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Genomic evidence of a previously undetected *Peromyscus truei* invasion on San Clemente Island, California

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Museum genomics (museomics) provide powerful tools for detecting cryptic diversity in natural history collections, including previously undetected invasions. We analyzed genomic and morphological data from 75 *Peromyscus* specimens collected during the Channel Islands Biological Survey (1939-1941), a series of expeditions on the California Channel Islands spearheaded by the Natural History Museum of Los Angeles County (LACM). Most of these specimens were confirmed as native Channel Island deer mice (*P. gambelii* subspp.), but two specimens from San Clemente Island (SCL) were re-identified as *P. truei*, a species never reported before on the Channel Islands. Using study skins, complete mitogenomes, and low coverage whole-genome data, we confirmed these identifications, and our phylogenetic analyses determined that these *P. truei* individuals are closely related to California mainland populations. We also placed these species within the subfamily Neotominae, including the first mitogenome of a native Channel Island deer mouse. Additional morphological data reveal several more likely *P. truei* specimens, indicating the existence of a substantial populations of this species in 1939. Combined with the presence of other non-native rodents on San Clemente Island (*Reithrodontomys megalotis* and *Microtus californicus*), these findings suggest a possible co-introduction from San Diego County during the 1930s via hay shipments. Our results have important implications for conservation management on San Clemente Island, and potentially Santa Rosa Island, where some specimens appear phenotypically inconsistent with *P. gambelii*. This study highlights the value of molecular tools for reassessing historic collections, especially in dynamic systems subject to high levels of anthropogenic modification.

Keywords: Channel Islands, cryptic diversity, island invasion, museomics, *Peromyscus*.

El estudio genómico de ejemplares de museo (museómica) es una herramienta poderosa para detectar diversidad críptica en colecciones de historia natural, incluidas invasiones previamente no detectadas. Obtuvimos datos genómicos y morfológicos de 75 ejemplares de *Peromyscus* colectados durante el Channel Islands Biological Survey (1939-1941), una serie de expediciones a las Islas del Canal de California encabezadas por el Natural History Museum de Los Angeles County (LACM). La mayoría de estos ejemplares fueron confirmados como ratones ciervo nativos de las Islas del Canal (*P. gambelii* subsp.), excepto dos ejemplares de la Isla San Clemente (SCL) que fueron reidentificados como *P. truei*, una especie nunca antes reportada para las Islas del Canal. El análisis de pieles de estudio, mitogenomas completos y datos del genoma completo de baja cobertura, permitió confirmar estas identificaciones. Los análisis filogenéticos mostraron que los ejemplares de *P. truei* están estrechamente relacionados con poblaciones continentales de California. Asimismo, incluimos estas especies dentro de la subfamilia Neotominae, incorporando el primer mitogenoma del ratón ciervo de las Islas del Canal. Datos morfológicos adicionales indicaron que varios ejemplares probablemente corresponden a *P. truei*, lo que sugiere la existencia de una población sustancial en 1939. Junto con la presencia de otros roedores no nativos en SCL (*Reithrodontomys megalotis* y *Microtus californicus*), estos hallazgos sugieren una posible co-introducción desde el Condado de San Diego durante la década de 1930 mediante envíos de pacas de heno. Nuestros resultados tienen implicaciones importantes para la gestión y conservación en SCL y, potencialmente en Isla Santa Rosa, donde algunos ejemplares parecen ser fenotípicamente inconsistentes con *P. gambelii*. Este estudio destaca el valor de las herramientas moleculares para reevaluar colecciones históricas, especialmente en sistemas dinámicos con altos niveles de modificación antropogénica.

Palabras clave: Diversidad críptica, invasión insular, Islas del Canal, museómica, *Peromyscus*.

Natural history collections (NHC) house irreplaceable records of global biodiversity spanning more than two centuries and increasingly provide the context needed to establish pre-perturbation baselines for threatened populations (Suarez and Tsutsui 2004; Benham and Bowie 2022). By coupling specimens with modern analytical tools, NHC enable retrospective assessments of changes of geographic distribution, phenology, morphology, and genetic diversity over time, often driven by anthropogenic impacts (Meineke *et al.* 2019). Critically, museum genomics (museomics) of historical DNA can also pinpoint the origins and pathways of non-native taxa, resolving the number of introductions, their timing and spread (Kim *et al.* 2023), informing conservation responses to pathogens, disease vectors, and other biosecurity threats (e.g., O'Hanlon *et al.* 2018). As genetic barcoding and genomic tools are applied more broadly, NHC are revealing cryptic invasions events that have gone unrecognized in the natural history literature, and consequently, unaccounted for in conservation management decisions (e.g., Provan *et al.* 2008; Goedknegt *et al.* 2018).

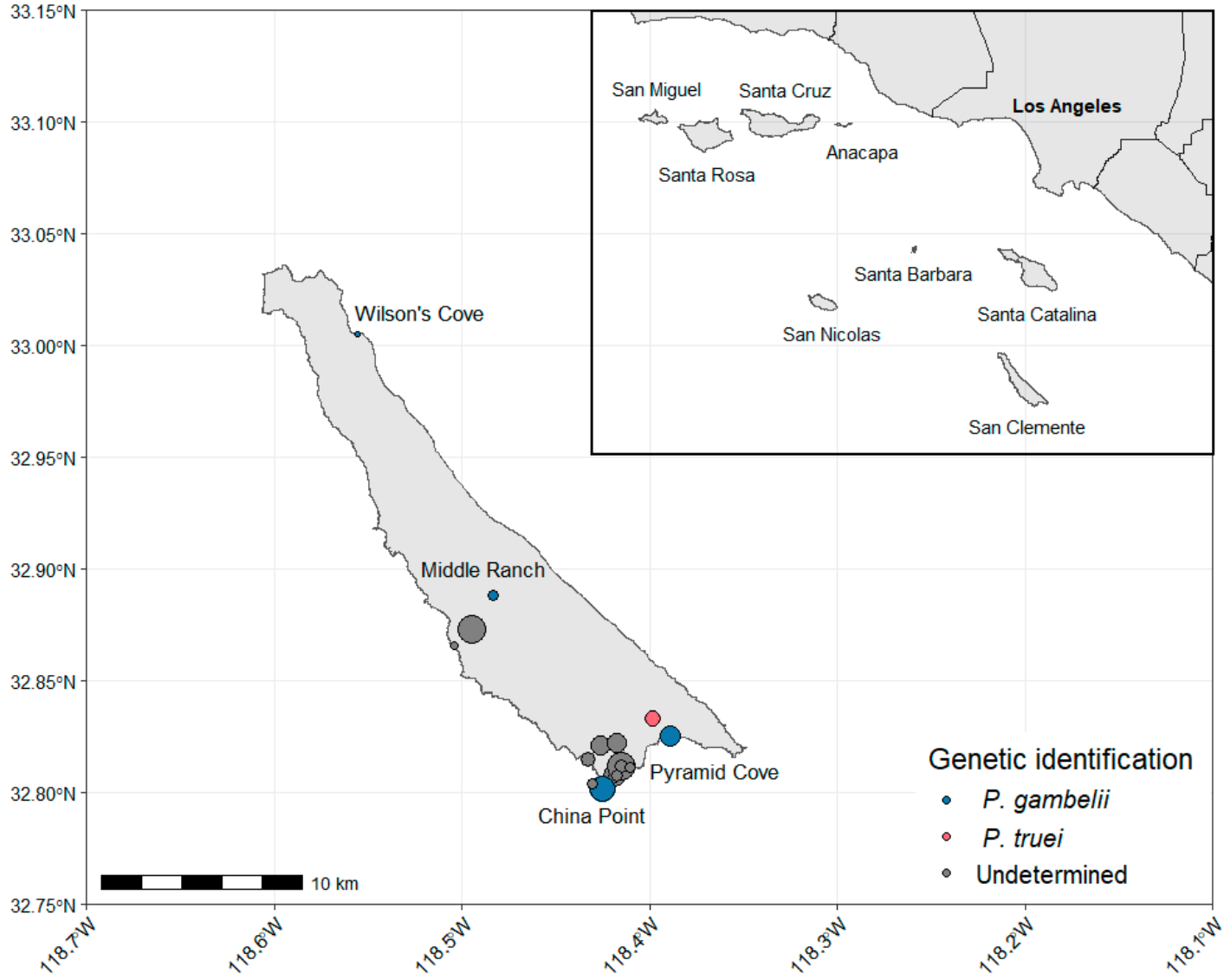

Figure 1. Collecting localities of 287 *Peromyscus* specimens from San Clemente Island, USA, during the Channel Islands Biological Survey (1939-1941). Dot size indicates the number of specimens collected at each site. Colors denote whether sequenced specimens were genetically identified as endemic *P. gambelii clementis* or introduced *P. truei*. Inset: Map of the Channel Islands Archipelago relative to mainland southern California.

The California Channel Islands, an isolated, near-shore archipelago, harbor exceptional endemic biodiversity and a rich archeological record reflecting over 13,000 years of human occupation on the northern islands and at least 9,500 years on the southern islands (Erlandson *et al.* 2011). Despite never being connected to the mainland, long-term human use, historical ranching, and 20th-century military activity have produced complex biogeographic legacies, including introduction of commensal and domestic animals and episodic translocations among islands and with the mainland.

