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RESEARCH PAPER

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DNA barcoding of Philippine cave-dwelling bats (Chiroptera) in Tabaco cave using the cytochrome c oxidase subunit I (COI) gene

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ABSTRACT

DNA barcoding utilizing the cytochrome c oxidase subunit I (COI) gene was employed to identify the cave-dwelling bats in Tabaco cave, Sta. Teresita, Cagayan, Philippines, an unexplored site for molecular bat research. This study integrated preliminary morphological classification with confirmatory COI barcoding to identify species within this understudied assemblage. Three species from two families were identified: *Hipposideros ater* and *Hipposideros lekaguli* (Hipposideridae), and *Miniopterus australis* (Miniopteridae). Molecular validation corrected initial morphological assignments for several specimens, demonstrating high sequence similarity with reference sequences in the genetic databases, thereby resolving ambiguities within cryptic species complexes. The findings underscore the limitations of relying solely on morphology for species delineation in groups with overlapping phenotypic traits, such as *Hipposideros* and *Miniopterus*. This research provides the first molecular assessment of Tabaco cave's bat community and highlights the critical role of integrative taxonomy, combining genetic data with morphological examination, for accurate biodiversity assessment. The results establish essential baseline data for the conservation of Philippine chiropteran diversity and advocate for an integrated framework to inform evidence-based conservation strategies for these ecologically pivotal and threatened taxa.

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INTRODUCTION

The Philippines, a recognized megadiverse nation, harbors more than 75% of global biodiversity within ecosystems renowned for exceptional species richness and a high degree of endemism (Pitchay and Torrentira, 2022). Its documented fauna exceeds 100,000 animal species (Ramachandran, 2023), among which bats (order Chiroptera) form the most diverse mammalian group (Tanalgo and Dela Cruz, 2026; Cruz and Pader, 2018). These species extensively inhabit the limestone karst caves that punctuate the major islands of the Philippines (Cruz and Pader, 2018). Moreover, Chiroptera is the second most diverse mammalian order worldwide (Hao *et al.,* 2024). The island of Luzon, a major biogeographic region renowned for its rich ecological communities and mammalian diversity, houses the world's highest concentration of unique bat species (Heaney *et al.,* 2016; Vallejo, 2014), with current records listing at least 57 species (Pader *et al.,* 2017).

Bats are ecologically pivotal organisms. They provide critical services such as pollination, seed dispersal, insect population control, and nutrient cycling via guano deposition (Jeyapraba *et al.,* 2023; Ramirez-Francel *et al.,* 2021). Despite their ecological significance, bat populations face escalating threats from habitat degradation, anthropogenic disturbances, and climate change, which are projected to alter their abundance and distribution (Tanalgo *et al.,* 2025; Castillo-Figueroa, 2020; Frick *et al.,* 2019). Effective conservation planning, therefore, relies on accurate species identification and a clear understanding of population status (Hu *et al.,* 2025). Traditional morphological identification of bats, however, can be challenging due to cryptic diversity and phenotypic plasticity, particularly in poorly studied regions (Wilson and Mittermeier, 2019; Cruz and Pader, 2018). Consequently, molecular techniques like DNA barcoding have become pivotal tools for reliable species identification, assessment of biodiversity, and discovery of cryptic species (Alam *et al.,* 2024; Gawade, 2024; Chac and Thinh, 2023). For molecular analysis targeting species-level differentiation, the cytochrome c oxidase subunit I (COI) gene serves as an ideal biological marker due to its rapid mutation rate, enabling the distinction of closely related species while remaining conserved among conspecifics and congenerics (Labonete *et al.,* 2025; Alam *et al.,* 2024; Kurata *et al.,* 2024; Liu *et al.,* 2016; Wilson-Wilde *et al.,* 2010). This gene is the standard marker used in DNA barcoding to identify species and to evaluate evolutionary relationships and genetic diversity across varied animal taxa (Alam *et al.*, 2024; Kurata *et al.*, 2024; Bacus *et al.,* 2021; Hebert *et al.,* 2003). The adherence to this marker enables standardized protocols, which promotes global comparability and data sharing among researchers.

