Revalidation of *Manis aurita*, based on integrative morphological and genomic evidence

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ABSTRACT

Pangolins face severe conservation threats globally, making accurate taxonomy essential for their protection. Previous genomic research on the Chinese pangolin (*M. pentadactyla*) identified two deeply divergent lineages (MPA and MPB), suggesting underestimated species diversity. The recent description of *M. indoburmanica* for the MPB lineage, however, did not assess its relationship with historical names, particularly the subspecies *M. p. aurita*, leaving the group's taxonomic status uncertain. To resolve this issue, we employed an integrative framework, analyzing genomic and morphological data from museum specimens to clarify the validity and relationship of these taxa. Our results demonstrate that the MPB lineage, which encompasses *M. indoburmanica*, is geographically restricted to the southern Himalayas, a range congruent with the type locality of *M. aurita* and distinct from other *M. pentadactyla* populations. Genomic analyses confirm this Himalayan lineage diverged ~1.2 Ma and has remained largely isolated since, with only minimal gene flow. Furthermore, morphometric analyses of both cranial and external features, including the *aurita* holotype, reveal consistent and significant differentiation between the Himalayan lineage and *M. pentadactyla sensu stricto*. Collectively, this congruent evidence unequivocally supports the revalidation of the Himalayan pangolin as a distinct species, *Manis aurita* Hodgson, 1836, representing the fifth extant species in the genus. This taxonomic revision provides a critical foundation for species-specific conservation strategies and enhances wildlife forensic capabilities by creating a robust genetic baseline to trace the provenance of illegally traded products.

Keywords: *Manis aurita*, Integrative taxonomy, Phylogenomics, Morphometrics, Conservation genetics

INTRODUCTION

Pangolins (Order Pholidota) are unique mammals characterized by their keratinized scales, an extraordinary trait among mammals (Challender et al., 2019). These animals face severe threats including habitat loss and extensive illegal trade, which has resulted in dramatic population declines (Challender et al., 2020b; Zhang et al., 2020; Zhang et al., 2022). Consequently, all pangolin species are listed under Appendix I of the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) and are recognized as Evolutionarily Distinct and Globally Endangered (EDGE) species (Zoological Society of London, 2014). Accurate species identification, clarification of species distribution, and estimation of population sizes and genetic load are essential for effective conservation efforts.

Until recently, eight extant pangolin species were recognized: four in Africa and four in Asia (Gaubert et al., 2018). All Asian species belong to the genus *Manis*, including Chinese pangolin (*M. pentadactyla*), Indian pangolin (*M. crassicaudata*), Sunda pangolin (*M. javanica*), and Philippine pangolin (*M. culionensis*). Recent genomic studies revealed cryptic genetic and taxonomic diversity within Asian pangolins. For instance, genome sequencing of confiscated scales uncovered a cryptic lineage, provisionally named “mysteria”, for which no voucher specimens or precise locality data exist (Gu et al., 2023). Moreover, analyses of broad sampling within *M. pentadactyla* have revealed distinct clades, indicating the existence of an undescribed species.

The Chinese pangolin is distributed across a broad range, extending from Nepal in the west to the eastern coast of China, with insular populations on Hainan and Taiwan islands. Latitudinally, its range extends from central China southward to Southeast Asia (Challender et al., 2020a). This broad distribution is divided by geographic barriers, such as the mountains of southwestern

China and southward-flowing river systems, which likely drive genetic divergence among geographic populations (He & Jiang, 2014; Koju et al., 2017). Accordingly, Hu et al. (2020a) identified two major clades within *M. pentadactyla*, namely, MPA and MPB. While recent studies have found additional subclades closely related to MPA in China and Southeast Asia (Wang et al., 2022; Wei et al., 2024), MPB remains the most genetically divergent lineage, and its geographic origin has been enigmatic. Initially, the MPB clade was known almost exclusively from specimens confiscated along the Sino-Myanmar border, suggesting a Myanmar origin. This inference was tentative, as the area is a major wildlife trafficking hub (Nijman et al., 2016; Zhang et al., 2017; Bashyal et al., 2021; Gomez et al., 2023; Koju & Tamang, 2025). However, recent studies found occurrences of MPB in Nepal, South Tibet and northeastern India (Koju, 2018; Shrestha et al., 2020; Hogan et al., 2025; Wangmo et al., 2025).

Historically, three subspecies of *M. pentadactyla* were recognized: the nominate subspecies *M. p. pentadactyla* Linnaeus, 1758 described based on specimens from Taiwan (Corbet & Hill, 1992); *M. p. pusilla* Allen, 1906 from the Hainan Island; and *M. p. aurita* Hodgson, 1836 from the central Nepal (Wilson & Mittermeier, 2018). While the former two have been subject to extensive genetic studies (Gaudin et al., 2009; Hu et al., 2020a; Wang et al., 2022; Heighton et al., 2023; Wei et al., 2024), and their evolutionary relationships as well as distribution in China and SE Asia has been confirmed (Hu et al., 2020a; Wei et al., 2024), the taxonomy and evolutionary history of *M. p. aurita* remains unclear.

Recently, Wangmo et al. (2025) describe a new species, *Manis indoburmanica*, from South Tibet, which highlights several challenges in modern taxonomy. The recognition of this new species is based solely on the mitochondrial genome, a data source susceptible to introgression, incomplete lineage sorting, and maternal inheritance bias (Funk & Omland, 2003; Ballard &

Whitlock, 2004; Toews & Brelsford, 2012). Furthermore, the work lacks a comprehensive morphological comparison with *M. pentadactyla*, thus failing to establish a clear morphological boundary for *M. indoburmanica*. Critically, as noted by Zijlstra (2025), the authors did not evaluate whether their samples correspond to existing historical names like *M. p. aurita* (Hodgson, 1836) or *M. assamensis* (Fitzinger, 1872), leaving the novelty of the taxon in question. Such challenges underscore the necessity of integrative taxonomic approaches that incorporate genome-wide data, robust morphological comparisons with both *M. pentadactyla* and *M. p. aurita* (Padial et al., 2010; Schlick-Steiner et al., 2010; Fujita et al., 2012).

To resolve this taxonomic uncertainty, we employed an integrative taxonomic framework combining genomic and morphological evidence. Our genomic analyses incorporated topotypical specimens of *M. p. aurita*, while our morphological comparisons included an examination of the external characteristics of its type specimen. The objective of this study was to evaluate whether pangolins from South Asia correspond to the subspecies *aurita* and, if so, whether their degree of divergence supports elevation to full species status. Our analyses reveal clear and pronounced differentiation from *M. pentadactyla* across both genetic and morphological datasets, providing robust support for recognizing this lineage as the distinct species *Manis aurita* Hodgson, 1836.

MATERIAL AND METHODS

Taxon sampling and sequencing

DNA was extracted from tissue samples (n=18) and purified using the Dneasy blood and tissue kit (Qiagen). Genomic DNA was sheared to ~350 bp fragments using a Covaris LE220R-plus system (Covaris, USA), followed by end-repair, A-tailing, and adapter ligation. Libraries were amplified by PCR, purified with AMPure XP beads.

Destructive sampling was conducted using skin specimens deposited in the National Museum of Natural History, the Smithsonian Institution (USNM), Field Museum of Natural History (FMNH); American Museum of Natural History (AMNH) and University of Michigan, Museum of Zoology (UMMZ) in the United States. Sterile practices were employed with routine bleaching, instrument sterilization, and changing of PPE to prevent any cross contamination between specimens. Samples of 25 mg of material were placed in sterile cryovials or 1.5mL tubes and transferred to a dedicated Historic DNA processing facility at the Smithsonian Institution's Museum Support Center where DNA extraction was performed via Qiagen MinElute or Investigator kits following the manufacturer's protocol. Single-stranded library preparation was performed with the SRSLY Pico Plus Kit (Claret Biosystems®) utilizing half reactions. Libraries had dual indexed iTru style adapters ligated to each sample and amplified for 18 cycles of PCR. Following amplification, samples were visualized on a High-Sensitivity Tape Station (Agilent), and pooled in equimolar ratios for sequencing.

Sequencing was performed on an Illumina NovaSeq X platform to generate 150 bp paired-end (PE150) reads. Raw FASTQ reads were processed with fastp v0.24.0 (Danecek et al., 2021) to remove adapter contamination and poly-G tails, trimming bases with Phred score ≤ 5. Reads containing > 10 % ambiguous bases or > 50 % low-quality bases were discarded. We supplemented our dataset with 48 available genome re-sequencing data including 24 *M. pentadactyla*, 19 *M. javanica*, 2 *M. crassicaudata*, 1 *Phataginus tricuspis*, and 1 *Smutsia gigantea* (**Table S1**).

