

VIROLOGICA SINICA

Electronic Supplementary Material

Chevrier's Field Mouse (*Apodemus chevrieri*) and Père David's Vole (*Eothenomys melanogaster*) in China Carry Orthohepeviruses that form Two Putative Novel Genotypes Within the Species *Orthohepevirus C*

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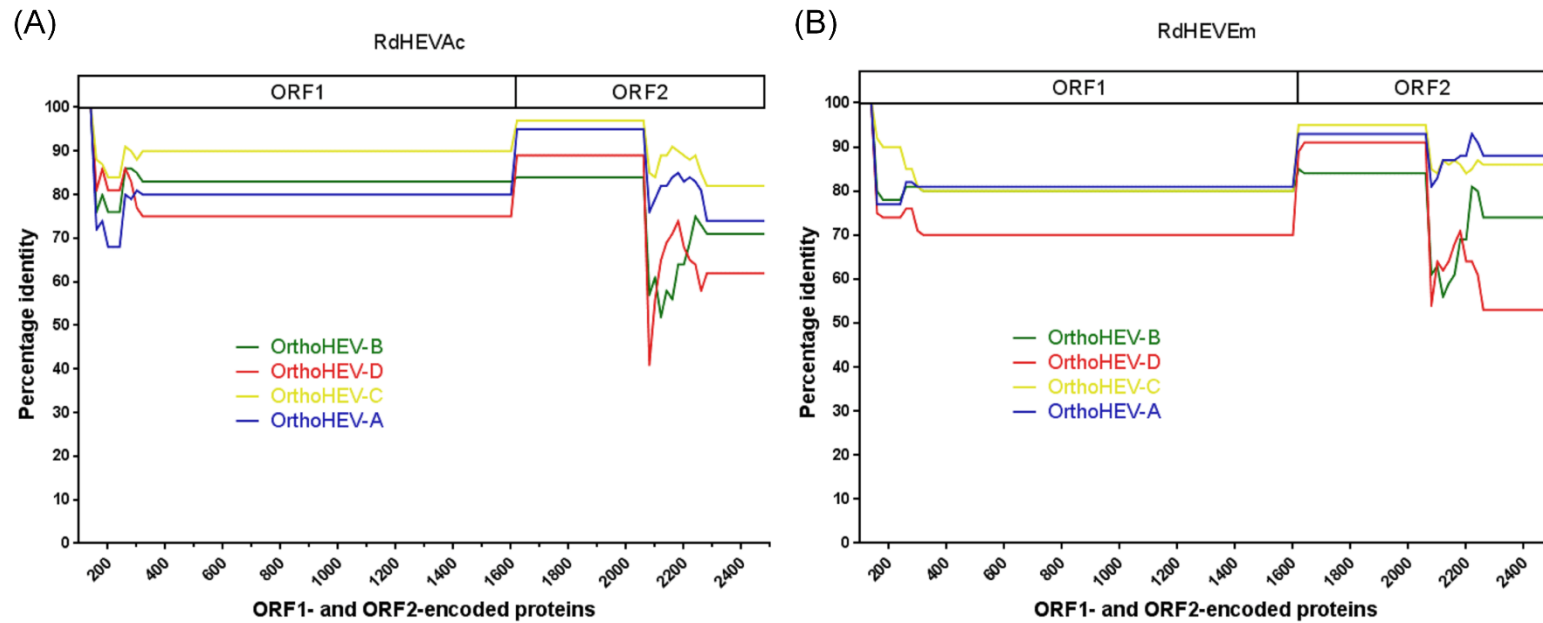


Figure S1. Amino acid identity plot. The complete ORF1 and ORF2 were translated, concatenated, and compared to reference strain of *Orthohepevirus A* to *D*. The GenBank accession numbers are as follows: M73218, M74506, AF082843, AJ272108, AB573435, AB602441, and KJ496143 for *Orthohepevirus A*; AY535004 for *Orthohepevirus B*; GU345042 and JN998606 for *Orthohepevirus C*; and JQ001749 for *Orthohepevirus D*. The uncorrected amino acid identity was plotted with a sliding window size of 200 and a step size of 20 amino acids. A schematic representation of concatenated ORF1 and ORF2 is shown at the top. (A) RdHEVAc. (B) RdHEVEm.