Despite the established utility of DNA barcoding, in the Philippines, many cave ecosystems and their chiropteran inhabitants remain profoundly understudied from a molecular perspective (Quibod *et al.,* 2019). While pioneering studies have applied DNA barcoding to fruit bats (e.g., Bacus *et al.,* 2021; Luczon *et al.,* 2019) and some cave-dwelling species in Central Luzon (Pader *et al.,* 2017), vast geographical and taxonomic gaps persist. This is particularly true for Region 2 (Cagayan Valley), which contains numerous understudied caves and lacks any molecular studies on bat fauna. Tabaco Cave in Sta. Teresita, Cagayan, is one such significant yet unexplored site for molecular faunal research. Prior to this study, no DNA barcoding had been conducted on the bat assemblage within this cave.

To address these regional and methodological gaps, this study was conducted to obtain a survey of the cave-dwelling bat community in Tabaco Cave. The objectives of this research were to perform a preliminary morphological characterization of collected bat specimens and validate and confirm these morphological identifications through definitive species identification using DNA barcoding of the COI gene. This work provides the first molecular assessment of Tabaco Cave's bats, thereby contributing essential baseline data for the conservation and systematic understanding of Philippine chiropteran diversity.

MATERIALS AND METHODS

Study area

Tabaco Cave. Luga, Sta. Teresita, Cagayan. 18°12'55.2"N; 121°52'41.5"E. Alt. ca. 33 m. Length: 163 m. This is an important cave (class III) in Sta. Teresita, Cagayan. It consists of a single NE-SW-directed main gallery with two entrances and a daylight hole in the NE section of the cave, as well as several impressive chambers. The cave was formed in a phreatic environment as witnessed by tubular cross-sections. The 20-meter-wide by 5-meter-high NE entrance leads to an entrance chamber with nice calcite decoration and a floor covered by sediment with only a few boulders. About 70 meters from the entrance a daylight hole in the roof of the cave marks the beginning of a smaller cave section that has a low subsidiary entrance to the north. Behind the short narrow cave section the main gallery opens again to a width of 6-8 meters by a height of 5-8 meters. The gallery soon opens to a huge circular chamber with a diameter of 30 meters with a little pool of water at its deepest point. At the SW end of the chamber a low passage continues with a pool of water but soon terminates in a boulder-filled dead-end.

Ethical statement and permits

The research protocol received formal approval (IREB Protocol No. 2024-10-18) from the Institutional Ethics Review Board of Isabela State University on December 4, 2024. All procedures adhered to principles of ethical wildlife research. Prior to fieldwork, the researcher secured the necessary clearance from the Local Government Unit of Sta Teresita, Cagayan, Philippines, and Wildlife Gratuitous Permit by the Department of Environment and Natural Resources (DENR) Regional Office 2, which authorized the capture, handling, and transport of specimens for scientific purposes.

Specimen collection and preservation

Bat sampling was conducted in Tabaco Cave (Luga, Sta. Teresita, Cagayan). Following safety protocols, the researcher and the field assistants utilized Level A Personal Protective Equipment (PPE), including full-body protective suits, puncture-resistant gloves, face shields or masks, and respirators, to mitigate zoonotic risks. Bats were captured using mist nets (Benitez *et al.,* 2021) strategically deployed at cave entrances.

Upon capture, only a single voucher specimen per species was retained for further analysis while all non-target individuals were immediately released at the site of capture.

Representative of each species was selected with the aid of standard taxonomic keys and bat identification references, ensuring one specimen per species (Ingle *et al.,* 1992; Heaney *et al.,* 2010). For each voucher specimen, standard morphometric data were recorded using digital calipers (to the nearest 0.1 mm) (Schmieder *et al.,* 2015). Their body mass (measured to the nearest 0.1 g using a spring balance) was also recorded. Measurements included head-body length (HBL: from the snout to the tail base), forearm length (FL: elbow to wrist), ear length (EL: base to distal tip), tail length (TL: tail base to the tip), tibia length (TBL: knee to ankle), and hind foot length (HL: heel to the tip of the longest digit/toe), following established protocols (Schmieder *et al.,* 2015). Ear width (EW) and thumb length were also measured. Specimens were photographed, assigned unique catalog numbers (JCC005/E–JCC008/H), fixed in 10% formalin, and ultimately preserved in 70% ethanol for long-term deposition at the Andres Biwag Learning Center Mini Museum, Isabela State University Cabagan Campus, Isabela, Philippines.

Morphological identification

Initial species identification was performed in the field using standard taxonomic keys for Philippine bats (Ingle *et al.,* 1992; Heaney *et al.,* 2010). All preliminary identifications were subsequently verified by an expert curator affiliated with the Vertebrate Museum, Institute of Biology, College of Science, University of the Philippines Diliman, Quezon City, Philippines.

