et al.* 2018, Giri *et al.* 2019). A similar case of erroneous generic allocation due to high morphological divergence was observed in the case of *Mictopholis austeniana* Annandale, 1908. The species has had a complex history of generic allocations until recently when Gowande *et al.* (2021) demonstrated with molecular data that

*Mictopholis austeniana* is a member of the genus *Japalura* and not a *Pseudocalotes* sensu Mahony (2010). For a complete taxonomic history of *Japalura austeniana*, see Mahony (2010) and Gowande *et al.* (2021). *Japalura austeniana* appears to be rare and restricted to higher elevation (>1600 m) montane forests across Arunachal Pradesh in India (Athreya 2006, Das & Das 2007, Agarwal *et al.* 2010, Gowande *et al.* 2021) and Medog Country in China (Wang *et al.* 2019b).

As part of an ongoing study on the reptiles of Arunachal Pradesh, we collected a specimen from Eaglenest Wildlife Sanctuary (WLS) that we first attributed to *Japalura austeniana*. However molecular as well as additional morphological data for the specimen suggest that the population can be distinguished from *J. austeniana sensu stricto*. A search through the Zoological Survey of India's collection revealed another specimen from the vicinity of Eaglenest WLS that was morphologically similar, which further confirmed the distinctiveness of the population from western Arunachal Pradesh. That population is herein described as a new species based on these two specimens.

## Material and methods

**Morphology:** One unique specimen was collected by hand, euthanized, and fixed in 6% formalin. It was later washed with water and stored in 70% ethanol. That specimen was deposited in the collection of the National Centre for Biological Sciences, Bangalore, as the paratype. All examined specimens were measured using a Mitutoyo™ digital calliper. Descriptive style and morphometric / morphological characteristics were recorded following Sadasivan *et al.* (2018). The following measurements were taken: snout–vent length (SVL, from tip of snout to anterior border of cloaca), head length (HL, from snout tip to posterior border of tympanum), head width (HW, distance from left to right outer edge of the head at its widest point), head height (HH, dorsoventral distance from top of head to underside of jaw at transverse plane intersecting angle of jaws), snout–eye length (SE, from snout tip to anterior border of orbit), eye to tympanum (ET, from posterior border of orbit to anterior border of tympanum), jaw length (JL, from rostrum to corner of jaw), interorbital width (IO, transverse distance between anterodorsal corners of left and right orbits), nares to eye (NE, distance from the anterior edge of orbit to

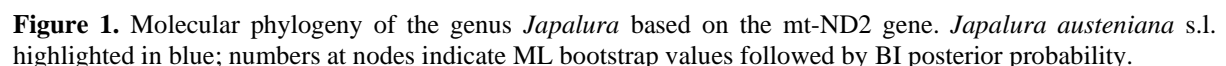
posterior edge of naris), snout width/internasal distance (IN, transverse distance between left and right nares), tympanum diameter (TD, greatest diameter of tympanum), orbit diameter (OD, distance between anterior and posterior margins of orbit), femur length (FEL, length of femur from groin to knee), crus length (CL, length of crus (tibia) from knee to heel), trunk length (TrL, from forelimb insertion to hind limb insertion), trunk width (TrW, width midway between the fore and hind limb insertions), tail length (TL, from posterior border of cloacal opening to tip of tail), and tail width (TW, at tail base). Meristic characters were counted for multiple individuals for each species.

The following meristic characters were scored: midbody scale rows (MBS, number of scale rows around the trunk at midbody), ventral scales (VEN, number of scales from below mental to anterior border of cloaca), fourth toe lamellae (LAM4, number of 4th toe lamellae, from 1st lamella at the digit's cleft to the most distal enlarged lamella), supralabials (SL, posterior end defined by the last enlarged scale that contacts the infralabials at the corner of mouth), infralabials (IL, posterior end defined by the posterior-most enlarged scales that contact the supralabials at the corner of the mouth), ventral scales on the belly (VENB, number of scales posterior to the dewlap to the anterior border of cloaca), vertebral scales (VS, number of scales above the vertebral column counted from the mid-dorsal first nuchal spine to a level directly above the cloacal opening), crest scales (CrS, number of erect enlarged scales from the nape to corresponding region above the cloaca). Institution acronyms were used as follows: NRC, National Research Collections of the National Centre for Biological Sciences (NCBS), Bangalore; ZSI, Zoological Survey of India, Kolkata.

**Molecular methods.** Total genomic DNA was extracted from the thigh muscle tissue using QIAGEN DNeasy kits following protocols directed by the manufacturer. Fragments of the mitochondrial NADH dehydrogenase 2 (ND2) was amplified using the primers L4437 5'-AAGCTTTCGGGCCCCATACC-3' and H5540 5'-TTTAGGGCTTTGAAGGC-3' (Macey *et al.* 1997). A 12 µl reaction was set containing 5 µl of Qiagen Taq PCR Master Mix, 4 µl of water, 0.5 µl of each primer and 2 µl template DNA, carried out with an Eppendorf Mastercycler Nexus GSX1. Thermo-cycle profile used for amplification were as follows: 94 °C for 15

Markov chains were sampled every 500 generations, for 20 million generations. At the end of the run, the standard deviation of the split frequencies was less than 0.05, and the analysis was not continued further. A total of 25% of trees were discarded as burn-in, and an effective sampling size was tested with Tracer v.1.7 (Rambaut *et al.* 2014). The tree representing the best evolutionary hypothesis for the dataset was selected using a 50% majority consensus rule. Sequence genetic divergence was calculated in MEGAX with the p-distance option, and missing data were dealt with, with a pairwise deletion option.