Within this context, the Channel Islands Biological Survey (CIBS; 1939–1941) conducted the only comprehensive archipelago-wide survey to date, leading 13 expeditions and collecting thousands of specimens now curated at the Natural History Museum of Los Angeles County (LACM). San Clemente Island (SCL), the first island visited by CIBS, has experienced intensive sheep/goat ranching and US Navy activity, with documented ecological degradation followed by substantial eradication and restoration efforts (Keegan *et al.* 1994). These histories make CIBS holdings particularly valuable for reconstructing mid-20th century species composition and for detecting previously unrecognized introductions to the islands.

Island deer mice (*Peromyscus gambelii* sensu Greenbaum *et al.* 2017; 2019; Bradley *et al.* 2019) occur on all eight Channel Islands, each with morphologically and genetically distinct subspecies (Gill 1980; Ashley and Wills 1989; Pergams and Ashley 2002). Six island mouse subspecies had been described by the time of CIBS (Mearns 1897; Elliot 1903; Mearns 1907; Nelson and Goldman 1931), and CIBS mammalogist Jack von Bloeker would go on to describe the last two (von Bloeker Jr 1940; 1941). Their extensive Holocene history stretches at least 11,000 years, (Shirazi *et al.* 2018), likely driven by natural and human assisted dispersal, in addition to later contact with mainland lineages on the southern islands (Ashley and Wills 1989; Becker *et al.* 2025).

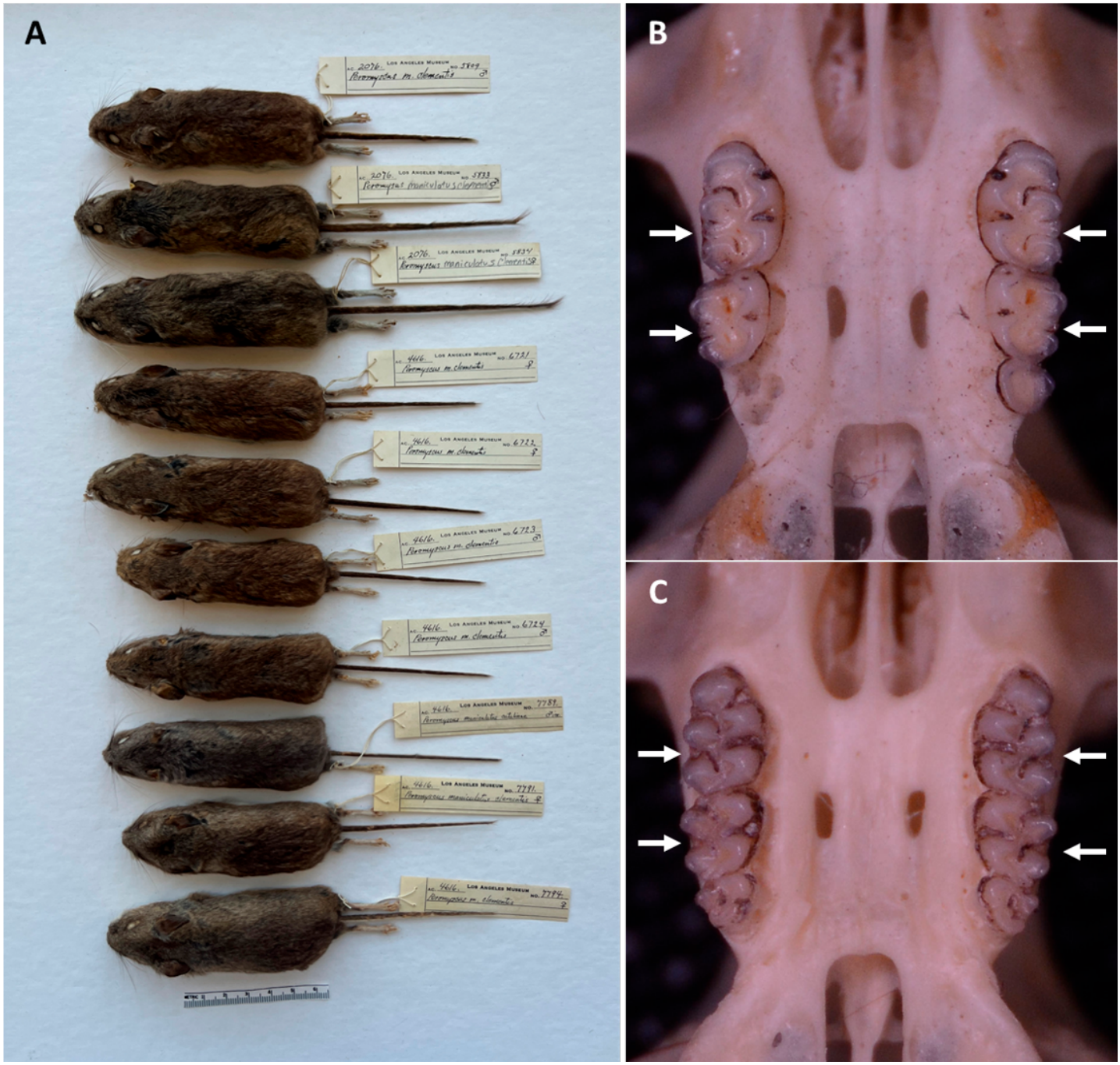

Figure 2. A) *Peromyscus* specimens from San Clemente Island, USA, collected during the Channel Islands Biological Survey (1939-1941) and housed at the Natural History Museum of Los Angeles County. Specimens LACM 5833 and LACM 5834 (second and third from the top, respectively) were re-identified as *P. truei* with genomic data. These specimens show morphological traits distinguishing them from the endemic *P. gambelii*, including longer tails with more densely furred tips, larger total body sizes, and larger ears. Original identifications from collector and CIBS mammalogist Jack von Bloeker appear in pen, while the specific and subspecific epithets in pencil were likely erroneously added later to LACM 5833 and LACM 5834. B) Upper molars of LACM 5834 exhibit diagnostic accessory cusps associated with *P. truei* (white arrows). C) Upper molars of LACM 6722 do not include these accessory cusps (absence indicated by white arrows), consistent with *P. gambelii* identification.

Recent introductions from other *Peromyscus* lineages have not been recorded on the Channel Islands, but given the archipelago's dynamic anthropogenic footprint and the presence of other introduced rodents (von Bloeker Jr 1967; Rick 2013), they may be under-documented. *Peromyscus* are a diverse group of morphologically similar animals which have been difficult to resolve with traditional tools (Platt *et al.* 2015; Castañeda-Rico *et al.* 2025), and contain frequently misidentified lineages (e.g., Light *et al.* 2021). Furthermore, field identification within *Peromyscus* relies on the geographic and ecological context of collection—information which is no longer useful in novel insular contexts. Lastly, rapid morphological adaptation to novel island habitats is common in rodents (e.g., Pergams *et al.* 2015), further impeding accurate identification of newly established populations and raising the possibility of cryptic introductions.

While conducting population genomic research with Channel Island deer mouse specimens (Becker in prep.), we recovered genomic data from two individuals on SCL (Figure

1) that were inconsistent with identification as *P. gambelii*. Here, we revisit the CIBS collections with museomics and morphology to interrogate this finding and reassess CIBS *Peromyscus* specimens. We analyze mitogenomes, low coverage whole-genome data, and study skins and skulls from 75 specimens collected during the CIBS to: 1) test for non-native *Peromyscus* lineages within historic Channel Island collections; 2) phylogenetically place newly identified lineages; 3) evaluate introduction pathways and management implications. We report the first evidence of *P. truei* on the Channel Islands, identify additional likely *P. truei* specimens on SCL consistent with an invasion of multiple individuals, and infer a probable co-introduction pathway via hay bales shipped from San Diego County on the California mainland. Our study demonstrates the power of genetic identification in dynamic systems such as the Channel Islands and underscores the importance of revisiting historical collections with genomic tools.

Materials and methods

Specimen subsampling. We subsampled 75 *Peromyscus* study skins housed in Natural History Museum of Los Angeles County (LACM) mammal collections (Supplemental Data SD1A), primarily to study historical *P. gambelii* population genomics (Becker in prep.). Using sterile techniques, we performed whole claw excision due to documented high performance for this sample type in rodent study skins (McDonough *et al.* 2018). These specimens were originally collected across the eight California Channel Islands during the Channel Islands Biological Survey from 1939-1941. All specimens were catalogued as *Peromyscus maniculatus*, with original specific locality data matching each corresponding island subspecies. Specimens were not morphologically examined during subsampling, since native island mice are the only extant recorded *Peromyscus* occurring on any of the Channel Islands. Ten specimens were sampled from San Clemente Island, including two that we are presently re-identifying as *P. truei* based on morphological and genomic evidence (Figure 2).

