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DATA NOTE

The genome sequence of *Rhynchonycteris naso, Peters, 1867 (Chiroptera, Emballonuridae, Rhynchonycteris)* [version 1; peer review: 3 approved]

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Abstract

We present a reference genome assembly from an individual male *Rhynchonycteris naso* (Chordata; Mammalia; Chiroptera; Emballonuridae). The genome sequence is 2.46 Gb in span. The majority of the assembly is scaffolded into 22 chromosomal pseudomolecules, with the Y sex chromosome assembled.

Keywords

Rhynchonycteris naso, genome sequence, chromosomal, Bat1K

Open Peer Review

Approval Status ✓ ✓ ✓

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Competing interests: NZ and BPO are employees of Paratus Sciences Corporation and are option holders. PP serves as consultant for Paratus Sciences Corporation. IAVT, MK, MN, GF,LA, NB, EJ, VT, JLG, MP, MM, ECT and SCV declare no competing interests.

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Species taxonomy

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Chiroptera; Yangochiroptera; Emballonuroidea; Emballonuridae; Emballonurinae; *Rhynchonycteris*; *Rhynchonycteris naso*[1–4].

Introduction

Emballonurid bats are aerial insectivores. They are found in Africa and Indo-Malayan, Australian, Neotropical, and Holarctic regions. Although typically found in tropical forest regions, a few species have been found in semiarid and desert regions[5].

The Emballonuridae family comprises two subfamilies: Taphozoinae and Emballonurinae. Emballonurinae consists of 14 genera and 55 species[6]. The genus *Rhynchonycteris* is within Emballonurinae and comprises a sole species: *Rhynchonycteris naso* (*Rhynchonycteris* is one of four monotypic genera in Emballonuridae) (Figure 1).

Rhynchonycteris naso, the proboscis bat, has been found in tropical regions in middle and south America from the south of Mexico to the north of Bolivia and center of Brazil[5]. Proboscis bats are found up to 1500 meters elevation, generally at less than 500 meters elevation, often in lowland tropical forest, close to water bodies[5]. They roost in an exposed manner on tree trunks or man-made structures in the vicinity of water[7]. Their grey and brown marbled coat makes them well camouflaged, they often look like tree bark (see Figure 2) or may be perceived as swaying leaves since they may form a single line along the tree's length (Figure 2A–B) and can be observed rocking back and forth[5,8]. They live in stable multi-male-multi-female groups of usually <40 individuals[7]. Male mating strategies are based on both direct female-defense and male territoriality[9,10]. A substantial proportion of males are philopatric[9].

Rhynchonycteris naso has been commonly referred to as long-nosed and or sharp-nosed bat in reference to the nose protruding from the rest of the face. They are small bats 36–48 mm body size with added ~11–17 mm of tail length, the forearm length is ~36–40 mm and they weigh around 3–6 g[5]. Although the family Emballonuridae is sometimes referred to as the "sac-winged bats", *R. naso* lacks wing sacs[7]. *R. naso* is classified in the IUCN Red List as a species of Least Concern.

Rhynchonycteris naso hunts small dipterans (such as mosquitoes, flies and caddisflies)[5,7]. The echolocation calls of *R. naso* are CF-FM with the CF component around 100 kHz during search flight[11]. The echolocation call frequency is lowered to 67 kHz during prey capture to maintain the peripheral acoustic view[12]. This strategy is different from the other members of the Emballonuridae family which use a constant frequency throughout the whole pursuit sequence.

Genome sequence report

The genome was sequenced from a single male *R. naso* collected on March 9th 2019, from a tree near the river in Gamboa, Panama (GPS coordinates: 9.1135734185584, -79.82011865195433). A total of 42x-fold coverage in