Table S1. Oligonucleotides used for orthohepevirus detection, complete genome sequencing, and viral quantification

^a Oligonucleotide	^b Sequence (5' -3')	Polarity	Use	Reference
HEV-F4228	ACYTTYTGTCYTYTITTTGGTCCITGGTT	+	Orthohepevirus detection	(Drexler et al., 2012)
HEV-R4598	GCCATGTTCCAGAYGGTGTTC	-		
HEV-R4565	CCGGGTTCCRCIGAGTGTTCCTTCCA	-		
HEV-F400	GGIMGIGAYGTICAGCGITGG	+	Rodent orthohepeviruses full-length genome amplification	(Drexler et al., 2012)
HEV-F795	GGCIRTIGGITGYCAYTTYGT	+		
HEV-F848	CCIATGCCITAYGTICCATCC	+		
HEV-R1045	GTCAKIAGICKIGARCARARIGC	-		
HEV-R1065	ATVCCICGIAGRATAIGTCATDAG	-		
HEV-R1075	GTIACYTTGTAYSWRATICCICGIAGRATAIGTCA	-		
HEV-F5760	CTGACGTTTTTCGACCTGTTCGT	+		
HEV-F5770	GCGTCTGTCCGGTGGGTTTTTC	+		
HEV-F5790	GGCCACAGTCCAACAATGTTC	+		
HEV-R5780	CTTATAGAAAACCCACCGACAGAC	-		
HEV-R5810	ATGTTGGAACATTGTTGGACTGTG	-		
HEV-R5960	GTYTCGACAGAGCGCCAICC	-		
HEV-R6473	CCIAGGTCTATRTCCTGTGIGG	-		
HEV-R6493a	TCCTGCTCRTGCTGRTTATCATARTCCTG	-		
HEV-R6493b	TCCTGGAGRTGCTGRTTATCAAARTCCTG	-		
HEV-F6376a	GTCTCGGCAATGGCGAGCC	+		
HEV-F6376b	GTGTCTGAGAACGGTGAGCC	+		
HEV-F6493a	CAGGAYTATGATAAYCAGCAYGAGCAGGA	+		
HEV-F6493b	CAGGAYTTTGATAAYCAGCAYCTCCAGGA	+		
HEV-R6865	CRGTRGTRTRTAATTRTARGGRTARCCRG	-		
RdHEVAc-F860	AAGTCTCAGGTAGTGTACGTC	+	Rodent orthohepeviruses full-length genome amplification	This study
RdHEVAc-HEV-F1030	GCTGCTCTAGGCTCATGACC	+		
RdHEVAc-HEV-F1517	GTGAGGACCTGAGTGATGAG	+		
RdHEVAc-HEV-R4115	AGGCAATCTGTCCACAATAGC	-		
RdHEVAc-HEV-R4265	CATCAACACACACTCCAATC	-		
RdHEVAc-HEV-R4780	CTGTAATACCTTGTAGCAAGT	-		
RdHEVAc-HEV-R5599	GACATCGGTGGACATTATAG	-		

RdHEVE _m -HEV-F947	TGCACGRTCCACYTTCCATG	+		
RdHEVE _m -HEV-F1004	GGTGTACAYTAGATGAYGAT	+		
RdHEVE _m -HEV-R3250	CTCGTGCACAGTTATAGCAG	-		
RdHEVE _m -HEV-R4322	AGCGGACCTTATYARATGGTAT	-		
RdHEVE _m -HEV-R4263	TTCAGCCATTATCTCACAYTC	-		
RdHEVE _m -HEV-R4290	CATARAGGCATRCCAACCTC	-		
5' RACE-HEV-R470	CCTGCAATTCTCAAATCCTCGGACAC	-		
5' RACE-HEV-R490	GGTGCAGCTCATGAAGCGAGTAGAG	-		
3' RACE-HEV-F6339	GGAGCTGARTATAAGCAGTCT	+		
3' RACE-HEV-F6457	GGACGAAGTGACTATTAAYGG	+		
HEV-qPCR-F	GTTGATGGCTGAAGCAGGTATG	+	Specific rodent orthohepevirus quantification	This study
HEV-qPCR-probe	FAM-ATGGATGTGGAAGTTGT-BHQ1	+		
HEV-qPCR-F	CCATGCCGACCTCAMYARATG	-		

^aNamed after the position in the reference sequence under GenBank accession number NC_001434.

^bR is G/A, Y is C/T, S is G/C, W is A/T, M is A/C, K is G/T, H is A/C/T, N is A/T/C/G, and I is inosine.