

Table S1. Lengths of CDSs and their encoded putative proteins, and GB nos. of CHeRI orbiviruses 1.0, 2.1, and 2.2.

CHeRI OrbV	Parameter	Segment Number and Gene ^c									
		1 (VP1)	2 (VP3)	3 (VP2)	4 (VP4)	5 (NS1)	6 (VP5)	7 (NS2)	8 (VP7)	9 (VP6)	10 (NS3)
1.0 (from animal OV682)	CDS length (bp) including stop codon	3,936	2,793	2,628	1,947	1,698	1,608	1,341	1,059	1,050	753
	Predicted protein length (aa)	1,311	930	875	648	565	535	446	352	349	250
	GenBank accession number	MK903619	MK903621	MK903620	MK903622	MK903626	MK903623	MK903627	MK903625	MK903624	MK903628
2.1 ^a (from animal OV610)	CDS length (bp) including stop codon	3,936	2,781	2,634	1,938	1,692	1,605	1,353	1,104	1,059	756
	Predicted protein length (aa)	1,311	926	877	645	563	534	450	367	352	251
	GenBank accession number	MK903629	MK903631	MK903630	MK903632	MK903636	MK903633	MK903637	MK903635	MK903634	MK903638
2.2 ^b (from animal OV682)	CDS length (bp) including stop codon	3,936	2,781	2,634	1,938	1,692	1,605	1,353	1,104	1,059	756
	Predicted protein length (aa)	1,311	926	877	645	563	534	450	367	352	251
	GenBank accession number	MK903639	MK903641	MK903640	MK903642	MK903646	MK903643	MK903647	MK903645	MK903644	MK903648

^aGenBank accession numbers of the corresponding CDS of co-infecting EHDV-2 virus: MK958987 - MK958996. ^bGenBank accession numbers of the corresponding CDS of co-infecting EHDV-2 virus: MK959007 - MK959016. ^cSeg.1, VP1 gene, encodes RdRp; Seg.2, VP3 gene, encodes T2 protein; Seg.3, VP2 gene, encodes major outer capsid protein; Seg.4, VP4 gene, encodes Cap; Seg. 5, NS1 gene, encodes Tup; Seg.6, VP5, encodes outer capsid protein VP5; Seg.7, NS2 gene, encodes ssRNA-binding protein; Seg. 8, VP7 gene, encodes immunodominant major serogroup-specific antigen; Seg.9, VP6 gene, encodes NTPase (helicase); Seg.10, NS3 gene, encodes for protein involved in release of virus particles from infected insect cells.

Table S2. Lengths of CDSs and their encoded putative proteins, and GB nos. of CHeRI orbiviruses 3.1, 3.2, and 3.3.

CHeRI OrbV	Parameter	Segment Number and Gene ^c									
		1 (VP1)	2 (VP3)	3 (VP2)	4 (VP4)	5 (NS1)	6 (VP5)	7 (NS2)	8 (VP7)	9 (VP6)	10 (NS3)
3.1 ^a (from animal OV617)	CDS length (bp) including stop codon	3,936	2,778	2,622	1,938	1,707	1,611	1,326	1,095	1,062	750
	Predicted protein length (aa)	1,311	925	873	645	568	536	441	364	353	249
	GenBank accession number	MK903649	MK903651	MK903650	MK903652	MK903656	MK903653	MK903657	MK903655	MK903654	MK903658
3.2 ^b (from animal OV867)	CDS length (bp) including stop codon	3,936	2,778	2,622	1,944	1,707	1,611	1,326	1,095	1,062	750
	Predicted protein length (aa)	1,311	925	873	647	568	536	441	364	353	249
	GenBank accession number	MK903659	MK903661	MK903660	MK903662	MK903666	MK903663	MK903667	MK903665	MK903664	MK903668
3.3 (from animal OV926)	CDS length (bp) including stop codon	3,936	2,778	2,622	1,944	1,707	1,611	1,326	1,092	1,062	750
	Predicted protein length (aa)	1,311	925	873	647	568	536	441	363	353	249
	GenBank accession number	MK903669	MK903671	MK903670	MK903672	MK903676	MK903673	MK903677	MK903675	MK903674	MK903678

