Supplementary Materials and Methods

Sample sources

Four samples of *M. gongshanensis*, including one antler, two skulls, and one skin, were obtained from northern Myanmar between 2016 and 2018, with permission (1567/XTBG/2017) from the Forest Research Institute, Forest Department Ministry of Environmental Conservation and Forestry of Myanmar. All samples were stored in 95% ethanol (Supplementary Table S2). Total genomic DNA was extracted using a TIANamp Genomic DNA Kit (Tiangen, Beijing, China). Specimens and DNA were deposited in the Southeast Asia Biodiversity Research Institute, Chinese Academy of Sciences, Myanmar Lab (Yezin, Nay Pyi Taw, Myanmar). Based on previous studies (Li et al., 2017; Martins et al., 2017; Zhang et al., 2004), 14 primers were designed to amplify mitogenomes of three samples. Primer synthesis and sequencing were conducted by Beijing Tianyi Huiyuan Bioscience and Technology Incorporation (Beijing, China). In addition, the mitochondrial gene cyt *b* of the fourth sample was amplified (Supplementary Table S2).

Data analysis

Sequences were edited using DNASTAR v.5.0 and aligned (mitogenomes and cyt *b* gene fragments in the same file) using default parameters in MAFFT v.7.245 (Rozewicki et al., 2019). Mitogenome sequences were assembled and annotated using software Geneious v 2019.1.1 (Kearse et al., 2012). Locations of genes were annotated by comparison with genes from *M. crinifrons* (NC_004577). Identical haplotypes were collapsed using DNASP v.5.10 (Rozas et al., 2017) by removing

missing/gap sites and invariant sites from the dataset and the median-joining network was reconstructed using Network v.4.6.1.4 (Leigh & Bryant, 2015) based on cyt *b* gene fragments for *M. gongshanensis*, *M. crinifrons*, and *M. feae*.

Phylogenies were reconstructed using two different methods: maximum-likelihood (ML) and Bayesian inference (BI). To assess the phylogenetic relationships of *Muntiacus*, complete and partial mitochondrial sequences of cyt *b* were downloaded from GenBank, and mitogenome sequences of *Tragulus kanchil* (JN632709) and *Elaphodus cephalophus* (DQ873526) were used as the outgroup according to Li et al. (2017). The best-fit model of nucleotide substitution for each marker was selected prior to analysis using the Akaike Information Criterion, implemented in the model selected by JModelTest 2 (Darriba et al., 2012). HKY+G was selected for mitochondrial DNA (mtDNA) sequences. Bayesian analyses were run in MrBayes v.3.2.2 (Ronquist et al., 2012) and consisted of two independent runs of 10 million generations, sampling trees every 100 generations under default priors. The average standard deviation of split frequencies between runs was always <0.001, indicating convergence. The first 25% of sampled trees were discarded as burn-in and the remaining topologies were combined to generate a 50% majority rule consensus tree. ML analysis was conducted using RAxML v.8.2.10 (Stamatakis, 2014) on the CIPRES Science Gateway (http://www.phylo.org). Rate heterogeneity and proportion of invariant sites were included as model parameters, with other options matching default settings. Support values for nodes and clades were estimated from 1 000 bootstrap replicates.

