VIRAL VARIANTS WITH ALTERED SUSCEPTIBILITY TO NUCLEOSIDE ANALOGS AND USES THEREOF

BACKGROUND OF THE INVENTION

FIELD OF THE INVENTION

The present invention relates generally to viral variants exhibiting reduced sensitivity to particular agents and/or reduced interactivity with immunological reagents. More particularly, the present invention is directed to hepatitis B virus (HBV) variants exhibiting complete or partial resistance to nucleoside analogs and/or reduced interactivity with antibodies to viral surface components including reduced sensitivity to these antibodies. The present invention further contemplates assays for detecting such viral variants, which assays are useful in monitoring anti-viral therapeutic regimens and in developing new or modified vaccines directed against viral agents and in particular HBV variants. The present invention also contemplates the use of the viral variants to screen for agents capable of inhibiting infection, replication and/or release of the virus.

DESCRIPTION OF THE PRIOR ART

Bibliographic details of the publications referred to by author in this specification are collected at the end of the description.

The reference to any prior art in this specification is not, and should not be taken as, an acknowledgment or any form of suggestion that that prior art forms part of the common general knowledge in any country.

Specific mutations in an amino acid sequence are represented herein as 'Xaa_1nXaa_2' where Xaa_1 is the original amino acid residue before mutation, n is the residue number and Xaa_2 is the mutant amino acid. The abbreviation 'Xaa' may be the three letter or single letter (i.e. 'X') code. The amino acid residues for Hepatitis B virus DNA polymerase are numbered with the residue methionine in the motif Tyr Met Asp Asp (YMDD) being

residue number 204 (Stuyver *et al., Hepatology 33:* 751-757, 2001). The amino acid residues for hepatitis B virus surface antigen are number according to Norder *et al.* (*J. Gen. Virol. 74:* 341-1348, 1993).

The term nucleoside analogs has been used in reference to both nucleotide and nucleoside analogs.

Hepatitis B virus (HBV) can cause debilitating disease conditions and can lead to acute liver failure. HBV is a DNA virus which replicates *via* an RNA intermediate and utilizes reverse transcription in its replication strategy (Summers and Mason, *Cell 29:* 403-415, 1982). The HBV genome is of a complex nature having a partially double-stranded DNA structure with overlapping open reading frames encoding surface, core, polymerase and X genes. The complex nature of the HBV genome is represented in Figure 1. The polymerase consists of four functional regions, the terminal protein (TP), spacer, reverse transcriptase (rt) and ribonuclease (RNAse).

The polymerase gene of HBV overlaps the envelope gene, mutations in the catalytic domain of the polymerase can affect the amino acid sequence of the envelope protein and *vice versa*. In particular, the genetic sequence for the neutralization domain of HBV known as the 'a' determinant, which is found within the HBsAg and located between amino acids 99 and 169, actually overlaps the major catalytic regions of the viral polymerase protein and in particular domains A and B.

The presence of an HBV DNA polymerase has led to the proposition that nucleoside analogs could act as effective anti-viral agents. Examples of nucleoside analogs currently being tested are penciclovir and its oral form (FAM) [Vere Hodge, *Antiviral Chem Chemother 4:* 67-84, 1993; Boyd *et al., Antiviral Chem Chemother. 32:* 358-363, 1987; Kruger *et al., Hepatology 22:* 219A, 1994; Main *et al., J. Viral Hepatitis 3:* 211-215, 1996] Lamivudine[(-)-β-2'-deoxy-3'-thiacytidine; (3TC or LMV) [Severini *et al., Antimicrobial Agents Chemother 39:* 1430-1435, 1995; Dienstag *et al., New England J Med 333:* 1657-1661, 1995]. New nucleoside analogs which have already progressed to

clinical trials include the pyriamidines Emtricitabine, ((-)-β-L-2'-3'-dideoxy-5-fluoro-3'-thiacydidine; FTC), the 5-fluoro derivative of 3TC, and Clevudine (1-(2-fluoro-5-methyl-β-L-arabino-furanosyl) uracil; L-FMAU), a thymidine analog. Like 3TC, these are pyrimidine derivatives with an unnatural "L"- configuration. Several purine derivatives have also progressed to clinical trials; they include Entecavir (BMS-200,475; ETV), a carbocyclic deoxyguanosine analog, diaminopurine dioxolane (DAPD), an oral pro-drug for dioxolane guanine ((-)-β-D-2-aminopurine dioxolane; DXG) and Adefovir dipivoxil, an oral prodrug for the acyclic deoxyadenosine monophosphate nucleoside analog Adefovir (9-[phosphonyl-methoxyethyl]-adenine; PMEA).

Whilst these agents are highly effective in inhibiting HBV DNA synthesis, there is the potential for resistant mutants of HBV to emerge during long term antiviral chemotherapy. In patients on prolonged LMV therapy key resistance mutations are selected in the rt domain within the polymerase at rtM204I/V +/- rtL180M. The nomenclature used for the polymerase mutations is in accordance with that proposed by Stuyver *et al.*, 2001, *supra*. Only LMV has been approved for use against chronic HBV infection. Lamivudine is a particularly potent inhibitor of HBV replication and reduces HBV DNA titres in the sera of chronically infected patients after orthotopic liver transplantation (OLT) by inhibiting viral DNA synthesis. LMV monotherapy seems unlikely to be able to control HBV replication in the longer term. This is because emergence of LMV-resistant strains of HBV seems almost inevitable during monotherapy and single therapy is generally inadequate to result in viral clearance *per se*.

ETV is also a potent inhibitor of HBV replication. ETV is an orally available cyclopentyl deoxyguanosine analog with activity against hepadnaviruses and herpesviruses. Preclinical studies indicate that ETV is a highly potent inhibitor of HBV in enzyme- and cell-based assays (Innaimo *et al., Antimicrobiol Agent Chem 44:* 1441-1448, 1997; Siefer *et al., Antimicrobiol Agent Chem 28;* 3200-3208, 1998; Yamanaka *et al., Antimicrobiol Agent Chem 43:* 190-193, 1999). ETV has also demonstrated efficacy against WHV in chronically-infected woodchucks (Colonno *et al., JID 184:* 1236-45 2001; Genovesi *et al., Antimicrobiol Agent Chem 42:* 3209-3217, 1998). A four week dose-escalation trial

indicated that ETV was well-tolerated and resulted in a 2.5 log_{10} mean reduction in viremia at the highest dose tested (1 mg/daily). LMV resistance mutations were reported to confer cross-resistance to ETV *in vitro*, although entecavir was still capable of inhibiting viral replication at higher doses; these data are somewhat surprising considering that ETV is not an L-nucleoside. ETV has been used successfully to treat patients with the LMV resistant HBV mutations. No specific ETV resistant mutations had been described.

Nucleoside analog therapy may be administered as monotherapy or combination therapy where two or more nucleoside analogs may be administered. The nucleoside analogs may also be administered in combination with other antiviral agents such as interferon or hepatitis B immunoglobulin (HBIG).

There is a need to identify nucleoside- and/or antibody-resistant variants of HBV. The rapid identification can lead to altered therapeutic protocols being pursued.

SUMMARY OF THE INVENTION

The abbreviations defined in Table 1 are used in the subject specification

TABLE 1

Abbreviations

ABBREVIATION	DESCRIPTION
3TC	(LMV); (-)-β-2'-deoxy-3'-thiacytidine
ADV	adefovir
DAPD	diaminopurine dioxolane
DXG	dioxolane guanine
ETV	entecavir
FAM	famciclovir
FTC	emtricitabine
HBIG	hepatitis B immunoglobulin
HBsAg	hepatitis B surface antigen
HBV	hepatitis B virus
LMV	lamividuine
PMEA	adefovir
RNAse	ribonuclease
rt	reverse transcriptase
YMDD	Tyr Met Asp Asp-a motif in the polymerase protein; where the Met residue is designated residue number 204 of the reverse transcriptase

Throughout this specification, unless the context requires otherwise, the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element or integer or group of elements or integers but not the exclusion of any other element or integer or group of elements or integers.

Nucleotide and amino acid sequences are referred to by a sequence identifier number (SEQ ID NO:). The SEQ ID NOs: correspond numerically to the sequence identifiers <400>1, <400>2, etc. A sequence listing is provided after the claims.

The positions of nucleotide and amino acid mutations identified using nomenclature from genotypes B, C or F where the methionine residue in the YMDD motif of the DNA polymerase was designated position 550 (see Australian Patent No. 734831). The nucleotide and amino acid positions given in the present specification are based on a new nomenclature where the methionine residue is YMDD is position 204 and is referred to as rtM204 where rt is an abbreviation for "reverse transcriptase".

In accordance with the present invention, HBV resistant variants were identified in a patient (patient A) with chronic hepatitis B treated with both LMV and ETV and a liver transplant patient (patient B) treated with ETV that had been previously treated with a number of nucleoside agents including LMV. In combination therapy, accordance with the present invention, resistant variants of HBV were identified, following LMV and ETV treatment, with mutations in the HBV DNA polymerase gene which reduce the sensitivity of HBV to these nucleoside analogs. Corresponding mutations in the surface antigen also occur. The identification of these HBV variants is important for the development of assays to monitor LMV and/or ETV resistance and/or resistance to other nucleoside analog therapeutic regimes and to screen for agents which are useful as alternative therapeutic agents. The mutations detected in the HBV isolated from patient A in key functional domains namely the rtI169T + rtV173L + rtL180M + rtM204V is demonstrated to have reduced sensitivity to ETV in functional assays.

The detection of such HBV variants is particularly important in the management of therapeutic protocols including the selection of appropriate agents for treating HBV infection. The method of this aspect of the present invention is predicated in part on monitoring the development in a subject of an increased HBV load in the presence of a nucleoside analog. The clinician is then able to modify an existing treatment protocol or select an appropriate treatment protocol accordingly.

One aspect of the present invention, therefore, is directed to an isolated HBV variant comprising a nucleotide mutation in a gene encoding a DNA polymerase resulting in at least one amino acid addition, substitution and/or deletion to the DNA polymerase and which exhibits decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs. Preferably, the DNA polymerase exhibits reduced sensitivity to ETV, or and ETV. The variant HBV comprises a mutation in an overlapping open reading frame in its genome in a region defined by one or more of domains F and A through E of HBV DNA polymerase.

The present invention further contemplates a method for determining the potential for an HBV to exhibit reduced sensitivity to ETV and/or LMV or optionally other nucleoside analogs by isolating DNA or corresponding mRNA from the HBV and screening for a mutation in the nucleotide sequence encoding HBV DNA polymerase resulting in at least one amino acid substitution, deletion and/or addition in any one or more of domains F and A through E or a region proximal thereto of the DNA polymerase and associated with resistance or decreased sensitivity to ETV and/or LMV. The presence of such a mutation is an indication of the likelihood of resistance to said entecavir and/or LMV. Preferably, the HBV variant exhibits reduced sensitivity to ETV, or both ETV and LMV.

The present invention also provides a composition comprising a variant HBV resistant to ETV and/or LMV and optionally other nucleoside analogs or an HBV surface antigen from the variant HBV or a recombinant or derivative form thereof or its chemical equivalent and one or more pharmaceutically acceptable carriers and/or diluents. Yet another aspect of the present invention provides a use of the aforementioned composition or a variant HBV comprising a nucleotide mutation in a gene encoding a DNA polymerase resulting in at least one amino acid addition, substitution and/or deletion to the DNA polymerase and a decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs in the manufacture of a medicament for the treatment and/or prophylaxis of hepatitis B virus infection.

The present invention also contemplates a method for determining whether an HBV strain exhibits reduced sensitivity to a nucleoside analog by isolating DNA or corresponding mRNA from the HBV and screening for a mutation in the nucleotide sequence encoding the DNA polymerase wherein the presence of the following mutations in the spacer region and the rt region: spacerL97I, spacerK115R, spacerH116L, spacerL128F, spacerS137G, spacerR139G, spacerF142S, rtY54H, rtL91I, rtA97V, rtY124H, rtH126R, rtS135Y, rtI169T, rtV173L, rtL180M, rtM204V, rtA21S, rtA38E, rtF122L, rtT128N, rtQ130P, rtT184G, rtS202I, rtH248N, rtY252L or combinations thereof or an equivalent one or more other mutation is indicative of a variant which exhibits a decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs.

The subject method may also be practiced by screening for a mutation in the nucleotide sequence encoding the DNA polymerase wherein the presence of the following mutations in the B or C domain of the rt region: rtI169T, rtV173L, rtL180M, rtT184G, rtS202I, rtM204V or combinations thereof or an equivalent one or more other mutations is indicative of a variant which exhibits a decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs.

It should be noted that mutants rtV173L, rtL180M and rtM204V correspond to mutants V519L, L526M, M550V and M550V, respectively in Australian Patent No. 734831 (using an earlier nomenclature system).

Still a further methodology comprises screening for a mutation in the nucleotide sequence encoding the envelope genes wherein the presence of the following mutations in the PreS1, PreS2 and S genes (changes in the overlapping reverse transcriptase region are indicated in parenthesis): PreS1N114D, PreS1 T115S, PreS2 F22L, PreS2 V39A, PreS2 P52L, sL89V, sT118A, sF161L (= rtI169T), sE164D (= rtV173L), sI195M (= rtM204V), sI208T, PreS1 E86Q, PreS1 N91K, PreS2 P41H, sQ30K, sP120T, sL176V, sV194F or combinations thereof or an equivalent one or more other mutation is indicative of a variant which exhibits a decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs.

The present invention also contemplates a method for determining whether an HBV strain exhibits reduced sensitivity to a nucleoside analog by isolating DNA or corresponding mRNA from the HBV and screening for a mutation in the nucleotide sequence encoding the DNA polymerase wherein the presence of the following mutations in the spacer region and the rt region: spacerL97I, spacerK115R, spacerH116L, spacerL128F, spacerS137G, spacerR139G, spacerF142S, rtY54H, rtL91I, rtA97V, rtY124H, rtH126R, rtS135Y, rtI169T, rtM250V, rtV173L, rtL180M, rtM204V, rtA21S, rtA38E, rtF122L, rtT128N, rtQ130P, rtT184G, rtS202I, rtH248N, rtY252L or combinations thereof or an equivalent one or more other mutation is indicative of a variant which exhibits a decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs.

The subject method may also be practiced by screening for a mutation in the nucleotide sequence encoding the DNA polymerase wherein the presence of the following mutations in the B or C domain of the rt region: rtI169T, rtV173L, rtL180M, rtT184G, rtS202I, rtM204V or combinations thereof or an equivalent one or more other mutations is indicative of a variant which exhibits a decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs.

It should be noted that mutants rtV173L, rtL180M and rtM204V correspond to mutants V519L, L526M, M550V and M550V, respectively in Australian Patent No. 734831 (using an earlier nomenclature system).