^aGenBank accession numbers of the corresponding CDS of co-infecting EHDV-2 virus: MK958997 - MK959006. ^bGenBank accession numbers of the corresponding CDS of co-infecting EHDV-2 virus: MK959017 - MK959026. ^cSeg.1, VP1 gene, encodes RdRp; Seg.2, VP3 gene, encodes T2 protein; Seg.3, VP2 gene, encodes major outer capsid protein; Seg.4, VP4 gene, encodes Cap; Seg. 5, NS1 gene, encodes Tup; Seg.6, VP5, encodes outer capsid protein VP5; Seg.7, NS2 gene, encodes ssRNA-binding protein; Seg. 8, VP7 gene, encodes immunodominant major serogroup-specific antigen; Seg.9, VP6 gene, encodes NTPase (helicase); Seg.10, NS3 gene, encodes for protein involved in release of virus particles from infected insect cells.

Table S3. GenBank accession numbers of orbivirus protein acid and nucleotide sequences used for phylogenetic analyses.

Orbivirus	VP1 (RdRp)		VP2 (outer capsid protein)		VP3 (T2)	
	Protein	Nucleotide	Protein	Nucleotide	Protein	Nucleotide
Big cypress orbivirus	AZK31312.1	MK105769.1	AVO64732.1	MF094110.1	AVO64733.1	MF094111.1
BTV	FJ969721.1	FJ969719.1	ACR58459.1	FJ969720.1	FJ969721.1	FJ969721.1
Changuinola virus	AFX73365.1	JQ610655.1	AFX73366.1	JQ610656.1	AFX73367.1	JQ610657.1
Chenuda virus	YP009158878.1	NC_027534.1	YP_009158881.1	NC_027537.1	YP009158879.1	NC_027535.1
CHeRI OrbV-1 OV682	QCQ85336.1	MK903619	QCQ85337.1	MK903620	QCQ85338.1	MK903621
CHeRI OrbV-2.1 OV610	QCQ85346.1	MK903629	QCQ85347.1	MK903630	QCQ85348.1	MK903631
CHeRI OrbV-2.2 OV862	QCQ85356.1	MK903639	QCQ85357.1	MK903640	QCQ85358.1	MK903641
CHeRI OrbV-3.1 OV617	QCQ85366.1	MK903649	QCQ85367.1	MK903650	QCQ85368.1	MK903651
CHeRI OrbV-3.2 OV926	QCQ85376.1	MK903659	QCQ85377.1	MK903660	QCQ85378.1	MK903661
CHeRI OrbV-3.3 OV867	QCQ85386.1	MK903669	QCQ85387.1	MK903670	QCQ85388.1	MK903671
Chobar Gorge virus	YP_009158901.1	NC_027553.1	YP_009158904.1	NC_027556.1	YP009158902.1	NC_027554.1
Corriparta virus	YP009507680.1	NC_038568.1	AGT51056.1	KC853044.1	YP009507675.1	NC_038564.1