Laboratory processing. Specimen subsamples were processed in a specialized ancient DNA facility with no exposure to PCR products or modern DNA. All laboratory work was conducted at the Center for Conservation Genomics (CCG), Smithsonian National Zoo and Conservation Biology Institute. We extracted samples with a modified ancient DNA silica-column protocol (McDonough *et al.* 2018), using either MinElute columns (Qiagen Inc., Valencia, CA, USA) or Zymo Spin Columns (Zymo Research, Irvine, CA, USA). DNA was quantified with 1x dsDNA High Sensitivity Qubit assays (Thermo Fisher, Waltham, MA, USA), and genomic libraries were prepared with the Santa Cruz Reaction customized for each sample's input quantity (Kapp *et al.* 2021). Libraries were indexed with KAPA uracil-tolerant polymerase (Roche Kapa Biosystems, Wilmington, MA, USA) in a modern DNA facility, using Tru-seq style indices. Indexing PCR cycle number was determined by performing quantitative PCR on diluted pre-PCR libraries (Kapp *et al.* 2021). In addition to these specimens, we also prepared genomic libraries with the same methods from a *P. truei truei* tissue sample (USNM 603235, coll. 2017) sheared DNA extract, which was previously sequenced for captured ultraconserved elements and the mitochondrial genome (Castañeda-Rico *et al.* 2025). Genomic libraries were quantified with Qubit and Tapestation High Sensitivity (Agilent Technologies, Santa Clara, CA, USA), equimolarly pooled with other projects, and quality controlled for insert size with Blue Pippin (Sage Science Inc., Beverly, MA, USA). Final pools were submitted for low-coverage paired-end sequencing (150bp PE, 300 cycles) on an Illumina NovaSeq X 25B flow cell (Illumina Inc., San Diego, CA, USA) at the Oklahoma Medical Research Foundation's Clinical Genomics Center.

Mitochondrial genome assembly and initial species identification. Raw sequences were trimmed for adapter content, quality, and length with default parameters in Trim Galore v0.6.10 (Martin 2011), and exact duplicates were removed with prinseq-lite.pl v0.20.4 (Schmieder and Edwards 2011). Mitochondrial genomes (mitogenomes) were assembled from the processed shotgun sequencing data in Geneious Prime® 2025.0.3 using the Geneious mapping algorithm with default parameters and up to five iterations. Initially, all sequences were mapped to the *Peromyscus maniculatus bairdii* reference mitogenome NC_039921, but final versions of the LACM 5833 and LACM 5834 *P. truei* mitogenomes were mapped to the reference *P. truei* mitogenome PP818778 (USNM 603235) for increased mapping quality. Any sites under 5X depth and all ambiguous bases in the consensus sequences for these mitogenomes were called as N. Annotations were transferred from the reference mitogenomes in Geneious and checked for premature stop codons and the presence of nuclear copies of mitochondrial DNA (NUMTs). Cytochrome *b* gene sequences were extracted from mitogenome assemblies for species identification and/or downstream analysis, since only one *P. truei* mitogenome (PP818778) and no island mouse (*P. gambelii* spp.) mitogenomes have previously been published. Initial species identifications were made by querying NCBI's core nucleotide database (core_nt) with cytochrome *b* sequences using BLASTN v2.17.0+ (Camacho *et al.* 2009). Of the confirmed island mouse specimens, we only included data from one SCL specimen (LACM 6722) in further molecular analyses to investigate differences between the *P. truei* collected with native *Peromyscus* on this island.

Nuclear DNA species identification. Since we obtained shotgun sequencing data from LACM 5833 and LACM 5834 as well as the specimen associated with the *P. truei* reference mitogenome (USNM 603235), we wanted to ensure that nuclear DNA also supported the species identification obtained from mitochondrial DNA. To do this, we used Kraken2 v2.1.3 (Wood and Salzberg 2014) to construct a custom database containing all available reference

genomes within the Neotominae subfamily: *P. maniculatus. bairdii* (HU_Pman_2.1), *P. m. sonoriensis* (mPerMan1.0.p), *P. leucopus* (UCI_PerLeu_2.1), *P. eremicus* (PerEre_H2_v1), *P. californicus* (ASM782708v3), *P. polionotus* (HU_Ppol_2), *P. melanophrys* (Pmel_10x_v1), *P. attwateri* (Patt_10x_v1), *P. nudipes* (Pnud_10x_v1), *P. aztecus* (Pazt_10x_v1), *Onychomys torridus* (mOncTor1.1), *O. arenicola* (OncAre_H1_v1), *O. leucogaster* (OncLeu_H2_v1), *Reithrodontomys megalotis* (mReiMeg1.0.p), *Neotoma floridana* (mNeoFlo1.hap1), *N. lepida* (ASM167557v1), *Scotinomys teguina* (ASM4990163v1). Since shotgun sequencing of museum specimens also frequently includes common contaminants, we also added the pre-made "bacteria", "human", and "UniVec_Core" libraries to prevent false hits. Because a genome for *P. truei* has not yet been assembled, we added the quality-checked, merged reads of the USNM 603235 tissue sample as representative sequences of this species. All validated reads from LACM 5833, 5834, and 6722 were queried against this custom database, and krakentools v1.2 (Lu *et al.* 2022) and krona v2.8.1 (Ondov *et al.* 2011) were used to visualize the results.

Whole mitogenome analysis and molecular dating. We conducted multiple whole mitogenome phylogenetic analyses with the three novel mitogenomes and previously published data to 1) robustly confirm the initial *P. truei* species identification of LACM 5833 and LACM 5834, 2) resolve the relationship between these specimens' mitochondrial haplotypes and closely related taxa, 3) and establish the position of *P. gambelii clementis* (LACM 6722).

We used MAFFT v7.490 plugin (Katoh and Standley 2013) in Geneious to align complete mitogenomes generated in this study and in Castañeda-Rico *et al.* (2025). Phylogenetic trees were obtained using Maximum Likelihood (ML) in IQTree v2.3.1 (Minh *et al.* 2020) and Bayesian Inference (BI) in MrBayes v3.2.7a (Ronquist and Huelsenbeck 2003) on partitioned mitogenome alignments. We used ModelFinder, as implemented in IQTree, to find the best-fit model for the ML analysis. IQTree was run with the best-fit models and partitions (TIM2+F+R4, GTR+F+I+R4, GTR+F+I+R5, GTR+F+I+R6, GTR+F+R4; five partitions) and 1000 ultrafast bootstrap replicates, with values of >95 indicating support. We used PartitionFinder 2.1.1 (Lanfear *et al.* 2017) with linked, corrected Akaike Information Criterion (AICc), and greedy parameters, to select the best model and partition scheme for the alignment. The search was limited to the models available in MrBayes. We defined the data block by codon position, tRNA, rRNA and D-loop selection. MrBayes was run with the best-fit model and partitions (GTR+I+G for each of the six partitions) for 50 million generations, with a burn-in of 25%, a sample frequency of 1000 generations, and 4 Markov chains Monte Carlo (MCMC). Posterior probabilities and final topologies result from 50% majority rule consensus trees, with a probability of >0.95 indicating support.

We estimated divergence times in BEAST2 v2.6.7 (Bouckaert *et al.* 2019) using a partitioned alignment. The best-fit model and partition scheme were selected with PartitionFinder 2.1.1, restricted to models available in BEAST and using linked, AICc, and greedy parameters. The data block was defined by codon position, tRNA, rRNA and D-loop selection. We ran the analysis with the best-fit models and partitions (GTR+I+G+X, TRN+I+G; six partitions) under an uncorrelated lognormal relaxed molecular clock model, a calibrated Yule speciation processes model, and with a randomly generated starting tree as priors. Calibrations were based on fossil records of 1) *Onychomys* sp. at ca. 4.85 million years ago (mya), 2) *Peromyscus* sp. at ca. 4.85 mya, and 3) *Reithrodontomys wetmori* at ca. 4.5 mya (see Castañeda-Rico *et al.* 2025). We performed two independent runs of 50 million iterations each, with sample frequency of 1000 iterations. Tracer v1.7.1 (Rambaut *et al.* 2018) was used to check convergence for the Effective Sample Size (ESS), and 25% burn-in was performed in each run. LogCombiner v2.6.6 and Tree Annotator v2.6.2, both packages in BEAST, were used to combine trees and to compile a maximum clade credibility tree with node heigh distribution.

All analyses were performed on the Smithsonian Institution High Performance Computing Cluster (Smithsonian Institution, https://doi.org/10.25572/SIHPC). Trees were visualized with ggtree (Yu *et al.* 2017) in R version R v.4.5.1 (R Core Team 2021).

Phylogeographic analysis of Peromyscus truei with cytochrome b. We conducted phylogeographic analysis with extracted cytochrome *b* genes of LACM 5833 and LACM 5834 and previously published *Peromyscus truei* sequences to infer the origins of the introduction of *P. truei* to SCL. We downloaded all sequenced cytochrome *b* gene fragments greater than 1000 bp from NCBI Genbank (n=82), which were all sequenced from wild-caught museum specimens with locality information. We only analyzed unique haplotypes (n=67) in addition to LACM 5833, LACM 5834, and the *P. truei* reference PP818778 (USNM 603235). We chose related outgroups based on the Neotominae mitogenome phylogeny (Castañeda-Rico *et al.* 2025): *P. gratus gratus* (AY376421), *P. gratus gentilis* (AY376420), *P. gratus zapotecae* (AY376423), *P. ochraventer* (PP818776), *P. attwateri* (ON528112), *P. nasutus* (PP818775). *P. pectoralis* (KY707309), and *Habromys ixtlani* (KY707304). The resulting dataset (n=78) was aligned with the MAFFT v7.490 plugin in Geneious.