**Molecular data.** Molecular phylogeny through the ML and BI resulted in comparable topologies with slight differences. The recovered phylogenetic relationships differ from those reported by Gowande *et al.* (2021) and Wang *et al.* (2019a) and suffer from having low to moderate support. The present analysis, which is solely based on the mitochondrial ND2 gene of 991 bp, recovered *Japalura variegata* Gray, 1853 basal to all members of the clade, *J. andersoniana* Annandale, 1905 was recovered sister to *J. austeniana* s.l. with moderate support (Fig. 1). *Japalura* cf. *andersoniana* is sister to *J. andersoniana* s.str. and *J. cf. andersoniana* from Eaglenest WLS with high support. The *Japalura* from Eaglenest (*J. cf. andersoniana*) shows a sequence divergence (*p*-distance) of 14% from *J. andersoniana* s.str. and 17% from *J. cf. andersoniana* from China.



## Systematics

### *Japalura mictophola* sp. nov.

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(Figs. 2–7, Table 1)

*Pseudocalotes austeniana* Mahony 2010 [*partim*]

*Mictopholis austeniana* Das & Das 2007: 45 [*partim*],

Manthey 2010: 111 [*partim*]

**Holotype.** Adult male, ZSI 24841, collected from Bomdila (27.262355°N, 92.419441°E, alt. 2,427m a.s.l.), West Kameng District, Arunachal Pradesh, India, by S. Sur; no precise date.

**Paratype.** Adult male, NRC-AA-8541, collected from near Lama Camp (27.161000°N, 92.460500°E, alt. 2,325m a.s.l.), Eaglenest Wildlife Sanctuary, West Kameng District, Arunachal Pradesh, India, by Mandar Sawant and Pushkar Phansalkar on 20 August 2021.

**Diagnosis.** A large-sized *Japalura*, reaching SVL of 92.9 mm with heterogeneous dorsum scalation and an exposed tympanum. Body laterally compressed and ventral scales subequal. Four large supra-tympanic scales and the males bear a distinct vertebral crest. Supra-tympanic scales are not in contact with orbital scales and are separated by two medium-sized smooth scales.

**Comparison.** *J. mictophola* sp. nov. is here compared with Indian congeners based on diagnostic non-overlapping characters: tympanum exposed (*vs* tympanum concealed in *J. andersoniana* and *Japalura variegata*), dorsal crest in males prominent [*vs* dorsal crest not prominent in *Japalura major*, *J. tricarinata* and *J. kumaonensis* (Annandale, 1907)], four enlarged supra-tympanic scales [*vs* enlarged supra-tympanic scales absent in *J. major* (Jerdon, 1870), *J. tricarinata* (Blyth, 1853), *J. kumaonensis*, *J. andersoniana* and *J. variegata*]. The new species is morphologically most similar to *J. austeniana* with which it shares heterogeneous dorsal scalation and a distinct row of enlarged supra-tympanic scales (Fig. 4). *Japalura mictophola* sp. nov. differs from *J. austeniana* in bearing four enlarged keeled supra-tympanic scales not in contact with orbital scales and separated by two medium-sized smooth scales (Fig. 4A) (*vs* four enlarged keeled supra-tympanic scales in contact with orbital scales in *J. austeniana* (Fig. 4B)) and lamellae on 4<sup>th</sup> toe 25 (*vs* 31 in *J. austeniana*). Enlarged keeled scales on the lateral aspect of the trunk in *J. mictophola* are relatively smaller than those in *J. austeniana* (Figs. 4C–D).

**Description of holotype.** The specimen is in a good state of preservation. The head of the specimen is curved to the left, the tail is coiled, and the posterior part of the trunk bears a small longitudinal ventral incision.

Adult male (SVL 84.5 mm). Head relatively long (HL/SVL ratio 0.31), longer than wide (HW/HL ratio 0.47), not depressed (HH/HL ratio 0.47), distinct from neck. Snout moderately long (SE/HL ratio 0.39), bluntly conical; longer than eye (OD/SE ratio 0.69). Eye large (OD/HL ratio 0.27); pupil round, eyelids covered with heterogeneous scales comprising of pentagonal, hexagonal and rounded scales, supraciliaries short. Snout obtusely pointed when viewed dorsally; rostral much wider than deep, bordered posteriorly by first supralabial, prenasal and dorsally by three small scales. Canthus rostralis and supraciliary edge moderately sharp, consisting of eight scales that gradually decrease in size from anterior to posterior. Nostrils positioned in the centre of a large, undivided nasal plate, each bordered by 6–7 scales (left side), including one prenasal, one postnasal and one supranasal, and in broad contact with rostral. Rostral and labial scales punctate. Seven rectangular, smooth supralabials, bordered above by a single row of larger, quadrangular, unkeeled scales. Loreal region concave, scales of the loreal region heterogeneous in size, flat, keeled, some roughly hexagonal. Scales on postorbital and temporal region homogeneous, imbricate, strongly keeled, and directed posteriorly and dorsally. Orbital scales small but not granular. Four large moderately-keeled postorbital scales from the posterior border of the orbit terminate at the supratympanic region; these four enlarged scales are not in contact with orbital scales and are interrupted by two medium sized smooth scales. Tympanum naked. Canthals enlarged, overlapping, becoming slightly smaller along subimbricate supraciliaries, protruding slightly laterally on supraorbital ridge. Scales on dorsal surface of snout, forehead, interorbital, and occipital region heterogeneous in size, and shape; mostly elongate, imbricate, smooth; those on snout smaller, rhomboidal, those on forehead largest, greatly elongate; supraorbital scales increase in size, becoming more elongate from supraciliaries to inner edges of orbits, of which the enlarged scales follow the curvature of the orbit posterolaterally; occipital region with slightly smaller, rounded, imbricate, and smooth scales. Parietal region with small as well as large scales lacking pineal eye. Mental shield narrower

