

# Detection of Batborne Hantaviruses, Laos, 2023–2024

## Appendix

### Taxa Information

Batborne hantaviruses 1–7 from Laos (large segment [L]: PQ585418–24, medium segment [M]: [PV034707-10], small segment [S]: [PV034711-14]). Other viruses: Longquan virus (LQUV Ra-25, L: JX465381, M: JX465397, S: JX465415), Huangpi virus (HUPV Pa-1, L: JX465369, S: JX473273), Mouyassue virus (MOYV KB576, L: JQ287716), Nova virus (NVAV Te34, L: KR072623, M: KR072622, S: KR072621), Ash River virus (ARRV MSB734418, L: EF619961, S: EF650086), Jemez Springs virus (JMSV MSB144475, L: FJ593501, M: FJ593500, S: FJ593499), Cao Bang virus (CBNV CBN3, L: EF543525.2, M: EF543526, S: EF543524), Seoul virus (SEOV IR80–39, L: NC\_5238, M: NC\_005237, S: NC\_005236), Sangassou virus (SANGV SA14, L: JQ082302, M: JQ082301, S: JQ082300), Dobrava virus (DOBV Greece, L: NC\_5235, M: NC\_005234, S: NC\_005233), Soochong virus-1 (SOOV SOO-1, L: DQ056292, M: AY675353, S: AY675349), Hantaan virus (HTNV 76–118, L: NC\_5222, M: NC\_005219, S: NC\_005218), Boginia virus (BOGV 2074, L: JX990965, M: JX990966), Tanganya virus (TGNV Tan826, L: EF050454, M: EF050453, S: EF050455), Azagny virus (AZGV KBM15, L: JF276228, M: JF276227, S: JF276226), Bowe virus (BOWV VN1512, L: KC631784, M: KC631783, S: KC631782), Jeju virus (JJUV SH42, L: HQ663935, M: HQ663934, S: HQ663933), Seewis virus (SWSV mp70, L: EF636026, M: EF636025, S: EF636024), Amga virus (ARTV Mukawa, L: KF974361, M: KF974359, S: KF974360), Kenkeme virus (KKMV MSB148794, L: GQ306150, M: GQ306149, S: GQ306148), Oxbow virus (OXBV Ng1453, L: FJ593497, M: FJ539167, S: FJ539166), Tigray virus (TIGV ET2121, L: KU934008, M: KU934009, S: KU934010), Asama virus (ASAV N10, L: EU929078, M: EU929075, S: EU929072), Tula virus (TULV M5320v, L: NC\_5226, M: NC\_005228, S: NC\_005227), Prospect Hill virus (PHV PH-1, L: EF646763, M: X55129, S: Z49098), Andes virus (ANDV Chile97, L: AF291704.5, M:

NC\_003467, S: NC\_003466), Sin Nombre virus (SNV NMH10, L: NC\_5217, M: NC\_005215, S: NC\_005216), Hokkaido virus (HOKV Kitahiyama, L: AB712372, M: AB676848, S: AB675463), Puumala virus (PUUV Sotkamo, L: NC\_5225, M: NC\_005223, S: NC\_005224), Rockport virus (RKPV MSB57412, L: HM015221, M: HM015219, S: HM015223), Hantavirus MGB/1209 (MGBV 1209, L: JN037851), Makokou virus (MAKV GB303, L: KT316176), Xuan son virus (XSV VN198264, L: JX912953, M: KU976427, S: KC688335), Laibin virus (LAIV BT20, L: KM102249, M: KM102248, S: KM102247), Đakrông virus (DKGV VN2913B72, L: MG663536, M: MG663535, S: MG663534), Quezon virus (OZNV INT1720, L: KU950715, M: KU950714, S: KU950713), Brno virus (BRNV 7, L: KX845680, M: KX845679, S: KX845678), Uluguru virus (ULUV FMNH158302, L: JX193697, M: JX193696, S: JX193695), Thottapalayam virus (TPMV VRC66412, L: EU001330, M: EU001329, S: AY526097), Imjin virus (MJNV CI05–11, L: EF641806, M: EF641798, S: EF641804), Kilimanjaro virus (KMJV FMNH174124, L: JX193700, M: JX193699, S: JX193698).