Still a further methodology comprises screening for a mutation in the nucleotide sequence encoding the envelope genes wherein the presence of the following mutations in the PreS1, PreS2 and S genes (changes in the overlapping reverse transcriptase region are indicated in parenthesis): PreS1N114D, PreS1 T115S, PreS2 F22L, PreS2 V39A, PreS2 P52L, sL89V, sT118A, sF161L (= rtI169T), sE164D (= rtV173L), sI195M (= rtM204V), sI208T, PreS1 E86Q, PreS1 N91K, PreS2 P41H, sQ30K, sP120T, sL176V, sV194F or combinations thereof or an equivalent one or more other mutation is indicative of a variant which exhibits a decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs.

Preferably, the variants are in isolated form such that they have undergone at least one purification step away from naturally occurring body fluid. Alternatively, the variants may be maintained in isolated body fluid or may be in DNA form. The present invention also contemplates infectious molecular clones comprising the genome or parts thereof from a variant HBV. The detection of HBV or its components in cells, cell lysates, cultured supernatant fluid and bodily fluid may be by any convenient means including any nucleic acid-based detection means, for example, by nucleic acid hybridization techniques or *via* one or more polymerase chain reactions (PCRs). The term "bodily fluid" includes any fluid derived from the blood, lymph, tissue or organ systems including serum, whole blood, biopsy and biopsy fluid, organ explants and organ suspension such as liver suspensions. The invention further encompasses the use of different assay formats of the nucleic acid-based detection means, including restriction fragment length polymorphism (RFLP), amplified fragment length polymorphism (AFLP), single-strand chain polymorphism (SSCP), amplification and mismatch detection (AMD), interspersed repetitive sequence polymerase chain reaction (IRS-PCR), inverse polymerase chain reaction (iPCR) and reverse transcription polymerase chain reaction (RT-PCR), amongst others. Reverse hybridization is a technique which is particularly useful in identifying specific nucleotides or nucleotide sequences. Other forms of detection include Northern blots, Southern blots, PCR sequencing, antibody procedures such as ELISA, Western blot and immunohistochemistry. A particularly useful assay includes the reagents and components required for immobilized oligonucleotide- or oligopeptide-mediated detection systems.

Another aspect of the present invention is directed to a variant HBV comprising a surface antigen having an amino acid sequence with a single or multiple amino acid substitution, addition and/or deletion or a truncation compared to a surface antigen from a reference or wild type HBV and wherein an antibody generated to the reference or wild type surface antigen exhibits an altered immunological profile relative to said HBV variant. One altered profile includes a reduced capacity for neutralizing the HBV. More particularly, the surface antigen of the variant HBV exhibits an altered immunological profile compared to a pre-treatment HBV where the variant HBV is selected for by a nucleoside analog of the

HBV DNA polymerase. The variant HBV of this aspect of the invention may also comprise a nucleotide sequence comprising a single or multiple nucleotide substitution, addition and/or deletion compared to a pre-treatment HBV.

The present invention extends to an isolated HBsAg or a recombinant form thereof or derivative or chemical equivalent thereof corresponding to the variant HBV. Generally, the HBsAg or its recombinant or derivative form or its chemical equivalent comprises an amino acid sequence with a single or multiple amino acid substitution, addition and/or deletion or a truncation compared to an HBsAg from a reference HBV and wherein an antibody directed to a reference HBV exhibits an altered immunological profile to an HBV carrying said variant HBsAg. In one embodiment, the altered immunological profile comprises a reduction in the ability to neutralize the variant HBV.

The present invention is predicated in part on the identification and isolation of variants of HBV that have a plurality of mutations and exhibit two or more characteristics selected from decreased or reduced sensitivity to one or more nucleoside analogs, a reduced level and/or functional activity of hepatitis B e antigen, or a reduced, abrogated or otherwise impaired immunological interactivity, relative to wild-type HBV. Thus, the identification of HBV variants with these mutational patterns is important *inter alia* for the development of assays to detect HBV variants and assays to screen for agents which are useful in treating and/or preventing infections by those variants and/or other HBV isolates and for the development of alternative therapeutic regimes for managing HBV infections.

Accordingly, one aspect of the present invention is directed to an isolated HBV variant comprising a plurality of nucleotide mutations that correlate with at least two characteristics selected from (a) resistance to one or more nucleoside analogs, (b) a reduced level and/or functional activity of hepatitis B e antigen, or (c) a reduced, abrogated or otherwise impaired immunological interactivity.

Another aspect of the present invention contemplates an isolated HBV variant comprising a plurality of nucleotide mutations that correlate with (a) resistance to one or more

nucleoside analogs, (b) a reduced level and/or functional activity of hepatitis B e antigen, and (c) a reduced, abrogated or otherwise impaired immunological interactivity.

Yet another aspect of the present invention provides an isolated HBV variant comprising a plurality of nucleotide mutations selected from two or more of (a) a nucleotide mutation in a gene encoding a DNA polymerase resulting in at least one amino acid addition, substitution and/or deletion to said DNA polymerase wherein said variant exhibits decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs, (b) a nucleotide mutation in a gene encoding a hepatitis B e antigen or in a transcriptional control element of said gene wherein said mutation results in a reduced level and/or functional activity of said hepatitis B e antigen, or (c) a nucleotide mutation in a gene encoding a hepatitis B polypeptide resulting in at least one amino acid addition, substitution and/or deletion to said polypeptide which reduces, abrogates or otherwise impairs its immunological interactivity.

Another aspect of the present invention contemplates a method for detecting an agent which exhibits inhibitory activity to an HBV by generating a genetic construct comprising a replication competent-effective amount of the genome from the HBV contained in a plasmid vector and then transfecting said cells with said construct, contacting the cells, before, during and/or after transfection, with the agent to be tested, culturing the cells for a time and under conditions sufficient for the HBV to replicate, express genetic sequences and/or assemble and/or release virus or virus-like particles if resistant to said agents; and the subjecting the cells, cell lysates or culture supernatant fluid to viral- or viral-component-detection means to determine whether or not the virus has replicated, expressed genetic material and/or assembled and/or been released in the presence of the agent. In a preferred embodiment, the plasmid vector in a baculovirus vector and the method comprises generating a genetic construct comprising a replication competent-effective amount of the genome from the HBV contained in or fused to an amount of a baculovirus genome effective to infect cells and then infecting said cells with said construct, contacting the cells, before, during and/or after infection, with the agent to be tested, culturing the cells for a time and under conditions sufficient for the HBV to replicate, express genetic

sequences and/or assemble and/or release virus or virus-like particles if resistant to said agent and then subjecting the cells, cell lysates or culture supernatant fluid to viral- or viral-component-detection means to determine whether or not the virus has replicated, expressed genetic material and/or assembled and/or been released in the presence of the agent.

In an alternative embodiment, the method comprises generating a continuous cell line comprising an infectious copy of the genome of the HBV in a replication competent effective amount such that said infectious HBV genome is stably integrated into said continuous cell line such as but not limited to 2.2.15 or AD, contacting the cells with the agent to be tested, culturing the cells for a time and under conditions sufficient for the HBV to replicate, express genetic sequences and/or assemble and/or release virus or virus-like particles if resistant to the agent and then subjecting the cells, cell lysates or culture supernatant fluid to viral- or viral-component-detection means to determine whether or not the virus has replicated, expressed genetic material and/or assembled and/or been released in the presence of the agent.

In an alternative embodiment, the present invention also contemplate a method for detecting an agent which exhibits inhibitory activity to an HBV polymerase in an *in vitro* polymerase assay. The HBV polymerase activity can be examined using established assays (Gaillard *et al.*, *Antimicrob Agents Chemother. 46(4)*: 1005-1013, 2002; Xiong *et al.*, *Hepatology. 28(6)*: 1669-73, 1998). The HBV polymerase may be a wild-type or reference HBV polymerase or mutant HBV polymerase.

In connection with these methods, the plasmid vector may include genes encoding part or all of other viral vectors such as baculovirus vectors or adenovirus vectors (see Ren and Nassal, *J. Virol. 75(3):* 1104-1116, 2001).

The identification of viral variants enables the production of vaccines comprising particular recombinant viral components such as polymerases or envelope genes PreS1, PreS2, S encoding for L, M, S proteins as well as therapeutic vaccines comprising

defective HBV variants. Rational drug design may also be employed to identify or generate therapeutic molecules capable of interacting with a polymerase or or envelope genes PreS1, PreS2, S encoding for L, M, S proteins or other component of the HBV. Such drugs may also have diagnostic potential.

A summary of sequence identifiers used throughout the subject specification is provided in Table 2.

TABLE 2

Summary of sequence identifiers

SEQUENCE ID NO:	DESCRIPTION
1	region F of HBV DNA polymerase (Formula I)
2	regions A to E of HBV DNA polymerase (Formula II)
3	primer (OS1)
4	primer (TTA3
5	primer (JM)
6	primer (TTA4)
7	primer (OS2)
8	primer SEQ2
9	primer TTA2
10	forward primer PC1
11	reverse primer PC2
12	HBV-specific molecule beacon primer
13-18	TR1 (Figure 4)
19-24	Pol Trans of TR1 (Figure 5)
25-30	HBsAg Trans of TR1 (Figure 6)
31	Pre-ETV (Figure 8)
32	On-ETV (Figure 8)
33	Pre-ETV (Figure 9)

SEQUENCE ID NO:	DESCRIPTION
34	On-ETV (Figure 9)
35	Pre-ETV (Figure 10)
36	Post-ETV (Figure 10)

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 is a diagrammatic representation showing the partially double stranded DNA HBV genome showing the overlapping open reading frames encoding surface (S), core (C), polymerase (P) and X gene.

Figure 2 is graphical representation of Patient A's clinical history including therapy regimen, HBV DNA viral load and alanine transaminase (ALT) levels.

Figure 3 is a diagrammatic representation of the chemical structure of entecavir.

Figure 4 is a representation showing comparison of the HBV nucleotide sequence encoding the catalytic region of the polymerase gene in sequential samples from Patient A during LMV monotherapy or LMV/entecavir combination therapy.

Figure 5 is a representation showing comparison of the deduced amino acid sequence of the catalytic region of the polymerase gene in sequential samples from Patient A during LMV monotherapy or LMV/entecavir combination therapy.

Figure 6 is a representation showing comparison of the deduced amino acid sequence of the envelope gene in sequential samples from Patient A during LMV monotherapy or LMV/entecavir combination therapy.

Figure 7 is a diagrammatic representation of a computer system for determining the potency value (P_A) of a variant HBV.

Figure 8 is a representation showing comparison of the HBV nucleotide sequence encoding the catalytic region of the polymerase gene in sequential samples from Patient B during LMV monotherapy (prior to ETV) and on ETV therapy.

Figure 9 is a representation showing comparison of the deduced amino acid sequence of the catalytic region of the polymerase gene in sequential samples from Patient B during LMV monotherapy (prior to ETV) and on ETV therapy.

Figure 10 is a representation showing comparison of the deduced amino acid sequence of the envelope gene in sequential samples from Patient B during LMV monotherapy (prior to ETV) and on ETV therapy.

Figure 11 is a graphical representation of HBV DNA replicative intermediates detected by quantitative PCR relative to the no drug control for both wild type virus and the HBV encoding the mutations at rtI169T+rtV173L+rtL180M+rtM204V.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

The present invention is predicated in part on the identification and isolation of nucleoside analog resistant variants of HBV following treatment of patients with ETV or LMV or ETV and LMV and optionally other nucleoside analogs. In particular, ETV, or ETV and LMV treated patients gave rise to variants of HBV exhibiting decreased or reduced sensitivity to ETV and/or LMV. Reference herein to "decreased" or "reduced" in relation to sensitivity to ETV and/or LMV includes and encompasses a complete or substantial resistance to the nucleoside analog as well as partial resistance and includes a replication rate or replication efficiency (yield phenotype) which is more than a wild-type in the presence of a nucleoside analog. In one aspect, this is conveniently measured by an increase in viral load to a level similar or greater than pre-treatment levels.

Accordingly, one aspect of the present invention is directed to an isolated HBV variant wherein said variant comprises a nucleotide mutation in a gene encoding a DNA polymerase resulting in at least one amino acid addition, substitution and/or deletion to said DNA polymerase and wherein said variant exhibits decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs.

Preferably, the decreased sensitivity is in respect of ETV, or both ETV and LMV.

In addition to a mutation in the gene encoding DNA polymerase, due to the overlapping nature of the HBV genome (Figure 1), a corresponding mutation may also occur in the gene encoding the surface antigen (HBsAg) resulting in reduced interactivity of immunological reagents such as antibodies and immune cells to HBsAg. The reduction in the interactivity of immunological reagents to a viral surface component generally includes the absence of immunological memory to recognize or substantially recognize the viral surface component. The present invention extends, therefore, to an HBV variant exhibiting decreased sensitivity to ETV and/or LMV and reduced interactivity of an immunological reagent to HBsAg wherein the variant is selected for following ETV and/or LMV combination or sequential treatment. The term "sequential" in this respect means ETV

followed by LMV or LMV followed by ETV or multiple sequential administrations of each of ETV and LMV or LMV and ETV.

A viral variant may, therefore, carry mutation only in the DNA polymerase or both in the DNA polymerase and the HBsAg. The term "mutation" is to be read in its broadest context and includes multiple mutations.

The present invention extends to a mutation and any domain of the HBV DNA polymerase and in particular regions F and A through E provided said mutation leads to decreased sensitivity to LMV and/or ETV. Region F of the HBV DNA polymerase is defined by the amino acid sequence set forth in Formula I [SEQ ID NO:1] below :

FORMULA I

L, B_1, B_2, D, W, G, P, C, B_3, B_4, H, G, B_5, H, B_6, I, R, B_7, P, R, T, P, B_8, R, V, B_9, G, G, V, F, L, V, D, K, N, P, H, N, T, B_{10}, E, S, B_{11}, L, B_{12}, V, D, F, S, Q, F, S, R, G, B_{13}, B_{14}, B_{15}, V, S, W, P, K, F, A, V, P, N, L, B_{16}, S, L, T, N, L, L, S*

wherein:

B_1 is L, or R, or I

B_2 is E, or D

B_3 is T, or D, or A, or N, or Y

B_4 is E, or D

B_5 is E, or K, or Q

B_6 is H, or R, or N,

B_7 is I, or T

B_8 is A, or S

B_9 is T or R

B_{10} is A, or T, or S

B_{11} is R, or T

B_{12} is V, or G

B_{13} is S, or I, or T, or N, or V

B_{14} is T, or S, or H, or Y

B_{15} is R, or H, or K, or Q

B_{16} is Q, or P;

and wherein S* is designated as amino acid 74.