Mitochondrial assembly and phylogenetic analyses

Mitochondrial genomes were assembled from 64 raw sequencing datasets, including data from 30 newly sequenced individuals and 34 previously published genomes of various pangolin

species. For these datasets, clean reads were processed for *de novo* assembly and annotation in MITOZ v3.6 (Meng et al., 2019), which employed Megahit with k-mer values of 21, 33, and 55. This final set of assembled mitogenomes was then augmented with five additional mitogenomes obtained from GenBank (**Table S2**). We aligned mitogenomes using MAFFT v7.5 (Katoh & Standley, 2013), and trimmed poorly aligned regions using Gblocks. We retained 12S, 16S rRNA, and 12 coding genes on the heavy chain for phylogenetic analyses. We also downloaded available mitochondrial 18 *CYTB* and 12 *COI* genes identified as *M. pentadactyla* from GenBank. We used IQ-TREE v2.1.3 to estimate the best-scoring Maximum-likelihood (ML) trees. ModelFinder was used to automatically determine the optimal partitioning scheme and substitution models under the Bayesian Information Criterion (–m MFP+MERGE). Node support was evaluated with 1,000 ultrafast bootstrap replicates.

Genome assembly and phylogenetic analyses

We aligned clean data to a *M. pentadactyla* reference genome (GCF_030020395.1) using BWA v0.7.17. The resulting SAM files were converted to coordinate-sorted BAMs and indexed with SAMtools v1.10 (Li et al., 2009). Duplicates were identified and flagged using MarkDuplicates tool of GATK v.4.6 (McKenna et al., 2010). Local realignment around indels was then performed using GATK's IndelRealigner to reduce false-positive variant calls. Per-sample gVCFs were generated with GATK's HaplotypeCaller and merged via CombineGVCFs. SNP calling was then executed with GenotypeGVCFs and SelectVariants to produce multisample VCF and isolate high-confidence SNP calls, respectively. We filtered SNP calls using GATK's VariantFiltration module with thresholds: QUAL < 30.0, QD < 2.0, MQ < 40.0, FS > 60.0, SOR > 3.0, MQRankSum < –12.5, ReadPosRankSum < –8.0, and SB ≥ –1.0. We applied VCFtools

v0.1.16 to remove SNPs with minor allele frequency < 2 % or depth outside the 2.5–97.5 percentile of the depth distribution (Danecek et al., 2011).

Phylogenetic relationships were inferred using three datasets: high-quality single nucleotide polymorphisms (SNPs) for autosomal and sex chromosomes as well as single-copy orthologous genes. For the SNP-based analyses, autosomal and sex chromosome SNP data were separately extracted from the filtered, high-quality multi-sample VCF. These datasets were converted to PHYLIP format using vcf2phylip v2.8. ML trees were constructed for both datasets using IQ-TREE v2.1.4 as mentioned above. For the ortholog-based analysis, we first identified 23,752 single-copy orthologs using OrthoFinder v2.5.4 (Emms & Kelly, 2015). These orthologs underwent stringent filtering based on GC content, sequence variability, proportion of missing data, and ambiguous bases, resulting in 7,852 high-quality loci. Each loci was individually aligned and a concatenated ML tree was constructed using IQ-TREE as mentioned above.

Genetic structuring analyses

To investigate population genetic structure, we utilized linkage-disequilibrium (LD)–pruned autosomal SNPs. LD pruning was performed in PLINK v1.90b6.21 using the –indep-pairwise 50 5 0.2 parameters (Purcell et al., 2007). We then performed PCA on mean-imputed genotypes in PLINK to extract the top ten principal components. To assess the statistical significance of the principal components, we applied the Tracy-Widom test implemented in EIGENSOFT v8.0.0 (Patterson et al., 2006). We applied PCA to all *Manis* samples and to *M. pentadactyla* sensu lato (which encompasses individuals later identified as *M. aurita*). To infer individual ancestry proportions, we ran ADMIXTURE v1.3.0 on the *M. pentadactyla* s.l. samples. We evaluated models for K (number of ancestral populations) from 1 to 10, and selected the optimal K to minimize cross-validation error (Alexander et al., 2009).

Molecular dating and population genetic analyses

Divergence times were estimated using *BEAST3 model (Douglas et al., 2022) as implemented in BEAST v2.7.7 (Bouckaert et al., 2019). First, we identified the 2,000 most genetically divergent loci from an initial pool of 7,852 filtered orthologs. These loci were then assessed for their conformity to a strict molecular clock using SortaDate v2.0 (Smith et al., 2018). The 200 orthologs that best fit the strict clock model were subsequently used for the divergence time estimation. The Bayesian inference employed a Birth–Death tree prior, a strict molecular clock, and the HKY+Γ substitution model. We employed two secondary calibrations derived from the molecular dating estimates of Gu et al. (2023). The analysis was constrained by setting priors on i) the crown-group pangolin divergence, set to 33.19 million years ago (Ma) (95% CI: 29.8–30.3 Ma), and ii) the divergence of Asian pangolins, set to 16.9 Ma (95% CI: 12.9–22.3 Ma). The Markov chain Monte Carlo (MCMC) analysis was run for 200 million generations. Convergence and parameter mixing were assessed in Tracer v1.7.2 (Rambaut et al., 2017), ensuring all key parameters achieved effective sample sizes (ESS) > 200.

Historical population dynamics were reconstructed using the Pairwise Sequentially Markovian Coalescent (PSMC) model (Li & Durbin, 2011). According to the estimated divergence time between *M. pentadactyla* and *M. aurita* (see Results), we estimated the mutation rate per generation assuming an average generation time of 7 years (IUCN SSC Pangolin Specialist Group, 2018). The analysis was run with the parameters -N25 -t15 -r5 -p "4+25*2+4+6", using the Manis *pentadactyla* genome (Hu et al., 2020a) as the reference for mapping. To assess the variability in demographic inferences, 100 bootstrap replicates were performed.

Levels of inbreeding were quantified by calculating the average inbreeding coefficient (FROH) for each individual. Long runs of homozygosity (ROH) were identified using PLINK v2.0

(Purcell et al., 2007) with the parameters --homozyg --homozyg-window-snp 20 --homozyg-kb 100. Individual FROH values were then calculated as the proportion of the autosomal genome covered by ROH, relative to the total autosomal SNP coverage, following McQuillan et al. (2008).

Geneflow analyses

To infer the direction and magnitude of historical gene flow among *Manis* species, we analyzed a high-quality SNP dataset from 52 samples representing the four *Manis* species using Dsuite v0.5 (Malinsky et al., 2021) and TreeMix v1.13 (Pickrell & Pritchard, 2012). We first filtered the SNP dataset to retain sites with ≤20% missing data using VCFtools (--max-missing 0.8). To quantify admixture, we used the Dtrios program in Dsuite to calculate D-statistics and f4-ratio statistics for all relevant population trios. *P. tricuspis* and *S. gigantea* were used as outgroups. Results were visualized with the dtools.py script. To model population splits and migration events, the filtered SNP data was first pruned for linkage disequilibrium (PLINK; --indep-pairwise 50 5 0.6), and the output was converted to TreeMix format using plink2treemix.py. We then ran TreeMix, exploring models with 0 to 5 migration edges (five replicates each). The optimal model was selected by evaluating the explained variance and residual plot fits. The resulting population graph was visualized using the R script plotting_funcs.R provided with TreeMix.

We used FastSimCoal v2.8 (Excoffier et al., 2021) to test potential gene flow between *M. pentadactyla* (MP) and *M. aurita* (MA). First, we used VCF file through easySFS to generated folded observed joint site frequency spectrum (JSFS). We constructed four demographic models to test gene flow scenarios: (1) early gene flow (range from 120,000 to 130,000 generations); (2)

recent gene flow (range from 1,000 to 20,000 generations); (3) continuous gene flow; and (4) no gene flow. For each tested demographic model, we performed 100 independent runs using 100,000 simulations, 40 expectation–maximization cycles, and a broad search range for parameters to determine the run with the best parameter estimates and maximum likelihood. Model comparisons were performed using the Akaike Information Criterion (AIC) to identify the model that best explains the observed data.