than rostral; gular scales smooth. Infralabials, mental, and a few gular scales punctate. A small dewlap-like appendage extending from the chin to the shoulders, ventrally spanning 22-23 scales. Dorsal crest present, 21 erect spines along the vertebral column from the nuchal to the mid-dorsum. The vertebral column bears 38 enlarged scales from the nuchals to the cloaca. Scales on nuchal region smaller, less than half the size of those on interorbital region, imbricate, smooth.

Body slender, 53 rows of heterogeneous scales around midbody. Scales in the anterior part of the trunk small, rounded, smooth and not depressed; these scales increase in size posteriorly, intermixed with 4-5 times larger, flat, strongly keeled scales. The keeled large scales in the dorsolateral aspect of the trunk have their keels directed upwards, whereas those in the ventrolateral aspect are directed downwards. Scales on the limbs subequal, similar in their dimensions and nature of keel to the trunk large-keeled scales, with the only exception being the ones on the elbow that are smaller in size. Fore and hind limbs relatively slender, tibia longer than forearm (CL/SVL ratio 0.24 vs FL/SVL ratio 0.14); digits moderately long, ending in strong, elongate, slightly recurved claw; interdigital webbing absent; subdigital lamellae entire, tri-mucronate, subdigital lamellae on right manus (I)10-(II)16-(III)20-(IV)17+\*(-V)13 (\*indicates damaged) and (I)12-(II)18-(III)25-(IV)25-(V)16 of right pes; relative length of fingers 4>3>2>5>1, toes 4>3>5>2>1. Fore and hind limbs covered above and below with regularly arranged, enlarged, pointed, strongly keeled scales. Enlarged projecting scale on thigh present.

Tail entire; tail base swollen; tail uniformly covered with similar sized, keeled, weakly pointed, regularly arranged, posteriorly directed imbricate scales, no enlarged subcaudal row.

**Colouration.** In preservative, the life colouration has entirely faded (Fig. 2). The specimen is in a shade of dark brown on the dorsum and light yellowish brown on the venter.

**Variation.** Some morphometric and meristic data are presented in Table 1. The paratype (Figs. 3–5) agrees with the holotype in most regards. The paratype was freshly collected, allowing us to describe its life colouration. The animal is green to yellowish green overall dorsally and yellow ventrally (Figs. 5A–C). The head and the anterior part of the body bear a few dark brown spots or streaks that are 1-2 scales wide. The middle of the trunk bears one broken transverse

band followed by a near-complete one. The limbs and the tail bear broad brown bands, and the fingers of the limbs are predominantly brown with a few patches of green.

**Etymology.** The specific epithet is a combination of two words, the Greek word *miktós* ‘μικτός’ meaning mixed, and the word *phola* (=scales) referring to the mixed (heterogeneous) scales on the dorsum of the species.