In this specification, reference is particularly made to the conserved regions of the DNA polymerase as defined by domains A to E. Regions A to E are defined by the amino acid sequence set forth in Formula II [SEQ ID NO:2] below (and in Australian Patent No. 734831):

FORMULA II

S Z_1 L S W L S L D V S A A F Y H Z_2 P L H P A A M P H L L Z_3 G S S G L Z_4 R Y V A R L S S Z_5 S Z_6 Z_7 X N Z_8 Q Z_9 Z_{10} X X X Z_{11} L H Z_{12} Z_{13} C S R Z_{14} L Y V S L Z_{15} L L Y Z_{16} T Z_{17} G Z_{18} K L H L Z_{19} Z_{20} H P I Z_{21} L G F R K Z_{22} P M G Z_{23} G L S P F L L A Q F T S A I Z_{24} Z_{25} Z_{26} Z_{27} Z_{28} R A F Z_{29} H C Z_{30} Z_{31} F Z_{32} Y M* D D Z_{33} V L G A Z_{34} Z_{35} Z_{36} Z_{37} H Z_{38} E Z_{39} L Z_{40} Z_{41} Z_{42} Z_{43} Z_{44} Z_{45} Z_{46} L L Z_{47} Z_{48} G I H L N P Z_{49} K T K R W G Y S L N F M G Y Z_{50} I G

wherein:

X is any amino acid;

Z_1 is N or D;

Z_2 is I or P;

Z_3 is I or V;

Z_4 is S or D;

Z_5 is T or N;

Z_6 is R or N;

Z_7 is N or I;

Z_8 is N or Y or H;

Z_9 is H or Y;

Z_{10} is G or R;

Z_{11} is D or N;

Z_{12} is D or N;

Z_{13} is S or Y;

Z_{14} is N or Q;

Z_{15} is L or M;

Z_{16} is K or Q;

Z_{17} is Y or F;

Z_{18} is R or W;

Z_{19} is Y or L;

Z_{20} is S or A;

Z_{21} is I or V;

Z_{22} is I or L;

Z_{23} is V or G;

Z_{24} is C or L;

Z_{25} is A or S;

Z_{26} is V or M;

Z_{27} is V or T;

Z_{28} is R or C;

Z_{29} is F or P;

Z_{30} is L or V;

Z_{31} is A or V;

Z_{32} is S or A;

Z_{33} is V or L or M;

Z_{34} is K or R;

Z_{35} is S or T;

Z_{36} is V or G;

Z_{37} is Q or E;

Z_{38} is L or S or R;

Z_{39} is S or F;

Z_{40} is F or Y;

Z_{41} is T or A;

Z_{42} is A or S;

Z_{43} is V or I;

Z_{44} is T or C;

Z_{45} is N or S;

Z_{46} is F or V;

Z_{47} is S or D;

Z_{48} is L or V;

Z_{49} is N or Q;

Z_{50} is V or I; and

M^* is amino acid 204;

and wherein the first S is designated as amino acid 75.

Preferably, the mutation results in an altered amino acid sequence in any one or more of domains F and A through E or regions proximal thereto of the HBV DNA polymerase.

Another aspect of the present invention provides an HBV variant comprising a mutation in an overlapping open reading frame in its genome wherein said mutation is in a region defined by one or more of domains F and A through E of HBV DNA polymerase and wherein said variant exhibits decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs.

In a related embodiment, there is provided an HBV variant comprising a mutation in the nucleotide sequence encoding a DNA polymerase resulting in an amino acid addition, substitution and/or deletion in said DNA polymerase in one or more amino acids as set forth in Formulae I [SEQ ID NO:1] and/or II [SEQ ID NO:2]:

FORMULA I

L, B_1, B_2, D, W, G, P, C, B_3, B_4, H, G, B_5, H, B_6, I, R, B_7, P, R, T, P, B_8, R, V, B_9, G, G, V, F, L, V, D, K, N, P, H, N, T, B_{10}, E, S, B_{11}, L, B_{12}, V, D, F, S, Q, F, S, R, G, B_{13}, B_{14}, B_{15}, V, S, W, P, K, F, A, V, P, N, L, B_{16}, S, L, T, N, L, L, S*

wherein:

B_1 is L, or R, or I

B_2 is E, or D

B_3 is T, or D, or A, or N, or Y

B_4 is E, or D

B_5 is E, or K, or Q

B_6 is H, or R, or N,

B_7 is I, or T

B_8 is A, or S

B_9 is T or R

B_{10} is A, or T, or S

B_{11} is R, or T

B_{12} is V, or G

B_{13} is S, or I, or T, or N, or V

B_{14} is T, or S, or H, or Y

B_{15} is R, or H, or K, or Q

B_{16} is Q, or P;

and

FORMULA II

S Z_1 L S W L S L D V S A A F Y H Z_2 P L H P A A M P H L L Z_3 G S S G L Z_4 R Y V A R L S S Z_5 S Z_6 Z_7 X N Z_8 Q Z_9 Z_{10} X X X Z_{11} L H Z_{12} Z_{13} C S R Z_{14} L Y V S L Z_{15} L L Y Z_{16} T Z_{17} G Z_{18} K L H L Z_{19} Z_{20} H P I Z_{21} L G F R K Z_{22} P M G Z_{23} G L S P F L L A Q F T S A I Z_{24} Z_{25} Z_{26} Z_{27} Z_{28} R A F Z_{29} H C Z_{30} Z_{31} F Z_{32} Y M* D D Z_{33} V L G A Z_{34} Z_{35} Z_{36} Z_{37} H Z_{38} E Z_{39} L Z_{40} Z_{41} Z_{42} Z_{43} Z_{44} Z_{45} Z_{46} L L Z_{47} Z_{48} G I H L N P Z_{49} K T K R W G Y S L N F M G Y Z_{50} I G

wherein:

X is any amino acid;
Z_1 is N or D;
Z_2 is I or P;
Z_3 is I or V;
Z_4 is S or D;
Z_5 is T or N;
Z_6 is R or N;
Z_7 is N or I;
Z_8 is N or Y or H;
Z_9 is H or Y;
Z_{10} is G or R;
Z_{11} is D or N;
Z_{12} is D or N;
Z_{13} is S or Y;
Z_{14} is N or Q;
Z_{15} is L or M;
Z_{16} is K or Q;
Z_{17} is Y or F;
Z_{18} is R or W;
Z_{19} is Y or L;

Z_{20} is S or A;

Z_{21} is I or V;

Z_{22} is I or L;

Z_{23} is V or G;

Z_{24} is C or L;

Z_{25} is A or S;

Z_{26} is V or M;

Z_{27} is V or T;

Z_{28} is R or C;

Z_{29} is F or P;

Z_{30} is L or V;

Z_{31} is A or V;

Z_{32} is S or A;

Z_{33} is V or L or M;

Z_{34} is K or R;

Z_{35} is S or T;

Z_{36} is V or G;

Z_{37} is Q or E;

Z_{38} is L or S or R;

Z_{39} is S or F;

Z_{40} is F or Y;

Z_{41} is T or A;

Z_{42} is A or S;

Z_{43} is V or I;

Z_{44} is T or C;

Z_{45} is N or S;

Z_{46} is F or V;

Z_{47} is S or D;

Z_{48} is L or V;

Z_{49} is N or Q;

Z_{50} is V or I; and

M^* is amino acid 204;

and wherein S* in Formula I is designated as amino acid 74 and the first S in Formula II is designated as amino acid 75;

and wherein said variant exhibits decreased sensitivity to ETV and/or LTV and optionally other nucleoside analogs. Preferably, the decreased sensitivity is to ETV, or both LMV and/or ETV.

Another preferred aspect of the present invention contemplates an HBV variant comprising a mutation in the nucleotide sequence encoding HBsAg resulting in an amino acid addition, substitution and/or deletion in said HBsAg in a region corresponding to the amino acid sequence set forth in Formulae I and II wherein said variant exhibits decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs.

More particularly, the present invention provides a variant HBV comprising a surface antigen having an amino acid sequence with a single or multiple amino acid substitution, addition and/or deletion or a truncation compared to a surface antigen from a reference or wild type HBV and wherein an antibody generated to the reference or wild type surface antigen exhibits reduced capacity for neutralizing said HBV variant, said variant selected by exposure of a subject to ETV and/or LMV in combination or sequential therapy.

The term "combination therapy" means that both ETV and LMV are co-administered in the same composition or simultaneously in separate compositions. The term "sequential therapy" means that the two agents are administered within seconds, minutes, hours, days or weeks of each other and in either order. Sequential therapy also encompasses completing a therapeutic course with one or other of ETV or LMV and then completing a second therapeutic course with the other of ETV or LMV.

Accordingly, another aspect of the present invention contemplates an HBV variant comprising a surface antigen having an amino acid sequence with a single or multiple

amino acid substitution, addition and/or deletion or truncation compared to the pretreatment HBV and wherein the surface antigen of the variant HBV exhibits an altered immunological profile compared to the pretreatment HBV where the said the variant HBV is selected for by a nucleoside analog of the HBV DNA polymerase, said variant selected by exposure of a subject to ETV and/or LMV in combination or sequential therapy.

In a related embodiment, the present invention provides an HBV variant comprising a nucleotide sequence comprising a single or multiple nucleotide substitution, addition and/or deletion compared to the pretreatment HBV and which HBV variant has a surface antigen exhibiting an altered immunological profile compared to the pretreatment HBV, said variant selected by exposure of a subject to ETV and/or LMV in combination or sequential therapy.

Preferably, the variants are in isolated form such that they have undergone at least one purification step away from naturally occurring body fluid. Alternatively, the variants may be maintained in isolated body fluid or may be in DNA form. The present invention also contemplates infectious molecular clones comprising the genome or parts thereof from a variant HBV. Furthermore, the present invention provides isolated components from the variant HBVs such as but not limited to an isolated HBsAg. Accordingly, the present invention provides an isolated HBsAg or a recombinant form thereof or derivative or chemical equivalent thereof, said HBsAg being from a variant HBV selected by exposure of a subject to ETV and/or LMV in combination or sequential therapy.

More particularly, yet another aspect of the present invention is directed to an isolated variant HBsAg or a recombinant or derivative form thereof or a chemical equivalent thereof wherein said HBsAg or its recombinant or derivative form or its chemical equivalent exhibits an altered immunological profile compared to an HBsAg from a reference HBV, said HBsAg being from a variant HBV selected by exposure of a subject to ETV and/or LMV in combination or sequential therapy.

Even more particularly, the present invention provides an isolated variant HBsAg or a recombinant or derivative form thereof or a chemical equivalent thereof wherein said HBsAg or its recombinant or derivative form or its chemical equivalent comprises an amino acid sequence with a single or multiple amino acid substitution, addition and/or deletion or a truncation compared to an HBsAg from a reference HBV and wherein a neutralising antibody directed to a reference HBV exhibits no or reduced neutralising activity to an HBV carrying said variant HBsAg, said HBsAg being from a variant HBV selected by exposure of a subject to ETV and/or LMV in combination or sequential therapy.

Preferred mutations in the HBV DNA polymerase include variants selected from patients with HBV recurrence following ETV and/or LMV treatment. Preferably, the treatment involves ETV or both ETV and/or LMV in combination or sequential therapy. Nucleoside analog treatment may occur in relation to a transplantation procedure (e.g. bone marrow transplantation (BMT) or OLT) or following treatment of patients diagnosed with hepatitis. Following selection of variants, viral loads are obtainable at levels greater than pre-treatment levels.

Preferred mutations in the HBV DNA polymerase include one or more of spacerL97I, spacerK115R, spacerH116L, spacerL128F, spacerS137G, spacerR139G, spacerF142S, rtY54H, rtL91I, rtA97V, rtY124H, rtH126R, rtS135Y, rtI169T, rtV173L, rtL180M, rtM204V, rtA21S, rtA38E, rtF122L, rtT128N, rtQ130P, rtT184G, rtS202I, rtH248N, rtY252L or combinations thereof or an equivalent one or more other mutation is indicative of a variant wherein said variant exhibits a decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs. It should be noted that the nomenclature system for amino acid positions is based on the methionine residues in the YMDD motif being designated codon rtM204. This numbering system is different to that in Australian Patent No. 734831 where the methionine residue in the YMDD motif within the polymerase gene is designated codon 550. In this regard, rtV173L, rtL180M and rtM204V correspond to V519L, L526M and M550V, respectively, in Australian Patent No. 734831. The term "SPACER" means a region that has been designated between two functional regions:

Terminal protein and reverse transcriptase. It provides the correct folding for the functional regions and no other specific function has been designated for this region. Corresponding mutations may also occur in envelope genes such as in one or more of PreS1, PreS2 and HBsAg. Particular mutations are as follows: PreS1 N114D, PreS1 T115S, PreS2 F22L, PreS2 V39A, PreS2 P52L, sL89V, s T118A, s 161L, sE164D, sI195M, sI208T PreS1 E86Q, PreS1 N91K, PreS2 P41H, sQ30K, sP120T, sL176V, sV194F or combinations thereof or an equivalent one or more other mutation is indicative of a variant wherein said variant exhibits a decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs. The mutations in gene encoding HBsAg at sF161L, sE164D, or sI195M also result in mutation in the in the polymerase gene rtI169T, rtV173L, or rtM204V respectively. Other corresponding mutations may occur in the rt such as spacerL97I, spacerK115R, spacerH116L, spacerL128F, spacerS137G, spacerR139G, spacerF142S, rtY54H, rtL91I, rtA97V, rtY124H, rtH126R, rtS135Y, rtI169T, rtV173L, rtL180M, rtM204V, rtA21S, rtA38E, rtF122L, rtT128N, rtQ130P, rtT184G, rtS202I, rtH248N, rtY252L or combinations thereof or an equivalent one or more other mutation is indicative of a variant wherein said variant exhibits a decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs.

The identification of the variants of the present invention permits the generation of a range of assays to detect such variants. The detection of such variants may be important in identifying resistant variants to determine the appropriate form of chemotherapy and/or to monitor vaccination protocols, or develop new or modified vaccine preparations.

Still another aspect of the present invention contemplates a method for determining the potential for an HBV to exhibit reduced sensitivity to ETV and/or LMV or optionally other nucleoside analogs, said method comprising isolating DNA or corresponding mRNA from said HBV and screening for a mutation in the nucleotide sequence encoding HBV DNA polymerase resulting in at least one amino acid substitution, deletion and/or addition in any one or more of domains F and A through E or a region proximal thereto of said DNA polymerase and associated with resistance or decreased sensitivity to ETV and/or LMV

wherein the presence of such a mutation is an indication of the likelihood of resistance to said ETV and/or LMV.