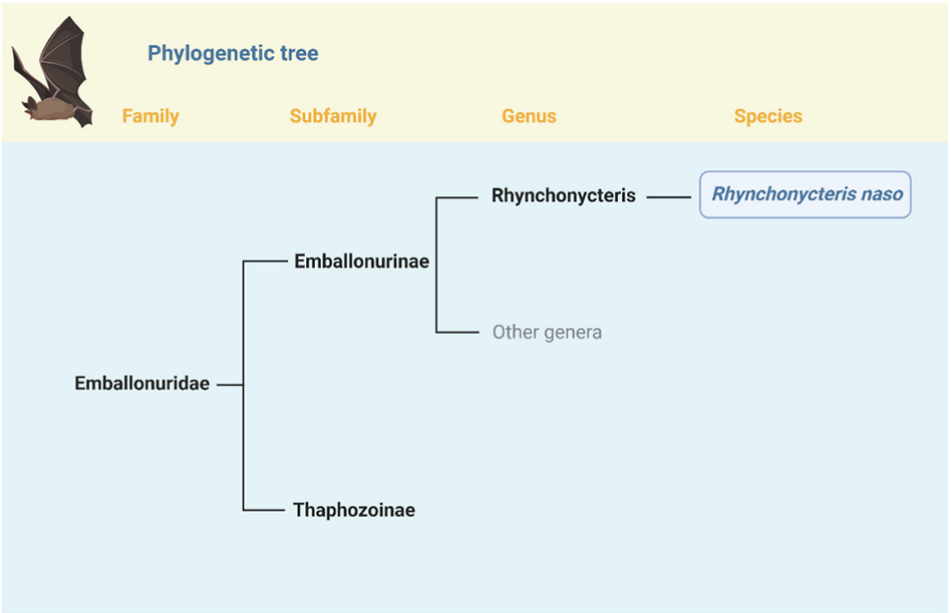

Figure 1. Position of *Rhynchonycteris naso* in the phylogeny of Emballonuridae. The bat *Rhynchonycteris naso* is the only species currently recognized in the genus *Rhynchonycteris*[13]. *Rhynchonycteris naso* belongs to the Subfamily Emballonurinae, which currently includes 14 genera and 55 species[6].

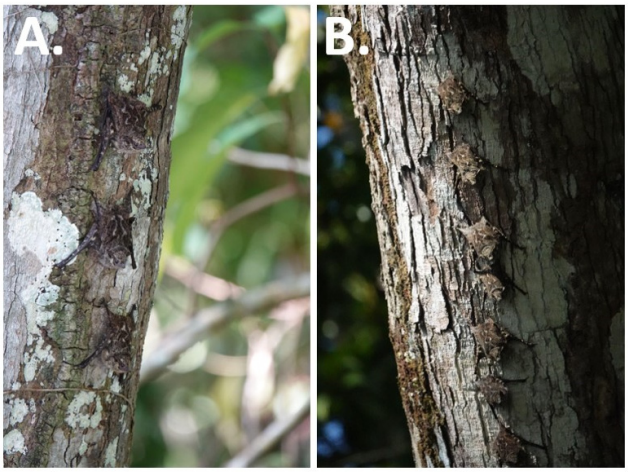

Figure 2. Proboscis bats, *Rhynchonycteris naso* Individuals of *R. naso*. (**A**–**B**) These bats roost in a line formation often on trees and near the water. They sometimes look like tree bark or lichen due to their grey and brown marbled coat and light stripes on their backs [Photos taken near a river close to Gamboa, Panama by Ine Alvarez van Tussenbroek].

Pacific Biosciences Hi-Fi long reads (contig N50 20 Mb) was generated after removal of all reads shorter than 10kb. Primary assembly contigs were scaffolded with chromosome conformation (Hi-C) data, which was also used to attain chromosome-level phasing[14]. The final assembly has a total length of 2.455 Gb in 40 sequence scaffolds with a contig N50 of 86 Mbp scaffold N50 of 286 Mbp (Table 1). The assembly has a BUSCO[15] completeness of 95.3% using the laurasiatheria reference set. Chromosomal pseudomolecules in the genome assembly of *Rhynchonycteris naso* are shown in Table 2.