Phylogenetic trees were built using ML (IQTree v2.3.1) and BI (MrBayes v3.2.7a) on unpartitioned cytochrome *b* alignments. We also used ModelFinder as implemented within IQTree to find the best models for both analyses. IQTree was run with the best-fit model (TIM2+F+G4) and 1000 ultrafast bootstraps, with a score of >95 indicating support. We ran MrBayes with the best-fit model (GTR+F+G4) for 20 million generations with a burn-in of 25%, a sample frequency of 1000, and 4 MCMC. Posterior probabilities and final topologies result from 50% majority rule consensus trees, with a probability of >0.95 indicating support.

Morphological analysis. We examined study skins of the SCL specimens included in our genomic analyses (Figure

2) and compared their original measurements to those of genetically confirmed *P. gambelii* and *P. truei* to other *Peromyscus* specimens collected during the CIBS across the Channel Islands. The goals of the morphological analyses were: 1) to determine whether LACM 5833 and LACM 5834 skins comported with morphological characters consistent with the genetic identification of *P. truei*, and 2) to detect any other putative misidentifications present in LACM Channel Island deer mice collections. We also examined a subset of skulls to assess dental traits diagnostic of *P. truei*, specifically the presence of accessory cusps (mesolophs) on upper molars (Ingles 1965).

Of the total 709 *Peromyscus* specimens collected during the CIBS and housed at LACM, we restricted analyses to the 703 specimens prepared by Jack von Bloeker to ensure measurement consistency. Juveniles and subadults were retained due to inconsistent age class labels, but two extreme outliers in tail or total length (due to tail damage) were removed, resulting in a final dataset of n=701 (Supplemental Data SD1B). This dataset includes 277 specimens caught on SCL, including those sequenced for genomic analysis. Since *P. truei* typically exhibits larger body size with longer tails proportional to their body size and larger ears compared to *P. gambelii*/*maniculatus* (Ingles 1965), we plotted the distribution of these traits using von Bloeker's original measurement data. Each island was treated as a separate population, and genetically confirmed individuals were concurrently plotted to visualize where *P. gambelii* and *P. truei* fell within island-specific distributions. These analyses were not performed to compare *P. gambelii* and *P. truei* specimens, but to better understand how our genetically identified individuals compared to the morphological variation found in each island *Peromyscus* population. To assess potential confounding effects of sexual dimorphism, pregnancy, and immaturity, we also plotted trait distributions by sex, known reproductive status, and recorded age class. All calculations and plots were made in R v.4.5.1 with tidyverse packages (Wickham *et al.* 2019).

Six specimens collected on SCL during the CIBS and now housed at the Santa Barbara Museum of Natural History were also examined, but were ultimately not included in this dataset as three of these specimens were originally identified as *Onychomys* and mistakenly re-labeled as *P. maniculatus*. We also examined 157 Channel Island *Peromyscus* specimens housed at the Smithsonian National Museum of Natural History (USNM) and collected in 1892-1931, prior to the CIBS. These specimens were largely collected before mammal body measurements were standardized, with many incomplete datapoints including few ear measurements. They were also prepared by several different collectors at multiple time points, so they were not included in the CIBS dataset. However, these collections remain an important reference point, and were still checked for diagnostic *P. truei* external characters such as high tail to body size ratios and tail tip fur density (Ingles 1965).

Results

Mitochondrial genome assembly and initial species identification. Mitogenomes from LACM 5833, 5834, and 6722 were successfully recovered from assembled shotgun data, with average depths of 70-104.4X (Supplemental Data SD2). However, likely structural variation in the D-loop led to low depth and poor assembly at the end of this region for the two *P. truei* samples. Reads were re-assembled with GetOrganelle to try to recover mitochondrial genomes without these small ambiguous regions, but this method resulted in 3-6 short contigs and did not cover the entire mitochondrial genome. Nonetheless, the final Geneious assemblies only contained 34-51 ambiguities, and variants in the rest of the mitochondrial genome were sufficient for downstream analysis. Annotated mitogenomes for these three specimens have been deposited in GenBank (PZ213495-PZ213497), and raw reads for these specimens and USNM 603235 can be found on the Sequence Read Archive (SRR37837849-SRR37837852; Supplemental Data SD1C).

The mitogenomes of LACM 5833 and LACM 5834 differed by 159 nucleotide positions, corresponding to a pairwise identity of 99.0%. Both haplotypes returned the same top BLAST hit: the *P. truei* reference mitochondrial genome (GenBank accession PP818778; voucher USNM 603235), with 96.04-96.22% pairwise identity. In contrast, the SCL island deer mouse (LACM 6722) matched most closely with a *P. maniculatus rufinus* voucher (USNM 603271, Figure 3), with a 96.25% pairwise identity. Pairwise identity between the *P. truei* collected on SCL and the *P. gambelii clementis* (LACM 6722) mitogenome was 86.5-86.7%.

The cytochrome *b* sequences extracted from LACM 5833 and 5834 were also unique, differing by nine nucleotide positions across a 1,144 bp region. Assemblies in this region were of high quality, with an average sequencing depth of 83-104X and a minimum depth of 53-55X. Neither haplotype had an identical match in the NCBI core_nt BLAST database; however, both showed high percent identity to multiple available vouchered *P. truei* specimens from California. The top BLAST hit for LACM 5833 was MVZ:Mamm:198610, a *Peromyscus truei montipinoris* collected in Kern County, CA (99.56%), with 30 total hits over 99% percent identity. For LACM 5834, the top BLAST hits were MVZ:Mamm:157332 and MVZ:Mamm:157330 (*Peromyscus truei gilberti)* collected in Berkeley, CA with 99.48% identity and 10 total hits over 99% percent identity.

The cytochrome *b* sequence extracted from LACM 6722 was 99.83% identical to previously sequenced island deer mice from San Clemente and Santa Catalina Islands (Becker *et al.* 2025). All other LACM *Peromyscus* subsampled from the CIBS expedition harbored either identical or very closely related haplotypes to previously reported Channel Island deer mouse cytochrome *b* sequences. Nine novel haplotypes were identified and deposited on GenBank (PZ213486-PZ213494; Supplemental Data SD1C). These sequences were generated primarily to confirm species identification in morphological re-examination of