Preferably, the assay detects one or more of the following mutations in the spacer region and/or the rt region: spacerL97I, spacerK115R, spacerH116L, spacerL128F, spacerS137G, spacerR139G, spacerF142S, rtY54H, rtL91I, rtA97V, rtY124H, rtH126R, rtS135Y, rtI169T, rtV173L, rtL180M, rtM204V, rtA21S, rtA38E, rtF122L, rtT128N, rtQ130P, rtT184G, rtS202I, rtH248N, rtY252L or combinations thereof or an equivalent one or more other mutation is indicative of a variant wherein said variant exhibits a decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs.

Accordingly, another aspect of the present invention produces a method for determining whether an HBV strain exhibits reduced sensitivity to a nucleoside analog, said method comprising isolating DNA or corresponding mRNA from said HBV and screening for a mutation in the nucleotide sequence encoding the DNA polymerase wherein the presence of the following mutations in the spacer region and the rt region: spacerL97I, spacerK115R, spacerH116L, spacerL128F, spacerS137G, spacerR139G, spacerF142S, rtY54H, rtL91I, rtA97V, rtY124H, rtH126R, rtS135Y, rtI169T, rtV173L, rtL180M, rtM204V, rtA21S, rtA38E, rtF122L, rtT128N, rtQ130P, rtT184G, rtS202I, rtH248N, rtY252L or combinations thereof or an equivalent one or more other mutation is indicative of a variant wherein said variant exhibits a decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs.

The preferred mutations in the reverse transcriptase are rtI169T, rtV173L, rtL180M, rtT184G, rtS202I, rtM204V or combinations thereof or an equivalent one or more other mutation is indicative of a variant wherein said variant exhibits a decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs.

Accordingly, another aspect of the present invention contemplates a method for determining whether an HBV strain exhibits reduced sensitivity to a nucleoside analog, said method comprising isolating DNA or corresponding mRNA from said HBV and

Even more particularly, the present invention provides an isolated variant HBsAg or a recombinant or derivative form thereof or a chemical equivalent thereof wherein said HBsAg or its recombinant or derivative form or its chemical equivalent comprises an amino acid sequence with a single or multiple amino acid substitution, addition and/or deletion or a truncation compared to an HBsAg from a reference HBV and wherein a neutralising antibody directed to a reference HBV exhibits no or reduced neutralising activity to an HBV carrying said variant HBsAg, said HBsAg being from a variant HBV selected by exposure of a subject to ETV and/or LMV in combination or sequential therapy.

Preferred mutations in the HBV DNA polymerase include variants selected from patients with HBV recurrence following ETV and/or LMV treatment. Preferably, the treatment involves ETV or both ETV and/or LMV in combination or sequential therapy. Nucleoside analog treatment may occur in relation to a transplantation procedure (e.g. bone marrow transplantation (BMT) or OLT) or following treatment of patients diagnosed with hepatitis. Following selection of variants, viral loads are obtainable at levels greater than pre-treatment levels.

Preferred mutations in the HBV DNA polymerase include one or more of spacerL97I, spacerK115R, spacerH116L, spacerL128F, spacerS137G, spacerR139G, spacerF142S, rtY54H, rtL91I, rtA97V, rtY124H, rtH126R, rtS135Y, rtI169T, rtM250V, rtV173L, rtL180M, rtM204V, rtA21S, rtA38E, rtF122L, rtT128N, rtQ130P, rtT184G, rtS202I, rtH248N, rtY252L or combinations thereof or an equivalent one or more other mutation is indicative of a variant wherein said variant exhibits a decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs. It should be noted that the nomenclature system for amino acid positions is based on the methionine residues in the YMDD motif being designated codon rtM204. This numbering system is different to that in Australian Patent No. 734831 where the methionine residue in the YMDD motif within the polymerase gene is designated codon 550. In this regard, rtV173L, rtL180M and rtM204V correspond to V519L, L526M and M550V, respectively, in Australian Patent No. 734831. The term "SPACER" means a region that has been designated between two functional

regions: Terminal protein and reverse transcriptase. It provides the correct folding for the functional regions and no other specific function has been designated for this region. Corresponding mutations may also occur in envelope genes such as in one or more of PreS1, PreS2 and HBsAg. Particular mutations are as follows: PreS1 N114D, PreS1 T115S, PreS2 F22L, PreS2 V39A, PreS2 P52L, sL89V, s T118A, s 161L, sE164D, sI195M, sI208T PreS1 E86Q, PreS1 N91K, PreS2 P41H, sQ30K, sP120T, sL176V, sV194F or combinations thereof or an equivalent one or more other mutation is indicative of a variant wherein said variant exhibits a decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs. The mutations in gene encoding HBsAg at sF161L, sE164D, or sI195M also result in mutation in the in the polymerase gene rtI169T, rtV173L, or rtM204V respectively. Other corresponding mutations may occur in the rt such as spacerL97I, spacerK115R, spacerH116L, spacerL128F, spacerS137G, spacerR139G, spacerF142S, rtY54H, rtL91I, rtA97V, rtY124H, rtH126R, rtS135Y, rtI169T, rtM250V, rtV173L, rtL180M, rtM204V, rtA21S, rtA38E, rtF122L, rtT128N, rtQ130P, rtT184G, rtS202I, rtH248N, rtY252L or combinations thereof or an equivalent one or more other mutation is indicative of a variant wherein said variant exhibits a decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs.

The identification of the variants of the present invention permits the generation of a range of assays to detect such variants. The detection of such variants may be important in identifying resistant variants to determine the appropriate form of chemotherapy and/or to monitor vaccination protocols, or develop new or modified vaccine preparations.

Still another aspect of the present invention contemplates a method for determining the potential for an HBV to exhibit reduced sensitivity to ETV and/or LMV or optionally other nucleoside analogs, said method comprising isolating DNA or corresponding mRNA from said HBV and screening for a mutation in the nucleotide sequence encoding HBV DNA polymerase resulting in at least one amino acid substitution, deletion and/or addition in any one or more of domains F and A through E or a region proximal thereto of said DNA polymerase and associated with resistance or decreased sensitivity to ETV and/or LMV

wherein the presence of such a mutation is an indication of the likelihood of resistance to said ETV and/or LMV.

Preferably, the assay detects one or more of the following mutations in the spacer region and/or the rt region: spacerL97I, spacerK115R, spacerH116L, spacerL128F, spacerS137G, spacerR139G, spacerF142S, rtY54H, rtL91I, rtA97V, rtY124H, rtH126R, rtS135Y, rtI169T, rtM250V, rtV173L, rtL180M, rtM204V, rtA21S, rtA38E, rtF122L, rtT128N, rtQ130P, rtT184G, rtS202I, rtH248N, rtY252L or combinations thereof or an equivalent one or more other mutation is indicative of a variant wherein said variant exhibits a decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs.

Accordingly, another aspect of the present invention produces a method for determining whether an HBV strain exhibits reduced sensitivity to a nucleoside analog, said method comprising isolating DNA or corresponding mRNA from said HBV and screening for a mutation in the nucleotide sequence encoding the DNA polymerase wherein the presence of the following mutations in the spacer region and the rt region: spacerL97I, spacerK115R, spacerH116L, spacerL128F, spacerS137G, spacerR139G, spacerF142S, rtY54H, rtL91I, rtA97V, rtY124H, rtH126R, rtS135Y, rtI169T, rtM250V, rtV173L, rtL180M, rtM204V, rtA21S, rtA38E, rtF122L, rtT128N, rtQ130P, rtT184G, rtS202I, rtH248N, rtY252L or combinations thereof or an equivalent one or more other mutation is indicative of a variant wherein said variant exhibits a decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs.

The preferred mutations in the reverse transcriptase are rtI169T, rtV173L, rtL180M, rtT184G, rtS202I, rtM204V or combinations thereof or an equivalent one or more other mutation is indicative of a variant wherein said variant exhibits a decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs.

Accordingly, another aspect of the present invention contemplates a method for determining whether an HBV strain exhibits reduced sensitivity to a nucleoside analog, said method comprising isolating DNA or corresponding mRNA from said HBV and

screening for a mutation in the nucleotide sequence encoding the DNA polymerase wherein the presence of the following mutations in the B or C domain of the rt region: rtI169T, rtV173L, rtL180M, rtT184G, rtS202I, rtM204V or combinations thereof or an equivalent one or more other mutation is indicative of a variant wherein said variant exhibits a decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs.

The detection of HBV or its components in cells, cell lysates, cultured supernatant fluid and bodily fluid may be by any convenient means including any nucleic acid-based detection means, for example, by nucleic acid hybridization techniques or *via* one or more polymerase chain reactions (PCRs). The term "bodily fluid" includes any fluid derived from the blood, lymph, tissue or organ systems including serum, whole blood, biopsy and biopsy fluid, organ explants and organ suspension such as liver suspensions. The invention further encompasses the use of different assay formats of said nucleic acid-based detection means, including restriction fragment length polymorphism (RFLP), amplified fragment length polymorphism (AFLP), single-strand chain polymorphism (SSCP), amplification and mismatch detection (AMD), interspersed repetitive sequence polymerase chain reaction (IRS-PCR), inverse polymerase chain reaction (iPCR) and reverse transcription polymerase chain reaction (RT-PCR), amongst others. Other forms of detection include Northern blots, Southern blots, PCR sequencing, antibody procedures such as ELISA, Western blot and immunohistochemistry. A particularly useful assay includes the reagents and components required for immobilized oligonucleotide- or oligopeptide-mediated detection systems.

One particularly useful nucleic acid detection system is the reverse hybridization technique. In this technique, DNA from an HBV sample is amplified using a biotin or other ligand-labeled primer to generate a labeled amplificon. Oligonucleotides immobilized to a solid support such as a nitrocellulose film are then used to capture amplified DNA by hybridization. Specific nucleic acid fragments are identified *via* biotin or the ligand. Generally, the labeled primer is specific for a particular nucleotide variation to be detected. Amplification occurs only if the variation to be detected is present. There

are many forms of the reverse hybridization assay and all are encompassed by the present invention.

Detecting HBV replication in cell culture is particularly useful.

Another aspect of the present invention contemplates a method for detecting an agent which exhibits inhibitory activity to an HBV by:

generating a genetic construct comprising a replication competent-effective amount of the genome from the HBV contained in a plasmid vector and then transfecting said cells with said construct;

contacting the cells, before, during and/or after transfection, with the agent to be tested;

culturing the cells for a time and under conditions sufficient for the HBV to replicate, express genetic sequences and/or assemble and/or release virus or virus-like particles if resistant to said agents; and

then subjecting the cells, cell lysates or culture supernatant fluid to viral- or viral-component-detection means to determine whether or not the virus has replicated, expressed genetic material and/or assembled and/or been released in the presence of the agent.

In a preferred embodiment, the plasmid vector may include genes encoding part or all of oher viral vectors such as baculovirus or adenovirus (Ren and Nassal, 2001, *supra*) and the method comprises:

generating a genetic construct comprising a replication competent-effective amount of the genome from the HBV contained in or fused to an amount of a baculovirus

genome or adenovirus genome effective to infect cells and then infecting said cells with said construct;

contacting the cells, before, during and/or after infection, with the agent to be tested;

culturing the cells for a time and under conditions sufficient for the HBV to replicate, express genetic sequences and/or assemble and/or release virus or virus-like particles if resistant to said agent; and

then subjecting the cells, cell lysates or culture supernatant fluid to viral- or viral-component-detection means to determine whether or not the virus has replicated, expressed genetic material and/or assembled and/or been released in the presence of the agent.

In an alternative embodiment, the method comprises:

generating a continuous cell line comprising an infectious copy of the genome of the HBV in a replication competent effective amount such that said infectious HBV genome is stably integrated into said continuous cell line such as but not limited to 2.2.15 or AD;

contacting the cells with the agent to be tested;

culturing the cells for a time and under conditions sufficient for the HBV to replicate, express genetic sequences and/or assemble and/or release virus or virus-like particles if resistant to the agent; and

then subjecting the cells, cell lysates or culture supernatant fluid to viral- or viral-component-detection means to determine whether or not the virus has replicated,

expressed genetic material and/or assembled and/or been released in the presence of the agent.

As indicated above, variants may also be detected with reference to the HBsAg (s gene) and Presl, Pres2 envelop genes. Preferred mutations in this regard include one or more of PreS1 N114D, PreS1 T115S, PreS2 F22L, PreS2 V39A, PreS2 P52L, sL89V, sT118A, s F161L, sE164D, sI195M, sI208T PreS1 E86Q, PreS1 N91K, PreS2 P41H, sQ30K, sP120T, sL176V, sV194F.

Accordingly, another aspect of the present invention contemplates a method for determining whether an HBV strain exhibits reduced sensitivity to a nucleoside analog, said method comprising isolating DNA or corresponding mRNA from said HBV and screening for a mutation in the nucleotide sequence encoding the envelope genes wherein the presence of the following mutations in the PreS1, PreS2 and HBsAg: PreS1 N114D, PreS1 T115S, PreS2 F22L, PreS2 V39A, PreS2 P52L, sL89V, sT118A, sF161L, sE164D, sI195M, sI208T PreS1 E86Q, PreS1 N91K, PreS2 P41H, sQ30K, sP120T, sL176V, sV194F or combinations thereof or an equivalent one or more other mutation is indicative of a variant wherein said variant exhibits a decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs.

The present invention is predicated in part on the identification and isolation of variants of HBV that have a plurality of mutations and exhibit two or more characteristics selected from decreased or reduced sensitivity to one or more nucleoside analogs, a reduced level and/or functional activity of hepatitis B e antigen, or a reduced, abrogated or otherwise impaired immunological interactivity, relative to wild-type HBV. Thus, the identification of HBV variants with these mutational patterns is important *inter alia* for the development of assays to detect HBV variants and assays to screen for agents which are useful in treating and/or preventing infections by those variants and/or other HBV isolates and for the development of alternative therapeutic regimes for managing HBV infections.

Accordingly, one aspect of the present invention is directed to an isolated HBV variant comprising a plurality of nucleotide mutations that correlate with at least two characteristics selected from (a) resistance to one or more nucleoside analogs, (b) a reduced level and/or functional activity of hepatitis B e antigen, or (c) a reduced, abrogated or otherwise impaired immunological interactivity.

Another aspect of the present invention contemplates an isolated HBV variant comprising a plurality of nucleotide mutations that correlate with (a) resistance to one or more nucleoside analogs, (b) a reduced level and/or functional activity of hepatitis B e antigen, and (c) a reduced, abrogated or otherwise impaired immunological interactivity.

Yet another aspect of the present invention provides an isolated HBV variant comprising a plurality of nucleotide mutations selected from two or more of (a) a nucleotide mutation in a gene encoding a DNA polymerase resulting in at least one amino acid addition, substitution and/or deletion to said DNA polymerase wherein said variant exhibits decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs, (b) a nucleotide mutation in a gene encoding a hepatitis B e antigen or in a transcriptional control element of said gene wherein said mutation results in a reduced level and/or functional activity of said hepatitis B e antigen, or (c) a nucleotide mutation in a gene encoding a hepatitis B polypeptide resulting in at least one amino acid addition, substitution and/or deletion to said polypeptide which reduces, abrogates or otherwise impairs its immunological interactivity.

