

# New Hepatitis E Virus Genotype in Bactrian Camels, Xinjiang, China, 2013

## Technical Appendix

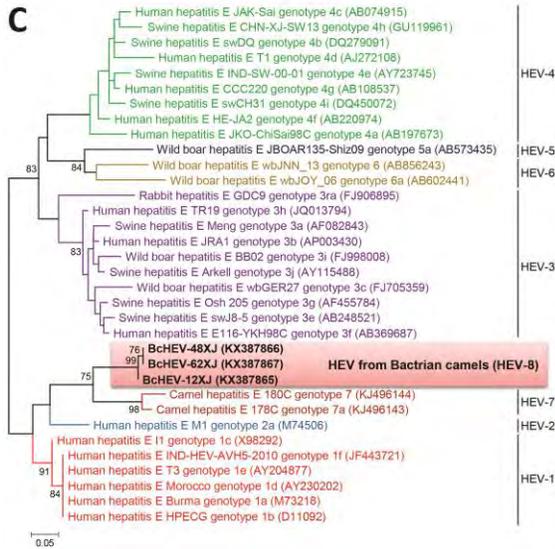
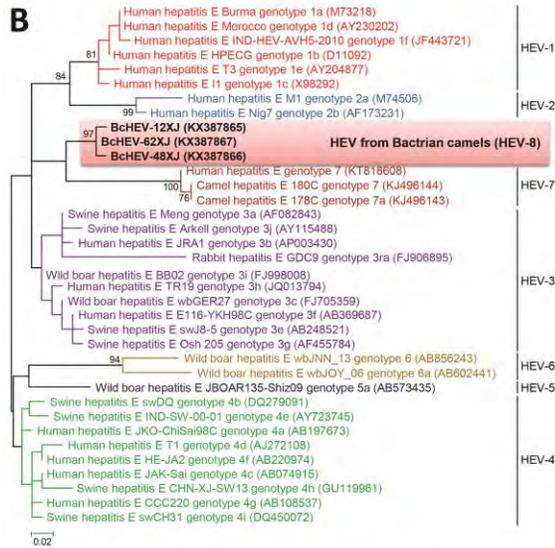
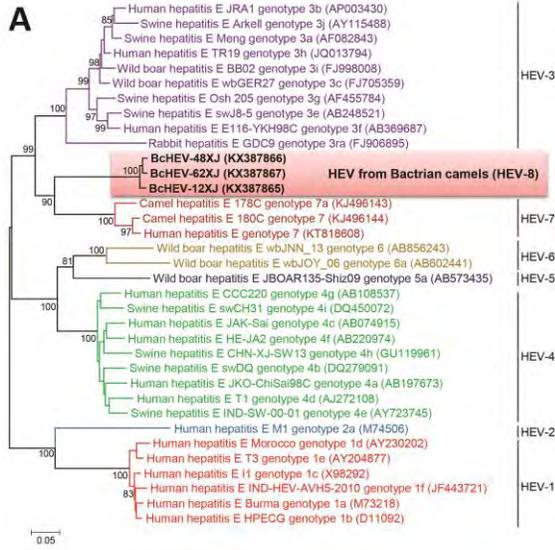
### Complete Genome Sequencing

Three complete genomes of Bactrian camel HEV (BcHEV) strains, including BcHEV-12XJ, BcHEV-48XJ and BcHEV-62XJ, were amplified and sequenced using the RNA extracted from the original specimens as templates. The RNA was converted to cDNA by a combined random-priming and oligo(dT) priming strategy. The cDNA was amplified by primers designed by multiple alignments of the genomes of other HEVs with complete genomes available. Additional primers were designed from the results of the first and subsequent rounds of sequencing (Table). The 5' ends of the viral genomes were confirmed by rapid amplification of cDNA ends using the 5'/3' RACE kit (Roche, Germany). Sequences were assembled and manually edited to produce final sequences of the viral genomes.

**Technical Appendix Table.** Primers for amplification of the three BcHEV genomes

Primers	5' to 3'
<b>Forward</b>	
LPW28520	GTTGTCTCAGCCAATGGCGA
LPW28892	CGAAGGCTTACGAATGTTGC
LPW29061	ATCCGTTGGTCATTGAGA
LPW29066	ACTGTTGAGCTTACAGTTG
LPW29070	TGCATGGTGTGTTGAGAATGA
LPW31223	CCGGCCCTACAGTCTTTCATAT
LPW31225	CCGCTAATCCTGGTGCTATTA
LPW29072	TGCTGGACTTGACTAACTCA
LPW31228	GTATTGCCTCTGAACTTGT
LPW31226	GTACGAAGCTGTATGAAGCTGCTCA
LPW31432	GAAGGGTCTGAGGTCGATT
LPW31299	GGCTGTAAGTGTGCTGTTCTT
LPW32175	CCATGTGTGGGAGTCCAA
<b>Reverse</b>	
LPW28521	GTAGTTTGGTCATACTCAGCAGC
LPW28893	CTGAGAATCAACCCGGTCA
LPW29062	CAACTGTAAGCTCAACAGT
LPW29067	CGAGTGAGTGCAACAATAGCA
LPW29071	GCTGAGAATCAACCCGGTCA
LPW31231	CTTACCAGAACCAGGGACA
LPW31233	CAGAACCCTTTCAGAGACTCCTT
LPW28521	GTAGTTTGGTCATACTCAGCAGC
LPW29077	GCCCTGAGTGTAAATCTCTT
LPW31233	CAGAACCCTTTCAGAGACTCCTT

LPW31433	GCATGTGCACGAGAAGATT
LPW32181	GCATAATTGGACGCCTCAG
LPW31433	GCATGTGCACGAGAAGATT



**Technical Appendix Figure.** Phylogenetic analyses of A) ORF1, B) ORF2, and C) ORF3 and other genotypes of HEVs (HEV-1 to HEV-7) within the species *Orthohepevirus A*. The trees were constructed using maximum likelihood method and the optimal substitution models of JTT+G+I+F, JTT+G+I and JTT+G were used for ORF1, ORF2 and ORF3, respectively. Amino acid residues 1–1743, 1–660 and 10–123 in ORF1, ORF2 and ORF3, numbered with reference to GenBank sequence M73218, were included in the analyses. For ORF1 and ORF3, the scale bars indicate the estimated number of substitutions per 20 aa. For ORF2, the scale bar indicates the estimated number of substitutions per 50 aa. The three strains of DcHEV with complete genomes sequenced in this study are in bold.