Table S1. Primers used for amplification and sequencing of complete HBV genomes.

Primer designation	Primer sequence
B-464S1	TTGCCCGTTTGTCCTCTAATTCCAGGATCC
B-464S2	TTGCCCGTTTGTCCTCTSATTCCAGGATCC
P2	AAAAAGTTGCATGRTGMTGG
P2L2	CCGGAAAGCTTGAGCTCTTCAAAAAGTTGCATGGTGCTGG
595F	CAC HTG TAT TCC CAT CCC A
179R	CCA ATT TMT GCY TAC AGC CTC
1584F	ACT TCG MBT CAC CTC TGC ACG T
2396R	GTC KGC GAG GYG AGG GAG TT
2331R	GGA AGY GTK GAY ARG ATA GGG GCA TT
1859F	ACT NTT CAA GCC TCC RAG CTG
2835R	GTT CCC AVG WAT AWG GTG AYC C
1877F	CTG TGC CTT GGR TGG CTT
gtA1-2792S1	GGAAACTACACGTAGCGCCTCATTTTG
gtA1-2792S2	GGAAACTACACGTAGCGCTTCATTTTG
B-874R1	ACCCCAACTTCCAATTACATAKCCCATGAA
B-874R2	RCCCCAACTTCCAATTATRTATCCCATGAA
B-874R4	GCCCCAACTTCCAATYACATATCCcATGAA
B-548R1	TTTTGTACAGCAACATGRGGGAAACATAGA
B-548R2	TTTTGTACAGCAACATGAGGGAATCATAGA
B-98R1	TTGACGAGATGTGAGAGGCARTATT
B-98R2	TTGACGATATGTGAGAGACAATATT
B-98R3	TTGACGATATGTGAGAGGCAATATT
B-98R4	TGGAGGAGATGGGAGAGGCAATATT

Table S2. Designation, genome length and position, and nucleotide length of the 5 ORFs in the sequenced complete HBV genomes.

Strains designation	Complete genomes N nucleotides	P gene (2307-1623) N nucleotides Deletions positions	S gene (2854-835)	Pre-C gene (1814-1900) N nucleotides (altered start codon)	C gene (1901-2458) N nucleo-tides	X gene (1374-1838)
Rw14-03	3167	2484 del 1-54	1149	87	552	465
Rw14-14	3167	2484 del 1-54	1149	87	558	465
Rw14-25	3221	2538	1203	87	558	465
Rw14-37	3221	2538	1170	87	558	465
Rw14-48	3221	2538	1203	87	558	465
Rw14-65	3221	2538	1203	87	558	465
Rw14-120	3221	2538	1203	87 (TTG)	558	465
Rw14-126	3221	2538	1203	87	558	465
Rw14-136	3167	2484 del 1-54	1149	87	558	465
Rw14-203	3221	2538	1203	87	558	465
Rw14-220	3233	2538	1203	87	558	408 12 nt insert between 1766 and 1777
Rw14-226	3158	2475 del 3051-3113	1140	87	558	465
Rw2003	3221	2538	1203	87	558	465
Rw2016	3221	2538	1203	87	558	465
Rw2079	3200	2517 del 1573-1590 del 3160-3163	1200	87	558	447 18 nt deletion between 1573 and 1590
Rw2086	3188	2505 del 22-54	1170	87	558	465
Rw2113	3221	2538	1203	87 (AAG)	558	465
Rw2157	3170	2487 del 1-51	1152	87 (TTG)	558	465
Rw2199	3182	2538	1203	87	558	426 39 nt deletion between 1736 and 1775
Rw2226	3167	2484 del 1-54	1149	87	558	465
Rw2244	3167	2484 del 1-54	1149	87	558	465
Rw3173	3221	2538	1203	87	558	465
Rw3531	3221	2538	1203	87	558	465

Figure S1. Branch from a UPGMA tree, based on 526 complete HBV genomes. The clades formed by each subgenotype of A are shown in the small tree to the left. The branch formed by subgenotype A3 complete HBV genomes is enlarged. The origin of strains from the same country is marked by brackets at the nodes, the origin of the other stains are given at the nodes. Strains with wild-type precore start codon and Kozak sequence preceding the precore start from patients with unknown HBeAg/anti-HBe status are marked by black squares at the nodes. Strains from HBeAg patients are marked by green squares. The strains marked with red or orange squares have either a changed precore start codon (red) or a changed Kozak sequence (orange). The figures below the branches refer to the bootstrap values of 1000 replicas.