The detection of amino acid variants of DNA polymerase is conveniently accomplished by reference to the amino acid sequence shown in Formulae I and II. The polymorphisms shown represent the variations shown in various databases for active pathogenic HBV strains. Where an HBV variant comprises an amino acid different to what is represented, then such an isolate is considered a putative HBV variant having an altered DNA polymerase activity.

The present invention further contemplates agents which inhibit ETV and/or LMV resistant HBV variants. Such agents will be particularly useful if long term treatment by ETV and/or LMV and/or optionally other nucleoside analogs is contemplated by the clinician. The agents may be DNA or RNA or proteinaceous or non-proteinaceous chemical molecules. Natural product screening such as from plants, coral and microorganisms is also contemplated as a useful potential source of masking agents. The agents may be in isolated form or in the form of a pharmaceutical composition and may be administered sequentially or simultaneously with the nucleoside analog.

Accordingly, another aspect of the present invention contemplates a method for detecting an agent which exhibits inhibitory activity to an HBV, exhibiting resistance or decreased sensitivity to ETV and/or LMV, said method comprising:

generating a genetic construct comprising a replication competent-effective amount of the genome from said HBV contained in a plasmid vector and then transfecting said cells with said construct;

contacting said cells, before, during and/or after transfection, with the agent to be tested;

culturing said cells for a time and under conditions sufficient for the HBV to replicate, express genetic sequences and/or assemble and/or release virus or virus-like particles if resistant to said agent; and

subjecting the cells, cell lysates or culture supernatant fluid to viral- or viral-component-detection means to determine whether or not the virus has replicated, expressed genetic material and/or assembled and/or been released in the presence of said agent.

Still another aspect of the present invention provides a method for detecting an agent which exhibits inhibitory activity to an HBV, exhibiting resistance or decreased sensitivity to ETV and/or LMV, said method comprising:

generating a genetic construct comprising a replication competent-effective amount of the genome from said HBV contained in or fused to an amount of a baculovirus genome effective to infect cells and then infecting said cells with said construct;

contacting said cells, before, during and/or after infection, with the agent to be tested;

culturing said cells for a time and under conditions sufficient for the HBV to replicate, express genetic sequences and/or assemble and/or release virus or virus-like particles if resistant to said agent; and

subjecting the cells, cell lysates or culture supernatant fluid to viral- or viral-component-detection means to determine whether or not the virus has replicated, expressed genetic material and/or assembled and/or been released in the presence of said agent.

Still another aspect of the present invention provides a method for detecting an agent which exhibits inhibitory activity to an HBV, exhibiting resistance or decreased sensitivity to ETV and/or LMV, said method comprising:

generating a genetic construct comprising a replication competent-effective amount of the genome from said HBV contained in or fused to an amount of a baculovirus genome effective to infect cells and then infecting said cells with said construct;

contacting said cells, before, during and/or after infection, with the agent to be tested;

culturing said cells for a time and under conditions sufficient for the HBV to replicate, express genetic sequences and/or assemble and/or release virus or virus-like particles if resistant to said agent; and

subjecting the cells, cell lysates or culture supernatant fluid to viral- or viral-component-detection means to determine whether or not the virus has replicated, expressed genetic material and/or assembled and/or been released in the presence of said agent.

Preferably, the HBV genome is stably integrated into the cells' genome.

Whilst the baculovirus vector is a particularly useful in the practice of the present invention, the subject invention extends to a range of other vectors such as but not limited to adenoviral vectors.

The present invention further extends to cell lines carrying genetic constructs comprising all or a portion of an HBV genome or a gene or part of a gene therefrom.

The present invention also provides for the use of the subject HBV variants to screen for anti-viral agents. These anti-viral agents inhibit the virus. The term "inhibit" includes antagonizing or otherwise preventing infection, replication, assembly and/or release or any intermediate step. Preferred anti-viral agents include nucleoside analogs, however, the present invention extends to non-nucleoside molecules.

In addition, rational drug design is also contemplated to identify or generate chemical molecules which either mimic a nucleoside or which interact with a particular nucleotide sequence or a particular nucleotide. Combinatorial chemistry and two hybrid screening are some of a number of techniques which can be employed to identify potential therapeutic or diagnostic agents.

In one example, the crystal structure of polymerase or the surface antigen is used to rationally design small chemical molecules likely to interact with key regions of the

molecule required for function and/or antigenicity. Such agents may be useful as inhibitors of polymerase activity and/or may alter an epitope on the surface antigen.

Several models of the HBV polymerase have been prepared due to the similarity with reverse transcriptase from HIV (Das *et al., J. Virol. 75(10):* 4771-4779, 2001; Bartholomeusz *et al., Intervirology 40(5-6):* 337-342 1997; Allen *et al., Hepatology 27(6):* 1670-1677, 1998). The models of the HBV polymerase can be used for the rational drug design of new agents effective against HBV encoding the resistant mutations as well as wild type virus. The rational drug that is designed may be based on a modification of an existing antiviral agent such as the agent used in the selection of the HBV encoding the mutations associated with resistance. Viruses or clones expressing HBV genomic material encoding the mutations may also be used to screen for new antiviral agents.

The above methods are particularly useful in identifying an inhibitor of a ETV- and/or LMV-resistant HBV. The present invention extends, therefore, to compositions of the inhibitors. The inhibitors may also be in the form of antibodies or genetic molecules such as ribozymes, antisense molecules and/or sense molecules for co-suppression or the induction of RNAi. Reference to RNAi includes reference to siRNA.

The term "composition" includes a "pharmaceutical composition".

The inhibitor is referred to below as an "active ingredient" or "active compound" and may be selected from the list of inhibitors given above.

The composition may include an antigenic component of the HBV, a defective HBV variant or an agent identified through natural product screening or rational drug design (including combinatorial chemistry).

Pharmaceutically acceptable carriers and/or diluents include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents and the like. The use of such media and agents for pharmaceutical active

substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active ingredient, use thereof in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions.

The pharmaceutical composition may also comprise genetic molecules such as a vector capable of transfecting target cells where the vector carries a nucleic acid molecule capable of encoding an aspartyl protease inhibitor. The vector may, for example, be a viral vector.

Pharmaceutical forms suitable for injectable use include sterile aqueous solutions (where water soluble) and sterile powders for the extemporaneous preparation of sterile injectable solutions. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dilution medium comprising, for example, water, ethanol, polyol (for example, glycerol, propylene glycol and liquid polyethylene glycol, and the like), suitable mixtures thereof and vegetable oils. The proper fluidity can be maintained, for example, by the use of superfactants. The preventions of the action of microorganisms can be brought about by various anti-bacterial and anti-fungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminium monostearate and gelatin.

Sterile injectable solutions are prepared by incorporating the active compounds in the required amount in the appropriate solvent with the active ingredient and optionally other active ingredients as required, followed by filtered sterilization or other appropriate means of sterilization. In the case of sterile powders for the preparation of sterile injectable solutions, suitable methods of preparation include vacuum drying and the freeze-drying technique which yield a powder of active ingredient plus any additionally desired ingredient.

When the active ingredient is suitably protected, it may be orally administered, for example, with an inert diluent or with an assimilable edible carrier, or it may be enclosed in hard or soft shell gelatin capsule, or it may be compressed into tablets. For oral therapeutic administration, the active ingredient may be incorporated with excipients and used in the form of ingestible tablets, buccal tablets, troches, capsules, elixirs, suspensions, syrups, wafers and the like. Such compositions and preparations should contain at least 1% by weight of active compound. The percentage of the compositions and preparations may, of course, b varied and may conveniently be between about 5 to about 80% of the weight of the unit. The amount of active compound in such therapeutically useful compositions is such that a suitable dosage will be obtained. Preferred compositions or preparations according to the present invention are prepared so that an oral dosage unit form contains between about 0.1 μg and 200 mg of active compound. Alternative dosage amounts include from about 1 μg to about 1000 mg and from about 10 μg to about 500 mg. These dosages may be per individual or per kg body weight. Administration may be per hour, day, week, month or year.

The tablets, troches, pills, capsules and the like may also contain the components as listed hereafter. A binder such as gum, acacia, corn starch or gelatin; excipients such as dicalcium phosphate; a disintegrating agent such as corn starch, potato starch, alginic acid and the like; a lubricant such as magnesium stearate; and a sweetening agent such as sucrose, lactose or saccharin may be added or a flavouring agent such as peppermint, oil of wintergreen or cherry flavouring. When the dosage unit form is a capsule, it may contain, in addition to materials of the above type, a liquid carrier. Various other materials may be present as coatings or to otherwise modify the physical form of the dosage unit. For instance, tablets, pills or capsules may be coated with shellac, sugar or both. A syrup or elixir may contain the active compound, sucrose as a sweetening agent, methyl and propylparabens as preservatives, a dye and a flavouring. Of course, any material used in preparing any dosage unit form should be pharmaceutically pure and substantially non-toxic in the amounts employed. In addition, the active compound(s) may be incorporated into sustained-release preparations and formulations.

As stated above, the present invention further extends to an isolated HBsAg from the HBV variants herein described. More particularly, the present invention provides an HBsAg or a recombinant form thereof or derivative or chemical equivalent thereof. The isolated surface component and, more particularly, isolated surface antigen or its recombinant, derivative or chemical equivalents are useful in the development of biological compositions such as vaccine formulations.

Yet another aspect of the present invention provides a composition comprising a variant HBV resistant to ETV and/or LMV and optionally other nucleoside analogs or an HBV surface antigen from said variant HBV or a recombinant or derivative form thereof or its chemical equivalent and one or more pharmaceutically acceptable carriers and/or diluents.

As indicated above, antibodies may be generated to the mutant HBV agents and used for passive or direct vaccination against infection by these viruses. The antibodies may be generated in humans or non-human animals. In the case of the latter, the non-human antibodies may need to be deimmunized or more specifically humanized prior to use. Deimmunized may include, for example, grafting complimentarity determining regions (CDRs) from the variable region of a murine or non-human animal anti-HBV antibody onto a human consensus fragment antibody binding (Fab) polypeptide. Alternatively, amino acids defining epitopes in the variable region of the antibody may be mutated so that the epitopes are no longer recognized by the human MHC II complex.

Insofar as ribozyme, antisense or co-suppression (RNAi) repression is concerned, this is conveniently aimed at post-transcription gene silencing. DNA or RNA may be administered or a complex comprising RNAi or a chemical analog thereof specific for HBV mRNA may be employed.

All such molecules may be incorporated into pharmaceutical compositions.

In another embodiment, the present invention provides a biological composition comprising a variant HBV or an HBsAg or L, M or S proteins from said variant HBV or a recombinant or derivative form thereof or its chemical equivalent.

Generally, if an HBV is used, it is first attenuated. The biological composition according to this aspect of the present invention generally further comprises one or more pharmaceutically acceptable carriers and/or diluents.

The biological composition may comprise HBsAg or like molecule from one HBV variant or the composition may be a cocktail of HBsAgs or L, M or S proteins or like molecules from a range of ETV- and/or LMV-resistant HBV variants. Similar inclusions apply where the composition comprises an HBV.

The present invention is further directed to the use of defective HBV variants in the manufacture of therapeutic vaccines to vaccinate individuals against infection by HBV strains having a particular nucleotide sequence or encoding a particular polymerase or surface antigen or L, M or S proteins.

In one embodiment, for example, an HBV variant may be identified having a particular mutation in its polymerase conferring resistance or decreased sensitivity to a nucleoside analog. This variant may then be mutated to render it defective, i.e. attenuated or unable to cause infection. Such a defective, nucleoside analog-resistant virus may then be used as a therapeutic vaccine against virulent viruses having the same mutation in its polymerase.

The subject invention extends to kits for assays for variant HBV resistant to ETV and/or LMV. Such kits may, for example, contain the reagents from PCR or other nucleic acid hybridization technology or reagents for immunologically based detection techniques. A particularly useful assay includes the reagents and components required for immobilized oligonucleotide- or oligopeptide-mediated detection systems.

Still another aspect of the present invention contemplates a method for determining the potential for an HBV to exhibit reduced sensitivity to ETV and/or LMV or optionally other nucleoside analogs, said method comprising isolating DNA or corresponding mRNA from said HBV and screening for a mutation in the nucleotide sequence encoding HBV DNA polymerase resulting in at least one amino acid substitution, deletion and/or addition in any one or more of domains F and A through E or a region proximal thereto of said DNA polymerase and associated with resistance or decreased sensitivity to ETV and/or LMV wherein the presence of such a mutation is an indication of the likelihood of resistance to said ETV and/or LMV.

An assessment of a potential viral variant is important for selection of an appropriate therapeutic protocol. Such an assessment is suitably facilitated with the assistance of a computer programmed with software, which *inter alia* adds index values (I_Vs) for at least two features associated with the viral variants to provide a potency value (P_A) corresponding to the resistance or sensitivity of a viral variant to a particular chemical compound or immunological agent. The I_Vs can be selected from (a) the ability to exhibit resistance for reduced sensitivity to a particular compound or immunological agent; (b) an altered DNA polymerase from wild-type HBV; (c) an altered surface antigen from wild-type HBV; or (d) morbidity or recovery potential of a patient. Thus, in accordance with the present invention, I_Vs for such features are stored in a machine-readable storage medium, which is capable of processing the data to provide a P_A for a particular viral variant or a biological specimen comprising same.

Thus, in another aspect, the invention contemplates a computer program product for assessing the likely usefulness of a viral variant or biological sample comprising same for determining an appropriate therapeutic protocol in a subject, said product comprising:

(1) code that receives as input I_Vs for at least two features associated with said viral agents or biological sample comprising same, wherein said features are selected from:

(a) the ability to exhibit resistance for reduced sensitivity to a particular compound or immunological agent;
(b) an altered DNA polymerase from wild-type HBV;
(c) an altered surface antigen from wild-type HBV; or
(d) morbidity or recovery potential of a patient;
(e) altered replication capacity (increased or decreased);

(2) code that adds said I_Vs to provide a sum corresponding to a P_V for said viral variants or biological samples; and

(3) a computer readable medium that stores the codes.

In a related aspect, the invention extends to a computer for assessing the likely usefulness of a viral variant or biological sample comprising same in a subject, wherein said computer comprises:

(1) a machine-readable data storage medium comprising a data storage material encoded with machine-readable data, wherein said machine-readable data comprise I_Vs for at least two features associated with said viral variant or biological sample; wherein said features are selected from:-

(a) the ability to exhibit resistance for reduced sensitivity to a particular compound or immunological agent;
(b) an altered DNA polymerase from wild-type HBV;
(c) an altered surface antigen from wild-type HBV; or
(d) morbidity or recovery potential of a patient;
(e) altered replication capacity (increased or decreased);

(2) a working memory for storing instructions for processing said machine-readable data;

(3) a central-processing unit coupled to said working memory and to said machine-readable data storage medium, for processing said machine readable data to provide a sum of said I_{VS} corresponding to a P_V for said compound(s); and

(4) an output hardware coupled to said central processing unit, for receiving said P_V.

