



Range extension of the Central American Red Brocket, *Mazama temama* (Kerr, 1792) (Artiodactyla, Cervidae), in Colombia

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Abstract

Mazama temama (Kerr, 1792) is a representative species of the northern Neotropics, but the geographic range limits for this species remain unclear. We report the southernmost record of *M. temama* from the southwestern Colombian Andes, increasing the previously known range of this species by more than 300 km. We obtained a cytochrome gene sequence (849 bp) which is 95% identical to samples from Mexico. This record raises the need for extensive sampling to obtain more complete information about the distribution of *M. temama* in northern Colombia.

Keywords

Andes, cytochrome-b, deer, distribution, range extension

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Introduction

Previous studies of deer diversification in the Neotropics have revealed an astonishing evolutionary history (Duarte et al. 2008). During the Great American Biotic Interchange (Woodburne 2010), a rapid diversification

occurred after different deer lineages migrated into South America (Duarte et al. 2008; Escobedo-Morales et al. 2016), giving rise to 15 currently recognized deer species in that continent (Burgin et al. 2020). Recent accounts

for Colombia have listed six to 11 species included in the genera *Mazama* Rafinesque, 1817, *Odocoileus* Rafinesque, 1832, and *Pudu* Gray, 1852 (Solari et al. 2013; Montenegro et al. 2019; Burgin et al. 2020). While recent genetic studies have elucidated the complex systematics of Neotropical deer (Duarte et al. 2008; Hassanin et al. 2012; Gutiérrez et al. 2015, 2017; Escobedo-Morales et al. 2016), information on the taxonomy and distribution of cervids in Colombia remain controversial.

The Central American Red Brocket Deer, *Mazama temama* (Kerr, 1792), distributed from Mexico to north-western Colombia (Bello-Gutiérrez et al. 2010), is restricted in its southern limit of its range to the Caribbean and Pacific regions in the departments of Chocó and Valle del Cauca (Montenegro et al. 2019). The presence of this species in the Colombian Andean region (Parque Nacional Chingaza, Cordillera Oriental) has been suggested based on genetic evidence from a specimen originally identified as *Odocoileus* (Hassanin et al. 2012) and later as *Mazama temama* (Escobedo-Morales et al. 2016; Gutiérrez et al. 2017) based on the high cytochrome-b sequence similarity with Mexican samples. Besides the efforts to clarify the distribution of *M. temama* in Colombia (Bello et al. 2016; Montenegro et al. 2019; Burgin et al. 2020), the distributional limits of this species in the country are unclear and based on limited evidence. Furthermore, there are no ecological studies of *M. temama* in Colombia (Montenegro et al. 2019), limiting national risk assessments. This also seems to be true for the global assessments which is Data Deficient due to taxonomic uncertainty (Bello et al. 2016). For those reasons, there is an increasing need for filling information gaps in the distribution of this and other deer species in Colombia, and the correct identification of specimens is crucial to document their genetic diversity in this part of their range. Here, we present a new record of *M. temama* that helps to clarify the presence of this species in northern South America.

Methods

We obtained incidental photographs of live specimens and a skull with adherent skin and soft tissue of one adult male found shot dead. The dead-collected specimen was deposited in the Museo de Historia Natural, Universidad de Caldas (MHN-UCa), Manizales, Caldas, Colombia. We took 14 linear measurements (Table 1) of the cranium and mandible following Gutiérrez et al. (2015), including: interorbital breadth (IB), frontal length (FL), intercondylar width (IW), zygomatic breadth (ZB), palatine-premaxillary length (PPL), basal length (BL), condylobasal length (CBL), greatest length of nasals (GLN), maxillary diastema-premaxillary length (MDPL), upper tooth row length (UTRL), occipital condyle-premolar length (COPL), lower tooth row length (LTRL), notch height (NH), and jaw length (JL), as well as antler length. Measurements were taken to the nearest 0.01 mm with digital calipers.

