

Supplementary materials

SUPPLEMENTARY TABLE 1

The dataset includes sequences from 69 distinct CoV genotypes, which have their origins in 17 different bat species. These genetic sequences have been obtained from GenBank and encompass the complete genome, polyprotein 1ab (ORF1ab), spike sequences of the CoVs, and the cytb gene sequences from the bat specimens.

The 17 bat hosts include individuals in the *Aselliscus stoliczkanus*, *Chaerephon plicatus*, *Hipposideros pratti*, *Miniopterus fuliginosus*, *Miniopterus magnate*, *Miniopterus pusillus*, *Myotis ricketti*, *Pipistrellus abramus*, *Rhinolophus affinis*, *Rhinolophus blasii*, *Rhinolophus ferrumequinum*, *Rhinolophus macrotis*, *Rhinolophus pearsoni*, *Rhinolophus pusillus*, *Rhinolophus sinicus*, *Tylonycteris pachypus*, and *Vespertilio superans*. For molecular characterization, cytochrome b (cytb) gene sequences from all sampled bats were sourced from GenBank. This mitochondrial gene has proven instrumental in achieving species-level resolution for mammalian phylogenies within the Order [1–3].

Table S1. Coronaviruses and bats sequences used for cophylogenetic analyses

Virus complete genome	Virus ORF1ab	Virus spike	Host	Host cyt b	Reference
KY417142	ATO98106	ATO98108	<i>Aselliscus stoliczkanus</i>	DQ888677	[4, 5]
JX993988	AGC74171(1a); AGC74177(1b)	AGC74176	<i>Chaerephon plicatus</i>	ON640662	[6, 7]
KF636752	AIL94214	AIL94216	<i>Hipposideros pratti</i>	OP894116	[8]
KJ473795	AIA62199	AIA62200	<i>Miniopterus fuliginosus</i>	AB085735	[9, 10]
KJ473796	AIA62205	AIA62206	<i>Miniopterus fuliginosus</i>	AB085735	[9, 10]
KJ473797	AIA62211	AIA62212	<i>Miniopterus fuliginosus</i>	AB085735	[9, 10]
KJ473798	AIA62219	AIA62220	<i>Miniopterus fuliginosus</i>	AB085735	[9, 10]
KJ473799	AIA62226	AIA62227	<i>Miniopterus fuliginosus</i>	AB085735	[9, 10]
KJ473800	AIA62233	AIA62234	<i>Miniopterus fuliginosus</i>	AB085735	[9, 10]
EU420138	ACA52163	ACA52164	<i>Miniopterus magnater</i>	ON640726	[7, 11]
EU420137	ACA52156	ACA52157	<i>Miniopterus pusillus</i>	MN366288	[11]
EU420139	ACA52170	ACA52171	<i>Miniopterus pusillus</i>	MN366288	[11]
KJ473806	AIA62245	AIA62246	<i>Myotis ricketti</i>	AB106608	[12, 13]
KJ473820	AIA62342	AIA62343	<i>Pipistrellus abramus</i>	AB085739	[8, 10]
EF065509	ABN10874	ABN10875	<i>Pipistrellus abramus</i>	AB085739	[10, 14]
KF569996	AHX37556(1a); AHX37557(1b)	AHX37558	<i>Rhinolophus affinis</i>	KP972690	[14?]
MK211376	QDF43824	QDF43825	<i>Rhinolophus affinis</i>	KP972690	[14, 15]