Any general or special purpose computer system is contemplated by the present invention and includes a processor in electrical communication with both a memory and at least one input/output device, such as a terminal. Such a system may include, but is not limited, to personal computers, workstations or mainframes. The processor may be a general purpose processor or microprocessor or a specialized processor executing programs located in RAM memory. The programs may be placed in RAM from a storage device, such as a disk or pre-programmed ROM memory. The RAM memory in one embodiment is used both for data storage and program execution. The computer system also embraces systems where the processor and memory reside in different physical entities but which are in electrical communication by means of a network. For example, a computer system having the overall characteristics set forth in Figure 7 may be useful in the practice of the instant invention. More specifically, Figure 7 is a schematic representation of a typical computer work station having in electrical communication (100) with one another *via,* for example, an internal bus or external network, a processor (101), a RAM (102), a ROM (103), a terminal (104), and optionally an external storage device, for example, a diskétte, CD ROM, or magnetic tape (105).

The present invention is further described by the following non-limiting Examples.

EXAMPLE 1

Overlapping genome of HBV

The overlapping genome of HBV is represented in Figure 1. The gene encoding DNA polymerase (P), overlaps the viral envelope genes, Pre-S1 and Pre-S2, and partially overlaps the X and core (C) genes. The HBV envelope comprises small, middle and large HBV surface antigens. The large protein component is referred to as the HBV surface antigen (HBsAg) and is enclosed by the S gene sequence. The Pre-S1 and Pre-S2 gene sequences encode the other envelope components.

EXAMPLE 2

Patient and Treatment

Patient A is a 44 year old male with chronic hepatitis B presented on Day 0 (9 July 1999) with raised serum HBV DNA levels (>2000 pg/ml) and was commenced on LMV treatment immediately (Figure 2). The patient A was HBsAg positive and anti-HBe positive. Following the initiation of LMV treatment the HBV DNA levels fell to 8 pg/ml over 54 days of therapy. The HBV DNA levels remained low until day 199 when there was a relapse in replication such that HBV DNA levels reached 1826 pg/ml. By Day 241 the serum ALT peaked at 741 IU/l. The HBV DNA was sequenced and LMV resistant virus was detected. The patient was then enrolled on Day 382 (24 July 2000) into a blinded ETV plus LMV clinical trial. HBV DNA levels only decreased to 33 pg/ml and the ALT decreased to 167 IU/ L by day 784. The patient was started on open label ETV plus LMV. However, both HBV DNA levels and ALT continued to rise and the HBV DNA was sequenced at day 894 (Figure 2).

Patient B Is a liver transplant patient. This patient has been treated with a number of nucleoside analogs including ganciclovir, famciclovir LMV and ETV. The patient was treated with LMV prior to ETV. The patient is currently on ETV treatment. During ETV treatment the HBV DNA levels were reduced to less than 5 pg/ml. At 532 days ETV treatment, that corresponds to 3857 days post transplant, there was a rise in the HBV DNA

levels to 993 pg/ml. The HBV DNA from this sample was further characterized by sequencing.

EXAMPLE 3

Detection of Viral Markers

Hepatitis B surface antigen (HBsAg), hepatitis B e antigen (HBeAg), anti-HBe and hepatitis B core antigen (HBcAg) specific IgG and IgM were measured using commercially available immunoassays (Abbott Laboratories, North Chicago, IL, USA). Hepatitis B viral DNA levels were measured using a capture hybridization assay according to the manufacturer's directions (Digene Hybrid Capture II, Digene Diagnostics Inc., Beltsville, MD). The manufacturers stated cut-off for detecting HBV viremia in clinical specimens was 0.7 x 10^6 copies/ml or 2.5 pg/ml, [Hendricks DA, *et al., Am J Clin Pathol 104:* 537-46, 1995].

EXAMPLE 4

Sequencing of HBV DNA

HBV DNA was extracted from 100µl of serum collected at 6 different time points (Figure 2) as described previously by Aye *et al., J Hepatol. 26:* 1148-53, 1997. Oligonucleotides were synthesized by Geneworks, Adelaide, Australia. Amplification of the HBV polymerase gene has been described by Aye *et al.*, 1997, *supra.*

The specific amplified products were purified using PCR purification columns from MO BIO Laboratories Inc (La Jolla, CA) and directly sequenced using Big Dye terminator Cycle sequencing Ready Reaction Kit (Perkin Elmer, Cetus Norwalk, CT). The PCR primers were used as sequencing primers, **OS1** 5'- GCC TCA TTT TGT GGG TCA CCA TA –3' (nt 1408-1430) [SEQ ID NO: 3], **TTA3** 5'-AAA TTC GCA GTC CCC AAA - 3'(nt2128-2145) [SEQ ID NO: 4], **JM** 5'- TTG GGG TGG AGC CCT CAG GCT - 3'(nt1676-1696) [SEQ ID NO: 5], **TTA4** 5' –GAA AAT TGG TAA CAG CGG –3'(nt

2615-2632) [SEQ ID NO: 6], **OS2** 5' TCT CTG ACA TAC TTT CCA AT 3' (nt 2798-2817) [SEQ ID NO: 7], to sequence the internal regions of the PCR products.

EXAMPLE 5

Analysis of HBV DNA

Patient A: The LMV resistant mutations at rtL180M and rtM204V were detected by sequencing by day 199 (Table 3). During the blinded phase of entecavir and LMV treatment, the mutation at rtV173L was also detected. A unique mutation in the B Domain at rtI169T was detected in combination with the two other B domain mutations at rtL180M and rtV173L as well as the mutation at rtM204V in the C domain. A number of other unique changes were also detected in the polymerase and in the overlapping envelope gene (Table 4, Figures 4, 5 and 6). These unique changes were compared to reference sequences from each of the seven genotypes A-G as well as a consensus sequence from pretreatment samples to determine unique changes.

Patient B: The sample at 532 days ETV treatment was sequenced and was compared to samples prior to ETV treatment (Figures 8, 9 and 10) Several polymerase mutations were detected in this sample including rtA21S, rtA38E, rtY54H, rtN76D, rtL91I, rtF122L, rtY124H, rtT128N, rtQ130P, rtL180M, rtT184G, rtS202I, rtM204V, rtH248N, rtY252L. At the start of ETV treatment the patient had been on LMV treatment and the mutations at rtL80M and M204V were detected (Figures 8, 9 and 10). The LMV mutations (rtL180M and rtM204V) were detected during ETV treatment even in the absence of the LMV selection pressure and these mutations may also contribute to ETV resistance. At the time of the virological breakthrough on ETV, the LMV selected mutations were still present as well as the mutations listed above. All the mutations listed were compared to reference sequences from each of the seven genotypes A-G as well as a consensus sequence from pretreatment samples to determine unique changes.

Patient B is HBeAg negative and the HBV isolated from this patient encoded a mutation in the precore gene at G1896A that results in a stop codon in the precore protein

precoreW28Stop. Mutations in other regions in the genome that included the precore mutation at G1896A may affect the replication fitness of HBV and the sensitivity to antiviral agents in combination with the mutation in the polymerase gene.

EXAMPLE 6

In vitro analysis of entecavir resistance

The sensitivity/resistance profile of HBV mutants to entecavir was examined *in vitro* using recombinant HBV/baculovirus. The procedure for analysing the resistance profile is outlined in the following Examples 7-14.

EXAMPLE 7

Cell culture

Sf21 insect cells were maintained in supplemented Grace's insect medium further supplemented with 10% v/v heat-inactivated fetal bovine serum (Gibco BRL, Gaithersburg, MD) in humidified incubator at 28 C with CO_2. HepG2 cells were maintained in minimal essential medium supplemented with 10% v/v heat-inactivated fetal bovine serum (MEM-FBS). HepG2 cells were grown in humidified 37°C incubators at 5% v/v CO_2.

EXAMPLE 8

Preparation of HBV/baculovirus transfer vector with specific point mutations

The recombinant HBV/baculovirus system used for antiviral testing has been previously described (Delaney *et al., Antimicrob Agents Chemother 45(6):* 1705-1013, 2001). In brief, the recombinant transfer vector was created by excising a fragment containing the 1.3x HBV genome construct and cloning it into the multiple cloning region of a baculovirus vector pBlueBac4.5 (Invitrogen, Carlsbad, CA). Point mutations were created by site directed mutagenesis using the commercial kits according to the manufacturers specifications (QuikChange, Stratagene). A HBV recombinant encoding the reverse

transcriptase mutations rtI169T + rtV173L + rtL180M + rtM204V. The nucleotide sequence of the plasmid and the point mutations generated by site directed mutagenesis were confirmed by sequencing using the ABI Prism Big Dye Terminator Cycle Sequencing Ready Reaction Kit according to the manufacturer's specifications (Perkin Elmer, Cetus Norwalk, CT).

EXAMPLE 9

Generation of recombinant baculoviruses containing the 1.3 HBV construct

Purified recombinant transfer vector and linear AcMNPV baculovirus DNA were co-transfected into Sf21 cells using the BacNBlue transfection kit from Invitrogen (Carlsbad, CA); recombinant viruses were isolated by plaque assay according to the manufacturer's instructions. A series of recombinant viruses were amplified from isolated plaques by infecting 100-mm dishes of Sf21 cells. Viral DNA was extracted from amplified viruses using standard procedures. Purified viral DNA was digested with restriction enzymes and then fractionated by electrophoresis in a 1% v/v agarose gel. Southern blotting was performed to determine which virus isolates contained the intact 1.3 HBV construct. A Boehringer Mannheim Random Prime DNA Labeling kit (Indianapolis, IN) was used to generate [P^{32}]-radiolabeled probes. A full-length double-stranded HBV genome was used as a template for all radiolabeled probes. Viral DNA sequence was confirmed by PCR amplification of the polymerase catalytic region using the sense primer 5'-GCC TCA TTT TGT GGG TCA CCA TA-3" [SEQ ID NO:3], (nucleotide 1408 to 1430 according to HBV Genebank Accession number M38454) and the antisense primer 5'-TCT CTG ACA TAC TTT CCA AT-3' [SEQ ID NO:6] (nucleotides 2817 to 2798 according to HBV Genebank Accession number M38454). The following primers were utilized for the sequencing of internal regions 5'- TGC ACG ATT CCT GCT CAA-3' [SEQ ID NO:8] (nucleotides 2345-2362 according to HBV Genebank Accession number M38454) and 5'-TTT CTC AAA GGT GGA GAC AG-3' [SEQ ID NO:9] (nucleotides 1790-1810 according to HBV Genebank Accession number M38454).

EXAMPLE 10

Preparative baculovirus amplification and purification

Baculoviruses were amplified by infecting suspension cultures of Sf21 cells in log phase at a multiplicity of infection (moi) of 0.5 pfu/cell. Infections were allowed to proceed until a majority of the cells in the flasks showed visible signs of infection (four to five days). Virions were concentrated from infected Sf21 medium by centrifugation at 80,000 x g and purified through a 20-60% w/v sucrose gradient. Purified virus was titrated in quadruplicate in Sf21 cells by end-point dilution. An aliquot of each high titer stock was used for DNA extraction. The polymerase gene was amplified and sequenced to confirm the presence of the site-directed mutagenesis as in Example 9

EXAMPLE 11

Infection of HepG2 cells with recombinant HBV expressing baculovirus

HepG2 cells were seeded at approximately 20-40% confluency and then were grown for 16-24 hours before infection. On the day of infection, triplicate plates of cells were trypsinized, and viable cell number was determined with a hemocytometer using Trypan blue exclusion. Average cell counts were calculated and used to determine the volume of high-titer viral stock necessary to infect cells at the indicated moi. HepG2 cells were washed one time with serum-free MEM to remove traces of serum. Baculovirus was diluted into MEM without serum to achieve the appropriate moi using volumes of 1.0, 0.5, and 0.25 ml to infect 100-mm, 60 mm, and 35-mm dishes, respectively. Baculovirus was adsorbed to HepG2 cells for one hour at 37°C with gentle rocking every 15 minutes to ensure that the inoculum was evenly distributed. The inoculum was then aspirated and HepG2 cells were washed two times with phosphate-buffered saline and refed MEM-FBS with or without various concentrations of agents.

EXAMPLE 12

Analysis of secreted HBV antigen

Detection of hepatitis Be antigen (HBeAg) was performed by radioimmunoassay and microparticle enzyme immunoassay using kits purchased from Abbott Laboratories (Abbott Park, IL, USA). Medium from HepG2 cells was collected, centrifuged at 6,000 g to remove cellular debris, transferred to clean tubes, and stored at 20°C until analysis. HBeAg values are expressed as fold of positive control. Medium samples were diluted appropriately so that radioimmunassay results were below positive control values for HBeAg.

EXAMPLE 13

Detection of intracellular replicative intermediates

HBV core particles were isolated from the cytoplasmic fraction of HepG2 cells lysed in 0.5% w/v NP-40. Cytoplasmic extracts were adjusted to 10 mmol/l McC12 and unprotected DNA was removed by an incubation to 500 g/ml Proteinase K for 1.5 hours at 37°C. HBV DNA in the samples were then extracted using commercial DNA extraction kits such as Qiagen (DNA extraction) or in-house methods using sequential phenol and chloroform extractions, and the nucleic acids were recovered by ethanol precipitation. Nucleic acids were resuspended in 50 µl /l TE (10 mmol/l Tris, 1 mmol/l ethylenediaminetetraacetic acid), normalized by OD260, and digested with 100 g/ml RNase (Boehringer Mannheim, Indianapolis, IN) for one hour at 37 °C before analysis by real-time PCR or electrophoresis and Southern blotting. After southern blot analysis a BioRad GS-670 imaging densitometer and the Molecular Analyst software (BioRad, Hecules California) was used to analyze suitable exposures of Southern blots. Densitometry data was fitted to logistic dose response curves using the TableCurve 2D software package from Jandel Scientific. Logistic dose response equations were used to calculate IC_{50} and IC_{90} values and co-efficients of variation.