We also extracted DNA from muscle samples with the Wizard® Genomic DNA Purification kit (Promega Corporation) following the manufacturer's instructions. Amplification of the mitochondrial cytochrome-b gene (cyt-b) was performed using the primer pair LGL765F and LGL766R, targeting a ≈1140 bp (Bickham et al. 1995, 2004). The final amplification reaction volume was 30 µL, which contained 20.24 µL ultrapure water, 3 µL 10× buffer, 0.9 µL MgCl₂ (50 mM), 2.4 µL dNTP mix (10 mM), 0.36 µL of each primer (25 µM), 1.2 U of Taq DNA Polymerase, and 2.5 µL DNA (approximately 110 ng of DNA). The amplification was performed on a Techne TCPLUS thermocycler: initial denaturation of 3 min at 94 °C, followed by 35 cycles of 95 °C for 45 s of denaturing, 50 °C for 40 s of annealing, 72 °C for 45 s of extension, completing the reaction with a final extension cycle at 72 °C for 7 min. The PCR products were quantified by fluorometry using a Quantus Fluorometer™ (Promega®). PCR products were sent to Macrogen Inc. (South Korea) for

Table 1. Cranial measurements of the new record of *Mazama temama* from Colombia. The measurements of the Neotype of *M. americana* and of several specimens of *M. rufina* were taken from Cifuentes-Rincón et al. (2020) and Gutiérrez et al. (2015), respectively.

Measurement	<i>Mazama temama</i>	<i>Mazama americana</i>	<i>Mazama rufina</i>
	MHN-UCa-M 1859	neotype	
Sex	Male	Male	Males and females
	Colombia		Colombia–Venezuela
Condylobasal length (CBL)	183.90	211.15	145.81–154.80
Basal length (BL)	170.44	197.73	136.23–149.36
Zygomatic breadth (ZB)	85.43	101.86	64.49–76.65
Greatest length of nasals (GLN)	65.45	70.53	31.51–54.09
Upper tooth row length (UTRL)	60.35	65.73	43.51–53.12
Interorbital breadth (IB)	44.77		32.10–42.82
Frontal length (FL)	55.24		48.63–68.48
Intercondylar width (IW)	36.34		29.33–34.63
Palatine-premaxillary length (PPL)	89.03		61.35–75.45
Occipital condyle-premolar length (COPL)	126.69		99.26–115.12
Lower tooth row length (LTRL)	65.08		48.95–57.46
Notch height (NH)	47.30		30.32–38.80
Jaw length (JL)	153.84		113.20–136.56
Maxillary diastema-premaxillary length (MDPL)	61.14		

purification and DNA sequencing. The sequencing chromatogram was evaluated and edited with the software Geneious Prime 2020.2.4 (<https://www.geneious.com>; Drummond et al. 2009). We compared the edited 849 bp *cyt-b* sequence by performing independent searches with the Basic Alignment Search Tool (BLAST) (Altschul et al. 1990) to obtain overall similarity and downloaded sequences of closely related taxa available in GenBank (Table 2) to conduct a phylogenetic analysis. For all analyses, we used *Alces alces*, *Capreolus capreolus* Linnaeus, 1758, and *Hydropotes inermis* (Gilbert et al. 2006; Hassanin et al. 2012; Gutiérrez et al. 2017) as outgroup taxa (Table 2). We aligned sequences using default options of ClustalW (Thompson et al. 1997), included in the program MEGA X (Kumar et al. 2018). Genetic distances for *cyt-b* were estimated using the *p*-distance method. We selected the best-fitting models of sequence evolution, using the Akaike Information Criterion (AIC) calculated with ModelFinder (Kalyaanamoorthy et al. 2017) in PhyloSuite (Zhang et al. 2020). We conducted phylogenetic analyses using maximum likelihood (ML) and Bayesian inference (BI). ML was conducted with IQ-TREE (Nguyen et al. 2015) under the TIM2+I+G4+F model for 5000 ultrafast bootstraps (Minh et al. 2013), as well as Shimodaira–Hasegawa-like approximate likelihood-ratio test (SH-like aLRT) for branches with 1000 replicates (Guindon et al. 2010), all included in PhyloSuite platform (Zhang et al. 2020). The BI was conducted in MrBayes 3.2.6 (Ronquist et al. 2012) under the GTR+F+G4 model; four parallel runs and four Markov chains were run for 15,000,000 generations and 25% of sampled data were discarded as burn-in. Finally, we used FigTree v. 1.4.3 to visualize the phylogenetic trees (Rambaut 2007).