Methods

The *R. naso* specimen was a male individual collected during a field expedition in Gamboa, Panama. *Rhynconycteris naso* was first identified by the roost location (a group of *R. naso* bats were hanging from a tree trunk in a line formation close to shallow waters). Furthermore, the shape of the face with a protruding nose, the gray-brown fur and the two light colored lines on the back of these bats determined the identification of this species as described previously (e.g. 9,16. After going on a boat by the river close to Gamboa, a roost was spotted on a tree near the water near a location previously investigated by locals under the supervision of the expert fieldworkers Mirjam Knörnschild and Martina Nagy. The bat was caught using a hand net and after confirmation of the sex it was placed in a fabric bag and taken to the laboratories at the Smithsonian Institute in Gamboa for tissue harvesting. Capture and sampling were done under the project proposal 2019-0301-2022 approved by the Smithsonian Tropical Research Institute and the STRI Animal Care and Use Committee (ACUC) and collection and export was conducted under the collecting field number issued by UNARGEN SC/A-3-19. All work was conducted with approval by the Panamanian Ministry of Environment (Mi Ambiente). Tissues were removed from the subject individual immediately following euthanasia and were flash-frozen in liquid nitrogen and stored in a freezer at -80°C until shipping on dry ice, maintaining the cold chain.

All efforts were made to minimize any suffering of the animal. The animal was subjected to minimal handling after capture, and it was held in a clean cloth bag after capture as per best practices for field containment of bats[17]. After species identification, the individual was euthanized humanely by experienced researchers while monitoring and prioritizing the reduction of stress and suffering of the animal. The animal was euthanized by overdose of isoflurane inhalation (Formula $CHF_2OCClHCF_3$, CAS number 26675-46-7; Manufacturer Piramal Critical Care, Supplier US Pharmacy Systems, Product code 5034-1FL-SOL-ORA). Euthanasia by isoflurane inhalation is a humane approved method that rapidly causes unconsciousness and eventually death upon inhalation. Bats euthanized by this method are rendered unconscious within seconds due to their high respiration rate, and death occurs within a minute or two with no significant suffering by the animal. The animal was tested for absence of breathing and reflexes. After breathing stops, isoflurane exposure was extended for one more minute. Confirmation of death was done immediately by decapitation. Tissue samples were dissected and immediately snap frozen using liquid nitrogen. A total of 21 samples were collected including brain, blood, liver, spleen, heart, lung, testes, muscle and kidney. All data were recorded and reported in accordance with the ARRIVE guidelines – see data availability section and Table 1.

DNA was extracted using Nanobind extraction from muscle tissue following the Circulomics Nanobind HMW DNA Extraction Protocol. Pacific Biosciences HiFi libraries were constructed according to the manufacturer's instructions. Hi-C data was generated using the Arima Hi-C+ High Coverage kit from the same muscle tissue sample. Sequencing was performed by the Genomic Operations DNA Pipelines at Paratus Sciences on Pacific Biosciences Sequel IIe (HiFi reads) and Illumina NextSeq 2000 (Hi-C) instruments.

Assembly was carried out following the Vertebrate Genome Project Galaxy pipeline v2.0[18]. A brief synopsis of the method is as follows: Genome size was estimated using GenomeScope2[19]. Hifiasm with Hi-C phasing was used for genome assembly (Cheng, Haoyu *et al.* 2021). The quality of the assembly was evaluated using Merqury[20] and BUSCO[21]. Scaffolding with Hi-C data (Rao, Huntley *et al.* 2014) was carried out with YaHS (Zhou, McCarthy *et al.* 2023). PretextView was implemented to generate a Hi-C contact map (Figure 3). Figure 4–Figure 6 were generated using BlobToolKit[22]. All bioinformatics software utilised for the *R. naso* analysis are depicted in Table 3.

Table 1. Genome data for *Rhynchonycteris naso*.

Project accession data	
Assembly identifier	GCA_031021685.1
Species	*Rhynchonycteris naso*
Specimen	rhynas1
NCBI taxonomy ID	249017
BioProject	PRJNA1076651, PRJNA1076652 Bat1K: Accession: PRJNA489245; ID: 489245
BioSample ID	SAMN39947078
Isolate information	Male [heart]
Raw data accessions	
Pacific Biosciences SEQUEL II	SRS20636215
Hi-C Illumina	SRS20636215
Genome assembly	
Assembly accession	GCA_037038545.1
Assembly of alternative accession	GCA_037038555.1
Span (Mb)	2455
Number of contigs	108
Contig N50 length (Mb)	86.3
Number of scaffolds	40
Scaffold N50 length (Mb)	287
Longest scaffold (Mb)	372

* BUSCO scores based on the laurasiatheria_odb10 BUSCO set using v5.0.0. C= complete [S= single copy, D=duplicated], F=fragmented, M=missing, n=number of orthologues in comparison.