EXAMPLE 14

Real-time PCR

For the real-time PCR based assay for HBV, HBV DNA was extracted from 200 µl of serum using the QIAamp DNA Mini Kit according to the manufacturer's instructions (QIAGEN GmbH, Hildens, Germany). Primers and a molecular beacon were designed for conserved nucleic acid sequences within the precore domain of the HBV genome to amplify and detect a 216-nucleotide product (Figure 1). Amplification was performed in a 50-µl reaction mixture containing 1.0 Taqman buffer A (Applied Biosystems, Foster City, CA), 3.0 mM MgCl, 0.4 pmol of each primer per µL, forward primer, PC1 (5'GGGAGGAGATTAGGTTAA3' [SEQ ID NO:10]) and reverse primer, PC2 (5'GGCAAAAACGAGAGTAACTC3' [SEQ ID NO:11]), 0.4 pmol of the HBV-specific molecular beacon per uL, (5'FAM-CGCGTCCTACTGTTCAAGCCTCCAAGCTGT GACGCG-DABCYL-3' [SEQ ID NO:12]; where FAM represents fluorophore 6-carboxyfluorescein and DABCYL, 4-dimethylaminophenylazobenzoic acid, a quenching chromophore) and 1.25U of AmpliTaq Gold DNA polymerase (Perkin-Elmer). PCR was performed using the ABI PRISM 7700 spectrofluorometric thermocycler (Applied Biosystems). The PCR program consisted of an initial cycle (95°C for 10 minutes) followed by 45 amplification cycles (94°C for 15 secs, 50°C for 30 secs, 72°C for 30 secs). The instrument detected and recorded the fluorescence spectrum of each reaction tube during the annealing phase.

An external standard was constructed by ligation of a 1.3 kB wild-type HBV plasmid (genotype D) into the pBlueBac plasmid vector (Hershey Medical Center, Hershey, PA). Quantification of the DNA concentration of the plasmid was determined by spectrophotometry. Duplicates of serial 10-fold dilutions of the plasmid ranging from 10_8 copies/ml to 100 copies/ml were included in each run in order to generate a standard curve. The copy number in each experimental reaction was determined by interpolation of the derived threshold cycle (C_T).

EXAMPLE 15

ETV treatments

ETV was resuspended in sterile water, aliquoted, and frozen at -20°C to avoid repeated freezing and thawing of the drug. Medium containing ETV was prepared daily as needed using fresh aliquots of 3TC. In experiments in which ETV treatment was initiated after viral infection, HepG2 cells were exposed to the indicated concentration of ETV immediately after infection with HBV baculovirus. In experiments utilizing pretreatment with ETV, cells were fed medium containing ETV 16 hours prior to HBV baculovirus infection, HBV baculovirus infection was also carried out in medium containing ETV, and cells were refed fresh medium containing ETV immediately after completion of the infection and washing procedures.

EXAMPLE 16

Antiviral testing performed with wild-type and HBV/baculovirus encoding rtIL69T + rtv173L + rtL180M + rtM204V

The graphical analysis of the dose effect of ETV on wild-type HBV and the quadruple mutant HBV are shown in Figure 11 using the quantitative real-time PCR results relative to wild type virus grown in the absence of ETV (0 μM ETV). ETV had the most pronounced effect on wild-type HBV replication as demonstrated by the reduction in HBV replicative intermediated detected by quantitative PCR at all ETV concentrations tested. In contrast, there was reduced sensitivity to ETV by the recombinant HBV encoding the quadruple mutant (rtI169T + rtV173L + rtL180M + rtM204V) especially at concentrations up to 0.5 μM ETV.

EXAMPLE 17

ETV

ETV (formerly BMS-200475 or SQ-34676) is a potent inhibitor of HBV replication. ETV is an cyclopentyl deoxyguanosine analog that has bio-oral available properties with activity

against hepadnaviruses and herpesviruses. The structure of ETV is shown in Figure 3 and its synthesis is described by Bisacchi *et al. (Bioorg. Med. Chem. Lit. 7:* 127-132, 1997). Preclinical studies indicate that entecavir is a highly potent inhibitor of HBV in enzyme- and cell-based assays (Innaimo *et al.,* 1997, *supra*; Siefer *et al.,* 1998, *supra*; Yamanaka *et al.,* 1999, *supra*. ETV was formerly described as BMS-200475 and SQ-34676.

Those skilled in the art will appreciate that the invention described herein is susceptible to variations and modifications other than those specifically described. It is to be understood that the invention includes all such variations and modifications. The invention also includes all of the steps, features, compositions and compounds referred to or indicated in this specification, individually or collectively, and any and all combinations of any two or more of said steps or features.

TABLE 3 Clinical, virological and HBV sequencing data summary for the patient A with increasing HBV viral loads while on LMV and ETV

Days Post LMV treatment	HBV DNA pg/ml	HBsAg	HBsAb	HBeAg	Anti-HBe	ALT IU/L	Treatment Protocol	Key Polymerase mutations detected by Sequencing
-143.00	>2000					n/a		
-107.00		detected		ND		399		
0.00							LMV (9/7/1999)	
54.00	8					510		
87.00	ND[1]					211		
115.00	ND			ND	+	106		
173.00	837					186		
199.00	1826					233		Sequenced: rtL180M, rtM204M/V[4]
241.00	930			ND	+	741		Sequenced: rtL180M,rtM204V
283.00	1631					334		
312.00	1539	+	ND	ND	+	238		
348.00	1605	+		ND	+	349		Sequenced rtL180M, rtM204V
382.00	1303	+	ND	ND	+	317	ETV *vs* LMV[2] 24/7/2000	00
397.00	131			ND	+	356		Sequenced rtL180M, rtM204V
495.00	44					205		
523.00	41					168		Sequenced rtV173V/L rtL180M, rtM204V,
784.00	33	+	ND	ND	+	167	ETV plus LMV[3] 22/8/01	
798.00	117					190		
826.00	75	+	ND	ND	+	215		
882.00	362	+	ND	ND	+	392		
894.00	192					597		Sequenced rtI169T, rtV173L, rtL180M rtM204V
902.00	246					627		

1. ND= not detected
2. Blinded phase of the study
3. Open label phase of the study
4. Nomenclature according to Stuyver *et al.*, 2001, *supra*

TABLE 4 Summary of HBV mutations in patient A treated with ETV and LMV

Sample name	Sample date	Days post LMV treatment	PCR Status	Genotype	Polymerase*	Surface
TR1	24/01/2000	199	1R PCR +ve	D	**rtL180M**** **rtM204V/M**	sA/V177A/V **sI195M/I**
TR2	6/3/2000	241	1R PCR +ve	D	**rtL180M** **rtV/M204V**	sA/V177A/V sL193S **sI/M195M**
TR3	21/6/2000	348	2R PCR +ve	D	**rtL180M** **rtM204V**	sV/A177V sS193S/L **sI/195M**
TR4	9/8/2000	397	2R PCR +ve	D	**rtL180M** **rtM204V**	sS/L177V **sI195M**
TR5	13/12/2000	523	2R PCR +ve	D	**rtV173V/L** **rtL180M** rtM204V	**sE164E/D** **sI195M**
TR6	18/12/2001	894	1R PCR +ve	D	spacerL97I spacerK115R spacerH116L spacerL128F spacerS137G spacerR139G spacerF142S rtY54H rtL91I **rtA97V** rtY124H rtH126R rtS135Y **rtI169T** **rtV173V/L** **rtL180M** **rtM204V**	preS1 N114 preS1 T115S preS2 F22L preS2 V39A preS2 P52L sL89V **sT118A** **sP127T** **sF161L** **sE164E/D** **sI/M195M**

* Nomenclature according to Stuyver *et al.*, 2001, *supra*

** Mutations in bold have not been detected in reference HBV genotypes, mutations not in bold are changes from the previous sample that are present in reference genotypes

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TABLE 4 Summary of HBV mutations in patient A treated with ETV and LMV

Sample name	Sample date	Days post LMV treatment	PCR Status	Genotype	Polymerase*	Surface
TR1	24/01/2000	199	1R PCR +ve	D	**rtL180M**** **rtM204V/M**	sA/V177A/V **sI195M/I**
TR2	6/3/2000	241	1R PCR +ve	D	**rtL180M** **rtV/M204V**	sA/V177A/V sL193S **sI/M195M**
TR3	21/6/2000	348	2R PCR +ve	D	**rtL180M** **rtM204V**	sV/A177V sS193S/L **sI/195M**
TR4	9/8/2000	397	2R PCR +ve	D	**rtL180M** **rtM204V**	sS/L177V **sI195M**
TR5	13/12/2000	523	2R PCR +ve	D	**rtV173V/L** **rtL180M** rtM204V	**sE164E/D** **sI195M**
TR6	18/12/2001	894	1R PCR +ve	D	spacerL97I spacerK115R spacerH116L spacerL128F spacerS137G spacerR139G spacerF142S rtY54H rtL91I **rtA97V** rtY124H rtH126R **rtS135Y,** **rtI169T,** **rtM250V** **rtV173V/L** **rtL180M** **rtM204V**	preS1 N114 preS1 T115S preS2 F22L preS2 V39A preS2 P52L sL89V **sT118A** **sP127T** **sF161L** **sE164E/D** **sI/M195M**

* Nomenclature according to Stuyver *et al.*, 2001, *supra*

** Mutations in bold have not been detected in reference HBV genotypes, mutations not in bold are changes from the previous sample that are present in reference genotypes

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CLAIMS

1. An isolated HBV variant wherein said variant comprises a nucleoside mutation in a gene encoding a DNA polymerase resulting in at least one amino acid addition, substitution and/or deletion to said DNA polymerase and wherein said variant exhibits decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs.

2. The isolated HBV variant of Claim 1 wherein said variant exhibits decreased sensitivity to ETV.

3. The isolated HBV variant of Claim 1 wherein said variant exhibits decreased sensitivity to both ETV and LMV.

4. The isolated HBV variant of any one of Claims 1 to 3 wherein said variant exhibits reduced interactivity to an immunological reagent specific to HBsAg.

5. The isolated HBV variant of Claim 1 wherein said variant comprises a mutation in domain F of the HBV DNA polymerase thereby conferring an altered amino acid sequence to the sequence set forth in Formula I (SEQ ID NO:1):

FORMULA I

L, B_1, B_2, D, W, G, P, C, B_3, B_4, H, G, B_5, H, B_6, I, R, B_7, P, R, T, P, B_8, R, V, B_9, G, G, V, F, L, V, D, K, N, P, H, N, T, B_{10}, E, S, B_{11}, L, B_{12}, V, D, F, S, Q, F, S, R, G, B_{13}, B_{14}, B_{15}, V, S, W, P, K, F, A, V, P, N, L, B_{16}, S, L, T, N, L, L, S*

wherein:

B_1 is L or R or I;

B_2 is E or D;

B_3 is T or D or A or N or Y;

B_4 is E or D;

B_5 is E or K or Q;

B_6 is H or R or N;

B_7 is I or T;

B_8 is A or S;

B_9 is T or R;

B_{10} is A or T or S;

B_{11} is R or T;

B_{12} is V or G;

B_{13} is S or I or T or N or V;

B_{14} is T or S or H or Y;

B_{15} is R or H or K or Q;

B_{16} is Q or P;

and wherein S* is designated as amino acid 74.

6. The isolated HBV variant of Claim 1 wherein said variant comprises a mutation in any one of domains A through E thereby conferring an altered amino acid sequence to the sequence set forth in Formula II (SEQ ID NO:2):

FORMULA II

S Z_1 L S W L S L D V S A A F Y H Z_2 P L H P A A M P H L L Z_3 G S S G L Z_4 R Y V A R L S S Z_5 S Z_6 Z_7 X N Z_8 Q Z_9 Z_{10} X X X Z_{11} L H Z_{12} Z_{13} C S R Z_{14} L Y V S L Z_{15} L L Y Z_{16} T Z_{17} G Z_{18} K L H L Z_{19} Z_{20} H P I Z_{21} L G F R K Z_{22} P M G Z_{23} G L S P F L L A Q F T S A I Z_{24} Z_{25} Z_{26} Z_{27} Z_{28} R A F Z_{29} H C Z_{30} Z_{31} F Z_{32} Y M* D D Z_{33} V L G A Z_{34} Z_{35} Z_{36} Z_{37} H Z_{38} E Z_{39} L Z_{40} Z_{41} Z_{42} Z_{43} Z_{44} Z_{45} Z_{46} L L Z_{47} Z_{48} G I H L N P Z_{49} K T K R W G Y S L N F M G Y Z_{50} I G

wherein:

X is any amino acid;
Z_1 is N or D;
Z_2 is I or P;
Z_3 is I or V;
Z_4 is S or D;
Z_5 is T or N;
Z_6 is R or N;
Z_7 is N or I;
Z_8 is N or Y or H;
Z_9 is H or Y;
Z_{10} is G or R;
Z_{11} is D or N;
Z_{12} is D or N;
Z_{13} is S or Y;
Z_{14} is N or Q;
Z_{15} is L or M;
Z_{16} is K or Q;
Z_{17} is Y or F;
Z_{18} is R or W;
Z_{19} is Y or L;
Z_{20} is S or A;
Z_{21} is I or V;
Z_{22} is I or L;
Z_{23} is V or G;
Z_{24} is C or L;
Z_{25} is A or S;
Z_{26} is V or M;
Z_{27} is V or T;

Z_{28} is R or C;

Z_{29} is F or P;

Z_{30} is L or V;

Z_{31} is A or V;

Z_{32} is S or A;

Z_{33} is V or L or M;

Z_{34} is K or R;

Z_{35} is S or T;

Z_{36} is V or G;

Z_{37} is Q or E;

Z_{38} is L or S or R;

Z_{39} is S or F;

Z_{40} is F or Y;

Z_{41} is T or A;

Z_{42} is A or S;

Z_{43} is V or I;

Z_{44} is T or C;

Z_{45} is N or S;

Z_{46} is F or V;

Z_{47} is S or D;

Z_{48} is L or V;

Z_{49} is N or Q;

Z_{50} is V or I; and

M^* is amino acid 204;

and wherein the first S is designated as amino acid 75.

7. The isolated HBV variant of Claim 5 or 6 wherein said variant further comprises an altered HBsAg.

8. The isolated HBV variant of Claim 5 or 6 or 7 wherein said variant exhibits reduced interactivity to an immunological reagent specific to HBsAg.

9. An isolated HBV variant comprising a mutation in the nucleotide sequence encoding HBsAg resulting in an amino acid addition, substitution and/or deletion in said HBsAg in a region corresponding to the amino acid sequence set forth in SEQ ID NO:1 or SEQ ID NO:2 and wherein said variant exhibits decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs.

10. The isolated HBV variant of Claim 9 wherein said variant exhibits decreased sensitivity to ETV.

11. The isolated HBV variant of Claim 9 wherein said variant exhibits decreased sensitivity to both ETV and LMV.

12. The isolated HBV variant of Claim 9 wherein an antibody specific for a wild-type HBsAg exhibits a reduced capacity to neutralize said HBV variant and wherein said HBV variant is selected by exposure of a subject to ETV and LMV in combination or sequential therapy.