To explore how the inclusion of the new records from Colombia determines the predicted geographic range for the species, we developed a species distribution model on MaxEnt software (Phillips et al. 2006, 2020). We searched for presence data in the Global Biodiversity Information Facility (GBIF) database (GBIF 2021),

including both specimens and human observations as well as records from the literature. The resulting database was curated to remove dubious records and duplicated locations (96 unique presence records). We used the 19 WorldClim variables (Fick and Hijmans 2017) at 2.5 arc-minutes resolution and delimited a buffer area of three geographic grades to the polygon resulting of the convex hull of the presence data. MaxEnt models were performed using 70% of the presence data as training, with default settings and 10 replicates, and logistic output were converted as binary maps using the minimum training presence and summarized to show coincidence areas of the replicates. Models were evaluated with NicheToolsBox tool (<http://shiny.conabio.gob.mx:3838/nichetoolb2/>) to determine if predictions were effectively different from a random one (Peterson et al. 2008).

Results

Mazama temama (Kerr, 1792)

New records. COLOMBIA – **Department of Nariño** • Municipality of Consacá, “Vereda” Cariaco Bajo, buffer zone of the Santuario de Flora y Fauna Galeras; 01.1787°N, 077.4619°W; 1700 m alt.; 01.IX.2018; Luis G. Lasso, LGL 071 leg.; ♂ adult male, skull, forefeet, and fragments of the skin; GenBank: MW880928; MHN-UCa-M 1859 (Fig. 1A) • **Department of Nariño** • Municipality of Consacá, Vereda San Rafael, Santuario de Flora y Fauna Galeras; 01.1661°N, 077.4442°W; ~2000 m alt.; 01.III.2011; Carola Lara, leg.; ♀ female, photographs alive (Fig. 1B).

Identification. A slender deer, reddish brown on the back with more grayish brown on neck, head, and hind and forefeet. The back is slightly bent and the rump is visibly high compared to the shoulders (Bello–Gutiérrez et al. 2010). The forehead has a tuft of long hair with dark ends. The skull is broad. The antlers are short (65.87 mm) and slightly curved. Antler length in males is approximately 50–96 mm (Groves and Grubb 2011). Other sympatric

Table 2. GenBank accession numbers for the *cyt-b* gene sequences used in this study. Accession numbers of sequences generated in this study are indicated in boldface type; all others were previously published and downloaded from GenBank.

Taxon	Accession numbers
<i>Mazama temama</i>	MW880928 (MHN-UCa-M 1859 Nariño-Colombia)
<i>Mazama temama</i>	KP954716–KP954721; KC146956; KC146958; KY928661
<i>Mazama temana</i> (identified in GenBank as <i>Odocoileus virginianus</i>)	JN632673 (Cundinamarca-Colombia)
<i>Odocoileus virginianus</i>	KY928662; KY928668; JN632671
<i>Odocoileus hemionus</i> (Rafinesque, 1817)	FJ188751
<i>Odocoileus hemionus</i>	FJ188881
<i>Mazama bororo</i> Duarte, 1996	DQ789187
<i>Mazama nana</i> (Hensel, 1872)	DQ789227
<i>Mazama americana</i>	DQ789220; DQ789230
<i>Mazama rufina</i>	LT546656–LT546658; NC_020721; KR107035; KR107038–KR107040
<i>Mazama nemorivaga</i> (F. Cuvier, 1817)	MN792634; MN792635; KY928658
<i>Mazama gouazoubira</i> (G. Fischer, 1814)	NC_020720; KY928656
<i>Alces alces</i> (Linnaeus, 1758)	NC_020677
<i>Capreolus capreolus</i> Linnaeus, 1758	NC_020684
<i>Hydropotes inermis</i> (Swinhoe, 1870)	JN632649