* *Rhynchonycteris naso* BUSCO scores based on laurasiatheria_odb10 BUSCO set v5.3.2.

Table 2. Chromosomal pseudomolecules in the genome assembly of *Rhynchonycteris naso*. ENA accession Chromosome Size (Mb) GC%. The chromosome number of *Rhynchonycteris naso* is 2n=22.

ENA Accession	Chromosome	Size (Mb)	GC%
SUPER_1	1	372.38	0.4189
SUPER_2	2	317.77	0.3968
SUPER_3	3	310.926	0.4063
SUPER_4	4	286.99	0.3953
SUPER_5	5	261.06	0.4168
SUPER_6	6	209.12	0.4066
SUPER_7	7	170.32	0.4314
SUPER_8	8	151.66	0.3915
SUPER_X	X	142.67	0.3867
SUPER_9	9	132.37	0.4223
SUPER_10	10	78.41	0.4207
SUPER_Y	Y	19.81	0.3984

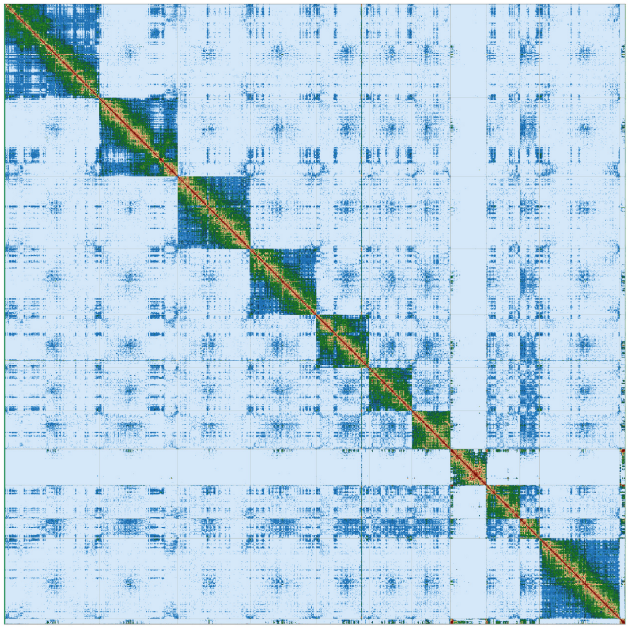

Figure 3. Hi-C Contact Map of the Rhynchonycteris naso haplotype 1 assembly with 11 scaffolds, visualized using PretextView. Scaffolds below 10 Mb were removed for creating the Hi-C Contact Map.