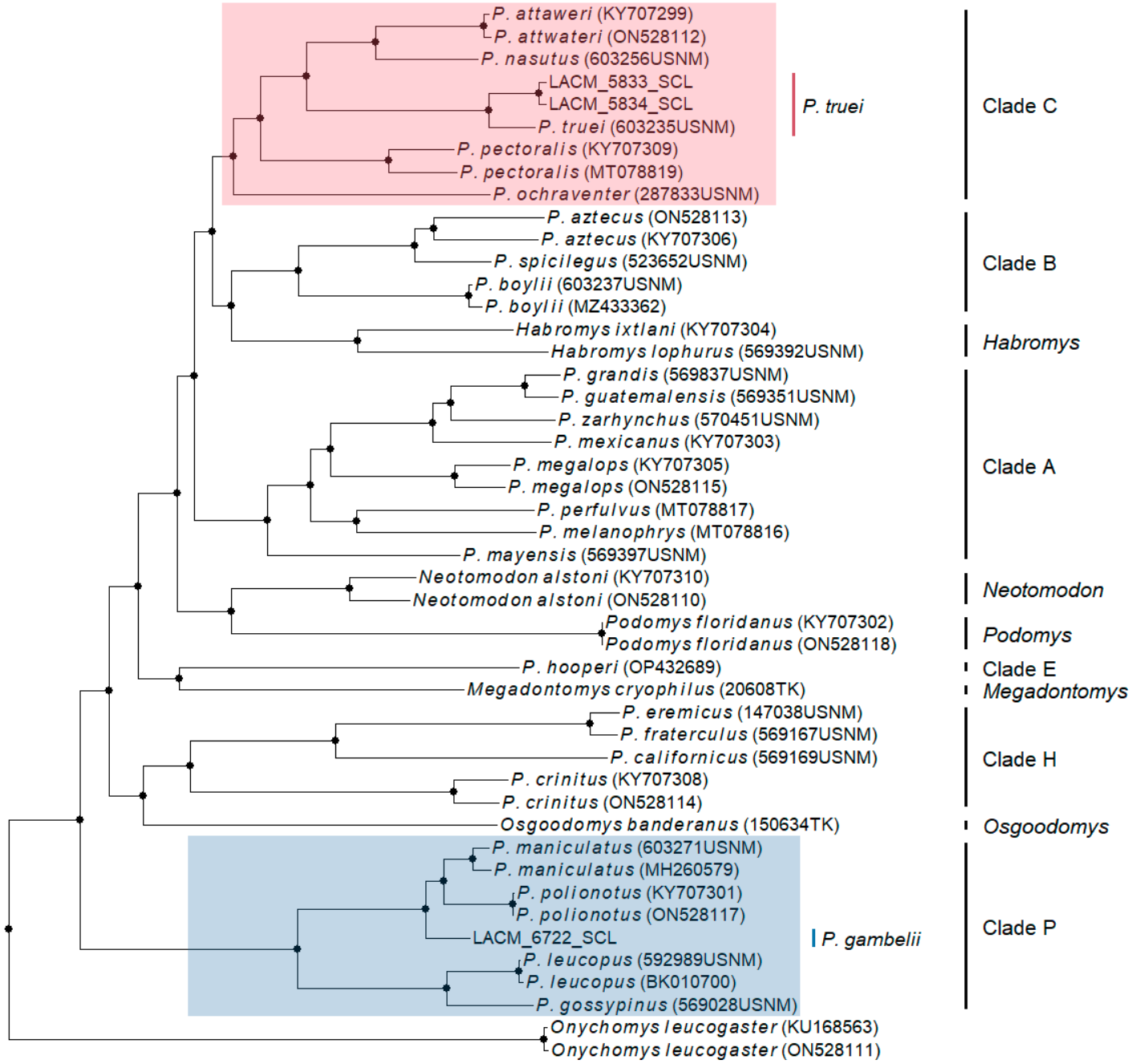

Figure 3. Bayesian mitogenome consensus tree showing positions of LACM 5833 and LACM 5834 (*P. truei*) and LACM 6722 (*P. gambelii clementis*), subset to the tribe Peromyscini and its sister genus (*Onychomys*). The *Peromyscus truei* species group is highlighted in red, and the *Peromyscus maniculatus* species group is highlighted in blue. Clade names and sequences are replicated from Castañeda-Rico *et al.* 2025. Nodes with black dots indicate high support with posterior probabilities >0.95.

specimens; no further molecular analysis were conducted on these samples.

Nuclear DNA identification. Validated shotgun reads from LACM 5833, 5834, and 6722 all contained high amounts of cricetid DNA (81-87%) according to the Kraken2 custom database search. Each library contained small numbers of human and bacterial reads and a significant number of unclassified reads (13-19%). This contamination is consistent with the age and preservation of the specimens (coll. 1939), and the unclassified reads may likely include fungi or other eukaryotic microbes found on study skins or pests present in collections (Raxworthy and Smith 2021). The highest species-resolved hit for LACM 5833 and 5834 was *P. truei*, with 31% of reads classified to this species. Despite our biased method of adding *P. truei* shotgun sequencing data to the custom database versus using an assembled genome like the other rodents, 22% of *P. gambelii clementis* reads were successfully classified as most related taxon of *Peromyscus maniculatus*, with a higher percentage of reads only classified to the genus level (43%). 1% of LACM 6722 reads were classified as *P. truei*, and 2% of LACM 5833 and 5834 reads were classified as *P. maniculatus*. These numbers are comparable to other Neotominae off-target classifications and seem likely driven by conserved regions of the genome between related species, rather than cross-contamination or hybridization (Supplemental Data SD3).

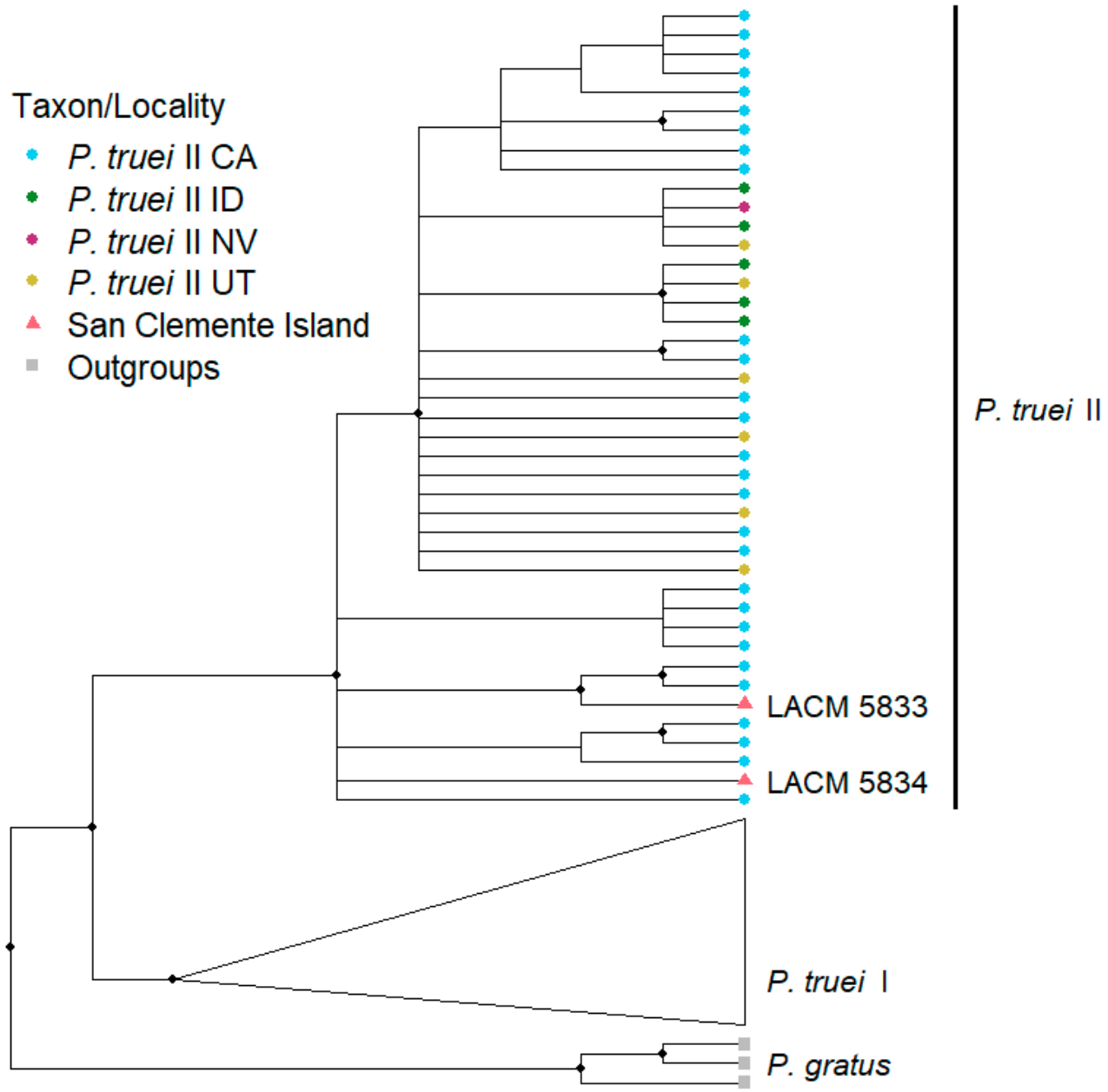

Figure 4. Bayesian cytochrome *b* consensus tree showing positions of LACM 5833 and LACM 5834 within *Peromyscus truei*. Clades are labeled in accordance with Hernández-Canchola *et al.* (2022). The *P. truei* II clade includes all haplotypes sequenced from California specimens. This phylogenetic tree has been subset to *P. truei* and its sister (*P. gratus*) for relevance. Nodes with black dots indicate high support with posterior probabilities >0.95.

Mitogenome phylogenetic analysis and molecular dating. In both BI and ML trees, LACM 5833 and LACM 5834 were recovered as sisters to each other and then sister to the *P. truei* reference mitogenome (USNM 603235), confirming the species identification as *P. truei* (Figure 3, Supplemental Data SD4-5). The reference genome is *P. truei truei*, which has previously been shown to belong to a separate clade from the western subspecies of *P. truei* (Hernández-Canchola *et al.* 2022). BEAST dated the split between the *P. truei truei* mitogenome and the LACM haplotypes to 512-670 kya, demonstrating significant distance between these two clades (Supplemental Data SD4).

LACM 6722 was recovered within the *Peromyscus maniculatus* species group (Clade P), sister to a clade of samples identified as *P. maniculatus rufinus*, *P. maniculatus bairdii*, and *P. polionotus* (1.0 posterior probability; 100 UF bootstrap). This position is consistent with previous placement of *P. gambelii* (Bradley *et al.* 2019; Greenbaum *et al.* 2019) and Channel Island mice specifically (Becker *et al.* 2025) within the *Peromyscus maniculatus* species group using cytochrome *b*. However, this position is not stable, since the relationship between *P. maniculatus* and *P. polionotus* is not resolved in the ML tree (92 UF bootstrap, Supplemental Data SD5), and in the BEAST tree, LACM 6722 is recovered as sister to the *P. maniculatus* mitogenomes only. This complex in general has been difficult to resolve and requires more loci to fully disentangle these relationships (Bradley *et al.* 2019; Castañeda-Rico *et al.* 2025). Nonetheless, BEAST dates the split between *P. gambelii clementis* and its sisters to 554-745 kya. This is