Figure 1. **A.** Lateral view of the skull of an adult male *Mazama temama* (MHN-UCa-M 1859; condylobasal length: 183.9 mm), from Vereda Cariaco Bajo, Municipality of Consacá, Department of Nariño, Colombia. **B.** Photograph of a live *M. temama* individual taken from Galeras Flora and Fauna Sanctuary, Department of Nariño, Colombia. **C.** Adult male *Odocoileus* sp. from the Central Andes of Colombia; note the branched antlers. **D.** Adult male *Mazama rufina* from the Central Andes of Colombia (MHN-UCa-M 3345); note the darker coloration, the black coloration on rostrum, fore and hindfeet, and smaller size than *M. temama*.

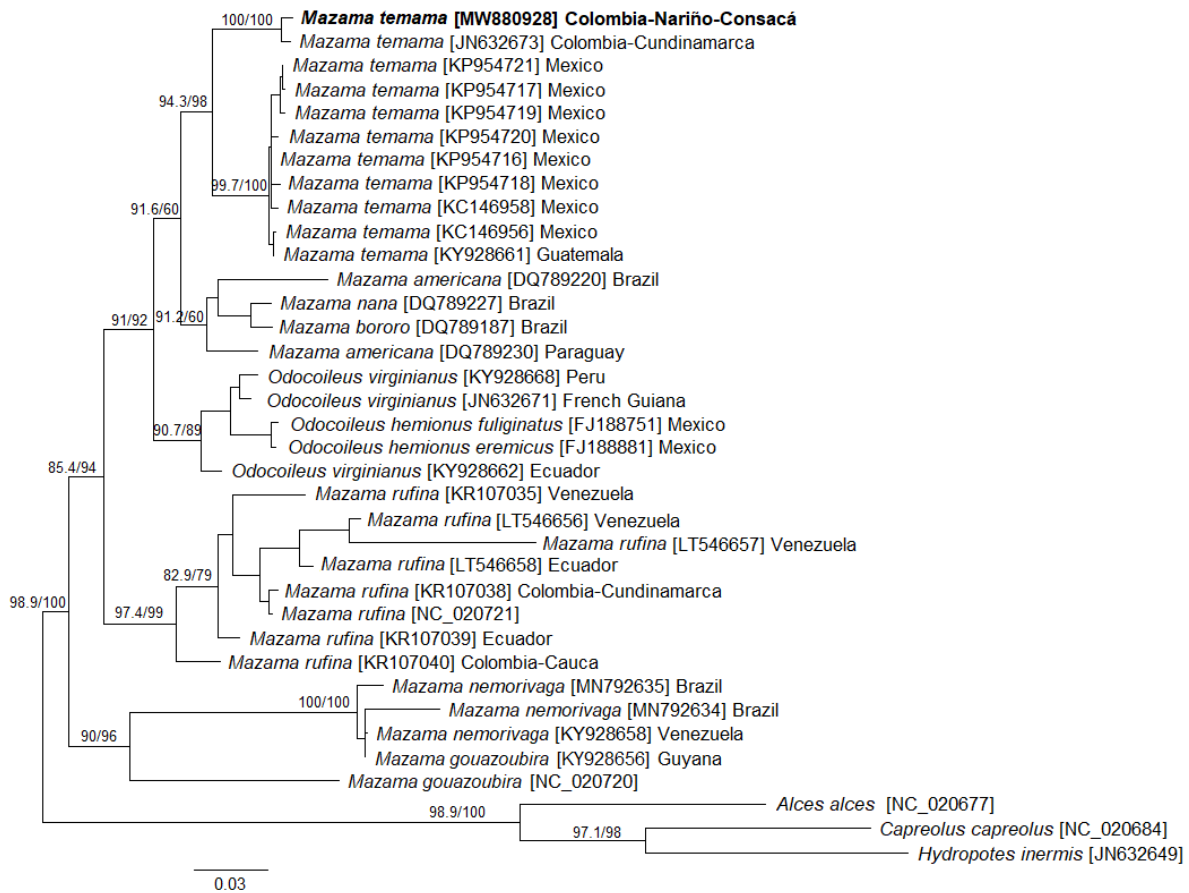


Figure 2. Maximum likelihood phylogenetic tree reconstruction based on a 849 bp fragment of the mitochondrial cyt-b gene of deer specimens using the TIM2+I+G4+F nucleotide substitution model. Values at nodes represent ultrafast bootstraps values and Shimodaira–Hasegawa–like approximate likelihood-ratio test (SH-like aLRT), respectively.