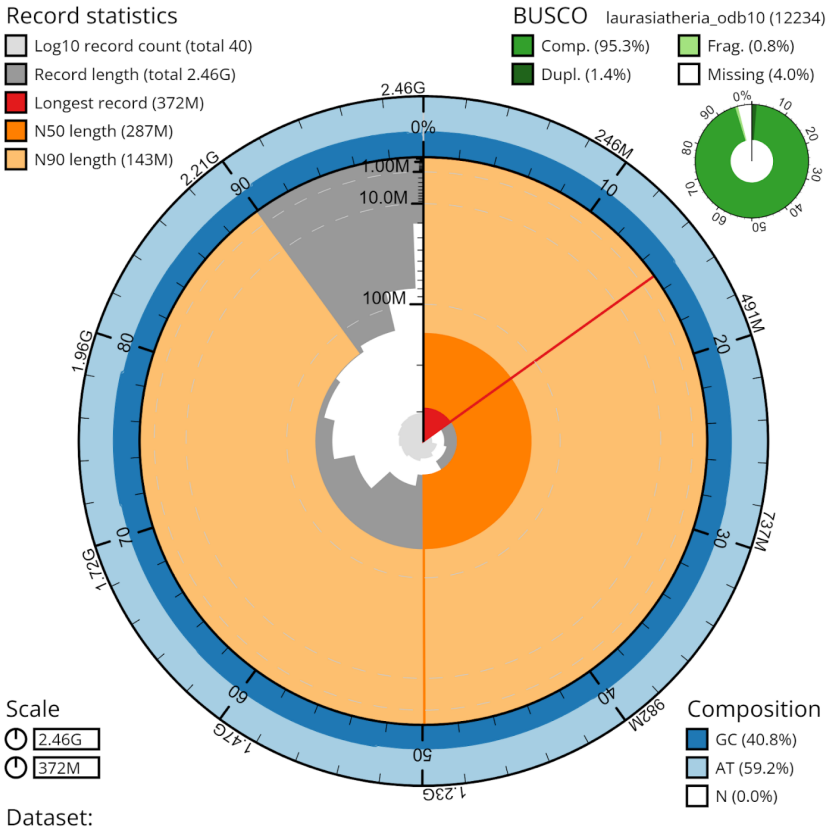

Figure 4. Genome assembly metrics generated using blobtoolkit for the *Rhynchonycteris naso* genome assembly. The larger snail plot depicts scaffold statistics including N50 length (bright orange) and base composition (blue). The smaller plot shows BUSCO completeness in green.

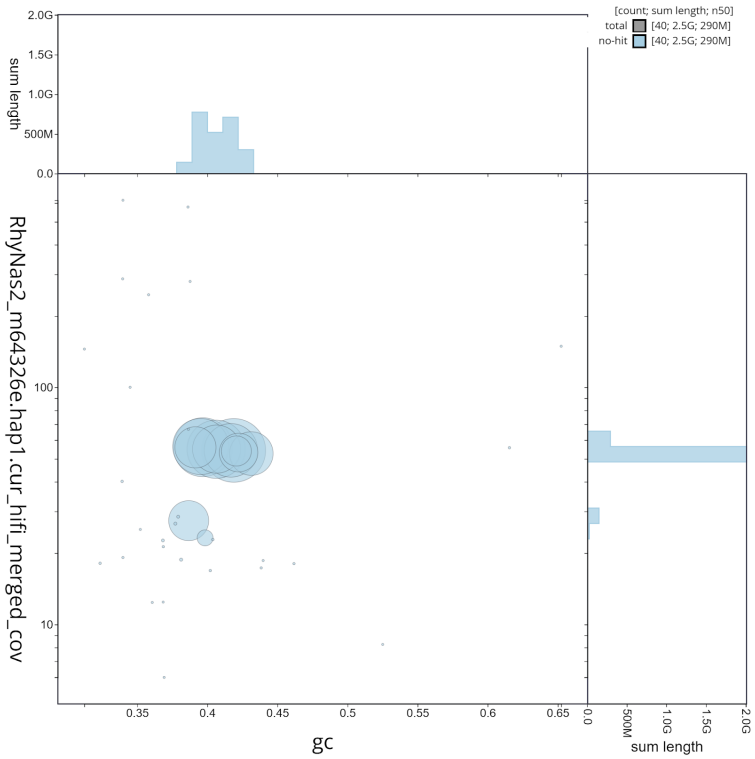

Figure 5. GC coverage plot generated for the *Rhynchonycteris naso* assembly using blobtoolkit. Individual chromosomes and scaffolds are represented by each circle. The circles are sized in proportion to chromosome/scaffold length. Histograms show the sum length of chromosome/scaffold size along each axis. Color of circles indicate taxonomic hits of each Phylum represented in the assembly.