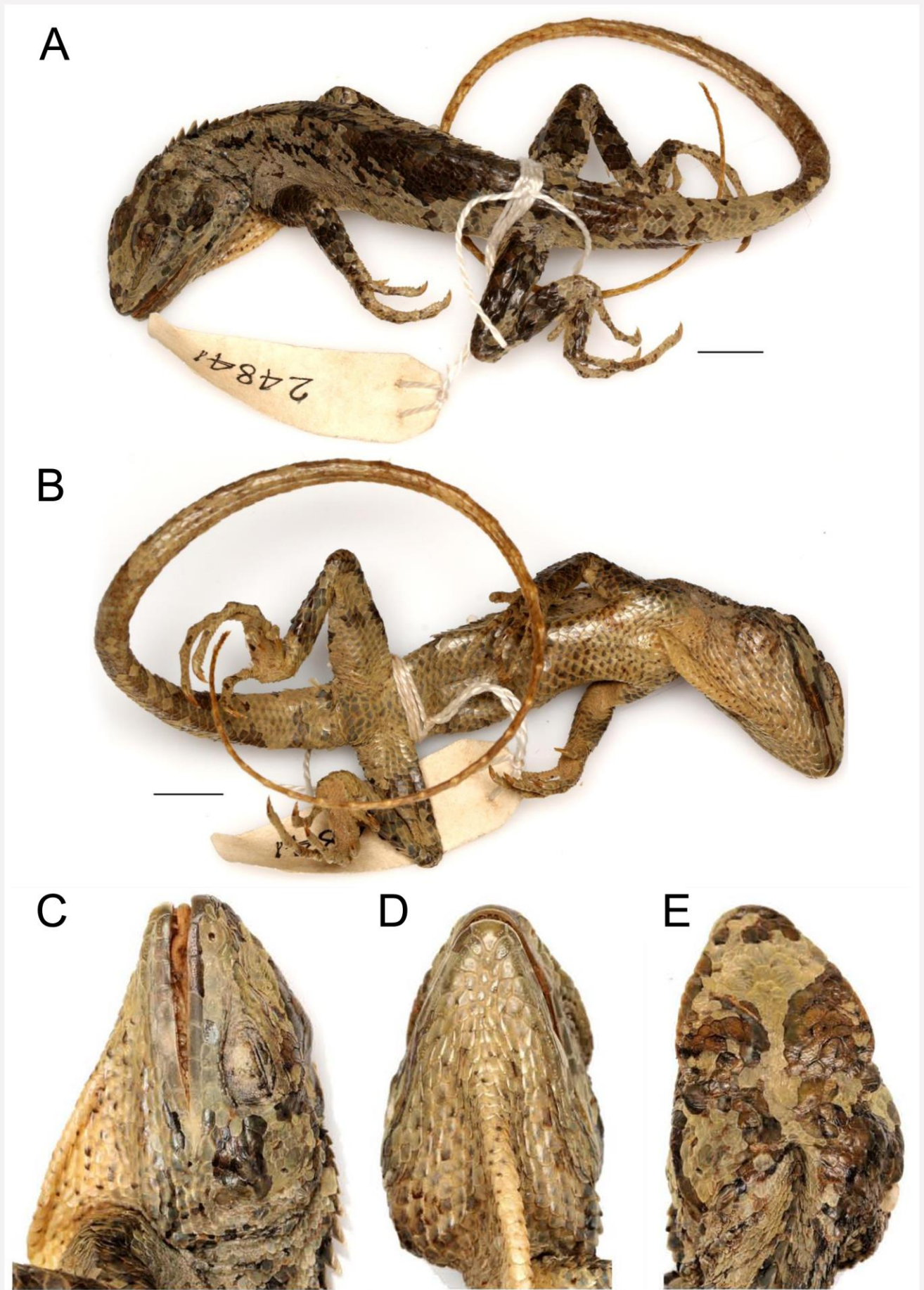
**Table 1.** Morphometric and meristic data for the type specimens of *Japalura mictophola* sp. nov. \* = incomplete tail/digit.

	<i>Japalura mictophola</i> sp. nov.		<i>Japalura austeniana</i>
	holotype	paratype	holotype
	ZSI 24841	NCBS NRC-AA- 8541	ZSI 3976
SVL	84.5	92.9	94
TrL	35	41.8	31.8
HL	26	29.7	–
HH	12.2	13.7	15.4
HW	15.7	20.1	17.5
FEL	11.9	15.3	16.9
CL	20.4	23.8	19.5
TrW	12.3	20.6	–
IO	10.6	14.3	–
IN	5.4	6.2	–
SE	10.2	12.7	9.8
NE	6.1	8.4	7.7
OD	7	5.1	4.8
ET	6.9	7.8	5.2
TD	2.9	3.9	4
TW	8.2	10.1	–
TL	210	237	75*
SL R/L	7/8	7/7	6/7
IL R/L	8	8/8	8/8
lamellae manus	10-16-20- 17*-13	10-16-20- 23-13	10-16-22- 22-15
lamellae pes	12-18-25- 25-16	12-17-26- 25-16	10-17-22- 24-15
MBS	51	52-53	51
CrS	35	32	33