Animal species: *Aselliscus stoliczkanus* (KU161570), *Hipposideros pomona* (JX912954), *Hipposideros ruber* (EU934474), *Taphozous melanopogon* (LC406449), *Rousettus amplexicaudatus* (KU950716), *Rhinolophus affinis* (JX465358), *Nyctalus noctula* (JX570902), *Neoromicia nanus* (JQ287717), *Pipistrellus abramus* (JX465352), *Nycteris hispida* (HQ693722), *Myosorex geata* (JX193701), *Myosorex zinki* (JX193702), *Suncus murinus* (DQ630386), *Crocidura lasiura* (KJ004674), *Crocidura shantungensis* (HQ663932), *Crocidura obscurior* (JF276229), *Crocidura theresae* (DQ521043), *Crocidura douceti* (KC684929), *Anourosorex squamipe* (AB175090), *Sorex cecutiens* (KF974362), *Sorex roboratus* (AB175128), *Sorex cinereus* (FJ667512), *Sorex monticolus* (FJ667514), *Sorex araneus* (FJ667524), *Neomys fodiens* (KC537797), *Urotrichus talpoides* (EU918371), *Scalopus aquaticus* (HM461914), *Talpa europaea* (FJ715340), *Neurotrichus gibbsii* (FJ595237), *Apodemus agrarius* (AB303225), *Apodemus flavicollis* (JF819967), *Apodemus peninsulae* (AB073811), *Rattus norvegicus* (AB355903), *Hylomyscus simus* (DQ212188), *Stenocephalemys albipes* (AF518346), *Myodes glareolus* (JX477304), *Myodes rufocanus* (LC406450), *Microtus pennsylvanicus* (AF119279), *Microtus arvalis* (AY220770), *Oligoryzomys longicaudatus* (AF346566), *Peromyscus maniculatus* (AF119261). The sequences were derived from the National Center for Biotechnology Information GenBank database (<https://www.ncbi.nlm.nih.gov/genbank/>).

## References

1. Arai S, Aoki K, Son NT, Tú VT, Kikuchi F, Kinoshita G, et al. Đakrông virus, a novel mobatvirus (*Hantaviridae*) harbored by the Stoliczka's Asian trident bat (*Aselliscus stoliczkanus*) in Vietnam. *Sci Rep.* 2019;9:10239. [PubMed https://doi.org/10.1038/s41598-019-46697-5](https://doi.org/10.1038/s41598-019-46697-5)
2. Klempa B, Fichet-Calvet E, Lecompte E, Auste B, Aniskin V, Meisel H, et al. Hantavirus in African wood mouse, Guinea. *Emerg Infect Dis.* 2006;12:838–40. [PubMed https://doi.org/10.3201/eid1205.051487](https://doi.org/10.3201/eid1205.051487)