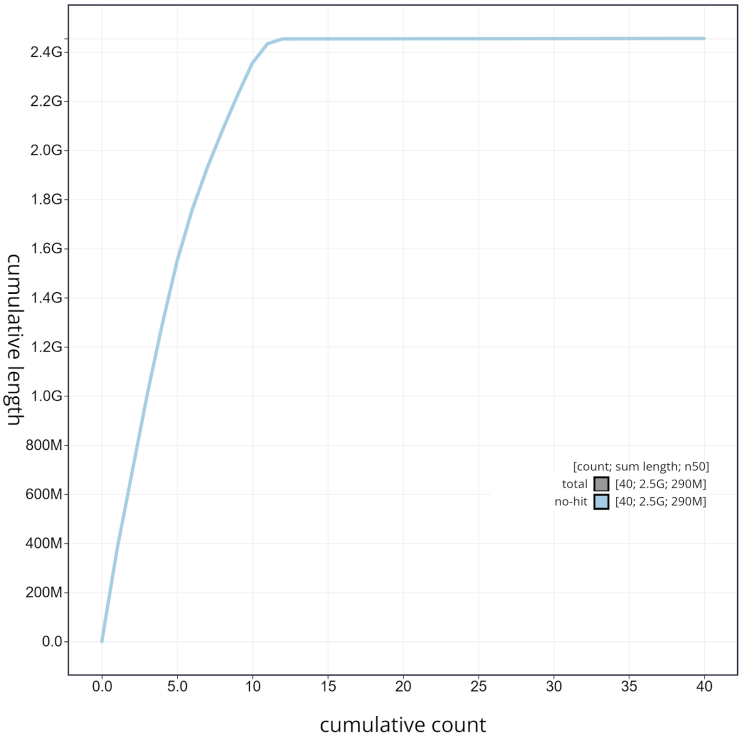

Figure 6. Cumulative sequence plot generated for the *Rhynchonycteris naso* assembly using blobtoolkit. The grey line shows the cumulative length for all chromosomes/scaffolds in the assembly. Colored lines represent Phylum represented in the assembly.

Table 3. Software tools used.

Software tool	Version	Source
bamUtil	1.0.15	https://genome.sph.umich.edu/wiki/BamUtil:_bam2FastQ
MultiQC	1.13	https://github.com/ewels/MultiQC
Genomescope	2.0	https://github.com/tbenavi1/genomescope2.0
hifiasm	0.19.3	https://github.com/chhylp123/hifiasm
purge_dups	1.2.6	https://github.com/dfguan/purge_dups
BUSCO	5.3.2	https://busco.ezlab.org/
Merqury	1.3	https://github.com/marbl/merqury
Assembly-stats	17.02	https://github.com/rjchallis/assembly-stats
Arima-HiC Mapping Pipeline	-	https://github.com/ArimaGenomics/mapping_pipeline
YaHS	1.1	https://github.com/c-zhou/yahs
HiGlass	1.11.7	https://github.com/higlass/higlass
samtools	1.9	https://www.htslib.org/
PretextView	-	https://github.com/sanger-tol/PretextView/tree/master
BUSCO	5.7.0	https://busco.ezlab.org/
BlobToolKit	4.3.5	https://github.com/blobtoolkit/blobtoolkit
pbmm2	1.13.1	https://github.com/PacificBiosciences/pbmm2
Blast	2.15.0+	https://blast.ncbi.nlm.nih.gov/Blast.cgi

Data availability

The *Rhynchonycteris naso* genome sequencing initiative is part of the Bat1K genome sequencing project. The genome assembly is released openly for reuse. Underlying data may be available for non-commercial research purposes upon request. Please email info@batbio.org for more information.

The genome assembly for *Rhynchonycteris naso* (proboscis bat) can be found in the European Nucleotide Archive and NCBI.

The assembly accession number at NCBI is GCA_031021685.1, and more details can be accessed through this link: https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_031021685.1/.

NCBI BioProject: Rhynchonycteris naso isolate: mRhyNas1 *(proboscis bat)*. Accession number: PRJNA945050, http://identifiers.org/ncbiprotein:PRJNA945050[23] under the Bat1K BioProject PRJNA489245.

The genome assembly can be found in the European Nucleotide Archive: Rhynchonycteris naso (proboscis bat). Accession number GCA_037038555, https://www.ebi.ac.uk/ena/browser/view/GCA_037038555.1[24].

All raw sequence data and the assembly have been deposited in the ENA (PRJNA1076651, PRJNA1076652) and NCBI (raw data). Data accession identifiers are SAMN39947078.

Data accession identifiers are reported in Table 1.

References

1. Wied-Neuwied MZ: **Reise nach Brasilien in den Jahren 1815 bis 1817**. 1820.
Reference Source
2. Peters WCH: **Über die zu den Gattungen Mimon und Saccopteryx gehörigen Flederthiere**. 1867; 478.
Reference Source
3. Teeling EC, Springer MS, Madsen O, *et al.*: **A molecular phylogeny for bats illuminates biogeography and the fossil record.** *Science.* 2005; **307**(5709): 580–4.
PubMed Abstract | Publisher Full Text
4. Meredith RW, Janečka JE, Gatesy J, *et al.*: **Impacts of the cretaceous terrestrial revolution and KPg extinction on mammal diversification.** *Science.* 2011; **334**(6055): 521–4.
PubMed Abstract | Publisher Full Text