EHDV	YP003240108.1	NC_013396.1	YP_003240109.1	NC_013397.1	YP003240110.1	NC_013398.1
Equine encephalosis virus	HQ630904.1	ADU57359.1	HQ630903.1	ADU57366.1	HQ630902.1	ADU57373.1
Eubenangee virus	JQ070378.1	AFH41511.1	NC_038588.1	YP009507701.1	JQ070376.1	AFH41511.1
Great Island virus	NC_014523.1	YP003896059.1	NC_014526.1	YP_003896062.1	NC_014522.1	YP003896058.1
Guangxi orbivirus	NC_040479.1	YP009551623.1	MG020126.1	AXS78000.1	NC_040478.1	YP009551622.1
Kammavanpettai virus	AXF35757.1	MG770350.1	AXF35760.1	MG770353.1	AXF35759.1	MG770352.1
Kemerovo virus	AGG68141.1	KC288130.1	ADZ96232.1	HQ266594.1	KC288131.1	KC288131.1
Koyama Hill virus	BAP18633.1	AB894484.1	BAP18633.1	AB894486.1	BAP18632.1	AB894485.1
Lebombo virus	AFX73376.1	JQ610665.1	AFX73378.1	JQ610667.1	AFX73377.1	JQ610666.1
Mobuck virus	AGX89720.1	KF296322.1	AGX89721.1	KF296323.1	YP008719913.1	NC_022627.1
Okhotskiy virus	ATW68806.1	KY023329.1	ATW68809.1	KY023332.1	ATW68807.1	KY023330.1
Orungo virus	AFX73387.1	JQ610675.1	AFX73389.1	JQ610677.1	AFX73389.1	JQ610677.1
Palyam virus	YP052935.1	NC_005990.1	YP052931.1	NC_005986.1	YP052934.1	NC_005989.1
Parry's lagoon virus	ANH10670.1	KU724110.1	ANH10672.1	KU724112.1	ANH10671.1	KU724111.1
PHSV	YP460038.1	NC_007748.1	ABB72772.1	DQ248059.1	YP460039.1	NC_007749.1
Sathuvachari virus	AGE32260.1	KC432629.1	AGE32261.1	KC432630.1	KC432631.1	KC432631.1
St Croix River virus	YP_052942.1	NC_005997.1	YP_052944.1	NC_005999.1	YP052943.1	NC_005998.1
Tribeč virus	ADZ96219.1	HQ266581.1	AIA24281.1	KJ574045.1	HQ266582.1	HQ266582.1
Umatilla virus	YP009047258.1	NC_024503.1	YP009047260.1	NC_024505.1	YP009047259.1	NC_024504.1
Wad Medani virus	YP009158877.1	NC_027533.1	QBP34453.1	MH571967.1	YP009158883.1	NC_027539.1
Wallal virus	YP008658416.1	NC_022553.1	YP_008658417.1	NC_022554.1	YP_008658418.1	NC_022555.1
Yunnan orbivirus	YP443925.1	NC_007656.1	AAW28769.1	AY701511.1	YP443926.1	NC_007657.1