Genomic Island of Differentiation

To identify genomic regions under divergent selection, we scanned the genomes of *M. pentadactyla* and *M. aurita*. We used Pixy v2.0 to calculate nucleotide diversity (π), fixation index (F_{ST}), and absolute genetic differentiation (d_{XY}) across 20 kb windows (Korunes & Samuk, 2021). Candidate genomic islands of divergence were defined as outlier windows concurrently in the top 5th percentile for both F_{ST} and d_{XY}. We extracted all genes within these outlier regions. Genes annotated only with LOC identifiers were annotated based on their high-confidence human orthologs, identified via BLASTP (Altschul et al., 1997). This gene set was then tested for Gene Ontology (GO) term enrichment using the R package clusterProfiler (Yu et al., 2012).

Morphometric analyses

We accessed specimens deposited in FMNH, USNM, UMMZ, British Museum of Natural History, UK (BMNH), Natural History Museum, Tribhuvan University (NHM-TU) Institute of Zoology, Guangdong Academy of Sciences, China (IOZ-GDAS), and Guangdong Wildlife Monitoring and Rescue Center, China (GWMRC) (**Table S1**). Fourteen external measurements were taken including full body length (abdominal) (FBLA), head body length (abdominal) (BLA), tail length (abdominal) (TLA), full body length (back) (FBLB), head body length (back)

(HBL), tail length (back) (TLB), ear length (EL), ear thickness (ET), middle claw length of the back foot (MCLBF), middle claw length of the forefoot (MCLFF), the distance of the first scale from the tip of the nose (DFSTN), the maximum number of scales in the back of the body (MNS), the single-sided number of tail edge scales (SNTE), length of hind foot (LHF), using soft tape rulers (accurate to 0.1 mm) for flexible dimensions and MNT-150 standard-type zinc alloy digital caliper (Model: MNT952101; DEGUQMNT, accuracy to 0.01 mm) for more precise linear features (**Supplementary Figure S3A**). This data includes 26 skin specimens for *M. pentadactyla* (n=8), *M. javanica* (n=12), *M. aurita* (n=6) and also includes the holotype of *M. aurita* (**Data S1**).

Twenty cranial measurements were conducted with MNT-150 standard-type zinc alloy digital caliper (accuracy to 0.01 mm), following (Gaubert & Antunes, 2005; Wu et al., 2005; Gaudin et al., 2009; Sulaiman et al., 2017; Igado et al., 2020; Morenikeji et al., 2022) including total skull length (TSL), nasal to foramen magnum base length (NFBL), premaxilla to palatine (PP), from Intersection between maxilla and palatine sutures to most posterior point of the palatine sutures(IMPS), tymapanic bulla (left) (TB), maximum width between lateral edge of auditory bulla (WSLB), skull height (H), width of Nasal Bone (WN), length of Nasal Bone (LN), dorsal gap between maxillary (dorsal) (GM), maximum width of Gap between maxillary (MWG), left maximal length of orbit left） (MO), distance between auditory bulla (DA), length of suture between parietal bone (DTEM), length of suture between frontal bone (DLOB), zygomatic process between maxilla and squamous bone left） (ZMS), length of foremen magnun occipitals (FMO), mandible length (left) (ML), the distance between condylar process (DCP), length of palatal process of premaxilla(LPP) (**Supplementary Figure S3B**). This data includes 44 skulls for *M. pentadactyla* (n=25), *M. javanica* (n=7), *Manis crassicaudata* (n=2), *M. culionensis* (n=3)

and *M. auritus* (n=7; **Data S2**). Sex was not considered in the analysis due to the absence of marked sexual dimorphism and the lack of information for some specimens. Specimen age was assessed based on body size, skull morphology, and available collection records. Juvenile and subadult individuals were excluded in the analysis. To ensure completeness of the data, we replaced missing values with the mean value calculated across specimens of the same species. We used the function prcomp () of stat to conduct principal component analysis (PCA) and Morpho to perform canonical variate analysis (CVA) on log□□-transformed variables. Finally, we conducted Levene's test for homogeneity of variances using the leveneTest () function and then performed Student's t-tests with t.test () to compare group means across taxa.

We downloaded 84 micro□CT scan data from Ferreira-Cardoso et al. (2019)**,** and scan 13 specimens, obtaining high□resolution micro□CT scans of 97 skulls for *M. pentadactyla* (n = 42), *M. javanica* (n = 38), *M. crassicaudata* (n = 12), *M. culionensis* (n = 3), and *aurita* (n = 2; **Table S2**). Raw DICOM stacks were imported into Materialise Mimics v19.0 for segmentation and construction of 3D cranial meshes. We placed 75 landmarks per mesh following Ferreira-Cardoso (2020; **Supplementary Figure S5).** After Procrustes alignment, we conduct principal component analysis (PCA) and canonical variate analysis (CVA) using MorphoJ v1.08 (Dryden & Mardia, 1993). Landmark selection was based on prior studies addressing mammalian taxa (Goswami, 2006; Hautier et al., 2017)

Scale coding

We generated scale-encoded heatmaps from 12 intact skins (nine *M. pentadactyla*, three *M. aurita*) to visualize variation following Algewatta et al. (2020); Guo et al. (2022) and Martin et al. (2024). In brief, we digitized the x-y coordinates of every scale in Excel, exported

standardized images into Photoshop v25, and overlaid all specimens per species to produce species-specific composite maps (**Data S3, S4**).

RESULT

Phylogenetic relationships and distribution of *Manis pentadactyla*

We firstly estimated the Asian pangolins' phylogeny using 68 mitogenomes (**Table S2**). The maximum likelihood (ML) tree is well-resolved, with every interspecific relationship strongly supported (i.e., bootstrap support [BS] = 100; **Figure 1A**). The topology aligns well with previous studies (Hu et al., 2020a; Wang et al., 2022; Gu et al., 2023; Wei et al., 2024; Wangmo et al., 2025), reaffirming *Manis pentadactyla* sensu lato (including all three subspecies *pentadactyla*, *pusilla*, and *aurita*) as the sister clade to all other Asian congeners. The putative taxon "mysteria" emerges as the immediate sister to *M. javanica*. *M. pentadactyla* s. l., is represented by 43 samples, clustered into two deeply diverged clades, corresponding to MPA and MPB identified in Hu et al. (2020a).

We further estimated maximum-likelihood trees using autosomal and sex-chromosome derived SNP and single-copy orthologues for a subset of samples (**Table S3**). The phylogenies derived from all three datasets are topologically identical (**Figure 1A, Supplementary Figures S1, S2**), mirroring the mitochondrial phylogeny. When projected the SNP of *Manis* species onto principal-component (PC) space, every *M. pentadactyla* s. l. sample falls into a tight cluster that is clearly distinct from the other congeneric species (**Figure 1B, 1C**). Restricting the analysis to *M. pentadactyla* s. l. reveals non-overlapping splitting between MPA and MPB along PC1 (Tracy-Widom test, $p = 1.09 \times 10^{-5}$; **Table S4**), underscoring consistent genomic differentiation despite their close relationship. The result of ADMIXTURE analysis echoes these patterns (**Figure 1D**). The lowest cross-validation error occurs at K = 2 (CV = 0.50), with marginal

increases at K = 3 and K = 4 (CV = 0.53 in both cases; **Table S5**). At K = 2, the inferred clusters correspond closely to MPA and MPB, with three individuals displaying minor ancestry from the opposite cluster. Taken together, the concordant mitochondrial and nuclear results support a robust validation of the split within *M. pentadactyla* sensu lato.