**Appendix Table 1.** Detailed sampling numbers\*

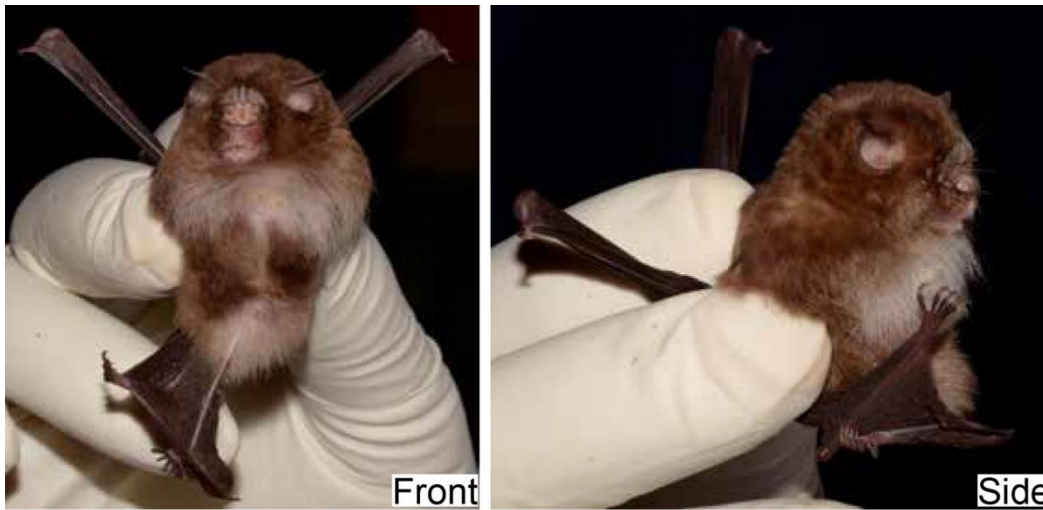
Species	Mission 1		Mission 2			Mission 3		Mission 4		Mission 5		Mission 6			Mission 7			Mission 8			Total
	-	Total	-	+	Total	-	Total	-	Total	-	Total	-	+	Total	-	+	Total	-	+	Total	
<i>Aselliscus stoliczkanus</i>	3	3	3	1	4	2	2	2	2	6	6	16	1	17	6	1	7	3	2	5	46
<i>Cynopterus bracyotis</i>												1	1								1
<i>Cynopterus horsfieldii</i>												5	5				1		1		6
<i>Cynopterus sphinx</i>			5		5							6	6	1		1	7	7			19
<i>Eonycteris spelaea</i>	3	3	1		1	1	1					6	6	4		4	4	4		4	19
<i>Hesperoptenus blanfordi</i>														1		1					1
<i>Hipposideros armiger</i>	2	2	1		1			1	1			1	1					4		4	9
<i>Hipposideros gentilis</i>	3	3	6		6	1	1	2	2	2	2	12	1	13	4		4	12	1	13	44
<i>Hipposideros khaokhouayensis</i>	1	1						1	1						2		2				4
<i>Hipposideros larvatus</i>	3	3	12		12	2	2	2	2	5	5				3		3	17		17	44
<i>Hipposideros scutinares</i>	2	2																1		1	3
<i>Kerivoula depressa</i>								1	1												1
<i>Lyroderma lyra</i>			1		1																1
<i>Macroglossus sobrinus</i>	1	1				2	2	2	2			2		2	4		4	1		1	12
<i>Megaderma spasma</i>			1		1	2	2					6		6				1		1	10
<i>Megaerops niphanae</i>			4		4	1	1											1		1	6
<i>Miniopterus magnater</i>	1	1				2	2	1	1						2		2				6
<i>Murina cyclotis</i>	1							2	2												2
<i>Murina eleryi</i>								1	1												1
<i>Murina feae</i>								1	1						1		1				2
<i>Myotis alticraniatus</i>	1	1				2	2	2	2						4		4				9
<i>Myotis annectans</i>	1	1													3		3				4
<i>Myotis laniger</i>	4	4	1		1	2	2	2	2	2	2				3		3				14
<i>Myotis muricola</i>	1	2						1	1						1		1				4
<i>Myotis sp.</i>			2		2					3	3							4		4	9
<i>Phoniscus jagorii</i>																		1		1	1
<i>Rhinolophus episcopus</i>								1	1												1

Species	Mission 1		Mission 2			Mission 3		Mission 4		Mission 5		Mission 6			Mission 7			Mission 8			Total
	-	Total	-	+	Total	-	Total	-	Total	-	Total	-	+	Total	-	+	Total	-	+	Total	
<i>Rhinolophus malayanus</i>	1	1	6		6	1	1	1	1			6		6	1		1	3		3	19
<i>Rhinolophus marshalli</i>	1	1																			1
<i>Rhinolophus microglobosus</i>	2	2	2		2			1	1						2		2				7
<i>Rhinolophus pearsonii</i>	2	2	5		5	2	2	2	2	1	1				5		5	2		2	19
<i>Rhinolophus perniger</i>	2	2						1	1						2		2	1		1	6
<i>Rhinolophus pusillus</i>	3	3	3		3	1	1	1	1	1	1	6		6	2		2	3		3	20
<i>Rhinolophus rex</i>			3		3							3		3	1		1				7
<i>Rhinolophus siamensis</i>	1	1										2		2							3
<i>Rhinolophus thomasi</i>	2	2	6		6	2	2	2	2	5	5	8		8	3		3	8		8	36
<i>Rousettus</i> sp.			2		2													1		1	3
<i>Sphaerias blanfordi</i>															2		2				2
<i>Tylonycteris fulvida</i>								2	2						1		1				3
<i>Tylonycteris tonkinensis</i>															1		1				1
<b>Total</b>	<b>41</b>	<b>41</b>	<b>64</b>	<b>1</b>	<b>65</b>	<b>23</b>	<b>23</b>	<b>32</b>	<b>32</b>	<b>25</b>	<b>25</b>	<b>80</b>	<b>2</b>	<b>82</b>	<b>59</b>	<b>1</b>	<b>60</b>	<b>75</b>	<b>3</b>	<b>78</b>	<b>406</b>

\*Empty cells represent no available samples. -, negative; +, positive.