Table S4. Results of CHeRI OrbV-1-specific virus isolation and RT-PCR tests.

Virus	Tissue	Virus isolation in:		RT-PCR
		Vero E6 cells	C6/36 cells	
CHeRI OrbV-1 (from animal OV682)	cardiac blood	NT ^a	NT	POS
	heart	neg ^b	neg	neg
	kidney	neg	neg	neg
	liver	neg	neg	neg
	lung	neg	neg	neg
	spleen	neg	POS ^c	POS
	miscellaneous GI tract	neg	neg	neg

NT ^a, Not tested; neg ^b, negative (no virus isolated); POS ^c, Positive (virus isolated).

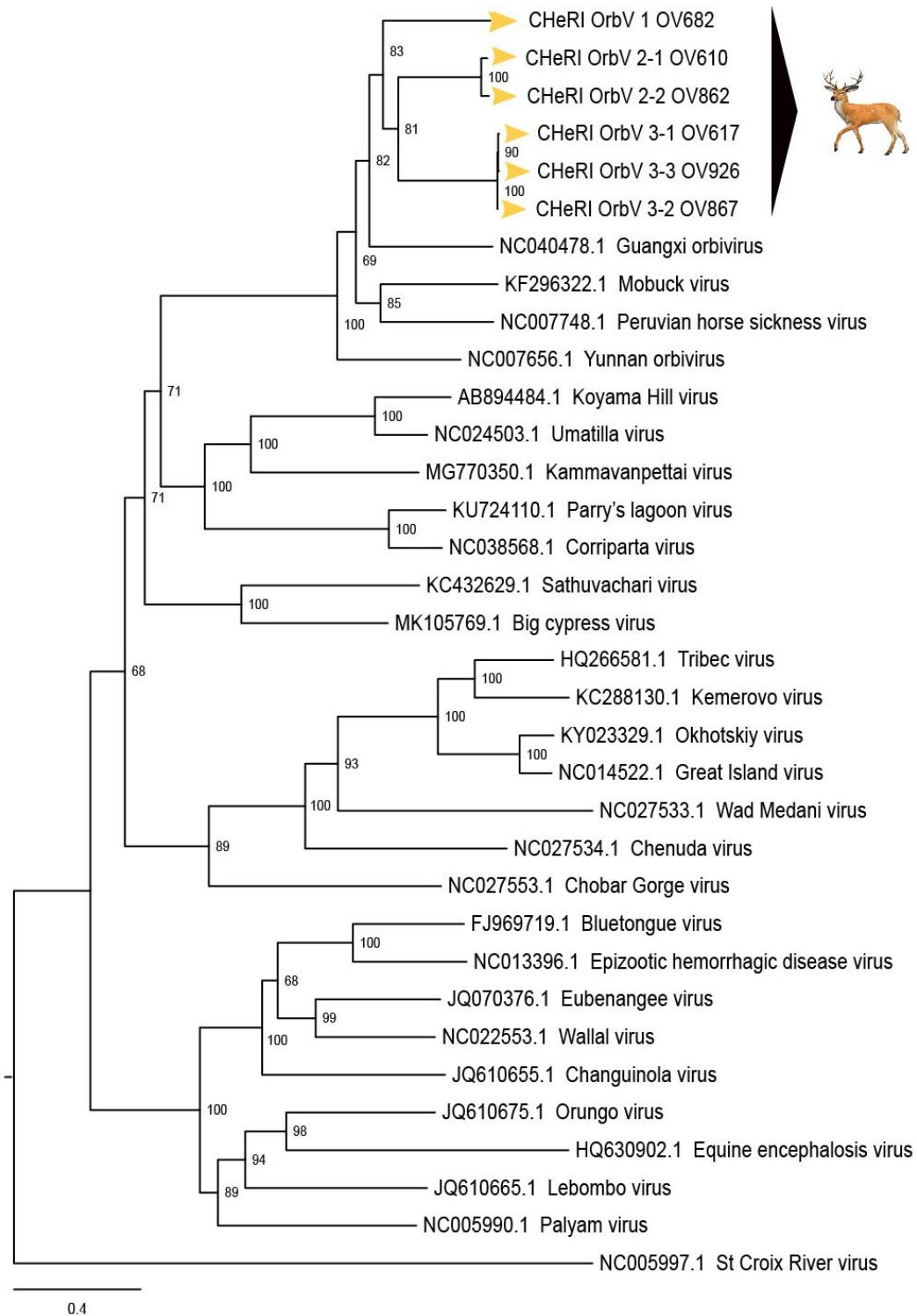
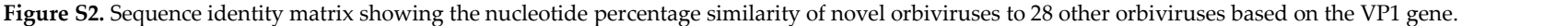


Figure S1. Maximum Likelihood phylogram depicting the relationship of novel orbiviruses to representatives of the *orbivirus* genus based on the nucleotide sequences of the gene RNA dependent RNA polymerase, VP1. Bootstrap values are given at each node and the branch lengths represent the number of inferred substitutions as indicated by the scale.