Collection of tissue samples

Prior to the preservation of bat specimens at the Andres Biwag Learning Center's biological mini museum, tissue samples were collected from captured bats. Specifically, 2 mm wing punches were excised from the plagiopatagium (wing membrane) using sterile biopsy tools (Boston *et al.,* 2012). The excised tissue samples from each bat were immediately preserved in separate sterile vials containing molecular-grade 100% ethanol to maintain nucleic acid integrity (Luczon *et al.,* 2019). The 4 vials, representing each collected specimen, were labeled JCC005/E through JCC008/H. For transport, the vials were securely sealed and moved under controlled conditions to the laboratory for subsequent DNA extraction and analysis.

Molecular identification

The preserved tissue samples were submitted to the DNA Barcoding Laboratory, University of the Philippines Diliman, for molecular identification. The laboratory's protocols included: DNA extraction from tissue samples using the Isolate II Genomic DNA Kit (Bioline); amplification of the cytochrome c oxidase subunit I (COI) gene using the primers VF1 (5'-TTCTCAACCAACCACAARGAYATYGG-3') and VR1 (5'-TAGACTTCTGGGTGGCCRAARAAYCA-3') established by Ivanova *et al.* (2007); and performance of PCR reactions in 20 µL volumes consisting of 10 µL HS RedMix, 6.7 µL ultrapure water, 0.65 µL of each primer (10 µM), and 2 µL of DNA. The amplified samples were sent to Macrogen (South Korea) for bidirectional sequencing. The resulting sequences obtained from Macrogen were assembled and trimmed using the Staden package (Staden *et al.,* 1999). Specimens were analyzed and identified using BLAST in GenBank, and the BOLD identification engine was also utilized to match sample sequences against a verified COI database.

RESULTS

Table 1 presents the morphometric and biological trait data of field-collected bats, which were essential for morphological identification. Table 2 shows the results of the morphological and molecular identification of the four collected bats, conducted by experts from the University of the Philippines Diliman. Fig. 1-3 provide photographs, conservation status, and diagnostic characteristics of the three successfully identified cave bats based on the identification keys of Heaney *et al.* (2010).

The collected bat specimens (JCC005/E and JCC008/H) were definitively identified as *Hipposideros ater*. This species is commonly known as the Common Dusky Round-leaf Bat, Bicolored Leaf-nosed Bat, Common Dusky Leaf-nosed Bat, or Dusky Leaf-nosed Bat.

Furthermore, this species is listed as Least Concern on The IUCN Red List of Threatened Species (Armstrong, 2021). The morphometric measurements (Table 1) and observed phenotypic traits of the specimens also aligned with the standard taxonomic keys of *H. ater* detailed by Heaney *et al.* (2010) and Ingle and Heaney (1992). As described by these authors, *H. ater* is a small bat species characterized by the following morphological measurements (in mm): total length 71-81; tail length 27-36 (typically 28-32); hind foot 7-9; ear 17-20; forearm 38-43. Body mass ranges from 5-7 g. It possesses large ears and a prominent noseleaf. Pelage coloration is variable within populations, ranging from dark brown to orange. Dorsal fur is distinctly bicolored: the distal one-third of each hair is dark brown or orange, contrasting with a pale tan to near-white basal two-thirds. Ventral pelage is similarly bicolored but with less intensely pigmented tips and a darker tan base. The noseleaf is small, narrower than the muzzle, and lacks lateral leaflets; the internarial septum is swollen basally. *Hipposideros ater* can be distinguished from several congeners by the following combination of traits. *H. pygmaeus* is smaller (total length 60-67 mm; forearm 38-40 mm; ear 11-15 mm) and possesses two pairs of lateral leaflets on the anterior noseleaf. *H. bicolor* is slightly larger (forearm 42-45 mm) and has a single pair of lateral leaflets. *H. coronatus* is notably larger (forearm 47-51 mm), with an elongated rostrum and unpigmented lower legs and foot soles. *H. obscurus* (forearm 42-47 mm) has a shorter tail (18-21 mm) and two pairs of lateral leaflets. *H. cervinus* is significantly larger in overall size.