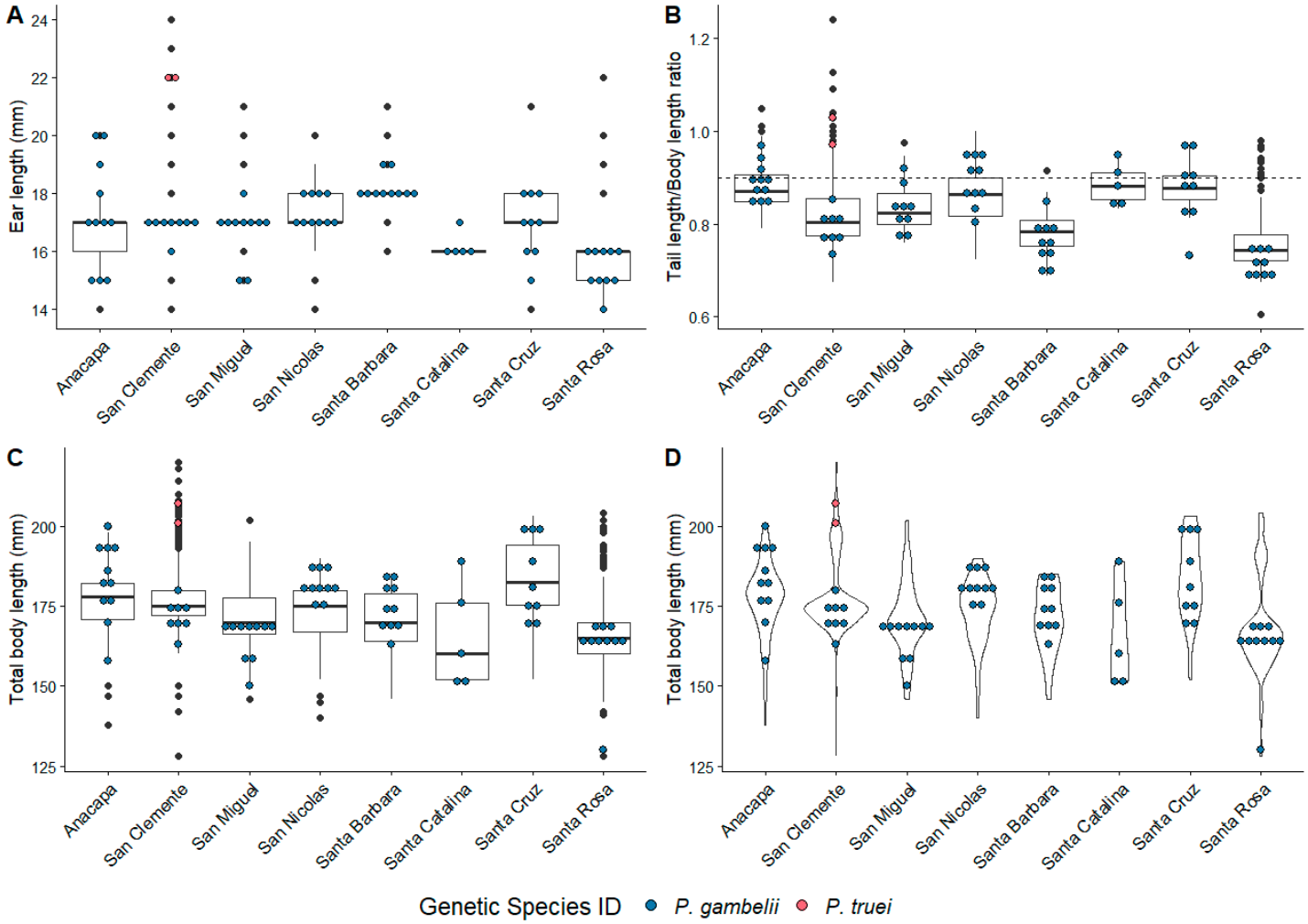

Figure 5. Distribution of study skin measurements recorded from Channel Islands Biological Survey specimens (n=701) prepared by Jack von Bloeker, including 75 genetically identified individuals, endemic *P. gambelii* (blue) and introduced *P. truei* (red), across each of the Channel Islands. A) Boxplot of ear length (mm). B) Boxplot of tail length to body length ratio; dashed line at 0.9 indicates threshold distinguishing *P. truei* from *P. gambelii* (Ingles 1965). C) Boxplot of total body length including tail (mm). D) Violin plot of total body length including tail (mm).

notably a shorter time than the 1.8 mya split previously estimated with cytochrome *b* (Bradley *et al.* 2019).

Cytochrome b phylogeographic analysis. Phylogenetic analysis of *P. truei* cytochrome *b* haplotypes recovered the two major clades identified by Hernández-Canchola *et al.* (2022). The *P. truei* I clade includes the *P. t. truei* reference mitogenome from New Mexico and other specimens from Arizona, Colorado, New Mexico, Oklahoma, Texas, and Utah (Figure 4). The *P. truei* II clade comprises specimens from California, Idaho, Nevada, and Utah. While we did not examine these specimens to verify their subspecies assignment within each clade, the observed geographic structuring is consistent with previous findings (Hernández-Canchola *et al.* 2022). The *P. truei* I clade was not resolved in the ML tree (Supplemental Data SD6), but *P. truei* II was supported in both ML and BI trees.

LACM 5833 and LACM 5834 were recovered in the *P. truei* II clade, which also contained all other specimens collected in California. We did not recover fine phylogeographic structure within the major clades, with polytomies in both ML/BI trees, limiting our ability to identify a source population for the *P. truei* caught on SCL. LACM 5833 is sister to haplotypes associated with MVZ specimens caught in Berkeley, CA, as suggested by the BLAST search, but this relationship only had support in the BI tree. The phylogenetic position of LACM 5834 was not resolved within the *P. truei* II clade.

Morphological analysis. LACM 5833 and LACM 5834 are much larger than the other SCL *Peromyscus* we sequenced (Figure 2) and have diagnostic features associated with *P. truei*. Their total body sizes are over 200 mm in total length (201, 207), with high tail to body ratios (0.97, 1.0), large ears (22 mm each), and visibly denser fur at the tip of the tail (Figure 2A). While the teeth of LACM 5833 were too worn for analysis, LACM 5834 exhibits distinct mesolophs/accessory cusps on its molars (Figure 2B), consistent with *P. truei* dental characters (Ingles 1965). By contrast, the specimens genetically confirmed as *P. gambelii clementis* have a median total body size of 172 ± 5.2 mm, a tail to body ratio of 0.79 ± 0.04, an ear length of 17 ± 0.4 mm, no tail tufting, and no accessory cusps (Figure 2C). The median measurements for these values across the 277 SCL specimens are relatively consistent with these specimens, but with high standard deviations: 175 ± 12.2 mm total length, 0.80 ± 0.08 tail/

body ratio, and 17 ± 2.0 mm ear length. Boxplots of this population demonstrate that abnormally large specimens are not limited to LACM 5833 and LACM 5834; there are a significant number of outliers with much larger total body lengths, tail ratios, and ear sizes (Figure 5A-C). In fact, this distribution is nearly bimodal, with few specimens of intermediate size, and the genetically identified *P. truei* specimens clustering with other outliers (Figure 5D). We did observe densely furred tail tips in some of these specimens, but this character is inconsistent and dependent on specimen preparation and preservation.

Across the Channel Islands, median measurements and distributions differed between island populations, consistent with prior morphological studies. While SCL specimens were either distributed solidly below or above the 0.9 tail/body length ratio used in differentiating *P. truei* and *P. maniculatus* (Ingles 1965), this value overlapped with the distribution of other islands. Santa Cruz Island contained the largest individuals, with total body size of genetically confirmed *P. gambelii* specimens comparable to the outliers on SCL. Some sporadic large specimens with long tails collected on Anacapa, San Nicolas, Santa Barbara, and Santa Catalina were also genetically confirmed as *P. gambelii*. By contrast, the median measurements of Santa Rosa Island deer mice were the smallest of any island, but also contained many large outlier specimens, none of which were sequenced. The measurements of these outliers were generally not as high as the SCL outliers and overlapped with distributions on other islands (Figure 5C). Nonetheless, the violin plot of Santa Rosa Island total body length was the only other island to show a more bimodal distribution like SCL (Figure 5D). Some outliers for total body length on SCL, Anacapa, San Miguel, and San Nicolas were pregnant when collected (Supplemental Data SD7A), but sexual dimorphism did not explain any general size distribution patterns (Supplemental Data SD8). Many, but not all, small-bodied outliers were recorded as immature, and three outliers for high total body length on SCL were also immature individuals (Supplemental Data SD7B).

Study skins housed at the Smithsonian National Museum of Natural History and collected before the CIBS contain few abnormally large specimens, except on Santa Cruz Island (Supplemental Data SD9), where large-bodied island mice have previously been documented. Of the six specimens from the Santa Barbara Museum of Natural History Museum collected during the CIBS, three were *Onychomys* specimens which had been incorrectly re-labeled as P. maniculatus (SBMNH:MAM:7621; SBMNH:MAM:9202-9203; Supplemental Data SD10). Of the *Peromyscus* specimens, two (SBMNH:MAM:7619, SBMNH:MAM:7620) were large-bodied (total length 198, 192 mm, respectively) with large ears (19 mm) and intermediate tail size (0.9, 0.88 tail/body ratio; Supplemental Data SD11). These measurements are consistent with descriptions of both *P. maniculatus* and *P. truei* (Ingles 1965). Neither specimen displayed dense fur at their tail tips of (Supplemental Data SD10), yet both were substantially larger than the median SCL island deer mouse.