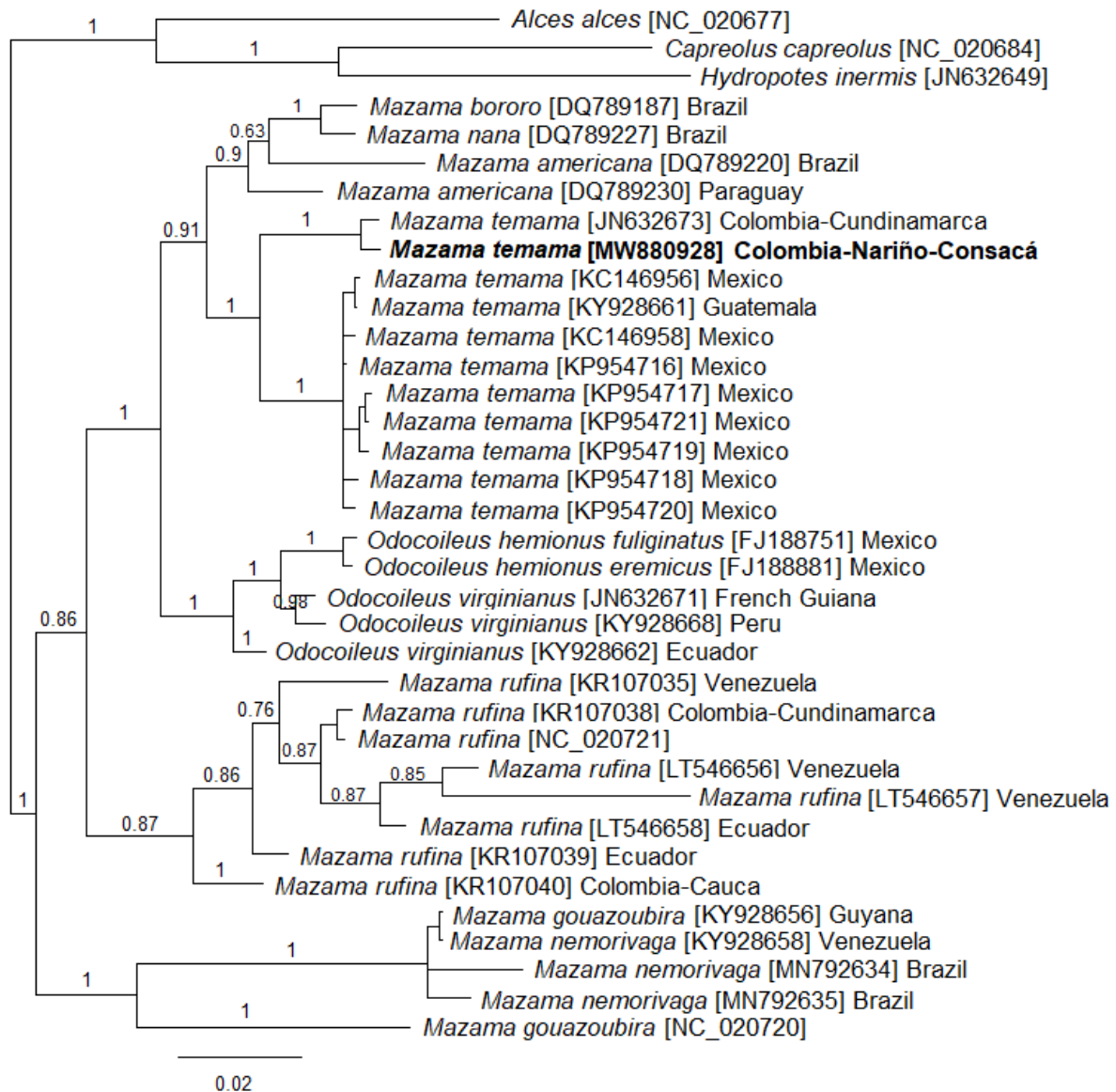


Figure 3. Phylogenetic tree based on an 849 bp fragment of the mitochondrial cyt-b gene of deer specimens, obtained by Bayesian inference (BI) using the GTR+F+G4 substitution model. Numbers above the nodes correspond to Bayesian posterior probabilities.

species from mid to highland elevations found in Colombia (Fig. 1C, D) are *Odocoileus* sp. which have branched antlers, and *Mazama rufina* (Pucheran, 1851) with smaller body size and skull (CBL: 145–159 mm) and has a narrower and substantially deeper lacrimal fossa (variable in *M. temama*), with darker fur on rostrum. Our specimen is also smaller in all cranial measurements than *M. americana* (Erxleben, 1777) (Cifuentes-Rincón et al. 2020), which has bigger body size (Table 1) and more reddish pelage.

The BLAST query recovered sequences from GenBank with similarity of 99.17% (accession number JN632673) and 95.36% (accession numbers KC146956, KC146958, KY928661). The origin of the samples was Colombia (JN632673, Department of Cundinamarca, but the locality is questionable), Mexico (KC146956, KC146958), and Guatemala (KY928661), all of them identified as *M. temama* (Escobedo-Morales et al. 2016;

Gutiérrez et al. 2017). The genetic distances between Colombian sequences in respect to Mexican and Guatemalan sequences are 4.6 and 5.4 %, respectively (Table 3; Figs. 2, 3).

Our species distribution models showed an average AUC ratio of 1.7 and $p < 0.001$, suggesting a predictive power far from random. The majority of them (up to seven of 10 replicates) predict potential distribution areas within Colombia through the western slope of the Cordillera Occidental. The new records presented here belong to an area where average matches within one geographic degree ratio showed an approximate value of four. Over-prediction areas seem to predict the occurrence of this species beyond the eastern slope of the Andes (Fig. 4).

Discussion

Our *Mazama temama* records extend the southernmost

Table 3. Average intraspecific (on the diagonal) and interspecific (below the -) distances based on *p*-distances for *cyt-b* sequences.