Table 1. Morphometric and biological trait data of field-collected bats

Species no.	Sex	Weight	HBL	FL	EL	EW	TL	TBL	HL	Thumb length
Tabaco cave (Luga, Sta Teresita, Cagayan)										
JCC005/E	M	7	40mm	45.8mm	21.4mm	14.0mm	17.6mm	21.4mm	9 mm	4.1mm
JCC006/F	M	23	62.6mm	68.3mm	30.7mm	22.5mm	40.9mm	27.1mm	11.7mm	5.8mm
JCC007/G	M	5	37.1mm	34.3mm	10.8mm	8.9mm	34.7mm	14.3mm	7.3mm	3.8mm
JCC008/H	M	5	35.1mm	39.8mm	17mm	13.6mm	27.9mm	17.6mm	7.5mm	2.4mm

Table 2. Results of the morphological and molecular identification of the 4 collected bats

Sample label	Morphological identification	Molecular identification					
		GenBank species match	% match	Accession number	Bold database species match	% match	Sample ID
JCC005/E	*Rhinolophus arcuatus*	*Hipposideros pomona*	91.17	HM540598	*Hipposideros ater*	99.84	Private
JCC006/F	*Hipposideros lekaguli*	*Hipposideros lekaguli*	95.99	MW981434	No match	N/A	N/A
JCC007/G	*Miniopterus paulus*	*Miniopterus fuliginosus*	89.05	MH523628	*Miniopterus australis*	99.69	Private
JCC008/H	*Hipposideros antricola*	*Hipposideros pomona*	90.85	MN056566	*Hipposideros ater*	99.19	Private

Fig. 1. *Hipposideros ater* (Templeton in Blyth, 1848)

Fig. 2. *Hipposideros lekaguli* (Thonglongya and Hill, 1974)

Fig. 3. *Miniopterus australis* (Tomes, 1858)

The collected bat specimen (JCC006/F) was definitively identified as *Hipposideros lekaguli*. This species is commonly known as the Large Asian Round-leaf Bat. Moreover, it is listed as Near Threatened on The IUCN Red List of Threatened Species (Csorba *et al.,* 2019). The morphometric measurements (Table 1) and observed phenotypic traits of the specimen aligned with the standard taxonomic keys of *H. lekaguli* detailed by Heaney *et al.* (2010) and Ingle and Heaney (1992). As described by these authors, *H. lekaguli* is one of the most distinctive bats in the Philippines, distinguished by its large noseleaf featuring a trilobed posterior portion inflated into three conspicuous "pockets" and two lateral leaflets flanking the anterior noseleaf. Key identification features include a total length of 115 mm, tail length of 40-43 mm, hind foot measuring 12 mm, ear length of 27-32 mm, forearm length of 64-72 mm, and a weight of 21 g. It is notably differentiated from *Hipposideros diadema*, which is significantly larger (forearm 77-88 mm) and lacks the trilobed, inflated pockets on the posterior noseleaf. All other *Hipposideros* species in the region are substantially smaller in size, further emphasizing the unique morphological and metric traits of this bat.

The collected bat specimen (JCC007/G) was definitively identified as *Miniopterus australis*. This species is commonly known as the Little Long-fingered Bat or Little Bent-winged Bat. Additionally, it is listed as Least Concern on The IUCN Red List of Threatened Species (Armstrong, 2021). The morphometric measurements (Table 1) and observed phenotypic traits of the specimen aligned with the standard taxonomic keys of *M. australis* detailed by Heaney *et al.* (2010) and Ingle and Heaney (1992). As described by these authors, the species, consistent with all *Miniopterus*, displays very dark brown fur that is longer over the shoulders and head compared to the rest of the body, a short, blunt tragus broadest at the tip, and a wing structure where the tip of the longest digit folds tightly backward against the adjacent wing membrane-a defining trait referenced in its English common name. Key diagnostic measurements include a total length of 81-91 mm, tail 34-43 mm, hind foot 7-9 mm, ear 9-11 mm, forearm 34-39 mm, and a weight of 5-6 g. It is distinguished from related species by size and morphological details. *Miniopterus schreibersii* is larger (total length 101-112 mm, forearm 42-46 mm), while *M. tristis* is significantly larger still. Among *Myotis* species, *M. muricola* is smaller (total length 69-79 mm, forearm 30-34 mm) and possesses a long, slender tragus. *Myotis ater* is similar in size but has a longer ear (14-15 mm) and a slender tragus. *Pipistrellus javanicus* differs in its shorter fur, broad, swollen-appearing muzzle, and a tragus that is short and blunt but not broadest at the tip. These distinctions in size, tragus shape, and other appendage features aid in precise identification.