**Appendix Table 2.** List of primers used for the amplification of partial small, medium, and large segments

Primer name	Sequences, 5'-3'	Strand	Reference
<b>Small segment</b>			
S_clust0_man0_L	AAAAGGAGGTRGCAYTRGCA	Forward	This study
S_clust0_man1_R	TCTGCATCCATATCRTCCCAAGA	Reverse	This study
S_clust1_man2_L	ATTGAGGARCCWTCTGGTGCA	Forward	This study
S_clust1_man1_R	CCCCTAGTAGTATGCTCCYTAGT	Reverse	This study
<b>Medium segment</b>			
M_clust0_man1_L	TSTGCCAAAGGATYGACACAGA	Forward	This study
M_clust0_man1_R	GCYGCCARCAYAACATTCTA	Reverse	This study
T-M1199F	TAAVTTCAMCAACATGTC	Forward	(1)
T-M1485R	CCAGCCAAARCARAATGT	Reverse	(1)
<b>Large segment</b>			
HAN-L-F1	ATGTAYGTBAGTGCWGATGC	Forward	(2)
HAN-L-R1	AACCADTCWGTGCCRTCATC	Reverse	(2)
HAN-L-F2	TGCWGATGCHACIAARTGGTC	Forward	(2)
HAN-L-R2	GCRTCRTCWGARTGRTGDGCAA	Reverse	(2)