Species	1	2	3	4	5	6	7	8	9	10	11	12	13
1 <i>Mazama temama</i> (accession MW880928; Nariño, Colombia)	-												
2 <i>Mazama temama</i> identified as <i>Odocoileus virginianus</i> (accession JN632673; Cundinamarca, Colombia)	0.008	-											
3 <i>Odocoileus virginianus</i>	0.065-0.074	0.059-0.068	0.011-0.026										
4 <i>Odocoileus h. fuliginatus</i>	0.071	0.068	0.025-0.038	-									
5 <i>Odocoileus h. eremicus</i>	0.075	0.071	0.024-0.037	0.005	-								
6 <i>Mazama temama</i>	0.046-0.052	0.046-0.054	0.056-0.080	0.070-0.075	0.073-0.078	0.001-0.010							
7 <i>Mazama bororo</i>	0.067	0.067	0.054-0.072	0.064	0.069	0.053-0.056	-						
8 <i>Mazama nana</i>	0.068	0.066	0.055-0.071	0.068	0.073	0.051-0.057	0.016	-					
9 <i>Mazama americana</i>	0.062-0.081	0.063-0.081	0.050-0.074	0.062-0.073	0.064-0.076	0.050-0.073	0.039-0.055	0.038-0.054	0.052				
10 <i>Mazama rufina</i>	0.056-0.118	0.045-0.116	0.052-0.118	0.071-0.123	0.074-0.125	0.057-0.123	0.067-0.116	0.065-0.112	0.063-0.118	0.005-0.103			
11 <i>Mazama nemorivaga</i>	0.117-0.130	0.119-0.133	0.104-0.133	0.123-0.133	0.124-0.133	0.102-0.122	0.098-0.113	0.094-0.116	0.090-0.112	0.063-0.123	0.012-0.025		
12 <i>Mazama gouazoubira</i>	0.118-0.130	0.113-0.120	0.102-0.119	0.117-0.123	0.120-0.124	0.109-0.121	0.113-0.115	0.116	0.082-0.114	0.081-0.123	0.001-0.107	0.107	
13 <i>Alces alces</i>	0.123	0.124	0.108-0.122	0.132	0.133	0.122-0.133	0.124	0.123	0.115-0.126	0.106-0.130	0.122-0.132	0.125-0.132	-

geographic range of this species by approximately 300 km from the closest localities in Colombia (Montenegro et al. 2019). Furthermore, our species distribution models suggest the likely presence of this species in Ecuador (Fig. 4). The *cyt-b* sequence generated here also confirms the presence of the species in Colombia (Figs. 2, 3), as suggested in previous studies (Hassanin et al. 2012; Gutiérrez et al. 2017). In addition, this is only the second *cyt-b* sequence generated from any *M. temama* specimen from South America and the only one with a voucher specimen properly deposited in a museum collection (MHN-UCa-M 1859). The previous *cyt-b* record from Colombia did not have a voucher specimen and was misidentified as belonging to *Odocoileus virginianus* (Zimmermann, 1780) (Hassanin et al. 2012), but our phylogenetic reconstructions cast no doubt on its assignment to *M. temama* as suggested by Escobedo-Morales et al. (2016) and Gutiérrez et al. (2017). The morphometric data obtained from our voucher specimen also confirms this taxonomic designation, as the range of variation of the cranial measurements also falls within the range of specimens from Central America available in the literature (Allen 1916; Bello-Gutiérrez et al. 2010).

Our records also confirm the presence of *M. temama* in the Department of Nariño where other cervids such as *Mazama americana* have been previously documented (Ramírez-Chaves et al. 2010). However, *M. americana* has been recently restricted to Brazil and French Guiana (Cifuentes-Rincón et al. 2020). The distribution limits of *M. temama* in Colombia are still preliminary and require additional records. Our predictive models suggest that

climatic conditions in the Nariño region could be a marginal habitat for the species. Additionally, we consider this contribution as a first step towards the revision of the taxonomy, systematics, and biogeography of cervids of Colombia. Finally, we also suggest the need for new integrative assessments of the diversity of cervids in Colombia to clarify the diversity and threats that this charismatic group of mammals face in this country.