DISCUSSION

The identification process integrated a preliminary morphological classification with definitive validation through DNA barcoding of the cytochrome c oxidase subunit I (COI) gene. The study further confirmed and supported species identities from DNA barcoding by corroborating molecular results, which exhibited reliable percent matches, with morphological data. A comparison of the molecularly identified species and the actual specimens' morphometric measurements against the identification keys of Heaney *et al.* (2010) demonstrated an alignment between the molecular identification and morphological assessment. Ultimately, the integration of genetic and morphological evidence provided a more holistic understanding of bat taxonomy.

This alignment between methods was directly demonstrated for JCC006/F (*H. lekaguli*). For the remaining specimens, molecular data were accorded precedence due to high sequence similarity (>95%) in reference databases, which was subsequently corroborated by re-examined morphological traits consistent with standard taxonomic keys (Heaney *et al.,* 2010). For instance, JCC005/E and JCC008/H (initially morphologically classified as *R. arcuatus* and *H. antricola*) exhibited 99.84% and 99.19% matches with *H. ater* in the Barcode of Life Data Systems (BOLD), surpassing the ~91% match with *H. pomona* in GenBank. Similarly, JCC007/G (initially morphologically aligned with *M. paululus*) had a 99.69% match with *M. australis* in BOLD, contrasting with the 89.05% match to *M. fuliginosus* in GenBank. These results underscore the critical role of molecular validation in correcting or refining morphological assignments.

The need for such corrections underscores the persistent challenge in chiropteran studies that reliable species identification, a cornerstone of ecological and conservation work, is inherently difficult due to widespread cryptic diversity (Mayo and Monro, 2022; Mulvaney *et al.,* 2023). Reliance solely on morphology, particularly superficial or non-systematic assessments of subtle phenotypic differences like fur color or wing morphology, can obscure the delineation species boundaries (Trail, 2021). This is evident in complexes such as *Hipposideros* corroborated by the findings of this study, where *H. ater*, *H. antricola*, and *H. diadema* exhibit overlapping external characteristics (Heaney *et al.,* 2010; Ingle *et al.,* 1992) despite being genetically distinct (Murray *et al.,* 2012).

Additionaly, *Miniopterus* species such as *M. eschscholtzii* and *M. schreibersii* (bent-winged bats) share near-identical phenotypes (Heaney *et al.,* 2010; Ingle *et al.,* 1992) despite significant genetic divergence. This genetic divergence of the two *Miniopterus sp.* was demonstrated through COI barcoding and aligns with the research of Wilson and Mittermeier (2019). DNA barcoding effectively mitigates these challenges by quantifying genetic divergence, thereby revealing lineages that are morphologically cryptic (Mulvaney *et al.,* 2023; Ahmed *et al.,* 2022; Mota *et al.,* 2022).

While powerful, it is important to recognize that the efficacy of DNA barcoding is contingent upon comprehensive and accurately curated reference databases (Shneyer and Rodionov*,* 2025). Limitations arise when queried sequences lack close matches in repositories like GenBank or BOLD, and misclassification may occur when sequence similarities do not meet arbitrarily defined thresholds, such as the commonly applied >95% COI match criterion.

Discrepancies in top matches between databases, as observed for some specimens in this study, highlight potential ambiguities and underscore that molecular results should not be interpreted in isolation. In such contexts, integrative taxonomy, including the synthesis of genetic data with detailed morphological examination, morphometrics, ecological data, and voucher specimen examination, becomes indispensable for robust species delimitation (Bemis *et al.,* 2023; Sheth and Thaker, 2017).

Therefore, the application of integrative taxonomy holds profound implications for conservation biology. Accurate species delineation enables the protection of evolutionarily distinct lineages, ensuring conservation resources or strategies prioritize genetically unique taxa rather than broad morphospecies (Nielsen *et al.,* 2023). Effective habitat management also depends on precise identification as ecologies differ significantly (Nielsen *et al.,* 2023). Furthermore, in disease ecology, precisely identifying reservoir host species is critical for understanding zoonotic transmission dynamics (Nguyen *et al.*, 2025; Plowright *et al.,* 2016). Finally, vouchered specimens with associated genetic sequences enhance public databases, resolving taxonomic ambiguities and building a more reliable foundation for future research (Bemis *et al.,* 2023).

CONCLUSION

This study successfully identified the cave-dwelling bats of Tabaco Cave, Cagayan, using an integrative approach combining morphological assessment with COI-based DNA barcoding. Three species—*Hipposideros ater*, *Hipposideros lekaguli*, and *Miniopterus australis*—were confirmed. Molecular evidence proved essential in resolving taxonomic ambiguities, correcting several initial morphological misidentifications and highlighting the prevalence of cryptic diversity within Philippine bat fauna.