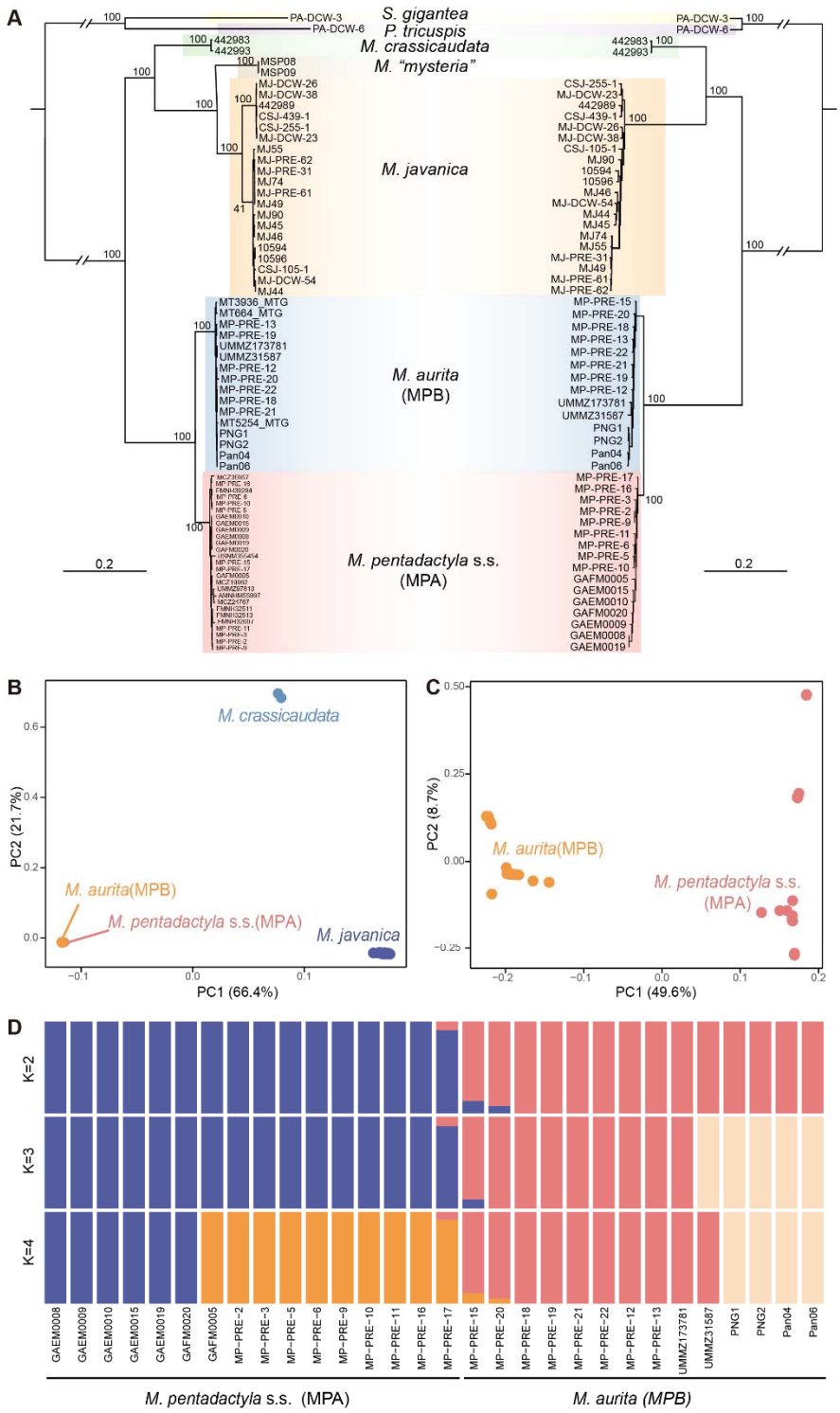

Figure 1: Phylogenomic relationships and population structure of pangolins. (A) Maximum likelihood (ML) phylogenies based on complete mitochondrial genomes (left) and autosomal nuclear single-nucleotide polymorphisms (SNPs) (right). Numbers at the nodes represent bootstrap support values. The scale bars indicate the number of substitutions per site. (B)

Principal Component Analysis (PCA) of genomic SNP data showing the separation of four *Manis* species. (C) PCA focused on the *M. pentadactyla* s.l. illustrating the clear genetic differentiation between *M. pentadactyla* s.s. (MPA) and *M. aurita* (MPB). Values in parentheses on each axis indicate the percentage of total variance explained by that principal component. (D) Population structure of the *M. pentadactyla* species complex as inferred by ADMIXTURE, for K=2 to K=4 assumed ancestral populations. Each vertical bar represents an individual, and its colored segments show the proportion of that individual's ancestry from each of the K inferred clusters.

To define the geographic distribution of the MPB clade, we augmented our dataset with publicly available mitochondrial *CYTB* and *COI* sequences representing *M. pentadactyla* s.l. A phylogenetic analysis of this expanded dataset confirmed the same backbone topology as our initial trees (**Figure 2A**). Critically, this analysis placed sequences from specimens described as *Manis indoburmanica* (from South Tibet) firmly within the MPB clade. Furthermore, every MPB haplotype with a reliable geographic origin was traced to either Assam, South Tibet, China or Nepal, a region that includes the collection locality of Hodgson's *aurita* topotype from central Nepal (**Figure 2B**). This direct association of the MPB clade with the *aurita* topotype provides evidence to assign this lineage, geographically rooted in Himalaya, to *M. aurita*.

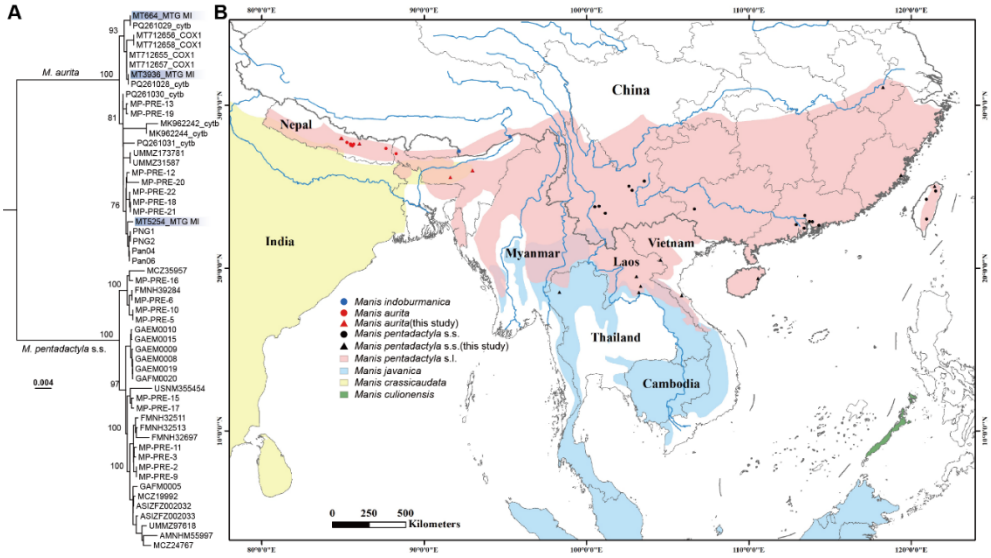

Figure 2:Mitochondrial phylogeny and geographic distribution of the *Manis pentadactyla* species complex. (A) Maximum likelihood phylogeny constructed from an expanded dataset of

mitochondrial sequences (complete mitogenomes and partial CYTB and COX1 fragments), incorporating publicly available data. Numbers at the nodes represent bootstrap support values. The scale bar indicates the number of substitutions per site. Note that specimens described as *M. indoburmanica* (MI, highlighted in green) nest firmly within the *M. aurita* (MPB) clade. (B) Geographic distribution map for specimens with reliable locality information (see Table S1). Circles represent data obtained from previous studies while triangles data collected in this study. Shaded areas denote the approximate ranges of Asian pangolin species based on distribution data from the IUCN Red List.

Morphometric evidence for the distinctiveness of *M. aurita*

To assess whether *M. aurita* is morphologically distinct from the *M. pentadactyla* sensu stricto (including subspecies *pentadactyla* and *pusilla*) and thus merits recognition as a separate species, we employed linear measurements-based and three-dimensional landmark-based geometric morphometric analyses (**Table S6**). Principal Component Analysis (PCA) of 20 cranial measurements for 44 specimens positioned *M. pentadactyla* s. l. within a morphospace that showed partial overlap with the Indian pangolin (*M. crassicaudata*) but remained clearly separated from the Sunda (*M. javanica*) and Philippine (*M. culionensis*) pangolins (**Figure 3A**; **Supplementary Figures S3; S4A, S4B**). Along PC1, which accounted for 39.4% of the shape variance and primarily reflected overall cranial size, specimens identified as *M. aurita* consistently occupied the positive extreme. This placement indicates that *M. aurita* possesses a significantly larger skull, and proportionally shorter palatine when compared to *M. pentadactyla* s.s. (**Tables S7A-6C**).