## Discussion

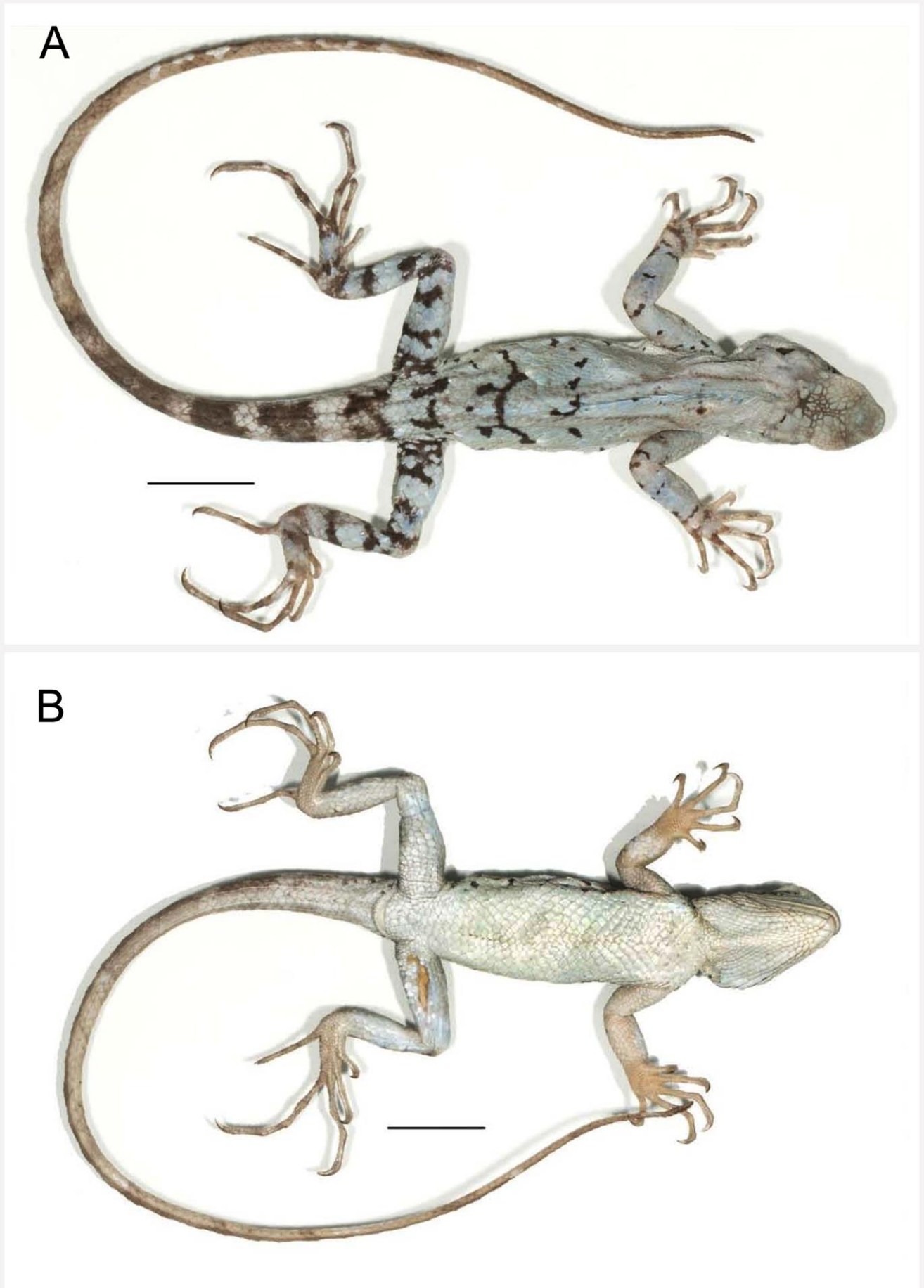
Molecular data generated for the paratype of the new species confirms its placement as a distinct species and that *Japalura austeniana* sensu Gowande *et al.* (2021) is a member of the genus *Japalura*, thus invalidating the genus *Mictopholis* to which it was attributed when first described by Smith (1935). The new species is

## Plate 1



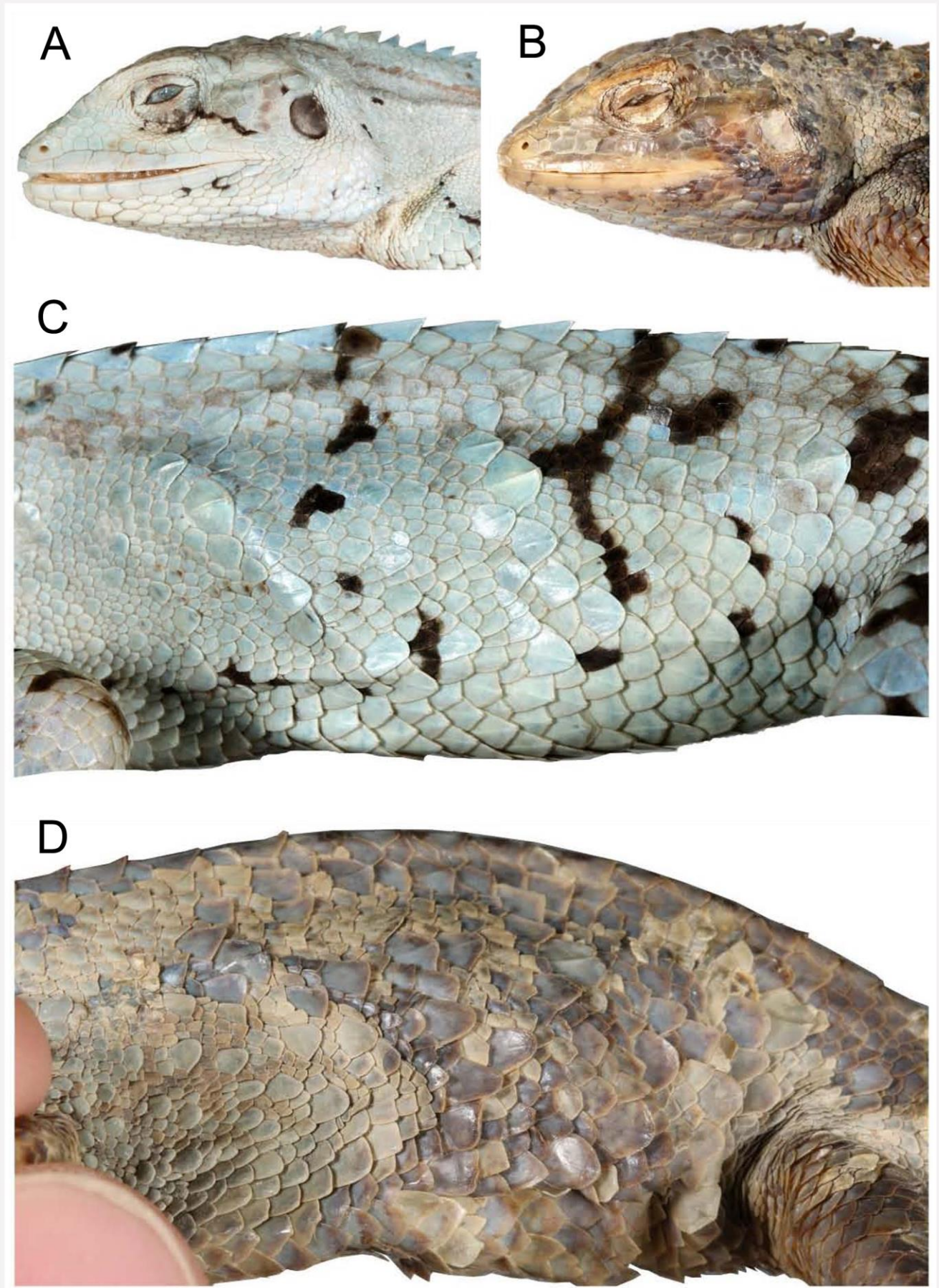
**Figure 2.** *Japalura mictophola* sp. nov. male (holotype, ZSI 24841): (A) dorsal and (B) ventral views of full body, scale: 20 mm; and (C) lateral, (D) ventral, and (E) dorsal views of the cephalic region; © Photo: ZAM