The study provides the first DNA barcode reference for bats in Tabaco Cave, contributing valuable baseline data for a previously unexplored region. It also reinforces the reliability of COI barcoding while emphasizing the importance of integrating molecular and morphological data for accurate species delineation.

These findings have important implications for biodiversity conservation and public health. Accurate species identification supports targeted conservation strategies, improves ecological understanding, and aids in monitoring potential zoonotic reservoirs. To build on this work, further integrative surveys, long-term monitoring, and community-based conservation initiatives are recommended to ensure the protection of these ecologically significant species and their habitats.

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REFERENCES

Ahmed S, Ibrahim M, Nantasenamat C, Nisar MF, Malik AA, Waheed R, Ahmed MZ, Ojha SC, Alam MK. 2022. Pragmatic applications and universality of DNA barcoding for substantial organisms at species level: A review to explore a way forward. BioMed Research International, Article 1846485. https://doi.org/10.1155/2022/1846485

Alam M, Abbas K, Usmani N, Mustafa M, Husain A. 2024. A comprehensive review on DNA barcoding for species identification across diverse taxa. Munis Entomology and Zoology Journal **19**(2), 1057–1072

Armstrong KN. 2021. *Hipposideros ater*. The IUCN Red List of Threatened Species, e.T80457009A22097974. https://doi.org/10.2305/IUCN.UK.2021-3.RLTS.T80457009A22097974.en

Bacus M, Burgos S, Elizagaque H, Malbog K, Responte M, Gamalo L, Achondo MJM, Murao L. 2021. Pilot fecal DNA barcoding on selected fruit bats in Davao City, Philippines. Philippine Journal of Science **150**, 545–555. https://doi.org/10.56899/150.02.19

Bemis KE, Girard MG, Santos MD, Carpenter KE, Deeds JR, Pitassy DE, Flores NAL, Hunter ES, Driskell AC, Macdonald KS III, Weigt LA, Williams JT. 2023. Biodiversity of Philippine marine fishes: A DNA barcode reference library based on voucher specimens. Scientific Data **10**, 411. https://doi.org/10.1038/s41597-023-02306-9

Benitez AJ, Ricardo-Caldera D, Atencia-Pineda M, Ballesteros-Correa J, Chacon-Pacheco J, Hoyos-Lopez R 2021. DNA barcoding of bats (Chiroptera) from the Colombian northern region. Mammalia **85**(5), 462–470. https://doi.org/10.1515/mammalia-2020-0138

Blyth E. 1864. Report of the curator, zoological department. The Journal of the Asiatic Society of Bengal **32**(4), 451–461. https://doi.org/10.5281/zenodo.16145124

Boston ESM, Puechmaille SJ, Scott DD, Buckley DJ, Lundy MG, Montgomery IW, Prodohl PA, Teeling EC. 2012. Empirical assessment of non-invasive population genetics in bats: comparison of DNA quality from faecal and tissue samples. Acta Chiropterologica **14**(1), 45–52. https://doi.org/10.3161/150811012X654259

Castillo-Figueroa D. 2020. Why bats matter: A critical assessment of bat-mediated ecological processes in the Neotropics. Tropical Conservation Science **13**, 1–15. https://doi.org/10.1177/1940082920943620

Chac L, Thinh B. 2023. Species identification through DNA barcoding and its applications: A review. Biology Bulletin **50**(11), 1143–1156. https://doi.org/10.1134/S106235902360229X

Cruz KJ, Pader L. 2018. Minalungao National Park hosts six Chiroptera species. International Journal of Biological, Pharmaceutical and Allied Sciences **7**(7), 4491–4502. https://doi.org/10.31032/IJBPAS/2018/7.7.4491

Csorba G, Bumrungsri S, Francis C, Bates P, Gumal M, Kingston T, Soisook P. 2019. *Hipposideros lekaguli*. The IUCN Red List of Threatened Species, e.T10144A22091565. https://doi.org/10.2305/IUCN.UK.2019-3.RLTS.T10144A22091565.en

Frick WF, Kingston T, Flanders J. 2019. A review of the major threats and challenges to global bat conservation. Annals of the New York Academy of Sciences **1469**(1), 5–25. https://doi.org/10.1111/nyas.14045

Gawade P. 2024. DNA barcoding based species classification using deep learning. International Journal of Scientific Research in Engineering and Management **8**, 1–5. https://doi.org/10.55041/IJSREM34462

Hao X, Lu Q, Zhao H. 2024. A molecular phylogeny for all 21 families within Chiroptera (bats). Integrative Zoology **19**(5), 989–998. https://doi.org/10.1111/1749-4877.12772

Heaney LR, Balete DS, Rickart EA. 2016. The mammals of Luzon Island: biogeography and natural history of a Philippine fauna. Johns Hopkins University Press.