Three-dimensional landmark-based geometric morphometric analyses of 75 cranial landmarks (**Table S6**) obtained from micro-CT scans also clearly distinguished *M. aurita* from *M. pentadactyla* s.s. along PC3 (**Figure 3B**, **Table S8A-8B**), but not PC1 or PC2 (**Supplementary Figures S4C, S4D**). Compared to *M. pentadactyla* s.s., *M. aurita* exhibits a relatively shorter yet broader nasal bone, a laterally expanded junction between the maxilla and palatine bones, a posteriorly positioned anterior point of the foramen magnum on the ventral occipital surface

(landmark 25, see **Table S6**; **Supplementary Figure S5**), and an anteriorly shifted M-shaped suture between the maxilla and palatine bones in ventral view, culminating in a shorter ventral maxilla (**Supplementary Figure S10C**).

To further substantiate the morphological separation between *M. aurita* and *M. pentadactyla* s.s., we conducted a PCA based on fourteen external body measurements including *M. aurita* and *M. pentadactyla* s.s. and *M. javanica.* A crucial aspect of this analysis was the inclusion of the *M. aurita* holotype (Natural History Museum, BMNH: 43.1.12.85), which notably lacks skull material. The results demonstrated a clear distinction: all specimens from South Tibet, Northeastern India and Nepal, including the *M. aurita* holotype, separated unequivocally from *M. pentadactyla* s.s. along both PC1 (accounting for 52.1% of variance) and PC3 (6.9% of variance) (**Figure 3C**; **Table S9A-9C**, **Supplementary Figures S4E, S4F**). The PCA-based separation is strongly supported by *t*-tests on individual cranial (**Figure 3D**, **Supplementary Figure S6A; Table S10**) and external measurements (**Figure 3E, Supplementary Figure S6B, Table S11**), which show *M. aurita* having significantly longer body lengths, tail lengths, larger hind feet, an extended snout and markedly smaller ears.

Finally, Canonical Variate Analyses (CVA) that using both cranial and external variables achieved 100% classification accuracy in separating *M. aurita* and *M. pentadactyla* s.s. (**Tables S12, S13, 14; Supplementary Figure. S7**). In contrast to these clear differences in skeletal and external body proportions, an analysis of scale characteristics using superimposed, scale-encoded heatmaps of 12 intact body skins (nine *M. pentadactyla* s. s. and *three M. aurita*) revealed no significant differences in either the total number of scale rows or their spatial distribution between the two taxa (**Supplementary Figure S8; Table S15**). Collectively, the consistent and pronounced size- and shape-based differences in both cranial and external morphology, strongly

demonstrate that *M. aurita* is morphologically distinct from *M. pentadactyla* s.s. supporting its full species status.

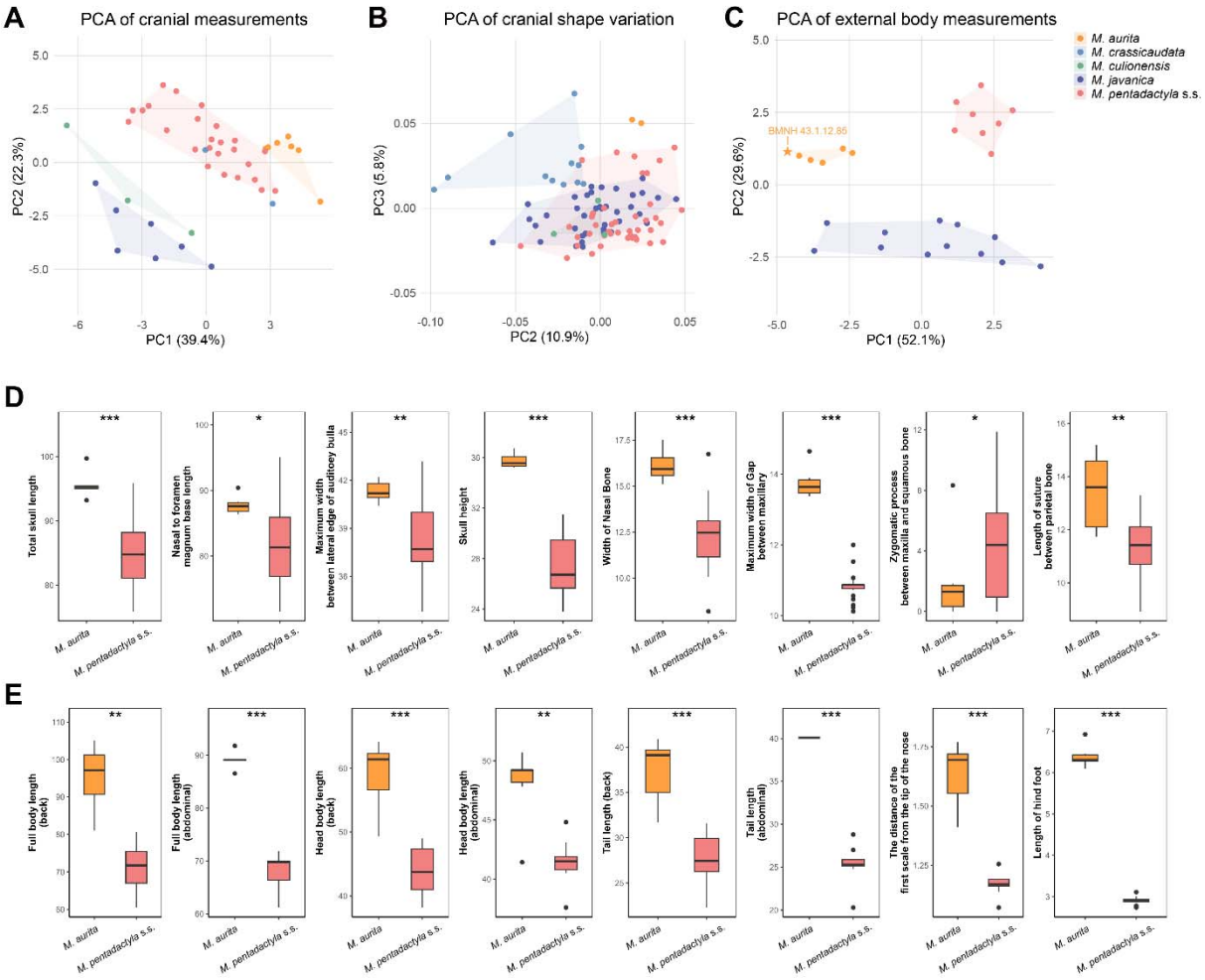

Figure 3: Morphometric analyses based on cranial and external morphology. (A) Principal Component Analysis (PCA) based on 20 linear cranial measurements (PC1 vs. PC2). (B) PCA of cranial shape variation derived from 75 3D geometric morphometric landmarks (PC2 vs. PC3). (C) PCA based on 14 external body measurements (PC1 vs. PC2). For all PCA plots (A-C), values in parentheses on the axes indicate the percentage of variance explained. Note the inclusion of the *M. aurita* holotype (BMNH: 43.1.12.85) in panel C, which clusters firmly with other *M. aurita* specimens. (D, E) Boxplots comparing key cranial (D) and external (E) measurements between the two taxa. Boxes depict the interquartile range (IQR) with the median indicated by the central line; whiskers extend to 1.5 times the IQR. Units are in millimeters (D) and centimeters (E). Statistical significance from Student's t-tests is denoted as: * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$. See Tables S5–S14 and Figures S4, S9, S10 for additional results.

Evolutionary and demographic history of *Manis aurita*

We estimated divergence time of pangolins using 200 selected clock-like single-copy orthologous genes. The most recent common ancestor (MRCA) of the genus *Manis* was dated to approximately 20.1 million years ago (Ma) (95% confidence interval [CI] = 17.5 to 22.6 Ma; **Figure 4A**), a finding consistent with Gu et al. (2023). *M. aurita* (MA hereafter) and *M. pentadactyla* s. s. (MP hereafter) diverged approximately 1.2 Ma (95% CI = 0.9 to 1.7 Ma), during the early Pleistocene. Pairwise Sequentially Markovian Coalescent (PSMC) analyses revealed MP maintained a larger effective population size (N□) than MA following their divergence (**Figure 4B**). After their split, the trajectory for MP was characterized by an initial decline, a subsequent period of prolonged stabilization since 1.0 Ma and a final, sudden drop around 50 ka. The trajectory for MA was broadly similar, showing stability until approximately 300 ka, at which point it entered a sustained decline.