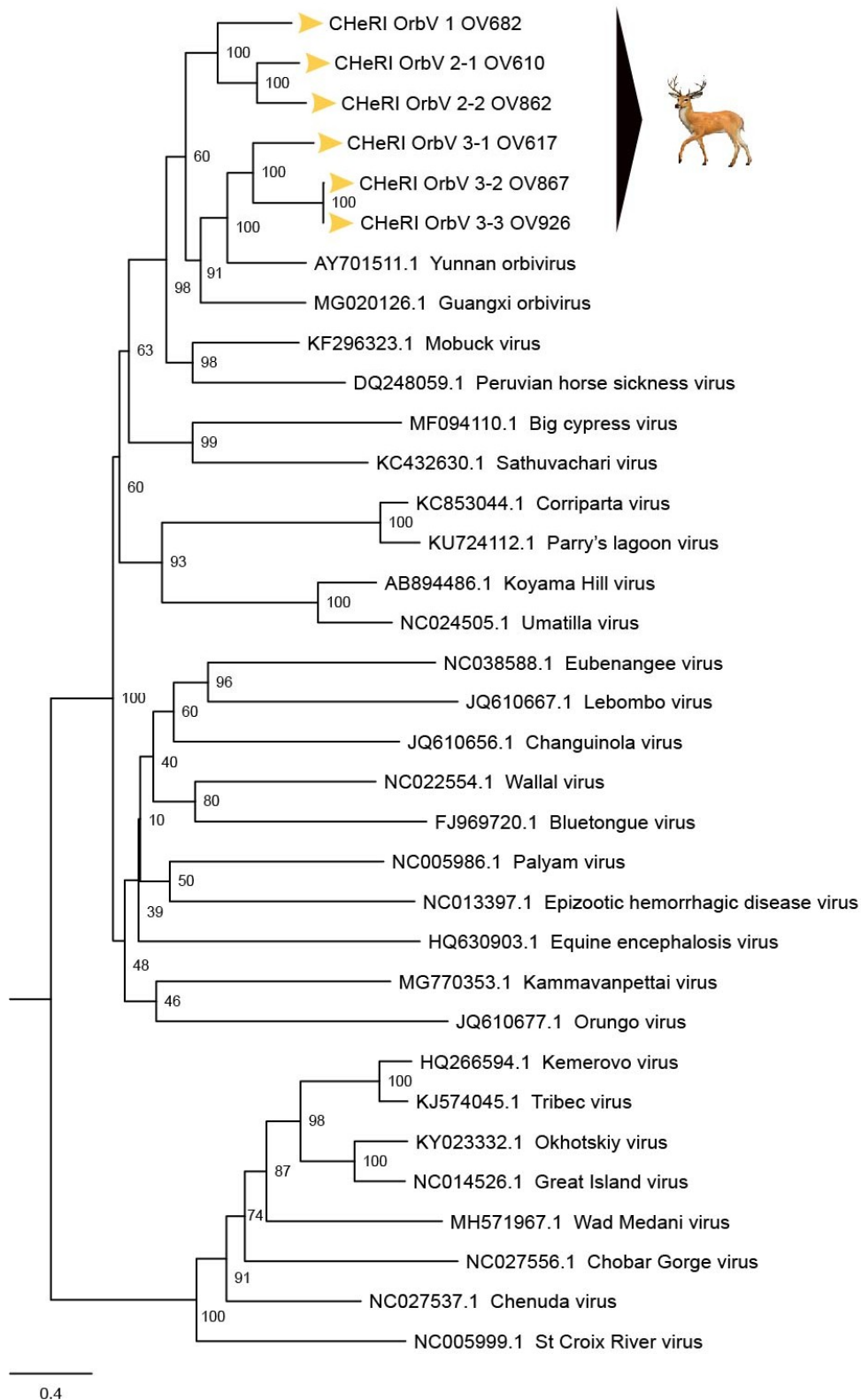


Figure S3. Maximum Likelihood phylogram depicting the relationship of novel orbiviruses to representatives of the *orbivirus* genus based on the nucleotide sequences of the gene for outer capsid protein VP2. Bootstrap values are given at each node and the branch lengths represent the number of inferred substitutions as indicated by the scale.