## Plate 2



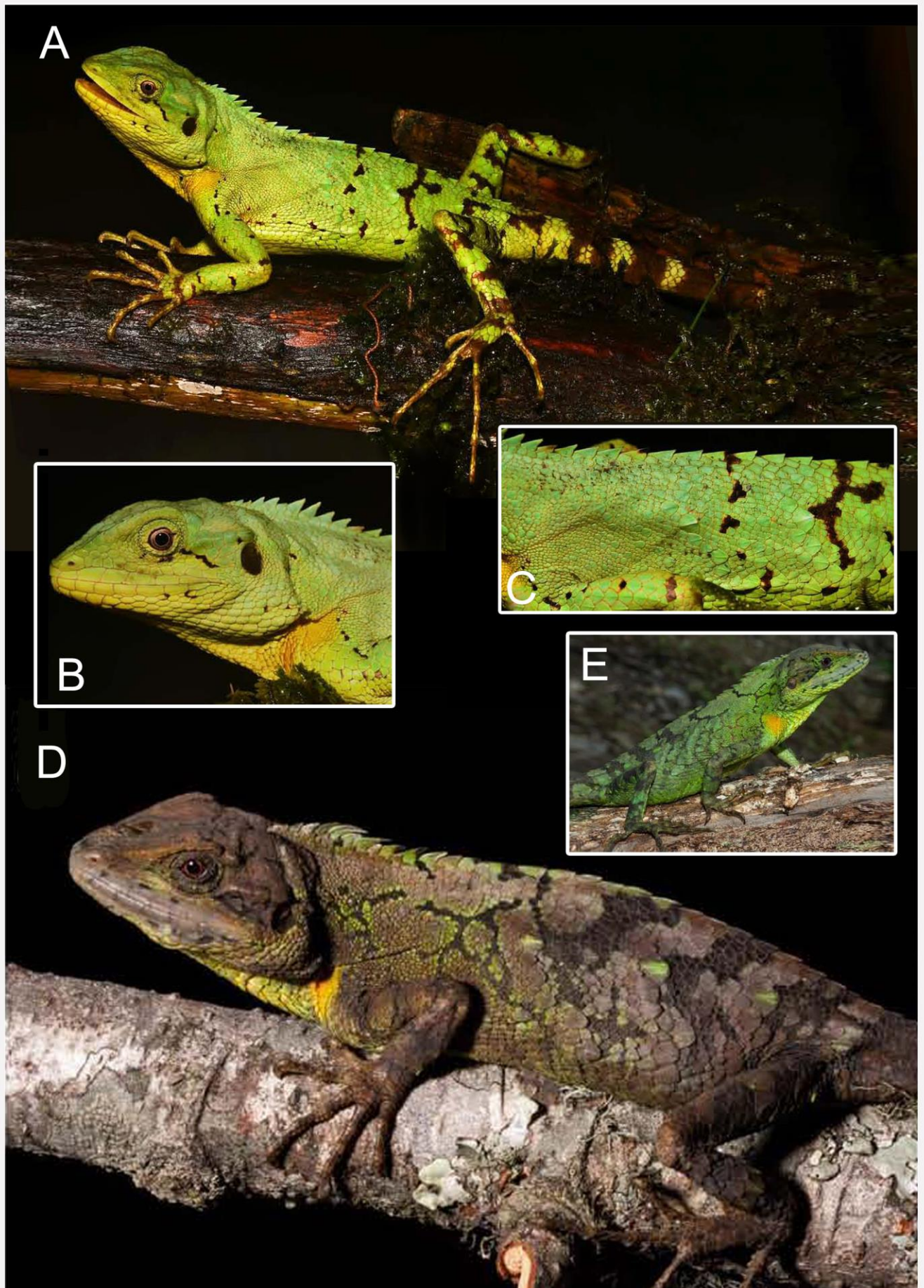
**Figure 3.** *Japalura mictophola* sp. nov. male (paratype, NRC-AA-8541): (A) dorsal and (B) ventral views of full body, scale: 20 mm; © Photo ZAM