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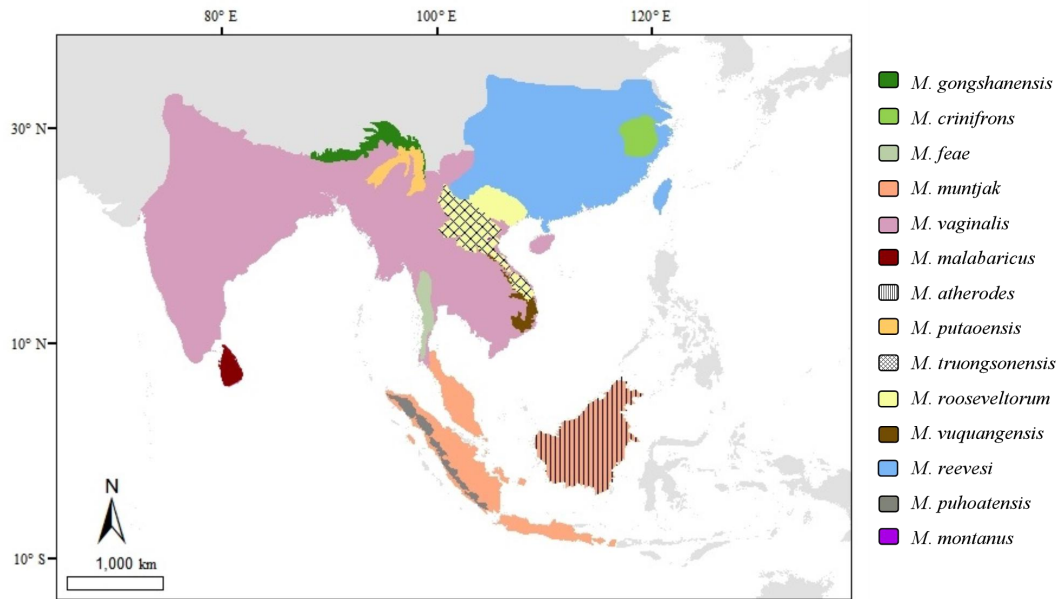
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SUPPLEMENTARY FIGURE LEGENDS

Supplementary **Figure S1** Currently accepted distribution of 14 muntjac species (IUCN). Map shows locations of *Muntiacus* species (adapted from: www.maps.iucnredlist.org).

Supplementary Table S1 Comparison of number of accepted *Muntiacus* species among four recent publications

Species name	Ma et al. (1986)	Groves & Grubb (2011)	IUCN (2018)	This study	Red List Category
M. muntjak (Zimmermann, 1780)	*M. muntjak*	*M. muntjak*	*M. muntjak*	*M. muntjak*	LC
M. vaginalis (Boddaert, 1785)		*M. vaginalis*	*M. vaginalis*	*M. vaginalis*	LC
M. aureus (Hamilton Smith, 1826)		*M. aureus*			
M. nigripes (G. M. Allen, 1930)		*M. nigripes*			
M. malabaricus (Lydekker, 1915)		*M. malabaricus*		*M. malabaricus*	
M. crinifrons (Sclate, 1885)	*M. crinifrons*	*M. crinifrons*	*M. crinifrons*	*M. crinifrons*	VU
M. gongshanensis (Ma et al., 1990)		*M. gongshanensis*	*M. gongshanensis*	*M. gongshanensis*	DD
M. feae (Thomas & Doria, 1889)	*M. feae*	*M. feae*	*M. feae*	*M. feae*	DD
M. vuquangensis (Tuoc et al., 1994)		*M. vuquangensis*	*M. vuquangensis*	*M. vuquangensis*	CR

M. rooseveltorum (Osgood, 1932)	*M. rooseveltorum*	*M. rooseveltorum*	*M. rooseveltorum*	*M. rooseveltorum*	DD
M. putaoensis (Amato et al., 1999)		*M. putaoensis*	*M. putaoensis*	*M. putaoensis*	DD
M. truongsonensis Giao et al., 1998)		*M. truongsonensis*	*M. truongsonensis*	*M. truongsonensis*	DD
M. reevesi (Ogilby, 1839)	*M. reevesi*	*M. reevesi*	*M. reevesi*	*M. reevesi*	LC
M. atherodes (Groves & Grubb, 1982)		*M. atherodes*	*M. atherodes*	*M. atherodes*	NT
M. montanus (Robinson & Kloss,1918)		*M. montanus*	*M. montanus*		DD
M. puhoatensis (Binh Chau, 1997)		*M. puhoatensis*	*M. puhoatensis*		DD
Total	5	16	13	12	

Number of recognized species ranges from 5 to 16. Red List category: LC, least concern; VU, vulnerable; DD, data deficient; CR, critically endangered; NT, near threatened.

