Nucleotide sequence of the VP1 gene from a Chinese strain of hepatitis A virus (HAV)

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Three independent cDNA clones were used to determine the sequence of the VP1 gene of HAV strain LCDC-1. The proposed proteolytic cleavage sites at the amino and carboxy termini of VP1 are indicated by the solid and broken arrows respectively (1-3). A striking feature of the LCDC-1 strain is the deletion of 18 nucleotides found exactly at the same region in the VP1 gene of HAS-15 HAV strain (4). These two VP1 proteins only differ in one amino acid, Ala at position 174 instead of Lys (4). Comparisons with four other HAV strains show highly conserved genetic relatedness of the VP1 genes. Other than the six amino acid deletion near the N-terminus, the LCDC-1 VP1 protein differs in 2 amino acids from the MBB and HM-175 proteins, and 3 amino acids from the CR-326 and the MS-1 sequences (5).

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CAG GTT GGA GAT GAT TCA GGA GGT TTC TCA ACA ACA GTT TCT ACA GAG CAG AAT GTT OCT GAT CCC CAA GTT GGC ATA --- --- --- --- --- AAA
Q V G D D S G G G F S T T V S T E Q N V P D P Q Q V G I K
GGG AAA GGC AAT AGG GGA AAG ATG GAT GTA TCA GGA GTG CAG GCA OCT GTG GGA GCT ATT ACA ACA ATT GAG GAT CCA GTT TTA GCA AAG AAA GTA OCT
G K A N R G K M D V S G V Q A P V G A I T T I E D P V L A K K V P
GAG ACA TTT OCT GAA TTG AAG OCT GCA GAA TCC AGA CAT ACA TCA GAT CAC ATG TCT ATT TAT AAA TTC ATG GCA AGG TCT CAT TTC TTG TGT ACT TTT
E T F P E L K P G E S R H T S D H M S I Y K F M G R S H F L C T F
ACT TTT AAT TCA AAC AAT AAA GAG TAC ACA TTT CCA ATA ACT CTG TCT TCG ACT TCT AAT OCT OCT CAT GGT TTA CCA TCA ACA TTA AGG TGG TTC TTT
T F N S N N K E Y T F P I T L S S T S N P P H G L P S T L R W F F
AAT TTG TTT CAG TTG TAT AGA GGA CCA TTG GAT TTG ACA ATT ATA ATC ACA GGA GGC ACT GAT GTG GAT GGT ATG GGC TGG TTT ACT CCA GTG GGC CTT
N L F Q L Y R G P L D L T I I I T G A T D V D G M A W F T P V G L
GCT GTC GAC ACC OCT TGG GTG GAA AAG GCG TCA GCT TTG TCT ATT GAT TAT AAA ACT GGC CTT GGA GCT GTT AGA TTT AAT ACA AGA AGA ACA GGG AAC
A V D T P W V E K A S A L S I D Y K T A L G A V R F N T R R T G N
ATT CAG ATT AGA TTG CCA TGG TAT TCT TAT TTG TAT GGC GTG TCT GGA CCA CTG GAT GGC TTG GGA GAT AAG ACA GAT TCT AAT TTT GGA TTG GTT TCT
I Q I R L P W Y S Y L Y A V S G A L D G L G D K T D S T F G L V S
ATT CAG ATT GCA AAT TAC AAT CAT TCT GAT GAA TAT TTG TCC TTT AGT TGT TAT TTG TCT GTC ACA GAG CAA TCA GAG TTC TAT TTC OCT AGA GCT CCA
I Q I A N Y N H S D E Y L S F S C Y L S V T E Q S E F Y F P R A P
TTA AAT TCA AAT GCT ATG TTG TCC ACT GAG TCC ATG ATG AGT AGA ATT GCA GCT GGA GAC TTG GAG TCA TCA GTG GAT GAT CCC AGA TCA GAG GAG GAC
L N S N A M L S T E S M M S R I A A G D L E S S V D D P R S E E D
AGA AGA TTT GAG AGT CAT ATA GAA TGT AGG AAA CCA TAT AAA GAA TTG ACA CTG GAG GTT GGC AAA CAA AGA CTC AAA TAT GCT CAG GAA GAG TTA TCA
R R F E S H I E C R P Y K E L R L E V G K Q R L K Y A Q E E L S
AAT GAA GTG CTT CCA OCT OCT AGG AAA ATG AAG GGG TTA TTT TCA CAA TCT
N E V L P P P R R K M K G L F S Q S

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