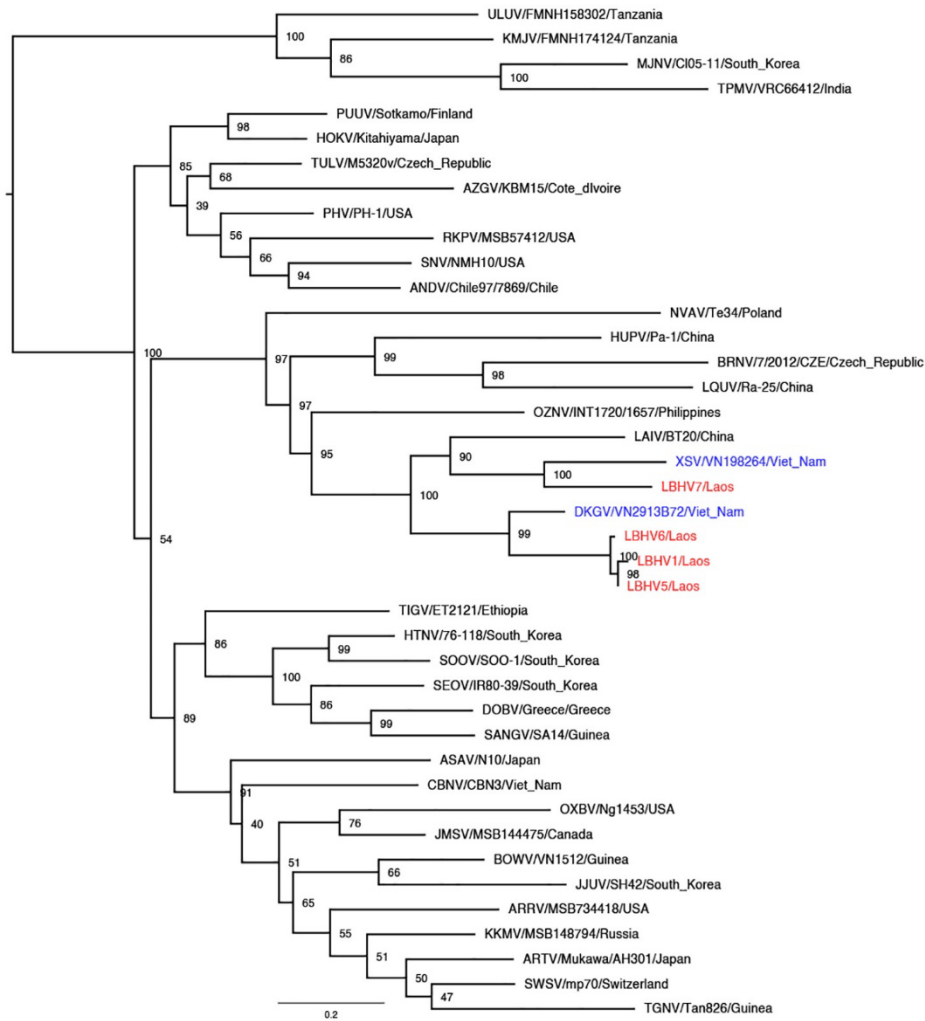


***Aselliscus stoliczkanus***

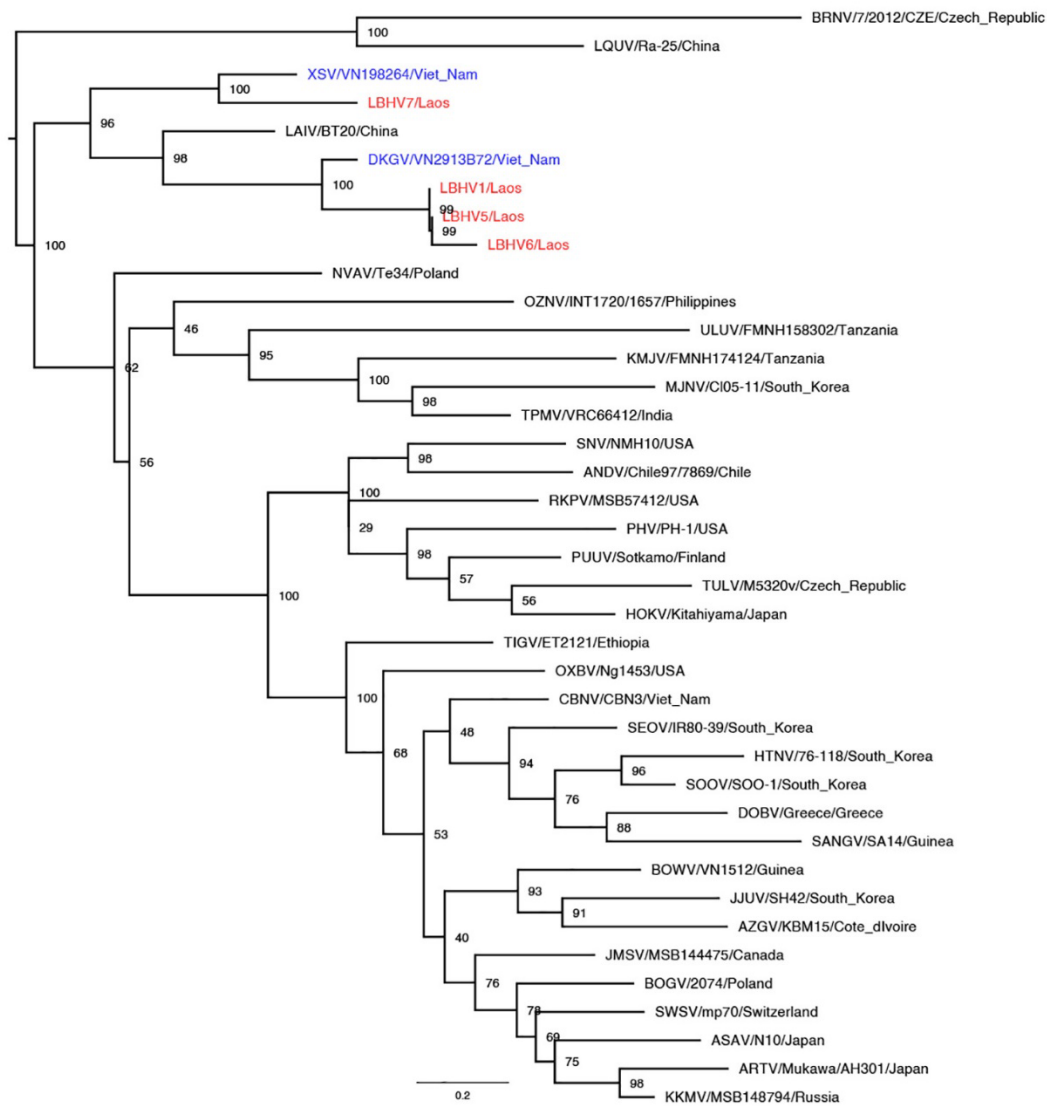


***Hipposideros gentilis***

**Appendix Figure 1.** Photos of bat species that tested positive for batborne hantaviruses from Laos, 2023–2024.



**Appendix Figure 2.** Phylogenetic tree of partial small (S) segments ( $\approx 200\text{--}700$  bp) from LBHV-1 and -5-7 and other hantaviruses. Tree tips highlighted in red represent hantaviruses detected in Laos, and tips highlighted in blue indicate strains from Vietnam. The maximum-likelihood tree was reconstructed with the same method in Figure 3.



**Appendix Figure 3.** Phylogenetic tree of partial medium (M) segments ( $\approx 200$ – $700$  bp) from LBHV-1 and -5–7 and other hantaviruses. Tree tips highlighted in red represent hantaviruses detected in Laos, and tips highlighted in blue indicate strains from Vietnam. The maximum-likelihood tree was reconstructed with the same method in Figure 3.