Heaney LR, Dolar ML, Balete DS, Esselstyn JA, Rickart EA, Sedlock JL. 2010. Synopsis of Philippine mammals. Field Museum of Natural History.

Hebert PDN, Cywinska A, Ball SL, deWaard JR. 2003. Biological identifications through DNA barcodes. Proceedings of the Royal Society B **270**(1512), 313–321. https://doi.org/10.1098/rspb.2002.2218

Hu Y, Zhou W, Hu Y, Wei F. 2025. Conservation evolutionary biology: a unified framework connecting biodiversity conservation. Molecular Biology and Evolution **42**(6), msaf122. https://doi.org/10.1093/molbev/msaf122

Ingle NR, Heaney LR. 1992. A key to the bats of the Philippine Islands. Fieldiana Zoology **69**, 1–440. https://doi.org/10.5962/bhl.title.3504

Ingle NR, Sedlock JL, Heaney LR. n.d. Bats of Mindanao Island, Philippines. Field Museum.

Ivanova NV, Zemlak TS, Hanner RH, Hebert PDN. 2007. Universal primer cocktails for fish DNA barcoding. Molecular Ecology Notes **7**(4), 544–548. https://doi.org/10.1111/j.1471-8286.2007.01748.x

Jeyapraba L, Margaret I, Addline D, Sakthi V. 2023. Prediction of foraging strategy of insectivorous bats through wing morphology. Iranian Journal of Fisheries Sciences.

Kurata S, Mano S, Nakahama N, Hirota SK, Suyama Y, Ito M. 2024. Development of mitochondrial DNA COI primer sets for DNA barcoding. Biodiversity Data Journal **12**, e117014. https://doi.org/10.3897/BDJ.12.e117014

Labonete HJP, Fulgencio BKR, Abatay MP, Ampang MP, Ancheta DJ, Gumal SJR, Jimenez EA, Modina RMR, Yongco JE, Tabugo SRM. 2025. Design and validation of corn-strain-specific primers for fall armyworm detection. Asian Journal of Agriculture **9**(2), 844–853.

Liu QN, Chai XY, Bian DD, Ge BM, Zhou CL, Tang BP. 2016. The complete mitochondrial genome of fall armyworm. Genes & Genomics **38**(2), 205–216. https://doi.org/10.1007/s13258-015-0346-6

Luczon AU, Ampo SAMM, Roño JGA, Duya MRM, Ong PS, Fontanilla IKC. 2019. DNA barcodes reveal high genetic diversity in Philippine fruit bats. Philippine Journal of Science **148**(S1), 133–140

Mayo SJ, Monro AK. 2022. Cryptic species: morphological stasis and hidden diversity. Cambridge University Press. https://doi.org/10.1017/9781009070553

Mota TFM, Fabrin TMC, Diamante NA, de Oliveira AV, Ortencio Filho H, Prioli AJ, Prioli SMAP. 2022. DNA barcode is efficient for identifying bat species. Journal of Mammalian Evolution **29**(1), 63–75. https://doi.org/10.1007/s10914-021-09563-8

Mulvaney J, Moir M, Cherry M. 2023. DNA barcoding reveals cryptic diversification among bats and birds. Biodiversity and Conservation **32**, 1–20. https://doi.org/10.1007/s10531-023-02737-1

Murray SW, Campbell P, Kingston T, Zubaid A, Francis CM, Kunz TH 2012. Molecular phylogeny of hipposiderid bats from Southeast Asia. Molecular Phylogenetics and Evolution **62**(2), 597–611. https://doi.org/10.1016/j.ympev.2011.10.021

Nielsen ES, Henriques R, Hanson JO, Kershaw F, Carvalho SB, Beger M, von der Heyden S 2023. Molecular ecology meets systematic conservation planning. Trends in Ecology & Evolution **38**(2), 143-153. https://doi.org/10.1016/j.tree.2022.09.006

Nguyen HTT, Lindahl JF, Bett B, Nguyen-Viet H, Lam S, Nguyen-Tien T, Unger F, Dang-Xuan S, Bui TX, Le HT, Lundkvist A, Ling J, Lee HS. 2025. Understanding zoonotic pathogens and risk factors from wildlife in Southeast Asia: a systematic literature review. Veterinary Quarterly **45(1)**, 1–17. https://doi.org/10.1080/01652176.2025.2475990