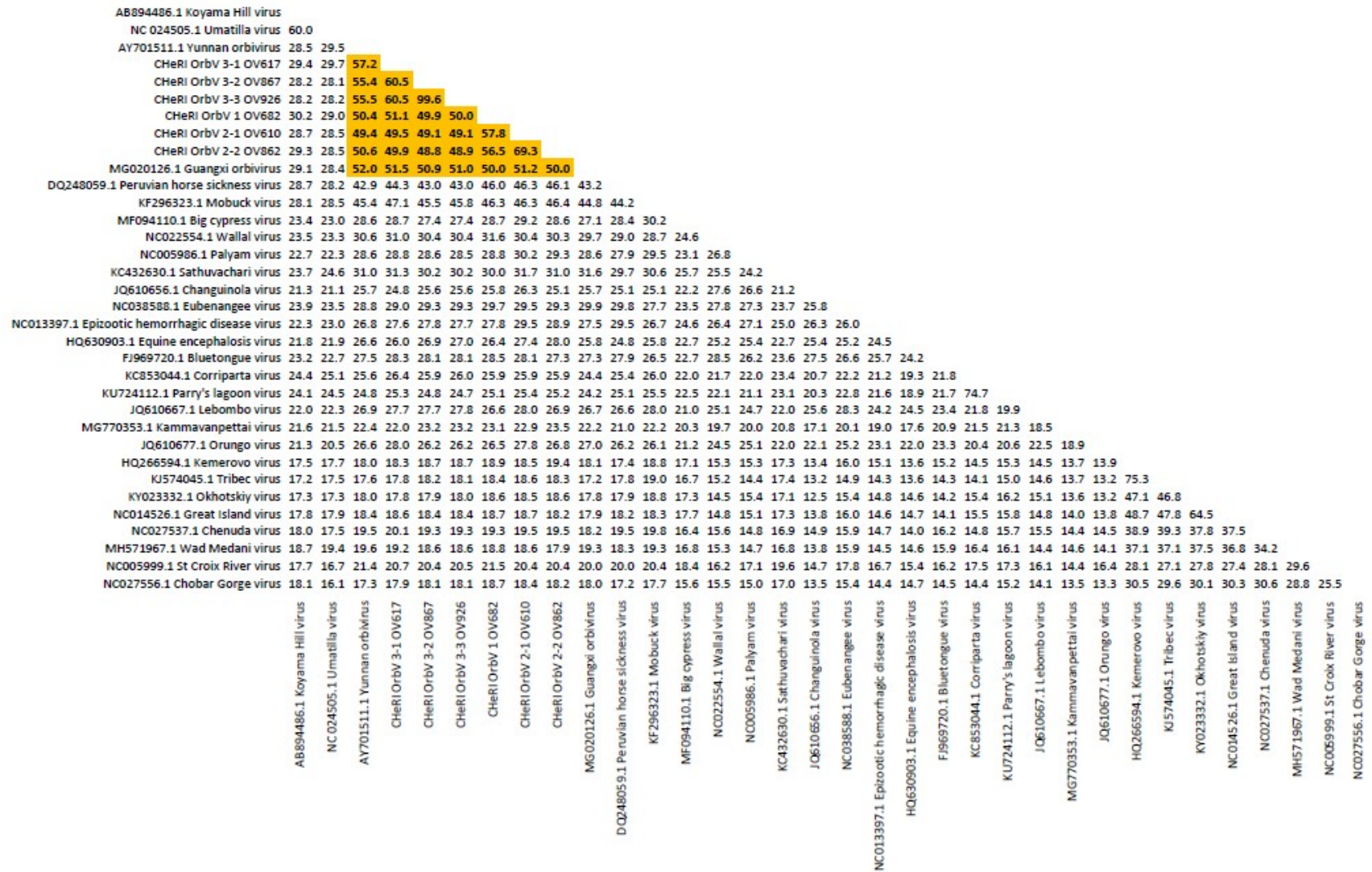


Figure S4. Sequence identity matrix showing the nucleotide percentage similarity of novel orbiviruses to 28 other orbiviruses based on the VP2 gene.