Continued on next page

Table S1 – continued from previous page

Virus complete genome	Virus ORF1ab	Virus spike	Host	Host cytb	Reference
MK211377	QDF43829	QDF43830	<i>Rhinolophus affinis</i>	KP972690	[14, 15]
MN996532	QHR63299	QHR63300	<i>Rhinolophus affinis</i>	KP972690	[14?]
GU190215	ADK66840	ADK66841	<i>Rhinolophus blasii</i>	MZ936290	[16, 17]
NC014470	YP003858583	YP003858584	<i>Rhinolophus blasii</i>	MZ936290	[16, 17]
KJ473807	AIA62251	AIA62252	<i>Rhinolophus ferrumequinum</i>	AB085731	[10, 13]
KJ473808	AIA62258	AIA62259	<i>Rhinolophus ferrumequinum</i>	AB085731	[10, 13]
KJ473811	AIA62276	AIA62277	<i>Rhinolophus ferrumequinum</i>	AB085731	[10, 13]
KJ473812	AIA62289	AIA62290	<i>Rhinolophus ferrumequinum</i>	AB085731	[10, 13]
KJ473813	AIA62299	AIA62300	<i>Rhinolophus ferrumequinum</i>	AB085731	[10, 13]
DQ412043	ABD75330(1a); ABD75331(1b)	ABD75332	<i>Rhinolophus macrotis</i>	KX261916	[18]
DQ648857	ABG47068	ABG47069	<i>Rhinolophus macrotis</i>	KX261916	[18]
DQ071615	AAZ67050(1a); AAZ67051(1b)	AAZ67052	<i>Rhinolophus pearsoni</i>	JX502551	[19]
JX993987	AGC74164(1a); AGC74170(1b)	AGC74165	<i>Rhinolophus pusillus</i>	ON012504	[6, 20]
KU973692	ARO76381(1a)	ARO76382	<i>Rhinolophus pusillus</i>	ON012504	[6, 20, 21]
DQ022305	AAZ88865	AAZ88866	<i>Rhinolophus sinicus</i>	HM134917	[22]
DQ084199	AAZ41328	AAZ41329	<i>Rhinolophus sinicus</i>	HM134917	[22]
DQ084200	AAZ41339	AAZ41340	<i>Rhinolophus sinicus</i>	HM134917	[22]
Continued on next page					

Table S1 – continued from previous page

Virus plete genome	com- Virus ORF1ab	Virus spike	Host	Host cyt b	Reference
FJ588686	ACU31044	ACU31032	<i>Rhinolophus sinicus</i>	HM134917	[22, 23]
GQ153539	ADE34721	ADE34722	<i>Rhinolophus sinicus</i>	HM134917	[22, 24]
GQ153540	ADE34732	ADE34733	<i>Rhinolophus sinicus</i>	HM134917	[22, 24]
GQ153541	ADE34743	ADE34744	<i>Rhinolophus sinicus</i>	HM134917	[22, 24]
GQ153542	ADE34754	ADE34755	<i>Rhinolophus sinicus</i>	HM134917	[22, 24]
GQ153543	ADE34765	ADE34766	<i>Rhinolophus sinicus</i>	HM134917	[22, 24]
GQ153544	ADE34778	ADE34779	<i>Rhinolophus sinicus</i>	HM134917	[22, 24]
GQ153545	ADE34789	ADE34790	<i>Rhinolophus sinicus</i>	HM134917	[22, 24]
GQ153546	ADE34800	ADE34801	<i>Rhinolophus sinicus</i>	HM134917	[22, 24]
GQ153547	ADE34811	ADE34812	<i>Rhinolophus sinicus</i>	HM134917	[22, 24]
GQ153548	ADE34822	ADE34823	<i>Rhinolophus sinicus</i>	HM134917	[22, 24]
KC881005	AGZ48805	AGZ48806	<i>Rhinolophus sinicus</i>	HM134917	[22, 25]
KC881006	KC881006	AGZ48818	<i>Rhinolophus sinicus</i>	HM134917	[22, 25]
KF367457	AGZ48830	AGZ48831	<i>Rhinolophus sinicus</i>	HM134917	[22, 25]
KJ473814	AIA62309	AIA62310	<i>Rhinolophus sinicus</i>	HM134917	[8, 22]
KJ473815	AIA62319	AIA62320	<i>Rhinolophus sinicus</i>	HM134917	[8, 22]
KJ473816	AIA62329	AIA62330	<i>Rhinolophus sinicus</i>	HM134917	[8, 22]
KT444582	ALK02468	ALK02457	<i>Rhinolophus sinicus</i>	HM134917	[22, 26]
KY417143	ATO98118	ATO98120	<i>Rhinolophus sinicus</i>	HM134917	[4, 22]
Continued on next page					