Discussion

Mitochondrial genomes, low coverage nuclear data, and morphological characters of LACM 5833 and LACM 5834 confirm their identity as *P. truei*, not the endemic SCL deer mouse *P. gambelii clementis*. These specimens represent the first assembled mitogenomes from the western "*P. truei* Clade II" (*P.* cf. *martirensis*; Hernández-Canchola *et al.* 2022), which we estimate diverged from "*P. truei* Clade I" ~512-670 kya. Distinct mitogenome haplotypes indicate multiple individuals were introduced rather than a single pregnant female. Morphometric analysis of other CIBS specimens revealed additional individuals with ear and tail measurements consistent with *P. truei*, suggesting breeding *P. truei* populations on SCL in the 1930s. Although limited phylogeographic resolution at cytochrome *b* precludes pinpointing a source population of the detected invasion, the closest related haplotypes derived from mainland California *P. truei*. This pattern aligns with historical accounts of hay shipments introducing other rodents, including *Microtus californicus* and *Reithrodontomys megalotis* (von Bloeker Jr 1967), and underscores how human-mediated movements repeatedly reshaped island faunas.

Anthropogenic history of Channel Island rodents and San Clemente Island. The archaeological record shows that *P. gambelii* arrived on the Channel Islands after or concurrently with humans (Shirazi *et al.* 2018), suggesting that deer mice were inadvertently introduced some 13,000 years ago. Trade networks between the mainland and among the Island Chumash and Gabrielino/Tongva peoples living on the Channel Islands likely provided further opportunities for translocation (Johnson *et al.* 1983), which may also explain Holocene introductions of harvest mice (*Reithrodontomys megalotis*) on Santa Catalina and Santa Cruz Islands (Ashley 1989). Other mammals, such as the island fox and the Catalina ground squirrel, may have been intentionally translocated by Indigenous people (Collins 1991a; 1991b; Rick *et al.* 2009; 2019; 2024). However, in addition to these species which have lived on the Channel Islands for thousands of years, several rodents were repeatedly introduced during 19th-20th centuries along with other commensal and domestic animals: *Rattus norvegicus* on Catalina; *Rattus rattus* on Catalina, San Clemente, San Miguel, and Anacapa Island; *Mus musculus* on Catalina and San Clemente; *Microtus californicus* on Catalina and San Clemente, and *Reithrodontomys megalotis* on San Clemente (Rick 2013). While many islands experienced agricultural activity and mainland connectivity during this period, this especially rich rodent diversity on the SCL including adept island invaders like *Rattus* and *Mus* is striking.

While considered federal land since 1850, SCL was used primarily for private ranching operations until the US Navy assumed control in 1934. Today, Naval Base Coronado administers military operations on SCL, including extensive training facilities and the US Navy's last remaining ship-to-shore live firing range. Increasing military development during the 1930s was a motivating factor for the CIBS

team to begin expeditions on SCL as quickly as possible, according to their initial proposal for the survey (Laverty 2020). However, there had already been a long history of ecological deterioration on the island due to the impact of sheep and goat ranching. The San Clemente sheep company operated from at least 1879, grazing tens of thousands of sheep on the island. Feral goats, likely the most destructive of the animals introduced to SCL, were finally eradicated in 1991 by the US Navy, with over 29,000 total goats removed since 1972 (Keegan *et al.* 1994). CIBS botanist Meryl Dunkle wrote that, "The heavy grazing of sheep and goats in the past gave such a desolate appearance to the island that it seemed superficially of but little interest to the botanist" (Dunkle 1943). However, SCL is recognized today for harboring the highest number of endemic plants in the Channel Islands archipelago (Raven 1963), aided by Navy conservation and restoration efforts.

Today, proactive biosecurity measures are in place on the Channel Islands (e.g., Brenner *et al.* 2025), as stakeholders understand the potential for invasive species undermining meticulous conservation restoration efforts. Millions of dollars have been spent eradicating feral animals left behind from the ranching period, especially as these species have threatened charismatic endemics: feral goats on SCL degraded habitats for the loggerhead shrike (*Lanius ludovicianus mearnsi*) and island night lizard (*Xantusia riversiana reticulata*) (Scott and Morrison 1990; Keegan *et al.* 1994); feral ungulates on the northern Channel Islands indirectly led to hyperpredation on island foxes from golden eagles (Roemer *et al.* 2001; Coonan *et al.* 2014); feral cats on Santa Barbara and rats on Anacapa predated on the rare Scripps's murrelet (*Synthliboramphus scrippsi*) (McChesney and Tershy 1998; Whitworth *et al.* 2013). Invasive species and habitat degradation on Anacapa and SCL have also impacted island deer mice, resulting in the State of California recognizing these two subspecies, *P. g. anacapae* and *P. g. clementis*, as critically imperiled (California Natural Diversity Database 2026). Monumental eradication efforts led by collaborations between National Park Services, the US Navy, and conservation organizations have led to the recovery and delisting of many Channel Islands species from the endangered species act, including the island fox and island night lizard (US Fish and Wildlife Service 2014; 2016), and recently on SCL, a unique Bell's sparrow subspecies (*Artemisiospiza belli clementeae*) and four endemic plants (US Fish and Wildlife Service 2023).

Timing and pathways of introduction. Mammalogist Jack von Bloeker collected both native and introduced mammals during the CIBS, and attempted to infer their colonization histories in his comprehensive list of Channel Island mammals (von Bloeker Jr 1967). For example, he examined 28 *M. californicus* and 36 *R. megalotis* specimens from SCL, and determined that they were indistinguishable from geographically proximate mainland species (von Bloeker Jr 1967). He hypothesized that both of these species were inadvertently introduced by imported hay from San Diego County: "In April, 1939, I obtained information which supports this suggestion from a conversation with Mr. Theodore Murphy, United States Marshal, who was stationed on the island at that time and was the recipient of the hay as feed for his horse which he used in patrolling the island" (von Bloeker Jr 1967). These *Microtus* and *Reithrodontomys* were collected in geographic proximity to both confirmed *P. gambelii* and *P. truei* on southern SCL. In addition, six *Onychomys* specimens were also collected by von Bloeker in this area (LACM 6593- 6594, LACM 6596; SBMNH:MAM:7621, SBMNH:MAM:9202-9203), which are the only *Onychomys* individuals ever recorded on any of the Channel Islands (Knapp *et al.* 2021).

The co-localized collection of non-native *Microtus*, *Reithrodontomys*, and *Onychomys* on southern SCL indicates an active route for wild (not just commensal) rodent invasions from mainland California during the Channel Islands ranching era. Furthermore, von Bloeker's correspondence with Theodore Murphy, who was ranching on SCL prior to serving as US Marshal, supports hay shipments as the introduction pathway for at least two of these species. If *P. truei* arrived contemporaneously, its introduction likely occurred after 1926 when Murphy began activity on SCL. This timeline is concordant with earlier *Peromyscus* specimens (n=37) collected on SCL between 1894-1897 by Mearns, Anthony, and Gaylord from the International Boundary Commission, which are phenotypically consistent with *P. gambelii* (Supplemental Data SD9). Because localities for these earlier specimens are unrecorded, and CIBS sampling was concentrated at the island's southern end, our ability to infer the distribution or spread of *P. truei* remains limited.

Specimen identification and historical notes. Given von Bloeker's extensive experience collecting and identifying rodents across California, it is notable that he did not classify any SCL specimens as *P. truei*. Specimens such as LACM 5833 and 5834 exhibit distinct tail tips, diagnostic dental characters, and body size significantly larger than both Mearns's descriptions and von Bloeker's average *Peromyscus* specimens. Unfortunately, von Bloeker's complete field notes are unavailable, and because SCL mice had already been described as a subspecies, he did not formally analyze them as he did for Santa Rosa and Anacapa Islands. However, original tag labels suggest he may have recognized some of these large mice as atypical: while most were labeled "*Peromyscus maniculatus clementis*" or "*Peromyscus m. clementis*", the original pen labels of LACM 5833, 5834, and other specimens were solely labeled "*Peromyscus*" (Figure 2). Later curatorial staff added species and subspecies epithets in pencil, but von Bloeker himself appears not to have resolved these identifications. Notes from a 1941 expedition to SCL further support this interpretation: "Jack von Bloeker secured … a considerable number of the San Clemente white-footed mouse, *Peromyscus maniculatus clementis*. In addition, several examples of *Peromyscus*, *Reithrodontomys* and *Microtus*, not yet

determined, were taken, and are being given further study" (Comstock 1946). Some pencil annotations even list the species epithet such as "*boylii*" or "*californicus*", though no diagnostic characters for these species were observed in the specimens we examined. Nonetheless, we recommend molecular identification for these specimens, especially those with damaged teeth or without skulls, to definitively resolve this issue without further misidentifications.

Several unusually large *Peromyscus* specimens from Santa Rosa and Anacapa Islands share similar labeling patterns to those on San Clemente, with pen-labeled "*Peromyscus*" and pencil-marked "*boylii*". On Anacapa, four such specimens (LACM 7394-7397) were genetically confirmed *P. gambelii*, along with other individuals with outlier total body lengths (Figure 5C). von Bloeker himself noted large body sizes and tail lengths in his description of the Anacapa subspecies (von Bloeker Jr 1941), and large body sizes and tail lengths on Santa Cruz Island are consistent with known subspecific traits (Nelson and Goldman 1931), with multiple outliers for total body length genetically confirmed as *P. gambelii*.