## Plate 3



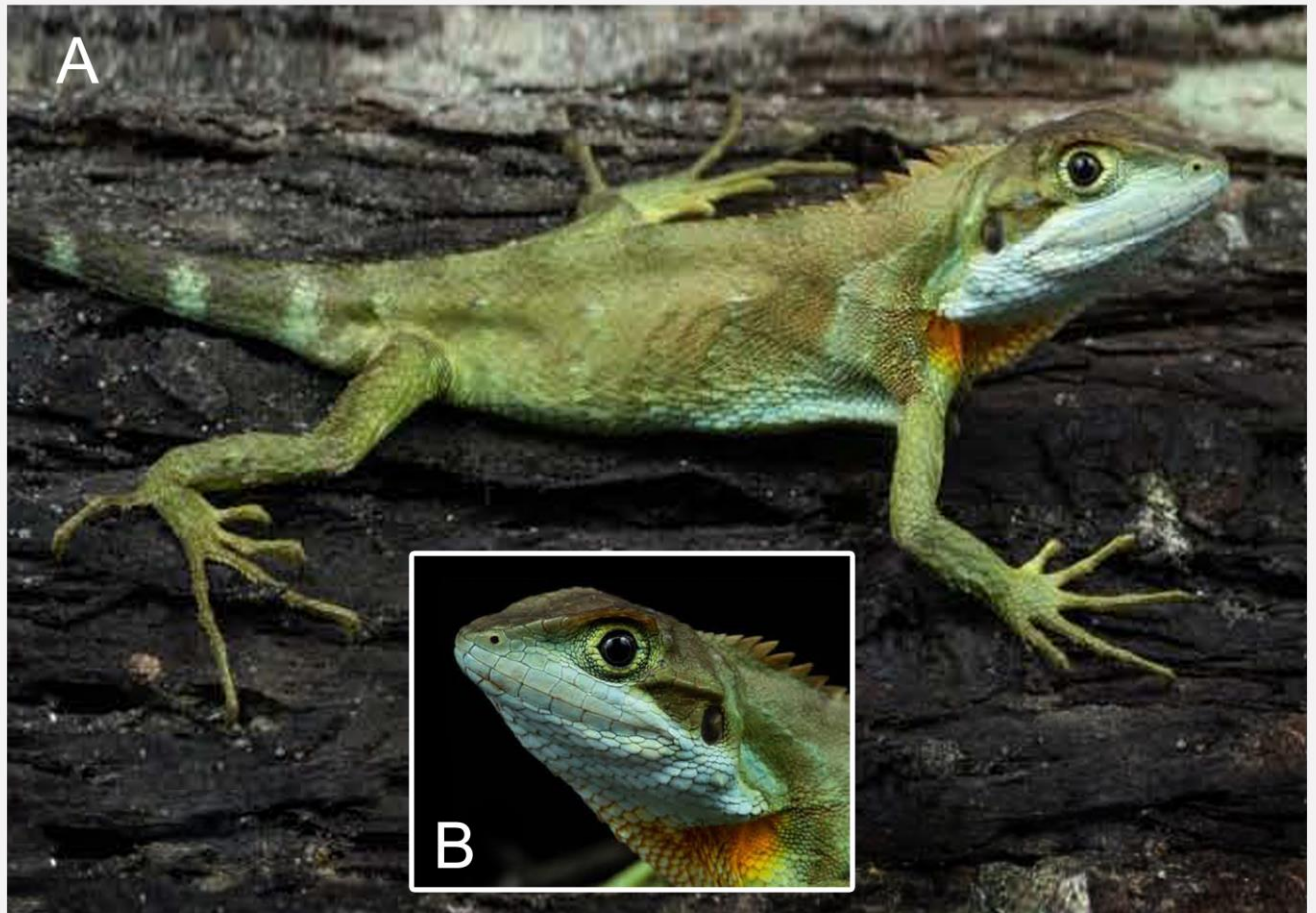
**Figure 4.** Comparison between *Japalura mictophola* sp. nov. (male paratype NRC-AA-8541) (A) lateral head (left) and (C) lateral trunk (left) and *Japalura austeniana* (male holotype ZSI 3976) (B) lateral head (left) and (D) lateral trunk (left); © Photo ZAM