5. Wilson DE, Mittermeier RA, Velik I: **Handbook of the mammals of the world, Volume 9: bats**. Lynx Edicions, 2019; 9.
Reference Source

6. Integrated Taxonomic Information System (ITIS): ***Rhynchonycteris naso*, Peters, 1867.** 2023.
Reference Source

7. Taylor M, Tuttle MD: **Bats: An illustrated guide to all species**. Smithsonian Books, 2019.
Reference Source

8. Knörnschild MHC, Moseley R, von Helversen O: **Remaining cryptic during motion—behavioral synchrony in the proboscis bat (*Rhynchonycteris naso*).** *Acta Chiropt.* 2009; **11**(1): 208–211.
Publisher Full Text

9. Nagy M, Günther L, Knörnschild M, *et al.*: **Female-biased dispersal in a bat with a female-defence mating strategy.** *Mol Ecol.* 2013; **22**(6): 1733–45.
PubMed Abstract | Publisher Full Text

10. Gunther L, Lopez MD, Knörnschild M, *et al.*: **From resource to female defence: the impact of roosting ecology on a bat's mating strategy.** *R Soc Open Sci.* 2016; **3**(11): 160503.
PubMed Abstract | Publisher Full Text | Free Full Text

11. Jung K, Kalko EAV, Von Helversen O: **Echolocation calls in Central American emballonurid bats: signal design and call frequency alternation.** *J Zool.* 2007; **272**(2): 125–137.
Publisher Full Text

12. Jakobsen L, Olsen MN, Surlykke A: **Dynamics of the echolocation beam during prey pursuit in aerial hawking bats.** *Proc Natl Acad Sci U S A.* 2015; **112**(26): 8118–23.
PubMed Abstract | Publisher Full Text | Free Full Text

13. Plumpton DL, Jones JJK: ***Rhynchonycteris naso*.** *Mamm Species.* 1992; (413): 1–5.
Publisher Full Text

14. Cheng H, Jarvis ED, Fedrigo O, *et al.*: **Haplotype-resolved assembly of diploid genomes without parental data.** *Nat Biotechnol.* 2022; **40**(9): 1332–1335.
PubMed Abstract | Publisher Full Text | Free Full Text

15. Simao FA, Waterhouse RM, Ioannidis P, *et al.*: **BUSCO: assessing genome assembly and annotation completeness with single-copy orthologs.** *Bioinformatics.* 2015; **31**(19): 3210–2.
PubMed Abstract | Publisher Full Text

16. Nyffeler M, Knornschild M: **Bat predation by spiders.** *PLoS One.* 2013; **8**(3): e58120.
PubMed Abstract | Publisher Full Text | Free Full Text

17. Kunz TH, Parsons S: **Ecological and behavioral methods for the study of bats**. 2nd edn ed. Baltimore: Johns Hopkins University Press, 2009.
Reference Source

18. Lariviere D, Abueg L, Brajuka N, *et al.*: **Scalable, accessible and reproducible reference genome assembly and evaluation in galaxy.** *Nat Biotechnol.* 2024; **42**(3): 367–370.
PubMed Abstract | Publisher Full Text | Free Full Text

19. Vurture GW, Sedlazeck FJ, Nattestad M, *et al.*: **GenomeScope: fast reference-free genome profiling from short reads.** *Bioinformatics.* 2017; **33**(14): 2202–2204.
PubMed Abstract | Publisher Full Text | Free Full Text

20. Nurk S, Walenz BP, Rhie A, *et al.*: **HiCanu: accurate assembly of segmental duplications, satellites, and allelic variants from high-fidelity long reads.** *Genome Res.* 2020; **30**(9): 1291–1305.
PubMed Abstract | Publisher Full Text | Free Full Text

21. Manni M, Berkeley MR, Seppey M, *et al.*: **BUSCO update: novel and streamlined workflows along with broader and deeper phylogenetic coverage for scoring of eukaryotic, prokaryotic, and viral genomes.** *Mol Biol Evol.* 2021; **38**(10): 4647–4654.
PubMed Abstract | Publisher Full Text | Free Full Text