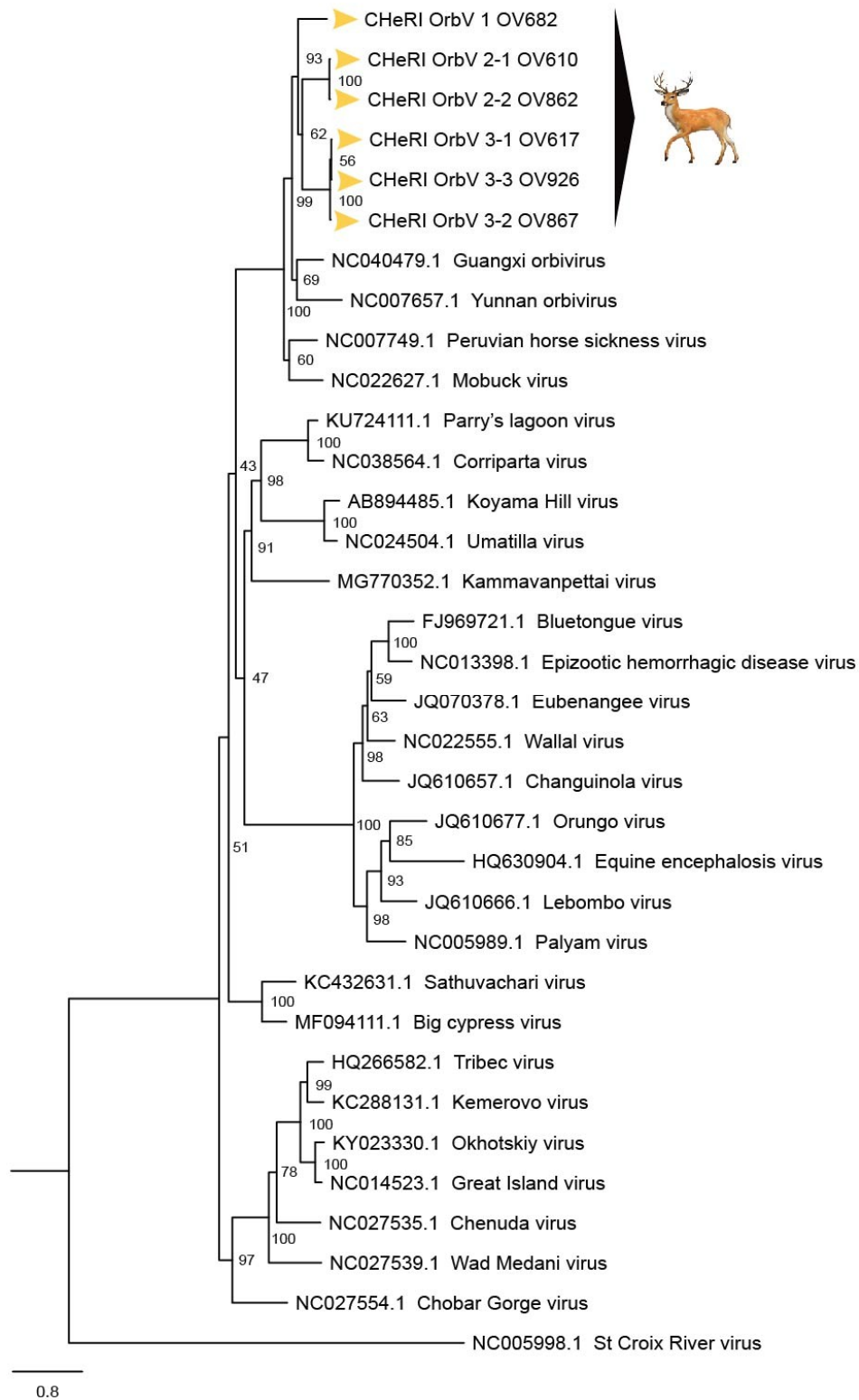


Figure S5. Maximum Likelihood phylogram depicting the relationship of novel orbiviruses to representatives of the *orbivirus* genus based on the nucleotide sequences of the gene for innermost subcore capsid protein VP3 (T2). Bootstrap values are given at each node and the branch lengths represent the number of inferred substitutions as indicated by the scale.