As both species experienced population declines and possess small effective population sizes (N_e), we evaluated whether population decline resulted from inbreeding. The histogram of ROH length (**Figure 4C**) shows that individuals of MP carry more medium- and long-tract ROHs (>100 kb) than those of MA, indicating a higher degree of recent inbreeding. Consistent with this, the median F_{ROH} in MP is ~0.0447, twice that of MA (~0.0228) (**Figure 4D**). This finding confirms that MP has undergone more recent inbreeding which may be related to the abrupt Ne drop in the recent past. It is also noteworthy that some individuals in both species exhibit very high FROH (> 0.1), suggesting pronounced inbreeding in certain populations such as *M aurita* near Kathmandu Valley (e.g., Dhading).

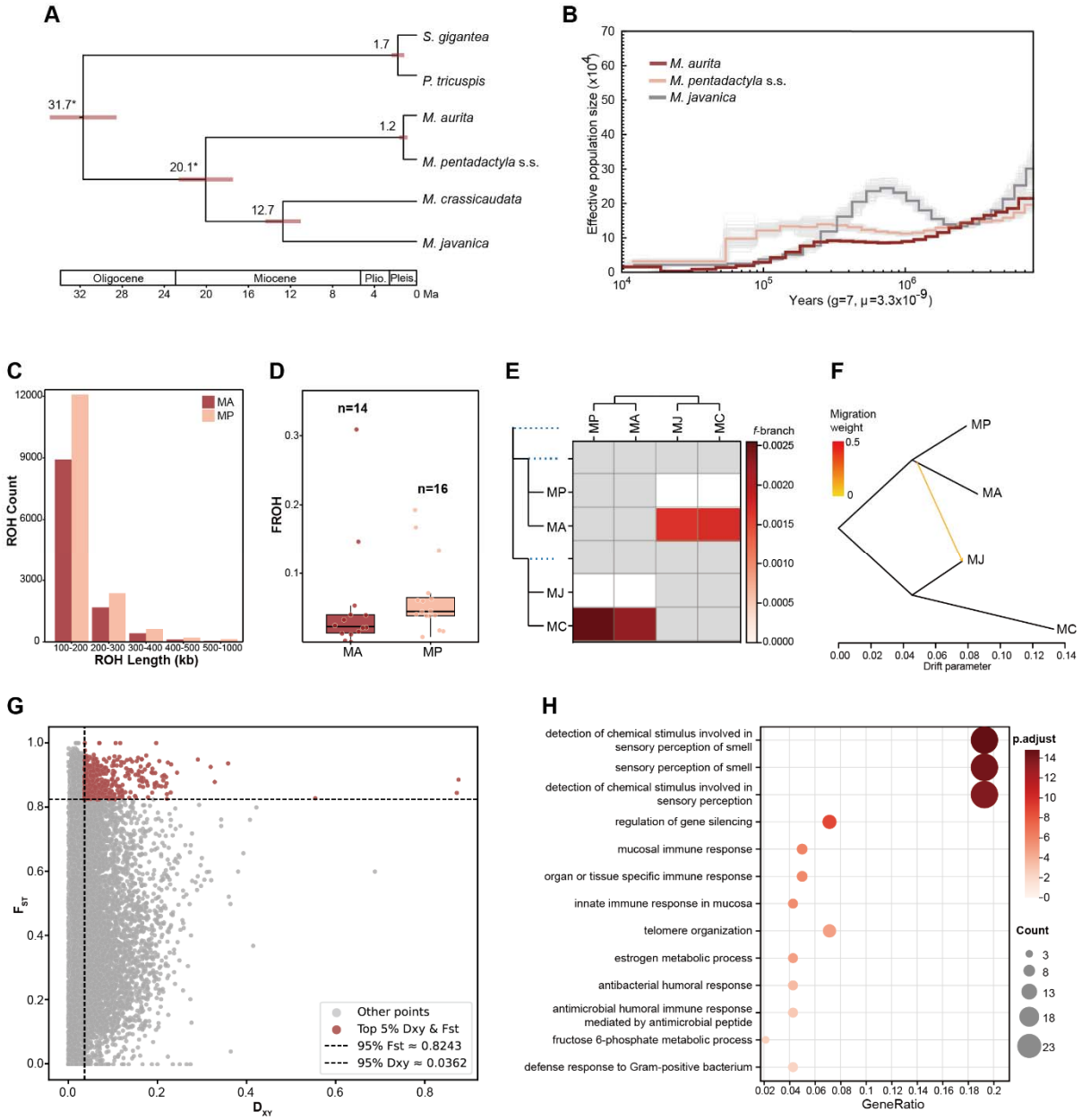

Figure 4: Divergence time, demographic dynamics, and genomic divergence of *Manis* species. (A) Divergence time estimates for pangolins based on 200 clock-like single-copy orthologous genes, inferred using *BEAST3. Numbers at nodes represent mean age estimates in millions of years (Ma), while the associated horizontal bars represent the 95% Confidence Intervals (CI). Asterisks indicate nodes used for calibration. (B) Historical effective population size (N□) trajectories for three species inferred using PSMC. Shaded areas represent 100 bootstrap replicates. (C-D) Comparison of recent inbreeding levels between *M. aurita* (MA) and *M. pentadactyla* s.s. (MP), showing (C) the distribution of Runs of Homozygosity (ROH) lengths and (D) the genome-wide fraction of ROH (F_{ROH}). (E-F) Interspecific gene flow analyses among four *Manis* species. MC: *M. crassicaudata*, MJ: *Manis javanica*. (E) Heatmap of Dsuite f-branch statistics, where warmer colors indicate stronger signals of admixture on a given branch. (F)

TreeMix population graph showing inferred drift and a migration event (arrow). (G-H) Genomic differentiation between *M. aurita* and *M. pentadactyla* s.s. (G) Manhattan plot of FST and dXY values, with dashed lines indicating the 95% outlier thresholds used to define genomic islands of divergence. (H) Gene Ontology (GO) enrichment analysis of genes within the identified genomic islands, revealing significant enrichment for terms related to olfactory functions. Dot size corresponds to gene count and color to statistical significance (p.adjust).

We subsequently investigated patterns of interspecific gene flow involving MA to assess the impact of current and historical range overlap with its congeners (**Figure 2B**). D-suite analyses indicated significant, albeit low-level, introgression from the Indian pangolin (*M. crassicaudata*) into both MP (f4-ratio ≈ 0.0025, p < 1x10-15) and MA (f4-ratio ≈ 0.0022, p < 1x10-15) (**Figure 4E; Table S16**). Evidence of introgression from MA into the Malayan pangolin (*M. javanica*) was also detected by Dsuite (f4-ratio ≈ 0.0017) and TreeMix (**Figure 4F**). In contrast, when we specifically examined gene flow between MP and MA post-divergence using fastsimcoal2, the analysis strongly favored a scenario of no gene flow over alternative models (ΔAIC > 2.9; **Table S17**). Collectively, these results indicate that while MA has experienced minimal introgression from other pangolin species, it has remained largely isolated from its sister species MP since their divergence.

Finally, we compared MA and MP genomes for signatures of local adaptation by calculating nucleotide diversity (π) and fixation index (F_{ST}), and absolute genetic differentiation (D_{XY}) (**Supplementary Figure S9**). Genomic islands of divergence were defined as windows in the top 5 % for both F_{ST} (>0.8575) and D_{XY} (>0.0373; **Figure 4G**). Gene Ontology (GO) enrichment analysis of genes within these identified islands revealed significant enrichment for terms related to olfactory functions, notably “detection of chemical stimulus involved in sensory perception of smell” and “sensory perception of smell” (**Figure 4H**).

DISCUSSION

The Revalidation of *M. aurita*

Despite accumulating molecular evidence suggesting overlooked, or cryptic species (Hu et al., 2020a; Wang et al., 2022; Wei et al., 2024), the taxonomy of *M. pentadactyla* s. l. lacked rigorous examination. Our mitochondrial and genome-wide phylogenomic analyses consistently reveal a divergence between *aurita* and *M. pentadactyla* s.s. at about 1.3 Ma (**Figure 4A**). The magnitude of this split surpasses commonly accepted thresholds for intraspecific variation (Rieseberg & Burke, 2001; Abreu et al., 2025; Van Elst et al., 2025). Complementing this genetic divergence, morphometric analyses identify consistent and diagnostic differences that distinguish *aurita* from *M. pentadactyla* s.s. (**Figure 3**). Cranially, *M. aurita* possesses a significantly larger overall skull with a proportionally shorter and broader nasal region compared to *M. pentadactyla* s.s. (**Supplementary Figures S10, S11, Table S9, Table S10**). External morphological differences are particularly clear and facilitate differentiation. For instance, *aurita* has obviously smaller ears than *M. pentadactyla*, a characteristic reflected in its original specific epithet (*aurita*, Latin for eared). On the other hand, our phylogenetic analysis fails to resolve *M. p. pentadactyla* and *M. p. pusilla* as two distinct evolutionary entities (**Figure 1A**).