Supplementary Table S2 Detailed information on mtDNA sequences used in this study

Species name	GenBank accession No.		Source material	Latitude & longitude	Haplotypes	References
	Mitogenome	cyt *b*				
M. gongshanensis	MW596243		Ziradam, Putao	27° 34' 43.67" N / 97° 5' 53.89" E	10 M	This study
M. gongshanensis	MW596244		Ziradam, Putao	27° 30' 43.67" N / 97° 24' 53.89" E	9 M	This study
M. gongshanensis		MW596246	Putao	27° 20' 31.20 "N / 97° 24' 3.60" E	11 I/M	This study
M. gongshanensis	MW596245		Hkakabo Razi	28° 19' 59.43" N / 97° 37' 19.12" E	7 M/C	This study
M. gongshanensis	MK882935		Gongshan, Yunnan China.		7 M/C	Zhang et al., 2019
M. gongshanensis		DQ445732			13 C	Chen et al., 2008
M. gongshanensis		DQ445733	Tibet, China,		4 C	Chen et al., 2008
M. gongshanensis		DQ445734			3 C	Chen et al., 2008
M. gongshanensis		DQ445735			12 C	Chen et al., 2008
M. gongshanensis		EF523661			5 I	James et al., unpublished
M. gongshanensis		EF523662	Namdapha, China		6 I	James et al., unpublished
M. gongshanensis		EF523663			8 I	James et al., unpublished
M. gongshanensis		EF523664			11 I/M	James et al., unpublished

Species	Accession	Location	Count	Reference
M. crinifrons	NC_004577		2	Li et al., unpublished
M. feae	MG857663		1	
M. feae	MG857664	Khao Kheow Open Zoo, Chon Buri, Thailand.	1	Srisodsuk et al., 2018
M. feae	NC_041100		1	
M. muntjak	KY052143			Martins et al., 2017
M. muntjak	KY052150			Martins et al., 2017
M. muntjak	KY052144			Martins et al., 2017
M. muntjak	KY052155			Martins et al., 2017
M. muntjak	KY052156			
M. muntjak	KY117560			Martins et al., 2017
M. muntjak	KY052141			Martins et al., 2017
M. vaginali	KY052084			Martins et al., 2017
M. vaginali	KY052088			Martins et al., 2017
M. vaginali	KY052104			Martins et al., 2017
M. vaginali	KY052105			Martins et al., 2017
M. vaginali	KY052114			Martins et al., 2017
M. vaginali	MH547032			Singh et al., 2018
M. vaginali	MK050505			Singh et al., 2018
M. vaginali	MK050506			Singh et al., 2018
M. vaginali	MK050507			Singh et al., 2018
M. malabaricus	KY052116			Martins et al., 2017

M. malabaricus	KY052117		Martins et al., 2017
M. atherodes	KY117559		Mohd et al., 2017
M. putaoensis	NC036430		Li et al., 2017
M. putaoensis		MF737181	Li et al., 2017
M. rooseveltorum		KJ425279	Le et al., 2014
M. truongsonensis		KJ425276	Le et al., 2014
M. vuquangensis	NC_016920		Alexandre et al., 2012
M. vuquangensis		AF042720	Giao et al., 1998
M. vuquangensis		KJ425275	Le et al., 2014
M. vuquangensis		KJ425283	Le et al., 2014
M. vuquangensis		KJ425284	Le et al., 2014
M. vuquangensis		KJ425285	Le et al., 2014
M. reevesi	KY117561		Mohdet al., unpublished
M. reevesi	NC_004069		
M. reevesi	NC_008491		Wang et al., unpublished
M. reevesi		AF042719	Giao et al., 1998
Tragulus kanchil	NC_020753		Hassanin et al., 2011
Elaphodus cephalophus	DQ873526		Alexandre et al., 2012