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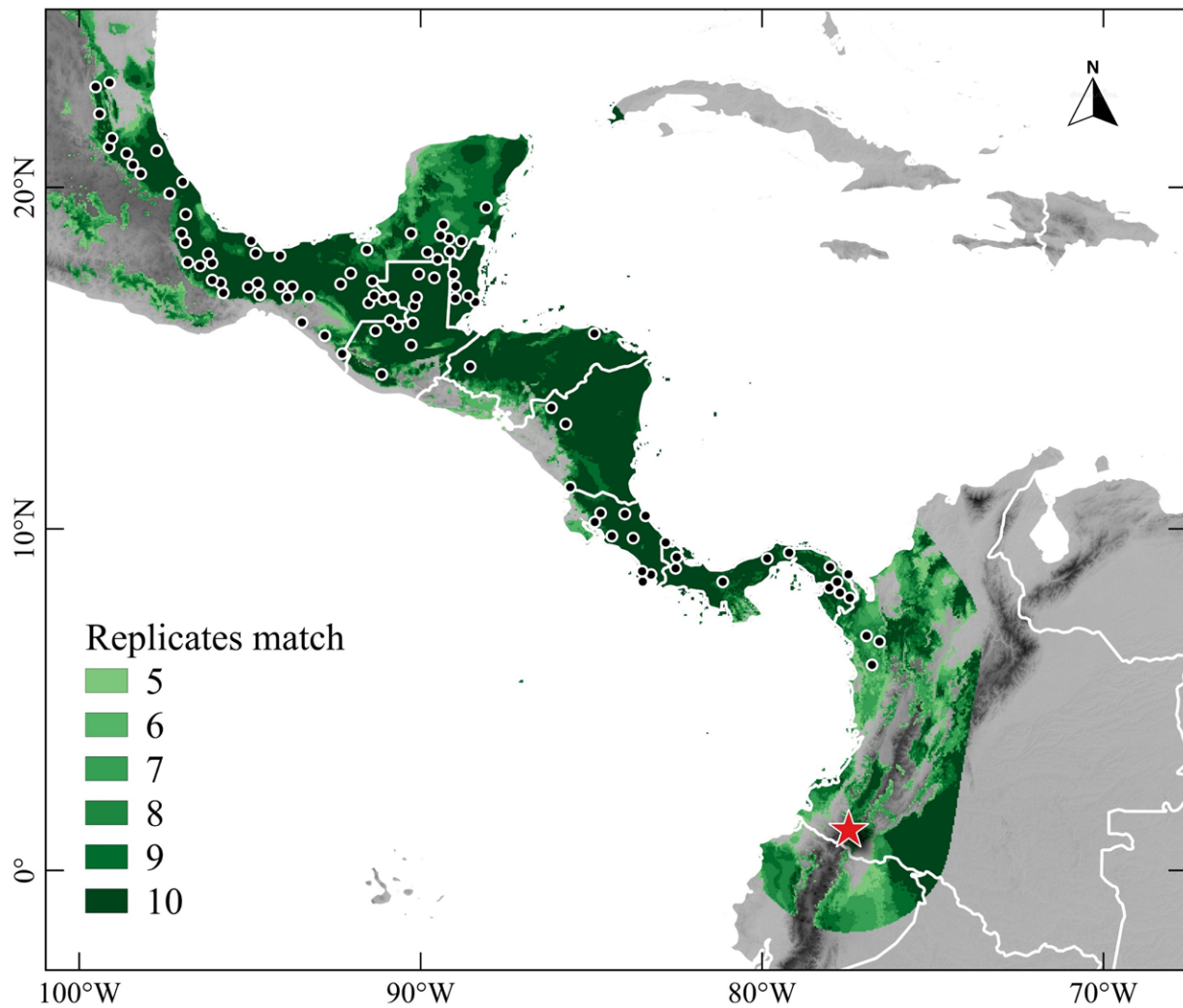


Figure 4. MaxEnt species distribution model of *Mazama temama*. New records in Colombia (red star) are based on one voucher specimen (MHN-UCa-M 1859) and photographs in this study. Additional localities are taken from literature and GBIF.

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