The distribution of *M. aurita* is associated with the Himalayan region (**Figure 2B**). It includes the type locality of *M. aurita* from central Nepal, as well as individuals from South Tibet recently described as *Manis indoburmanica* (Wangmo et al., 2025). In contrast, *M. pentadactyla* s.s. is predominantly found in South and Eastern China and Southeast Asia. This geographical separation is likely influenced by biogeographic barriers, such as the rivers run in north-south directions (e.g., the Brahmaputra River) (Lehman et al., 2006; Hu et al., 2020b) and the Arakan Mountains (Hinckley et al., 2024).

Collectively, the congruent evidence from our genetic, morphological, and distributional analyses unequivocally supports recognizing Hodgson's *aurita* as a distinct species. While Zijlstra (2025) previously argued for its revalidation, our study substantiates this view with broader and more integrative evidence. Consequently, in accordance with the Principle of Priority of the International Code of Zoological Nomenclature (ICZN), we reinstate *Manis aurita* Hodgson, 1836 as the valid name for this species. This action renders junior synonyms such as *Pholidotus assamensis* Fitzinger, 1872, and *Manis indoburmanica* Wangmo, Ghosh, Dolker, Joshi, Sharma and Thakur, 2025.

Evolutionary history of *M.* aurita

The population genetic and demographic analyses illuminate the evolutionary trajectory of *M. aurita* following its speciation. The ancestors of *M. aurita* and *M. pentadactyla* diverged in the early Pleistocene, period of, significant global climatic oscillations. Given that pangolins are generally warm-adapted species, with no historical fossil evidence suggesting their presence in northern China (Tong, 2007), the climatic shifts likely played a crucial role in driving the allopatric separation of the ancestor into western (Himalaya) vs. eastern (East/ South East Asia) refugium (Louys & Meijaard, 2010; Leonard et al., 2015; Hawkins et al., 2016; Camacho-Sanchez et al., 2017; Hinckley et al., 2023). Pangolins are highly olfactory-reliant mammals, exhibiting significantly enlarged olfactory bulb (Imam et al., 2018; Li et al., 2024), using smell to forage for ants and termites (DiPaola et al., 2020). As the *M. aurita* and *M. pentadactyla* adapted to their respective environments, certain OR genes, certain OR genes likely diverged under selection as supported in our GO enrichment analysis (**Figure 4H**).

The population of *M. aurita* decline started around 300 Ka and is consistent with the Penultimate Glaciation (~300–130 Ka), during which the climate cooled and dried (Colleoni et al., 2016; Ma

et al., 2022), likely leading pangolin habitats to contract. Notably, similar patterns are seen in other warm-adapted mammals in southern China (Li et al., 2025), such as the golden snub-nosed monkeys (Dai et al., 2024).

Our analyses further detected limited gene flow between *M. aurita* and two other Asian pangolins. The signal of introgression between *M. aurita* and *M. crassicaudata* (contributing to <0.25% of the genome) is unsurprising, given their sympatric ranges in southern Nepal and northeastern India. We also observed a similarly low level of gene flow between *M. aurita* and *M. javanica*, indicating that their distributions likely have overlapped at least historically. Despite these instances of historical admixture, the low level of gene flow indicates *M. aurita* has maintained its status as a distinct evolutionary entity.

It is noteworthy, in the admixture analysis, at both K=3 and K=4, *M. aurita* separated into two distinct genetic clusters: one comprising individuals from Nepal and the other comprising individuals from South Tibet and northeastern India, a pattern that indicates significant intraspecific subdivision (**Figure 1D**).

Conservation Implications

The formal recognition of *M. aurita* as a distinct species carries profound conservation significance. Its intrinsic vulnerability is underscored by a geographically restricted range, confined to the Himalayan–Indo-Burmese region, and a demographic history marked by a more pronounced and sustained population decline since the Middle Pleistocene compared to *M. pentadactyla*.

Despite the long-term population decline revealed by PSMC analyses, *M. aurita* on average exhibits lower levels of recent inbreeding than *M. pentadactyla* as evidenced by the results of ROH and FROH (**Figures 4C, 4D**). This likely reflects differing histories of anthropogenic

pressure nowadays; the less intensively developed landscapes of South Asia historically provided more contiguous refuge habitats compared to the range of *M. pentadactyla* in China and Southeast Asia, where has experienced intense human activity for centuries, leading to severe habitat fragmentation and the regional extinction of many medium-to-large mammal species (Brook et al., 2014; Goossens et al., 2016; Boonratana, 2020). However, it is noteworthy, *M. aurita* around Kathmandu valley exhibit extremely high inbreeding levels (i.e., FROH > 0.1), indicating that these populations are already facing severe inbreeding depression (**Figure**. **4D**). Conservation strategies must therefore prioritize the identification and management of these highly vulnerable populations to prevent local extinctions.

Overarching these intrinsic vulnerabilities is the critical threat from illegal wildlife trade. Genetic analyses of confiscated scales have repeatedly confirmed that *M. aurita* is a target (Hu et al., 2020a). Alarmingly, our findings also reveal that products from this species have infiltrated regulated traditional medicine markets (data from Xie et al. (2021); **Supplementary Figure S13**), demonstrating that illegally sourced materials are being laundered through formal supply chains. The comprehensive genomic dataset presented here, with its improved geographic coverage and inclusion of previously unsampled populations, provides an enhanced genetic baseline which will bolster wildlife forensics by allowing for greater precision in determining the geographic provenance of confiscated scales, thereby helping to pinpoint poaching hotspots.

Taxonomy

Manis aurita Hodgson, 1836 stat. nov.

Manis auritus Hodgson, 1836. Original description.

Manis aurita Waterhouse,1838

Phatages bengalensis Fitzinger, 1872

Pholidotus assamensis Fitzinger, 1872

Manis pentadactyla auritus Thomas 1918

Manis pentadactyla Ellerman & Morrison-Scott, 1951 (part)

Manis indoburmanica Wangmo, Ghosh, Dolker, Joshi, Sharma and Thakur, 2025

Holotype: BMNH 43.1.12.85, an adult (skin) collected by Brian Houghton Hodgson in 1836 from Central Nepal (**Supplementary Figure S11B**).

Emended diagnosis

Manis aurita can be diagnosed by the following combination of characters that distinguish it from all other Asian pangolins: the external pinna is small and distinctively flake-shaped. On the snout, the first row of head scales lies well behind the nasal tip, exposing a bare patch of naked skin (**Supplementary Figure S10A**); dorsal scales are smooth and trapezoidal with straight posterior margins, whereas the lateral scales near the abdomen are broad and shield-shaped (**Supplementary Figure S10B**). Cranially, the palatal process of the premaxilla extends posteriorly but measures less than half of the premaxillary midline length, and the incisive foramen does not extend to the premaxilla's posterior border. At its anterior end, the maxilla bulges laterally, creating nearly parallel lateral margins (**Supplementary Figure S10C**). The postglenoid foramen opens laterally within the central region of the postglenoid fossa. (**Supplementary Figure S10D**). Both the jugular and hypoglossal foramina are recessed yet remain distinct. Finally, the ventral surface of the occipital condyle is flat rather than convex (**Supplementary Figure S10C**).

Description

Manis aurita is an Asian pangolin with an elongated head, small ears, short limbs, and a tail shorter than half the body length. Its external pinna is small and flake-shaped. The head and body are covered in overlapping, exceptionally smooth keratin scales: dorsal scales are trapezoidal with straight posterior edges, while lateral abdominal scales are broad and shield-shaped. On the snout, the first row of head scales lies well behind the nasal tip, leaving a bare patch of skin. The ventral surface is pale brown and densely fringed with short, stiff hair bristles. Claws are moderately curved: the third (middle) claw on each forefoot is the longest, the first and fifth claws are noticeably shorter, and all hind-foot claws are shorter than those on the forefeet. Scale coloration in adults ranges from dark brown to chestnut; juveniles are slate-grey or grey-brown, with more bristles between scales.