## Plate 4

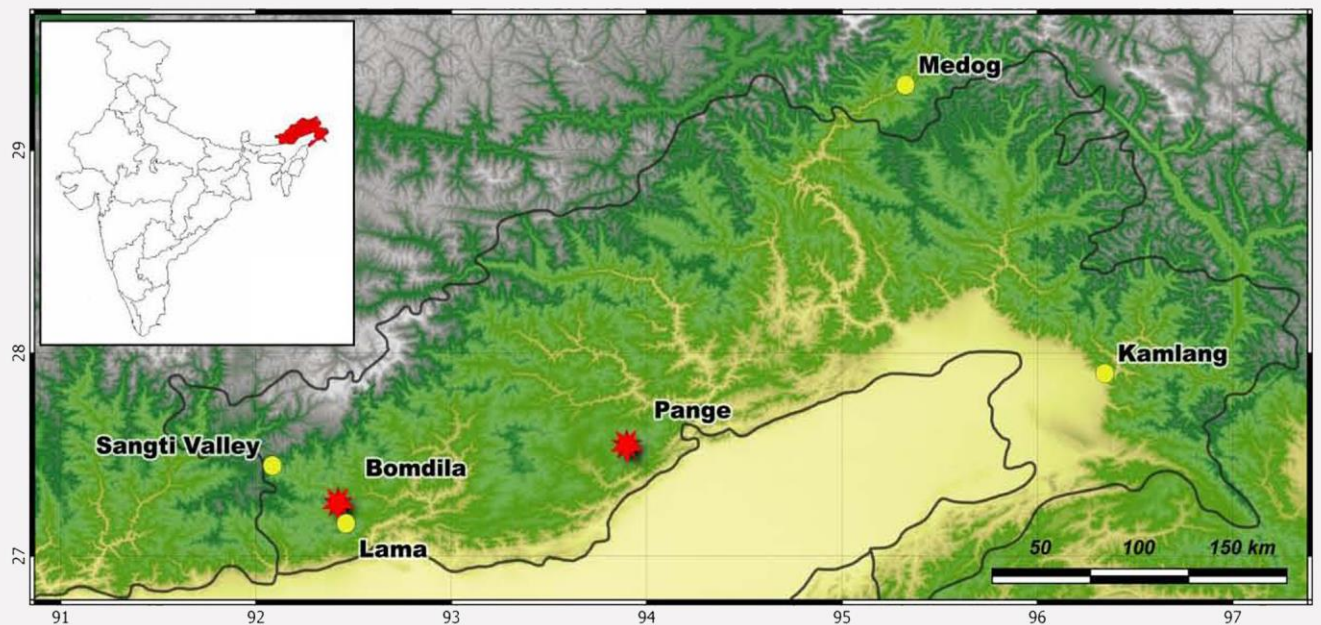


**Figure 5.** *Japalura mictophola* sp. nov. in life: lateral views of (A) full body, (B) head, and (C) trunk of male paratype (NRC-AA-8541) © Photo: MS; and (D, E) lateral full body (not collected) © Photo: I. Agarwal

## Plate 5



**Figure 6.** *Japalura austeniana* in life (not collected): (A) full body and (B) lateral head view © Photo: ZAM



**Figure 7.** The map of Arunachal Pradesh in India shows the known distribution of *Japalura austeniana* s.l.; type localities of *Japalura mictophola* sp. nov. at Bomdila, and *Japalura austeniana* s.s. at Dafla Hills near Harmatti are indicated by red stars.

morphologically similar to *J. austeniana* (Figs. 5D-E, 6A-B) from which it differs in having a sequence divergence of 14% on the ND2 gene. The two localities from where the sequences were generated are 150 km apart, both at an elevation above 2000 m (Fig. 7). The sequence of *Japalura* cf. *austeniana* from Medog Country, China (Wang *et al.* 2019b) is 17% divergent and likely represents another undescribed taxon. The low-elevation forests are likely a barrier to gene flow across these high-elevation montane-adapted lizards. Similar altitudinal restrictions are also observed in the newly described genus *Problepharus* Mirza, Bragin, Bhosale *et al.*, 2022 (Mirza *et al.* 2022) and in snakes of the genus *Trachischium* (Bhosale *et al.* 2019). On the other hand, low to mid-elevation species have a broader distributional range across Arunachal Pradesh, for example, *Cyrtodactylus arunachalensis* Mirza, Bhosale, Ansari *et al.*, 2021 (see Bhosale *et al.* 2020, Mirza *et al.* 2021) and other parts of northeast India, *Trimeresurus salazar* Mirza, Bhosale, Phansalkar *et al.*, 2020 and *Trimeresurus popeiorum* Smith, 1937 (see Mirza *et al.* 2020, 2023; Vogel *et al.* 2022).

The holotype ZSI 24841 housed in the collection of the Zoological Survey of India, Kolkata, has been mentioned in the literature by Das & Das (2007), Mahony (2010), Wang *et al.* (2019) and Gowande *et al.* (2021) and therefore was chosen as the holotype even though a fresh specimen was available.

Members of the genus *Japalura* s.l. (as defined by Smith 1935) represent a challenging taxonomic group of draconine lizards. The contribution by Wang *et al.* (2019a) presents a framework for further investigation of the systematics of *Japalura* s.str., especially by generating new molecular data. The molecular phylogenetic results recovered in the present work are at odds with those published by Wang *et al.* (2019a). This may be attributed to the single marker employed for the analysis in our work as opposed to the multigene analysis made by Wang *et al.* (2019a).

The Eastern Himalayas are said to host greater biodiversity in comparison with the central and western Himalayas, which are said to have a subset of the biodiversity of the Eastern Himalayas (Mani 1974). Furthermore, that area appears to be the centre of origin of several evolutionarily distinct lineages (Kamei *et al.* 2012, Xu *et al.* 2021, Mirza *et al.* 2022). The discovery of a new species of agamid from the region is not surprising as it has only been poorly

explored in terms of its reptilian diversity. The discovery of the new lizard described here was part of a second trip to document the reptilian diversity of Arunachal Pradesh, the first trip leading to the discovery of several undescribed species of reptiles. The high-elevation Eastern Himalayas montane forests possess isolated sky islands that each host distinct biota. Dedicated efforts to document the biodiversity of such high-elevation (>1800 m) montane forests as soon as possible would be desirable.

#### Author contributions

All the authors contributed equally. Conceived and designed the study: ZAM, GG & HP; conducted fieldwork: ZAM, GG, MS, HB, PP; Funding acquisition: ZAM, GG, HB & TT; Data curation and formal analysis: ZAM, GG & HP. All the authors reviewed and approved the final version of the manuscript.

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#### Research permits

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#### Appendix I. Sequence substitution model used for ML and BI phylogeny

Codon position	ML	BI
ND2 position 1	HKY+F+G4	HKY+I+G
ND2 position 2	HKY+F+G4	HKY+I+G
ND2 position 3	TN+F+G4	HKY+I+G

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