

# The complete nucleotide sequence of Hepatitis B virus, subtype adr (SRADR) and phylogenetic analysis

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We have cloned a genomic DNA of hepatitis B virus (HBV) and the complete DNA sequence was determined. The HBV (1) genomic DNA was purified from serum (2) in a patient with hepatitis who had HBe antigens (3) positive, and the adr subtype of HBV.

The constructed vector with the HBV genome (SRADR) and pUC18 was amplified in *Escherichia coli* strain DH5 alpha, purified and sequenced with dideoxy methods using a T7 Sequencing Kit (Pharmacia LKB Biotechnology, Sweden). The DNA sequence homologies were 99.0% with ADRA (4), 97.7% with ADRC (5), 97.5% with ADRCG (6). Alignment of the region P sequences from SRADR and other HBV defined in Figure 1. To determine the phylogenetic relationships among SRADR, and HPBVCG (Chimpanzee), and other HBV, we constructed evolutionary trees (7) for their pol sequences using both neighbor-joining methods (Figure 2) and UPGMA methods (Figure 3). In both methods, SRADR, ayr and seven previously reported isolates of subtype adr clustered in a closely related group.

## ACKNOWLEDGEMENT

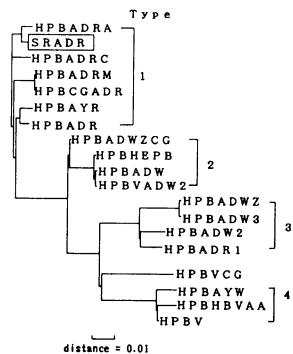
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(a) Type 2		(b) Type 4	
HPBAYW	ATGCCCTATCTTACACACTCCGGAGACTACTGTGTTAGACCCACAG----	HPBAYW	-----
HPBAYA	ATGCCCTATCTTACACACTCCGGAGACTACTGTGTTAGACCCACAG----	HPBAYA	S4
HPBY	ATGCCCTATCTTACACACTCCGGAGACTACTGTGTTAGACCCACAG----	HPBY	S4
HPBYCC	ATGCCCTATCTTACACACTCCGGAGACTACTGTGTTAGACCCACAG----	HPBYCC	S4
HPBAYWZC	ATGCCCTATCTTACACACTCCGGAGACTACTGTGTTAGACCCACAG----	HPBAYWZC	S4
HPBADR	ATGCCCTATCTTACACACTCCGGAGACTACTGTGTTAGACCCACAG----	HPBADR	S4
HPBADRC	ATGCCCTATCTTACACACTCCGGAGACTACTGTGTTAGACCCACAG----	HPBADRC	S4
HPBADRM	ATGCCCTATCTTACACACTCCGGAGACTACTGTGTTAGACCCACAG----	HPBADRM	S4
HPBCGADR	ATGCCCTATCTTACACACTCCGGAGACTACTGTGTTAGACCCACAG----	HPBCGADR	S4
HPBAYR	ATGCCCTATCTTACACACTCCGGAGACTACTGTGTTAGACCCACAG----	HPBAYR	S4
HPBADR	ATGCCCTATCTTACACACTCCGGAGACTACTGTGTTAGACCCACAG----	HPBADR	S4
HPBADWZCG	ATGCCCTATCTTACACACTCCGGAGACTACTGTGTTAGACCCACAG----	HPBADWZCG	1
HPBHEPB	ATGCCCTATCTTACACACTCCGGAGACTACTGTGTTAGACCCACAG----	HPBHEPB	1
HPBADW	ATGCCCTATCTTACACACTCCGGAGACTACTGTGTTAGACCCACAG----	HPBADW	1
HPBVADW2	ATGCCCTATCTTACACACTCCGGAGACTACTGTGTTAGACCCACAG----	HPBVADW2	2
HPBADWZ	ATGCCCTATCTTACACACTCCGGAGACTACTGTGTTAGACCCACAG----	HPBADWZ	2
HPBADW3	ATGCCCTATCTTACACACTCCGGAGACTACTGTGTTAGACCCACAG----	HPBADW3	3
HPBADW2	ATGCCCTATCTTACACACTCCGGAGACTACTGTGTTAGACCCACAG----	HPBADW2	3
HPBADR1	ATGCCCTATCTTACACACTCCGGAGACTACTGTGTTAGACCCACAG----	HPBADR1	3
HPBVCG	ATGCCCTATCTTACACACTCCGGAGACTACTGTGTTAGACCCACAG----	HPBVCG	4
HPBAYW	ATGCCCTATCTTACACACTCCGGAGACTACTGTGTTAGACCCACAG----	HPBAYW	4
HPBHVAA	ATGCCCTATCTTACACACTCCGGAGACTACTGTGTTAGACCCACAG----	HPBHVAA	4
HPBV	ATGCCCTATCTTACACACTCCGGAGACTACTGTGTTAGACCCACAG----	HPBV	4

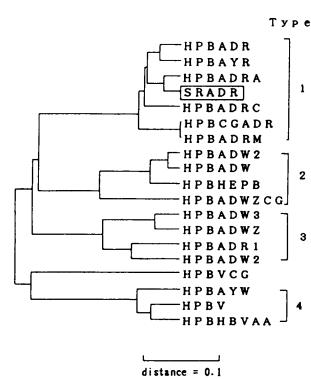
**Figure 1.** Alignment of the region P sequences from SRADR and other HBV. Identification of specific insertion of type 2 (1) and deletion of type 4 (b). Symbols (\*), Positions showing type 2-specific insertion; (+), positions showing type 4-specific deletion.

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**Figure 2.** Phylogenetic analysis of the region P sequences from various HBV (GenBank), including the newly isolated SRADR (boxed). The tree was constructed by the neighbor-joining method.



**Figure 3.** Phylogenetic analysis of the region P sequences from various HBV (GenBank), including the newly isolated SRADR (boxed). The tree was constructed by the UPGMA method.