The skull exhibits a relatively elevated and broad profile. The ventral palatal process of the premaxilla is short, measuring less than half the length of the premaxilla itself. The incisive foramen of the premaxilla does not contact the ventral projection of the maxilla. The vomer does not protrude at the midline on the ventral surface of the maxilla. The nasal bones are broad and terminate in a semicircular shape. The postglenoid foramen is positioned laterally. The pterygoid hamulus is short and does not extend beyond the ectotympanic bulla, which is rounded in shape. The palatine sutures form an M-shaped structure. The zygomatic process of the maxilla may either be connected to the zygomatic process of the squamosal via a bony rod-like structure or remain unconnected. The external and skull measurements are presented in **Supplementary Data 1, 2**, respectively.

The total number of body scales ranges from 538 to 596. From the neck to the tail base there are 254–274 scales arranged in 23–24 longitudinal and 15–17 transverse rows. The tail bears 140–153 scales: 80–94 on the dorsal surface organized into five transverse by 16–20 longitudinal

rows, and 50–63 on the ventral surface in three to five transverse by 18–20 longitudinal rows, with 17–19 scales along each lateral edge. The forelimbs carry 37–55 scales per side, while the hindlimbs have 32–41 scales per side.

Comparisons

Manis aurita (MA) and *M. pentadactyla* s.s. (MP) share a close morphological resemblance, exhibiting a similar number of body scales, typically uniform dark brown to deep chestnut. These scales are generally shield-shaped or trapezoidal and are interspersed with sparse hair bristles (**Supplementary Figure S11A**). This contrasts with *M. javanica*, whose scales on the tail tip, tail base, and ventral side are pale yellow, and which uniquely features a reversed growth direction in the last longitudinal scale row on its forelimbs. *M. crassicaudata* is set apart by its larger, earth-toned scales and the absence of interspersing hair bristles. *M. culionensis* is characterized by more numerous, elongated, and sharper-tipped scales that are dark brown and either leaf-shaped or shield-shaped. In MA and MP, the zygomatic process of the maxilla and the squamosal is sometimes connected via a bony rod to form a zygomatic arch. This contrasts with all other species, that lack a complete zygomatic arch. The palatal process of the premaxilla in MA and MP is notably short, not exceeding half the premaxilla's midline length, unlike in other species, where this process is longer (**Supplementary Figure S11B**). Additionally, the postglenoid foramen in MA and MP opens on the lateral aspect of the zygomatic process, differing from *M. javanica* and *M. culionensis*, where it opens posteriorly, and from *M. crassicaudata*, where its opening can be either posterior or lateral (**Supplementary Figure S11B**).

Compared to MP, MA typically attains a larger adult body size, with a total body length ranging from 81.0 to 105.1 cm (mean: 95.2 cm) compared to 60.5 to 80.6 cm in MP (mean: 71.2 cm).

MA also possesses a longer tail (31.7–40.9 cm, mean: 37.4 cm) than MP (22.3–31.6 cm, mean: 27.5 cm), and has larger foot surfaces, with hindfoot lengths averaging 6.4 cm versus 2.9 cm in MP. Furthermore, the external pinnae differ, with those of MA being distinctly smaller than in MP (**Figure**. 3E; **Supplementary Figure S6B**). The skull of MA is larger and taller than that of MP, with cranial width ranging from 93.2 to 99.7 mm (mean: 95.6 mm) and height from 35.2 to 36.3 mm (mean: 35.8 mm), compared to MP's cranial width of 75.9 to 95.9 mm (mean: 84.6 mm) and height of 23.8 to 31.5 mm (mean: 27.6 mm). Additionally, the maximum width of the gap between the maxillary bones is wider in MA (13.5–14.7 mm, mean: 13.8 mm) than in MP (10.1–12.0 mm, mean: 10.9 mm). The skull of MA is larger and taller than that of MP. This is reflected in a relatively smaller nasal length-to-width ratio in MA (approximately 1.9:1), indicating a broader nasal bone, whereas MP has a narrower nasal bone with a larger ratio (approximately 2.5:1), resulting in a comparatively slenderer nasal region (**Figure. 3D, Supplementary Figure S6A**). The anterior portion of the skull in MA is also broader and deeper; its maxillary region expands laterally, with the posterior lateral margins of this anterior expansion running nearly parallel. In contrast, the anterior part of the skull in MP is more elongated, contributing to a more triangular overall shape of the ventral skull surface. The palatine bone in MA is positioned more anteriorly than in MP. Specifically, the most posterior point of the palatine sutures in MA aligns approximately with the maxilla zygomatic process and squamosal zygomatic process junction. In MP, however, this point lies posterior to this junction. The occipital condyle also shows clear differences: in MP, it is distinctly prominent, whereas MA presents a relatively flat ventral condylar articular surface that extends posteriorly. The condylar articular facet is comparatively smaller in MP than in MA (**Supplementary Figure S11A**).

Distribution, habitat, and Conservation Statues

Manis aurita is distributed along the southern Himalayan foothills, with confirmed occurrences in Nepal, South Tibet and northeastern India (including Assam), southern Bhutan, and extending into southern Tibet. The species' altitudinal range spans from lowland areas to approximately 3,000 meters above sea level. The eastern extent of its distribution remains undefined, but the Arakan Mountains appear to represent the eastern geographic limit for this species (Hinckley et al., 2024). Further surveys are necessary to ascertain its potential presence in Myanmar.

Manis aurita predominantly inhabits mixed deciduous and evergreen forests. Key tree species in these habitats include *Shorea robusta*, *Schima wallichii*, *Castanopsis indica*, and *Alnus nepalensis*. *M. aurita* is also frequently observed in forested areas adjacent to human-modified landscapes, indicating some level of adaptability to disturbed environments (Dhital et al., 2020; Shrestha et al., 2021).

Despite protected under national laws such as the Nepal's National Parks and Wildlife Conservation Act (1973), India's Wildlife Protection Act (Schedule I, 1972), and internationally under CITES Appendix I, *M. aurita* remains a significant target for illegal wildlife traffickers in South Asia. For example, Kathmandu functions as a major transit hub for smuggled pangolin scales (Bashyal et al., 2021; Koju & Tamang, 2025). Similar trafficking pressures are evident in neighboring India and Bhutan, where challenges such as limited enforcement capacity and porous international borders facilitate cross-border smuggling operations.

DATA AVAILABILITY

All sequencing data were deposited in the National Center for Biotechnology Information (NCBI) database (BioProjectID ……), and Genome Sequence Archive (GSA) database (https://ngdc.cncb.ac.cn/gsa/) (accession number …….).

SUPPLEMENTARY DATA

Supplementary data to this article can be found online.

COMPETING INTERESTS

The authors declare that they have no competing interests

AUTHOR CONTRIBUTIONS

AUTHOR CONTRIBUTIONS

NPK: Conceptualization, Methodology, Investigation, Formal analysis, Visualization, Validation, Writing – original draft, Writing – review & editing. **ZZ**: Methodology, Investigation, Formal analysis, Visualization, Validation, Writing – original draft, Writing – review & editing. **GZ**: Methodology, Investigation, Formal analysis, Visualization, Validation, Writing – original draft, Writing – review & editing. **XH**: Methodology, Investigation, Formal analysis, Visualization, Validation. **ZY**: Methodology, Investigation, Formal analysis, Visualization, Validation. **XW**: Methodology, Investigation, Formal analysis, Visualization, Validation. **MTRH**: Formal analysis, Validation, Writing – original draft, Writing – review & editing. **CG**: Formal analysis, Validation, Writing – original draft, Writing – review & editing. **AH**: Formal analysis, Validation, Writing – original draft, Writing – review & editing. **MFCF**: Formal analysis, Validation, Writing – original draft, Writing – review & editing. **JL**: Formal analysis, Validation, Writing – original draft, Writing – review & editing. **DM**: Methodology, Investigation, Formal analysis, Visualization. **SB:** Methodology, Investigation, Formal analysis, Visualization **LH**: Formal analysis, Validation, Writing – original draft, Writing – review & editing. **WY**: Formal analysis, Validation, Writing – original draft, Writing – review & editing. **LL**: Formal analysis, Validation, Writing – original draft, Writing – review & editing. **AF**:

Methodology, Investigation, Resources, Visualization, Validation, Writing – review & editing. All authors read and approved the final version of the manuscript. **YH**: Methodology, Investigation, Resources, Visualization, Validation, Supervision, Funding acquisition, Project administration, Writing – review & editing. All authors read and approved the final version of the manuscript. **KH**: Conceptualization, Methodology, Investigation, Resources, Visualization, Validation, Supervision, Funding acquisition, Project administration, Writing – review & editing. All authors read and approved the final version of the manuscript.

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