SUPPLEMENTARY MATERIALS

Title: Detection and genetic characterization of hepatitis B and D viruses: a multi-site cross-sectional study of people who use illicit drugs in the Amazon region.

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Table S1. Information used for the construction of the phylogenetic trees of the hepatitis B virus (HBV) in this study.

Akaike information criterion (AIC)*	Bayesian Information Criterion (BIC)*
Model = TVM+I+G	Model = TPM3uf+G
Partition = 012314	Partition = 012012
-lnL = 14408.9885	-lnL = 4519.5605
K = 331	K = 86
FreqA = 0.2444	FreqA = 0.1630
FreqC = 0.2652	FreqC = 0.3115
FreqG = 0.2012	FreqG = 0.2650
FreqT = 0.2893	FreqT = 0.2605
R(a) [AC] = 2.3370	R(a) [AC] = 0.5556
R(b) [AG] = 4.3672	R(b) [AG] = 2.8769
R(c) [AT] = 1.2537	R(c) [AT] = 1.0000
R(d) [CG] = 0.4893	R(d) [CG] = 0.5556
R(e) [CT] = 4.3672	R(e) [CT] = 2.8769
R(f) [GT] = 1.0000	R(f) [GT] = 1.0000
p-inv = 0.3610	
Gamma shape = 0.5020	Gamma shape = 0.5330

*Information provided by the jModeltest2 software from the analysis of the alignment of the nucleotide sequences in this study and the reference sequences deposited at the NCBI.

Note: To test the robustness of the maximum likelihood tree topologies, 1,000 bootstrap replicates were performed. Bayesian analyzes consisted of two independent runs (Chain lengths of 2×10^6 Markov Chain Monte Carlo) with a total of 1,000 interactions and 10% burn-in.

Table S2. Information used for the construction of the phylogenetic trees of the hepatitis D virus (HDV) in this study.

Akaike information criterion (AIC)*	Bayesian Information Criterion (BIC)*
Model = TIM3+G	Model = TPM3uf+I+G
Partition = 012032	Partition = 012012
-lnL = 4518.5076	-lnL = 3809.7180
K = 87	K = 79
FreqA = 0.1709	FreqA = 0.1571
FreqC = 0.3017	FreqC = 0.3116
FreqG = 0.2741	FreqG = 0.2871
FreqT = 0.2533	FreqT = 0.2442
R(a) [AC] = 0.5553	R(a) [AC] = 0.5935
R(b) [AG] = 2.5338	R(b) [AG] = 2.8917
R(c) [AT] = 1.0000	R(c) [AT] = 1.0000
R(d) [CG] = 0.5553	R(d) [CG] = 0.5935
R(e) [CT] = 3.2090	R(e) [CT] = 2.8917
R(f) [GT] = 1.0000	R(f) [GT] = 1.0000
	P-inv = 0.3290
Gamma shape = 0.5340	Gamma shape = 1.7530

*Information provided by the jModeltest2 software from the analysis of the alignment of the nucleotide sequences in this study and the reference sequences deposited at the NCBI.

Note: To test the robustness of the maximum likelihood tree topologies, 1,000 bootstrap replicates were performed. Bayesian analyzes consisted of two independent runs (Chain lengths of 2×10^6 Markov Chain Monte Carlo) with a total of 1,000 interactions and 10% burn-in.