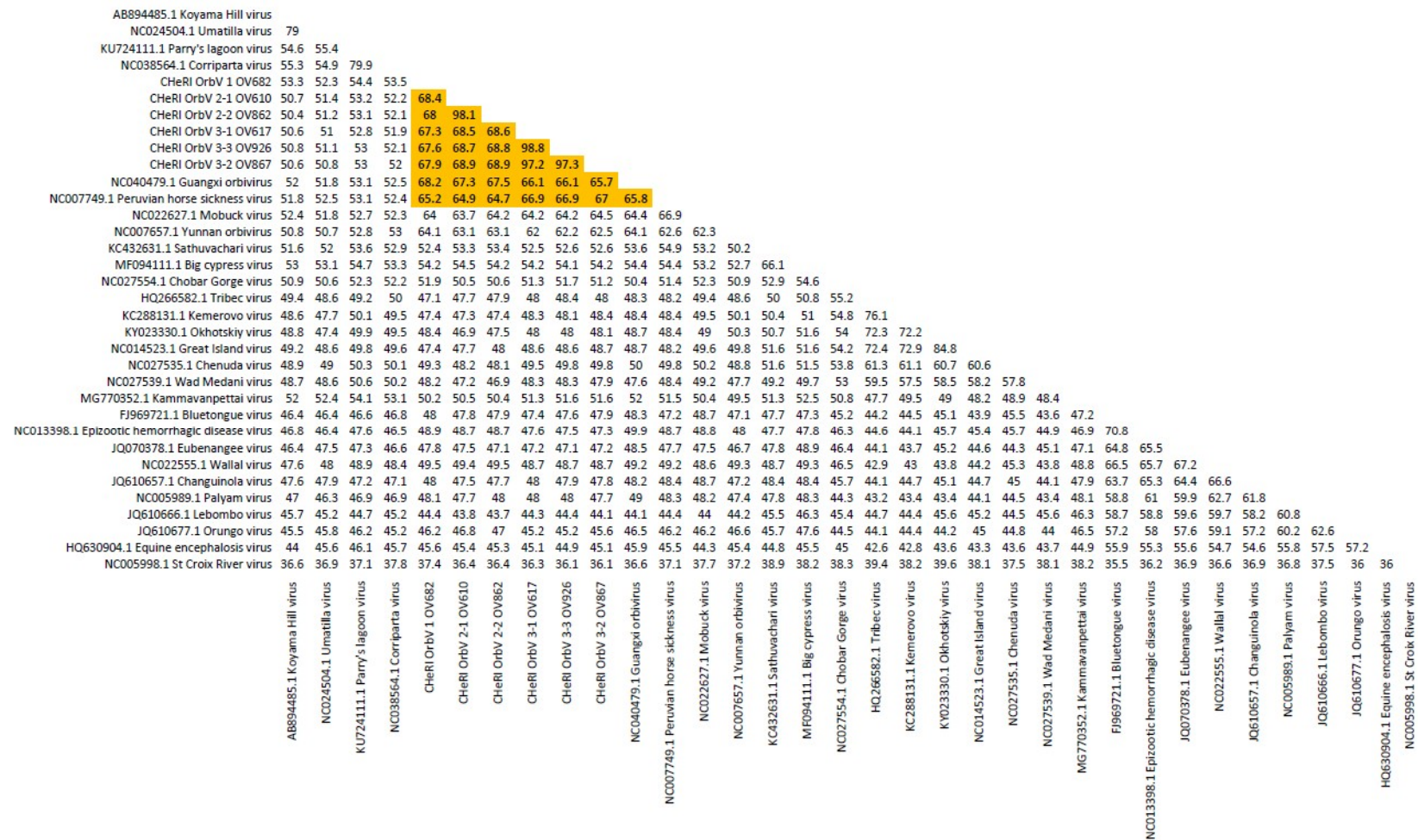


Figure S6. Sequence identity matrix showing the nucleotide percentage similarity of novel orbiviruses to 28 other orbiviruses based on the VP3 (T2) gene.