Santa Rosa Island presents a more ambiguous case. A significant series of large-bodied specimens collected in 1939 from Elderberry and Cherry Canyons were not genetically tested, and dental characters were inconclusive. von Bloeker described *P. m. sanctaerosae* as one of the smallest island mouse subspecies with uniquely short tails (von Bloeker Jr 1940), yet our morphological analysis identified several outliers exceeding 170 mm in total length. Comparing von Bloeker's reported specimen counts to current LACM holdings suggests that these outliers were excluded from his subspecies description, possibly because he did not consider them *P. m. sanctaerosae*. Their collection near Vail Ranch, where calves were routinely shipped for nearly a century, provides a plausible introduction pathway via livestock transport. Without genetic data or field notes, the identity of these large Santa Rosa mice remains unresolved.

Although we detected evidence of non-native *Peromyscus* on San Clemente and possibly Santa Rosa Islands using standard measurements, morphological identification in this group is inherently challenging. *Peromyscus* is highly diverse, with unresolved species complexes and substantial phenotypic variation that complicates differentiation among sympatric lineages (Rich *et al.* 1996; Platt *et al.* 2015; Castañeda-Rico *et al.* 2025). Channel Island deer mice also exhibit mild island gigantism making them larger than mainland forms (Collins *et al.* 1979; Gill 1980). These size differences reduce the utility of identification keys based on mainland *Peromyscus*, as exemplified by the many genetically confirmed island mice with a tail to body ratio of exceeding 0.9 (Figure 5C). Morphological plasticity on the Channel Islands further complicates identification (Pergams and Ashley 1999), though we minimized this by restricting analyses to specimens collected during the same three-year survey period. While von Bloeker likely suspected that unusually large *Peromyscus* on San Clemente were atypical, similar suspicions may have applied to outlier Anacapa and Santa Cruz specimens.

Implications and further directions. LACM 5833, LACM 5834, and other specimens may not have been correctly identified as *P. truei* because this species is not typically associated with island invasions. In fact, insular forms of *P. truei*, native or introduced, have never been reported. While some subspecies specialize in piñon-juniper habitats, California *P. truei* occupy a diversity of habitats, including chaparral on canyon slopes (Hoffmeister 1981), suggesting suitable habitat exists on the Channel Islands, even on comparatively depauperate SCL. Limited post-CIBS collecting makes it unclear whether *P. truei* populations persisted past the 1940s. Although *P. truei* is absent from published records and platforms like iNaturalist (Knapp *et al.* 2021), it is likely that Channel Island rodent identifications are rarely scrutinized beyond the generic level with only one known local *Peromyscus* species. Determining whether *P. truei* remains extant on SCL is critical, as introduced rodents may thrive in degraded habitats and threaten the critically imperiled endemic *P. gambelii clementis*. Monitoring is essential as restoration progresses to assess shifts in rodent communities. While eradication of black rats on Anacapa succeeded without negatively affecting native island deer mice populations (Howald *et al.* 2010; Ozer *et al.* 2011), similar efforts for *P. truei* on SCL would be impractical due to the island's large size and *P. truei*'s morphological similarity to native island deer mice.

Over 80 years after the CIBS, museum genomics has resolved long standing misidentifications within *Peromyscus*, confirming that large-bodied Anacapa and Santa Cruz specimens belong to endemic subspecies, while revealing a cryptic invasion of *P. truei* on SCL. Cytochrome *b* comparisons link these specimens to mainland California populations, consistent with the hypothesis that hay bales imported from San Diego during the 1930s may have inadvertently translocated multiple species of wild rodents (von Bloeker Jr 1967). Morphological evidence suggests *P. truei* may have formed substantial populations on SCL, and perhaps on Santa Rosa Island. We recommend molecular screening and comprehensive morphological analysis in collections and targeted field surveys to test identifications and better understand the scope of these introductions. Accurate identification is essential for conservation management on the Channel Islands, and for collections-based research in this taxonomically complex group.

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Declaration of Artificial Intelligence use

No generative AI tools were used in the preparation of this manuscript.

Author contributions

Madeleine A. Becker: Conceptualization, Formal Analysis, Funding Acquisition, Investigation, Visualization, Writing – Original Draft Preparation, Writing – Review & Editing; Kayce C. Bell: Data Curation, Investigation, Writing – Review & Editing; Selena Lopez-Ortiz: Formal Analysis, Visualization, Writing – Review & Editing; Jesús E. Maldonado: Conceptualization, Funding Acquisition, Resources, Supervision, Writing – Review & Editing; Cody W. Edwards: Funding Acquisition, Supervision, Writing – Review & Editing; Susette Castañeda-Rico: Conceptualization, Formal Analysis, Supervision, Visualization, Writing – Original Draft Preparation, Writing – Review & Editing.

Supplementary data

SD1. A) Measurements from Natural History Museum of Los Angeles County (LACM) Channel Island *Peromyscus* specimens collected during the Channel Islands Biological Survey (1939-1941), which were genetically sampled and morphologically examined. All metadata are derived from original study skin tags, except for tail to body size ratio, which was calculated from these measurements. B) Measurements from Natural History Museum of Los Angeles County (LACM) Channel Island Peromyscus specimens collected during the Channel Islands Biological Survey (1939-1941), which were morphologically examined but not genetically sampled. All metadata are derived from original study skin tags, except for tail to body size ratio, which was calculated from these measurements. C) GenBank and Sequence Read Archive accession numbers for annotated mitochondrial genomes, novel cytochrome b haplotypes, and shotgun genomic data generated.

SD2. Shotgun sequencing and mito-chondrial genome assembly statistics for San Clemente Island *P. truei* specimens (LACM 5833, LACM 5834), San Clemente Island mouse (*P. gambelii clementis*; LACM 6722), and reference *P. truei truei* (USNM 603235).

SD3. Kronagrams displaying classi-fication results of low coverage whole genome data, restricted to reads classified as *Peromyscus* at the genus level: A) LACM 5833 (*P. truei*), B) LACM 5834 (*P. truei*), and C) LACM 6722 (*P. gambelii clementis*).

SD4. Time-scaled mitogenome tree inferred by BEAST, showing the positions of LACM 5833 and LACM 5834 (*P. truei*) and LACM 6722 (*P. gambelii clementis*), subset to the tribe Peromyscini and its sister genus (*Onychomys*). Nodes are labeled with median estimated divergence time in millions of years, with green bars displaying the 95% confidence interval.

SD5. Maximum Likelihood mito-genome consensus tree showing positions of LACM 5833 and LACM 5834 (*P. truei*), and LACM 6722 (*P. gambelii clementis*), subset to the tribe Peromyscini and its sister genus (*Onychomys*). The *Peromyscus truei* species group is highlighted in red, and the *Peromyscus maniculatus* species group is highlighted in blue. Clade names and sequences are replicated from Castañeda-Rico *et al.* 2025. Nodes with black dots indicate high Ultrafast bootstrap support >95.

SD6. Maximum Likelihood cytochrome *b* consensus tree showing positions of LACM 5833 and LACM 5834 within *Peromyscus truei*. Clades are labeled in accordance with Hernández-Canchola *et al.* (2022). The *P. truei* II clade includes all haplotypes sequenced from California specimens. This phylogenetic tree has been subset to *P. truei* and its sister (*P. gratus*) for relevance. Nodes with black dots indicate high Ultrafast bootstrap support >95.

SD7. Distribution of study skin measurements from Channel Islands Biological Survey specimens (n=701) prepared by Jack von Bloeker. Boxplots of total body size by island (mm) with A) pregnant females foregrounded according to reproductive status as originally recorded on tags by von Bloeker, B) immature individuals foregrounded according to age class as originally recorded on tags by von Bloeker.

SD8. Distribution of study skin measurements from Channel Islands Biological Survey specimens (n=701) prepared by Jack von Bloeker. Boxplots of total body size (mm) by island and by sex.

SD9. Measurements from National Museum of Natural History (USNM) Channel Island *Peromyscus* specimens collected before the Channel Islands Biological Survey. All

metadata are derived from original study skin tags, except for tail to body size ratio, which was calculated from these measurements. Many specimen tags did not include complete metadata, resulting in missing data.

SD10. Santa Barbara Museum of Natural History (SBMNH) *Peromyscus* (SBMNH:MAM:7619-7620, SBMNH:MAM:7622) and *Onychomys* (SBMNH:MAM:7621, SBMNH:MAM:9202-9203;) specimens originally collected on San Clemente Island during the Channel Islands Biological Survey. *Onychomys* specimens had been erroneously re-labeled as *P. maniculatus* in collections.

SD11. Measurements of Santa Barbara Museum of Natural History (SBMNH) *Peromyscus* and *Onychomys* specimens originally collected on San Clemente Island during the Channel Islands Biological Survey. *Onychomys* specimens had previously been re-labeled as *P. maniculatus* in collections. All metadata are derived from original study skin tags, except for tail to body size ratio, which was calculated from these measurements.

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