Table S1 – continued from previous page

Virus plete genome	com- Virus ORF1ab	Virus spike	Host	Host cyt b	Reference
KY417144	ATO98130	ATO98132	<i>Rhinolophus sinicus</i>	HM134917	[4, 22]
KY417146	ATO98155	ATO98157	<i>Rhinolophus sinicus</i>	HM134917	[4, 22]
KY417147	ATO98167	ATO98169	<i>Rhinolophus sinicus</i>	HM134917	[4, 22]
KY417148	ATO98179	ATO98181	<i>Rhinolophus sinicus</i>	HM134917	[4, 22]
KY417149	ATO98191	ATO98193	<i>Rhinolophus sinicus</i>	HM134917	[4, 22]
KY417150	ATO98203	ATO98205	<i>Rhinolophus sinicus</i>	HM134917	[4, 22]
KY417151	ATO98216	ATO98218	<i>Rhinolophus sinicus</i>	HM134917	[4, 22]
KY417152	ATO98229	ATO98231	<i>Rhinolophus sinicus</i>	HM134917	[4, 22]
KY770858	ARI44798	ARI44799	<i>Rhinolophus sinicus</i>	HM134917	[22]
KY770859	ARI44803	ARI44804	<i>Rhinolophus sinicus</i>	HM134917	[22]
MG772933	AVP78030	AVP78031	<i>Rhinolophus sinicus</i>	HM134917	[22]
MG772934	AVP78041	AVP78042	<i>Rhinolophus sinicus</i>	HM134917	[22]
EF203065	ABQ57215	ABQ57216	<i>Rhinolophus sinicus</i>	HM134917	[22]
KJ473822	AIA62351	AIA62352	<i>Tylonycteris pachypus</i>	ON640722	[13]
EF065505	ABN10838	ABN10839	<i>Tylonycteris pachypus</i>	ON640722	[14]
KJ473821	AHY61336	AHY61337	<i>Vespertilio superans</i>	AB085738	[8, 10]