Pader LD, Banson CJGC, Pranilla WAP, Barroga KJD, Morales ND, Martin LO, Cumbe AP, Medel NFS, Ventura ZA, Battad ZG, Judan Cruz KG. 2017. DNA barcoding of chiropterans at Minalungao National Park, Nueva Ecija, Philippines. International Journal of Agricultural Technology **13**(7.3), 2341–2344

Pitchay RB, Torrentira MC Jr. 2022. Philippine biodiversity in a glance. American Journal of Humanities and Social Sciences Research **6**(6), 186-189

Plowright RK, Peel AJ, Streicker DG, Gilbert AT, McCallum H, Wood J, Baker ML, Restif O. 2016. Transmission or within-host dynamics driving pulses of zoonotic viruses in reservoir-host populations. PLoS Neglected Tropical Diseases **10**(8), e0004796. https://doi.org/10.1371/journal.pntd.0004796

Quibod MNR, Alviola P, de Guia AP, Cuevas V, Lit I, Pasion B. 2019. Diversity and threats to cave-dwelling bats in a small island in southern Philippines. Journal of Asia-Pacific Biodiversity **12**. https://doi.org/10.1016/j.japb.2019.06.001

Ramachandran S. 2023. Building back biodiversity. United Nations Development Programme. https://www.undp.org/philippines/blog/building-back-biodiversity

Ramirez-Francel LA, Garcia-Herrera LV, Losada-Prado S, Reinoso-Florez G, Sanchez-Hernandez A, Estrada-Villegas S, Lim BK, Guevara G. 2021. Bats and their vital ecosystem services: a global review. Integrative Zoology **17**(1), 2–22. https://doi.org/10.1111/1749-4877.12552

Schmieder DA, Benitez HA, Borissov IM, Fruciano C. 2015. Bat species comparisons based on external morphology: A test of traditional versus geometric morphometric approaches. PLOS ONE **10**(5), e0127043. https://doi.org/10.1371/journal.pone.0127043

Sheth BP, Thaker VS. 2017. DNA barcoding and traditional taxonomy: An integrated approach for biodiversity conservation. Genome **60**(7), 618-628. https://doi.org/10.1139/gen-2015-0167

Shneyer VS, Rodionov AV. 2025. 20 years of DNA barcoding: achievements and problems. Biochemistry (Moscow) **90**(11), 1602–1619. https://doi.org/10.1134/S0006297925602977

Staden R, Beal KF, Bonfield JK. 1999. The Staden package. In: bioinformatics methods and protocols, 115–130. https://doi.org/10.1385/1-59259-192-2:115

Tanalgo K, Dela Cruz K. 2026. BatMapPH: Philippine bat species occurrence database. Eco/Con Lab Biodiversity Synthesis+ Centre. https://doi.org/10.15468/x8vxpr

Tanalgo KC, Dela Cruz KC, Russo D. 2025. Susceptibility of bats to ecological and evolutionary traps. Biological Conservation **305**, 111110. https://doi.org/10.1016/j.biocon.2025.111110

Thonglongya K, Hill JE. 1974. A new species of *Hipposideros* (Chiroptera) from Thailand. Mammalia **38**(2), 285–294.

Tomes RF. 1858. A monograph of the genus *Miniopteris*. Proceedings of the Zoological Society of London **26**(1), 115-128. https://doi.org/10.1111/j.1469-7998.1858.tb06353.x

Trail PW. 2021. Morphological analysis: a powerful tool in wildlife forensic biology. Forensic Science International: Animals and Environments **1**, 100025. https://doi.org/10.1016/j.fsiae.2021.100025

Vallejo B. 2014. Biogeography of Luzon Island, Philippines. In: Telnov D (ed.), Biodiversity, biogeography and nature conservation in Wallacea and New Guinea **2**, 47-60. https://biostor.org/reference/245652

Wilson DE, Mittermeier RA. 2019. Miniopteridae. In: handbook of the mammals of the world: bats, 674–709. https://doi.org/10.5281/zenodo.5735202

Wilson-Wilde L, Norman J, Robertson J, Sarre S, Georges A. 2010. Current issues in species identification for forensic science and the validity of using the COI gene. Forensic Science, Medicine and Pathology **6**(3), 233-241. https://doi.org/10.1007/s12024-010-9172-y