

Electronic Supplementary Material

Novel HCV-Like Virus Detected in Avian Livers in Southern China and Its Implications for Natural Recombination Events

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Table S1. Primers used to sequence DuHV in this study

Primer Sequence (5'→3') [†]	Target Region (bp) [§]	Product length (bp)
F:GAAAGGGGGTGGGTCAGCCTTA R:CAGACCTCAGAAAAGCCGAA	13-1711	1699
F:GTGTTTGGCTTCTAACCAC R:CTATGACTCACCCAGCTAC	1559-2767	1209
F:TCCAGTTCACATCTTTGGC R:TAGCCAACGTCTTGAGG	2534-3867	1334
F:AGGTATTCCATCAAGTGAAAT R:CCATAACTGTTGCCTCTGGGA	3632-5280	1649
F:TCCCAGAGGCAACAGTTAT R:TAACGGTAGAGGAACCCAT	5260-7146	1887
F:TTCCCTTGGTATGCTTCGGTA R:GGATAGACACGTCCACCCA	7019-8470	1452
F:GTGTTATCATCGTCCAGACCT R:TACATGATCAACGCGTTTCGAC	8350-9791	1442
F:CAGTCTTGTGTATTACACCA R:GGCATTAAAACAACAGAAAAT	9713-11422	1710

[†]F: Forward primer; R: Reverse primer.

[§]Numbered according to the genomic sequence of DuHV strain HCL-2.

Table S2. The *P*-values for recombination events in the seven detection methods used in this study.

Method	<i>P</i> value	
	Event 1	Event 2
RDP	3.095×10^{-74}	1.344×10^{-4}
GENECONV	1.146×10^{-72}	3.560×10^{-4}
BootScan	2.818×10^{-77}	4.185×10^{-5}
MaxChi	7.081×10^{-23}	5.117×10^{-3}
Chimaera	2.329×10^{-23}	1.797×10^{-2}
SiScan	1.974×10^{-30}	>0.01
3Seq	8.881×10^{-16}	1.798×10^{-2}

Table S3. Unique amino acid substitutions and their viral protein locations in GD-61.

Unique Amino acid substitutions	Viral protein
A396V	E1
V536N, N576T, R594V, D596S, A626V, Q670K,	E2
I684V	
I784V, V805I	P7
A938C, I984V	NS2
A1421S, S1478N	NS3
V1787A, F1792Y, K1798R, V1834I, S1835A,	NS4B
R1858K	
V2029I, L2043I, V2047I, T2159S, Q2430K,	NS5A
S2434G, A/T2437P, P2440S, N/T2456D,	
E2464G, V2473T, S2494P, T2495K, T2496A,	
T2511S, G2516R, K2523E, E2524A, T2604A,	
E2636A, V2685T, A2692P, F2711C, I/N2718L,	
S2730T, V2738I, G2743S, F2744Y, I2745M,	
Y2766F, S2774G, S2775A, A2777K, S2781A,	
A2784T, I2786V, T2798A, A/V2805M, S2837G,	
A2838T, D2843S, T/S2850A, L2851M, S2895T,	
R/G2936K, N2939S, A/T2948S, S2952G,	
V/I2953M, V2958A, T2960A, T2981S, V2983T	