REFERENCES

1. T. D. Kocher, W. K. Thomas, A. Meyer, *et al.*, "Dynamics of mitochondrial dna evolution in animals: amplification and sequencing with conserved primers." *Proc. Natl. Acad. Sci.* **86**, 6196–6200 (1989).
2. R. D. Bradley and R. J. Baker, "A test of the genetic species concept: cytochrome-b sequences and mammals," *J. mammalogy* **82**, 960–973 (2001).
3. I. Agnarsson, C. M. Zambrana-Torrel, N. P. Flores-Saldana, and L. J. May-Collado, "A time-calibrated species-level phylogeny of bats (chiroptera, mammalia)," *PLoS currents* **3** (2011).
4. B. Hu, L.-P. Zeng, X.-L. Yang, *et al.*, "Discovery of a rich gene pool of bat sars-related coronaviruses provides new insights into the origin of sars coronavirus," *PLoS pathogens* **13**, e1006698 (2017).
5. G. Li, B. Liang, Y. Wang, *et al.*, "Echolocation calls, diet, and phylogenetic relationships of stoliczka's trident bat, *Aselliscus stoliczkanus* (hipposideridae)," *J. Mammal.* **88**, 736–744 (2007).
6. L. Yang, Z. Wu, X. Ren, *et al.*, "Novel sars-like betacoronaviruses in bats, china, 2011," *Emerg. infectious diseases* **19**, 989 (2013).
7. Z. Wu, Y. Han, Y. Wang, *et al.*, "A comprehensive survey of bat sarbecoviruses across china in relation to the origins of sars-cov and sars-cov-2," *Natl. Sci. Rev.* p. nwac213 (2022).
8. Z. Wu, L. Yang, X. Ren, *et al.*, "Orf8-related genetic evidence for chinese horseshoe bats as the source of human severe acute respiratory syndrome coronavirus," *The J. infectious diseases* **213**, 579–583 (2016).
9. J. Du, L. Yang, X. Ren, *et al.*, "Genetic diversity of coronaviruses in *Miniopterus fuliginosus* bats," *Sci. China Life Sci.* **59**, 604–614 (2016).
10. T. Sakai, Y. Kikkawa, K. Tsuchiya, *et al.*, "Molecular phylogeny of japanese rhinolophidae based on variations in the complete sequence of the mitochondrial cytochrome b gene," *Genes & Genet. Syst.* **78**, 179–189 (2003).
11. D. Chu, J. Peiris, H. Chen, *et al.*, "Genomic characterizations of bat coronaviruses (1a, 1b and hku8) and evidence for co-infections in *Miniopterus* bats," *J. Gen. Virol.* **89**, 1282–1287 (2008).
12. K. Kawai, M. Nikaido, M. Harada, *et al.*, "The status of the japanese and east asian bats of the genus *Myotis* (Vespertilionidae) based on mitochondrial sequences," *Mol. Phylogenetics Evol.* **28**, 297–307 (2003).
13. Z. Wu, L. Yang, X. Ren, *et al.*, "Deciphering the bat virome catalog to better understand the ecological diversity of bat viruses and the bat origin of emerging infectious diseases," *The ISME journal* **10**, 609–620 (2016).
14. P. C. Woo, M. Wang, S. K. Lau, *et al.*, "Comparative analysis of twelve genomes of three novel group 2c and group 2d coronaviruses reveals unique group and subgroup features," *J. virology* **81**, 1574–1585 (2007).
15. B. He, Y. Zhang, L. Xu, *et al.*, "Identification of diverse alphacoronaviruses and genomic characterization of a novel severe acute respiratory syndrome-like coronavirus from bats in china," *J. virology* **88**, 7070–7082 (2014).
16. M. Curran, M. Kopp, M. Ruedi, and J. Bayliss, "A new species of horseshoe bat (chiroptera: Rhinolophidae) from mount namuli, mozambique," *Acta Chiropterologica* **24**, 19–40 (2022).
17. J. F. Drexler, F. Gloza-Rausch, J. Glende, *et al.*, "Genomic characterization of severe acute respiratory syndrome-related coronavirus in european bats and classification of coronaviruses based on partial rna-dependent rna polymerase gene sequences," *J. virology* **84**, 11336–11349 (2010).
18. K. Sun, R. T. Kimball, T. Liu, *et al.*, "The complex evolutionary history of big-eared horseshoe bats (*Rhinolophus macrotis* complex): insights from genetic, morphological and acoustic data," *Sci. reports* **6**, 35417 (2016).
19. W. Li, Z. Shi, M. Yu, *et al.*, "Bats are natural reservoirs of sars-like coronaviruses," *Science* **310**, 676–679 (2005).
20. W. Wang, J.-H. Tian, X. Chen, *et al.*, "Coronaviruses in wild animals sampled in and around wuhan at the beginning of covid-19 emergence," *Virus evolution* **8**, veac046 (2022).
21. L. Wang, S. Fu, Y. Cao, *et al.*, "Discovery and genetic analysis of novel coronaviruses in least horseshoe bats in southwestern china," *Emerg. microbes & infections* **6**, 1–8 (2017).
22. S. K. Lau, P. C. Woo, K. S. Li, *et al.*, "Severe acute respiratory syndrome coronavirus-like virus in chinese horseshoe bats," *Proc. Natl. Acad. Sci.* **102**, 14040–14045 (2005).
23. J. Yuan, C.-C. Hon, Y. Li, *et al.*, "Intraspecific diversity of sars-like coronaviruses in rhinolo-

- phus sinicus and its implications for the origin of sars coronaviruses in humans," J. general virology **91**, 1058–1062 (2010).
24. S. K. Lau, K. S. Li, Y. Huang, *et al.*, "Ecoepidemiology and complete genome comparison of different strains of severe acute respiratory syndrome-related rhinolophus bat coronavirus in china reveal bats as a reservoir for acute, self-limiting infection that allows recombination events," J. virology **84**, 2808–2819 (2010).
 25. X.-Y. Ge, J.-L. Li, X.-L. Yang, *et al.*, "Isolation and characterization of a bat sars-like coronavirus that uses the ace2 receptor," Nature **503**, 535–538 (2013).
 26. X.-L. Yang, B. Hu, B. Wang, *et al.*, "Isolation and characterization of a novel bat coronavirus closely related to the direct progenitor of severe acute respiratory syndrome coronavirus," J. virology **90**, 3253–3256 (2016).