22. Challis R, Richards E, Rajan J, *et al.*: **BlobToolKit - interactive quality assessment of genome assemblies.** *G3 (Bethesda).* 2020; **10**(4): 1361–1374.
PubMed Abstract | Publisher Full Text | Free Full Text

23. Vernes S, *et al.*: ***Rhynchonycteris naso* isolate: mRhyNas1 (proboscis bat).** NCBI BioProject, [Dataset]. 2023.
http://identifiers.org/ncbiprotein:PRJNA945050

24. Vernes S, *et al.*: ***Rhynchonycteris naso* (proboscis bat).** European Nucleotide Archive, [Dataset]. 2024.
https://www.ebi.ac.uk/ena/browser/view/GCA_037038555.1

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Version 1

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✔ **Luciano Chaves Franco Filho**
Instituto Evandro Chagas, Ananindeua, Brazil

The Data Note presents a high-quality reference genome assembly for the proboscis bat, *Rhynchonycteris naso*, from the family Emballonuridae. The genome, covering around 2.46 Gb, is organized into 22 chromosomal pseudomolecules, including the Y chromosome. The assembly achieved a contig N50 of 86 Mb and a scaffold N50 of 287 Mb, demonstrating the completeness and accuracy of the genome sequence. This work contributes to the Bat1K project, aiming to sequence the genomes of all bat species, and provides valuable insights into the genetic makeup of *R. naso*, an insectivorous bat species found in tropical regions of Central and South America.

Is the rationale for creating the dataset(s) clearly described?
Yes

Are the protocols appropriate and is the work technically sound?
Yes

Are sufficient details of methods and materials provided to allow replication by others?
Yes

Are the datasets clearly presented in a useable and accessible format?
Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Next Generation Sequencing (NGS); Molecular biology; biodiversity and microbiome diversity

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Reviewer Report 04 September 2024

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Authors presented a exciting reference genome assembly from an individual male *Rhynchonycteris naso.* No doubt it will benefit the future genomic analyses on Emballonuridae and other.

However, I have 2 minor comments for its improvement:

1) The use of *Rhynchonycteris naso* Peters, 1867 is not correct. I think it should be *Rhynchonycteris naso* (Wied-Neuwied, 1820). Pls check "Mammal species of the World" for the further details.

2) "Rhynchonycteris" in the Fig. 1 should be italic (genera name).

Is the rationale for creating the dataset(s) clearly described?
Yes

Are the protocols appropriate and is the work technically sound?
Yes

Are sufficient details of methods and materials provided to allow replication by others?
Yes

Are the datasets clearly presented in a useable and accessible format?
Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Comparative genomics, Taxonomy, Evolutionary biology, Diversification, Bats

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Reviewer Report 02 September 2024

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Xiuguang Mao
School of Ecological and Environmental Sciences, East China Normal University, Shanghai, China

This manuscript presents a high-quality chromosome-scale assembly for *Rhynchonycteris naso* and also provides detailed characteristics about this species in the Introduction section.

I have two minor comments:

1) In Figure 1, 'Rhynchonycteris' should be italic.

2) "The final assembly has a total length of 2.455 Gb in 40 sequence scaffolds with a contig N50 of 86 Mbp scaffold N50 of 286 Mbp (Table 1)". But in Table 1, the scaffold N50 length is 287 Mb.

Is the rationale for creating the dataset(s) clearly described?
Yes

Are the protocols appropriate and is the work technically sound?
Yes

Are sufficient details of methods and materials provided to allow replication by others?
Yes

Are the datasets clearly presented in a useable and accessible format?
Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Comparative genomics, genome assembly, evolutionary biology, speciation, bats

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Comments on this article

Version 1

Reader Comment 13 Jul 2024

Victor Van Cakenberghe, Biology, Universiteit Antwerpen, Antwerp, Belgium

I think you should modify the title: Peters (1867) isn't the author for *Rhynchonycteris naso*. Peters described the genus *Rhynchonycteris*, but *Rhynchonycteris naso* was described as *Vespertilio Naso* by Wied-Neuwied (1820). So the correct title should be "The genome sequence of *Rhynchonycteris naso* (Wied-Neuwied, 1820) (Chiroptera, Emballonuridae, Rhynchonycteris)".

Competing Interests: No competing interests were disclosed.