13. The isolated HBV variant of Claim 1 or 9 comprising a mutation in the HBV DNA polymerase selected from spacerL97I, spacerK115R, spacerH116L, spacerL128F, spacerS137G, spacerR139G, spacerF142S, rtY54H, rtL91I, rtA97V, rtY124H, rtH126R, rtS135Y, rtI169T, rtV173L, rtL180M, rtM204V, rtA21S, rtA38E, rtF122L, rtT128N, rtQ130P, rtT184G, rtS202I, rtH248N, rtY252L or a combination thereof or an equivalent mutation.

14. The isolated HBV variant of Claim 1 or 9 or 13 comprising a mutation selected from PreS1 N114D, PreS1 T115S, PreS2 F22L, PreS2 V39A, PreS2 P52L, sL89V, sT118A, sI161L, sE164D, sI195M, sI208T PreS1 E86Q, PreS1 N91K, PreS2 P41H, sQ30K, sP120T,

sL176V, sV194F or a combination thereof or an equivalent mutation.

15. The isolated HBV variant of Claim 1 or 9 or 13 comprising a mutation selected from sF161L, sE164D and sI195M or a combination thereof or an equivalent mutation.

16. The isolated HBV variant of Claim 1 or 9 or 13 comprising a mutation selected from rtI169T, rtV173L, rtL180M, rtT184G, rtS202I and rtM204V or a combination thereof or an equivalent mutation.

17. A method for determining the potential for an HBV to exhibit reduced sensitivity to ETV and/or LMV or optionally other nucleoside analogs, said method comprising isolating DNA or corresponding mRNA from said HBV and screening for a mutation in the nucleotide sequence encoding HBV DNA polymerase resulting in at least one amino acid substitution, deletion and/or addition in any one or more of domains F and A through E or a region proximal thereto of said DNA polymerase and associated with resistance or decreased sensitivity to ETV and/or LMV wherein the presence of such a mutation is an indication of the likelihood of resistance to said ETV and/or LMV.

18. The method of Claim 17 wherein the mutation screened for is selected from spacerL97I, spacerK115R, spacerH116L, spacerL128F, spacerS137G, spacerR139G, spacerF142S, rtY54H, rtL91I, rtA97V, rtY124H, rtH126R, rtS135Y, rtI169T, rtV173L, rtL180M, rtM204V, rtA21S, rtA38E, rtF122L, rtT128N, rtQ130P, rtT184G, rtS202I, rtH248N, rtY252L or a combination thereof or an equivalent mutation.

19. A method for determining whether an HBV strain exhibits reduced sensitivity to a nucleoside analog, said method comprising isolating DNA or corresponding mRNA from said HBV and screening for a mutation in the nucleotide sequence encoding the DNA polymerase wherein the presence of the following mutations in the spacer region and the rt region: spacerL97I, spacerK115R, spacerH116L, spacerL128F, spacerS137G, spacerR139G, spacerF142S, rtY54H, rtL91I, rtA97V, rtY124H, rtH126R, rtS135Y, rtI169T, rtV173L,

rtL180M, rtM204V, rtA21S, rtA38E, rtF122L, rtT128N, rtQ130P, rtT184G, rtS202I, rtH248N, rtY252L or combinations thereof or an equivalent one or more other mutation is indicative of a variant wherein said variant exhibits a decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs.

20. The method of Claim 19 wherein the mutation screened for is selected from rtI169T, rtV173, rtL180M, rtT184G, rtS202I and rtM204V or a combination thereof or an equivalent mutation.

21. A method for determining whether an HBV strain exhibits reduced sensitivity to a nucleoside analog, said method comprising isolating DNA or corresponding mRNA from said HBV and screening for a mutation in the nucleotide sequence encoding the DNA polymerase wherein the presence of the following mutations in the B or C domain of the rt region: rtI169T, rtV173L, rtL180M, rtT184G, rtS202I, rtM204V or combinations thereof or an equivalent one or more other mutation is indicative of a variant wherein said variant exhibits a decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs.

22. A method for detecting an agent which exhibits inhibitory activity to an HBV, exhibiting resistance or decreased sensitivity to ETV and/or LMV, said method comprising:

generating a genetic construct comprising a replication competent-effective amount of the genome from said HBV contained in a plasmid vector and then transfecting said cells with said construct;

contacting said cells, before, during and/or after transfection, with the agent to be tested;

culturing said cells for a time and under conditions sufficient for the HBV to replicate, express genetic sequences and/or assemble and/or release virus or virus-like particles if resistant to said agent; and

subjecting the cells, cell lysates or culture supernatant fluid to viral- or viral-component-detection means to determine whether or not the virus has replicated, expressed genetic material and/or assembled and/or been released in the presence of said agent.

23. A method for detecting an agent which exhibits inhibitory activity to an HBV, exhibiting resistance or decreased sensitivity to ETV and/or LMV, said method comprising:

generating a genetic construct comprising a replication competent-effective amount of the genome from said HBV contained in or fused to an amount of a baculovirus genome effective to infect cells and then infecting said cells with said construct;

contacting said cells, before, during and/or after infection, with the agent to be tested;

culturing said cells for a time and under conditions sufficient for the HBV to replicate, express genetic sequences and/or assemble and/or release virus or virus-like particles if resistant to said agent; and

subjecting the cells, cell lysates or culture supernatant fluid to viral- or viral-component-detection means to determine whether or not the virus has replicated, expressed genetic material and/or assembled and/or been released in the presence of said agent.

24. A method for detecting an agent which exhibits inhibitory activity to an HBV, exhibiting resistance or decreased sensitivity to ETV and/or LMV, said method comprising:

generating a genetic construct comprising a replication competent-effective amount of the genome from said HBV contained in or fused to an amount of a baculovirus genome effective to infect cells and then infecting said cells with said construct;

contacting said cells, before, during and/or after infection, with the agent to be tested;

culturing said cells for a time and under conditions sufficient for the HBV to replicate, express genetic sequences and/or assemble and/or release virus or virus-like particles if resistant to said agent; and

subjecting the cells, cell lysates or culture supernatant fluid to viral- or viral-component-detection means to determine whether or not the virus has replicated, expressed genetic material and/or assembled and/or been released in the presence of said agent.

25. The method of Claims 22 or 23 or 24 wherein the HBV genome is stably integrated into the cells' genome.

26. A vaccine comprising an antigenic component of the HBV variant of any one of Claims 1 to 16 or an antibody thereto.

27. The vaccine of Claim 26 wherein the antigenic component is an HBsAg or PreS1 or PreS2.

28. The vaccine of Claim 26 wherein the antigenic component is a defective HBV variant.

29. The vaccine of Claim 26 comprising an antibody to HBsAg or PreS1 or PreS2.

30. A computer product for assessing the likely usefulness of a viral variant or biological sample comprising same for determining an appropriate therapeutic protocol in a subject, said product comprising:

(1) code that receives as input I_Vs for at least two features associated with said viral agents or biological sample comprising same, wherein said features are selected from:

(f) the ability to exhibit resistance for reduced sensitivity to a particular compound or immunological agent;
(g) an altered DNA polymerase from wild-type HBV;
(h) an altered surface antigen from wild-type HBV; or
(i) morbidity or recovery potential of a patient;
(j) altered replication capacity (increased or decreased);

(2) code that adds said I_Vs to provide a sum corresponding to a P_V for said viral variants or biological samples; and

(3) a computer readable medium that stores the codes.

31. A computer for assessing the likely usefulness of a viral variant or biological sample comprising same in a subject, wherein said computer comprises:

(1) a machine-readable data storage medium comprising a data storage material encoded with machine-readable data, wherein said machine-readable data comprise I_Vs for at least two features associated with said viral variant or biological sample; wherein said features are selected from:-

(a) the ability to exhibit resistance for reduced sensitivity to a particular compound or immunological agent;
(b) an altered DNA polymerase from wild-type HBV;
(c) an altered surface antigen from wild-type HBV; or
(d) morbidity or recovery potential of a patient;

(e) altered replication capacity (increased or decreased);

(2) a working memory for storing instructions for processing said machine-readable data;

(3) a central-processing unit coupled to said working memory and to said machine-readable data storage medium, for processing said machine readable data to provide a sum of said I_Vs corresponding to a P_V for said compound(s); and

(4) an output hardware coupled to said central processing unit, for receiving said P_V.

32. A composition comprising an agent capable of directly or indirectly inhibiting an HBV variant as defined in any one of Claims 1 to 16, said composition further comprising one or more pharmaceutically acceptable carriers and/or diluents.

33. The composition of Claim 32 wherein the agent is a recombinant protein from said HBV variant.

34. The composition of Claim 33 wherein the recombinant protein is HBsAg or PreS1 or PreS2.

35. The composition of Claim 32 wherein the agent is capable of inhibiting an HBV variant polymerase.

36. The composition of Claim 35 wherein the agent is identified by natural product screening or rational drug design.

37. The composition of Claim 32 wherein the agent is a defective HBV variant.

38. The composition of Claim 32 wherein the agent is an antibody directed to an HBV compound.

39. The composition of Claim 32 wherein the agent is a ribozyme, antisense molecule or sense molecule relative to an HBV gene.

CLAIMS

1. An isolated HBV variant wherein said variant comprises a nucleoside mutation in a gene encoding a DNA polymerase resulting in at least one amino acid addition, substitution and/or deletion to said DNA polymerase and wherein said variant exhibits decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs wherein the mutation in the DNA polymerase is selected from spacerL97I, spacerK115R, spacerH116L, spacerL128F, spacerS137G, spacerR139G, spacerF142S, rtY54H, rtL91I, rtA97V, rtY124H, rtH126R, rtS135Y, rtI169T, rtM250V, rtV173L, rtL180M, rtM204V, rtA21S, rtA38E, rtF122L, rtT128N, rtQ130P, rtT184G, rtS202I, rtH248N, rtY252L or a combination thereof or an equivalent mutation with the *proviso* that where the HBV variant is resistant to LMV alone, then the mutation is not rtV173L, rtL180M or rtM204V.

2. The isolated HBV variant of Claim 1 wherein the mutation in the DNA polymerase is selected from rtI169T, rtV173L, rtL180M, rtT184G, rtS202I, rtM204V and rtM250V or a combination thereof or an equivalent mutation.

3. An isolated HBV variant wherein said variant comprises a nucleoside mutation in a gene encoding a surface mutation resulting in at least one amino acid addition, substitution and/or deletion to said surface antigen and wherein said variant exhibits decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs wherein the mutation in the surface antigen is selected from PreS1 N114D, PreS1 T115S, PreS2 F22L, PreS2 V39A, PreS2 P52L, sL89V, sT118A, s161L, sE164D, sI195M, sI208T PreS1 E86Q, PreS1 N91K, PreS2 P41H, sQ30K, sP120T, sL176V, sV194F or a combination thereof or an equivalent mutation.

4. The isolated HBV variant of Claim 3 wherein the mutation in the surface antigen is selected from sF161L, sE164D and sI195M or a combination thereof

or an equivalent mutation.

5. The isolated HBV variant of Claim 1 or 2 or 3 or 4 wherein said variant exhibits decreased sensitivity to ETV.

6. The isolated HBV variant of Claim 1 or 2 or 3 or 4 wherein said variant exhibits decreased sensitivity to both ETV and LMV.

7. The isolated HBV variant of any one of Claims 1 to 6 wherein said variant exhibits reduced interactivity to an immunological reagent specific to HBsAg.

8. The isolated HBV variant of Claim 1 or 2 wherein said variant further comprises an altered HBsAg.

9. The isolated HBV variant of any one of Claims 1 to 8 wherein said variant exhibits reduced interactivity to an immunological reagent specific to HBsAg.

10. An isolated HBV variant comprising a mutation in the nucleotide sequence encoding HBsAg resulting in an amino acid addition, substitution and/or deletion in said HBsAg and wherein said variant exhibits decreased sensitivity to ETV and/or LMV and optionally other nucleoside analogs, wherein said mutation is selected from PreS1 N114D, PreS1 T115S, PreS2 F22L, PreS2 V39A, PreS2 P52L, sL89V, sT118A, s161L, sE164D, sI195M, sI208T PreS1 E86Q, PreS1 N91K, PreS2 P41H, sQ30K, sP120T, sL176V, sV194F or a combination thereof or an equivalent mutation.

11. The isolated HBV variant of Claim 1 wherein the mutation is selected from sF161L, sE164D and sI195M or a combination thereof or an equivalent mutation.

12. The isolated HBV variant of Claim 10 or 11 wherein said variant exhibits decreased sensitivity to ETV.

13. The isolated HBV variant of Claim 10 or 11 wherein said variant exhibits

decreased sensitivity to both ETV and LMV.

14. The isolated HBV variant of Claim 10 or 11 wherein an antibody specific for a wild-type HBsAg exhibits a reduced capacity to neutralize said HBV variant and wherein said HBV variant is selected by exposure of a subject to ETV and LMV in combination or sequential therapy.

15. A method for determining the potential for an HBV to exhibit reduced sensitivity to ETV and/or LMV or optionally other nucleoside analogs, said method comprising isolating DNA or corresponding mRNA from said HBV and screening for a mutation in the nucleotide sequence encoding HBV DNA polymerase resulting in at least one amino acid substitution, deletion and/or addition in any one or more of domains F and A through E or a region proximal thereto of said DNA polymerase and associated with resistance or decreased sensitivity to ETV and/or LMV wherein the presence of such a mutation is an indication of the likelihood of resistance to said ETV and/or LMV wherein the mutation is selected from spacerL97I, spacerK115R, spacerH116L, spacerL128F, spacerS137G, spacerR139G, spacerF142S, rtY54H, rtL91I, rtA97V, rtY124H, rtH126R, rtS135Y, rtI169T, rtM250V, rtV173L, rtL180M, rtM204V, rtA21S, rtA38E, rtF122L, rtT128N, rtQ130P, rtT184G, rtS202I, rtH248N, rtY252L or a combination thereof or an equivalent mutation with the *proviso* that where the HBV variant is resistant to LMV alone, then the mutation is not rtV173L, rtL180M or rtM204V.

16. The method of Claim 15 LMV wherein the mutation is selected from rtI169T, rtV173L, rtL180M, rtT184G, rtS202I rtM204V and rtM250V or a combination thereof or an equivalent mutation.

17. A method for determining the potential for an HBV to exhibit reduced sensitivity to ETV and/or LMV or optionally other nucleoside analogs, said method comprising isolating DNA or corresponding mRNA from said HBV and screening for a mutation in the nucleotide sequence encoding HBV surface antigen resulting in at least one amino acid substitution, deletion and/or addition in any one or more of domains F and A

through E or a region proximal thereto of said surface antigen and associated with resistance or decreased sensitivity to ETV and/or LMV wherein the presence of such a mutation is an indication of the likelihood of resistance to said ETV and/or LMV wherein the mutation is selected from PreS1 N114D, PreS1 T115S, PreS2 F22L, PreS2 V39A, PreS2 P52L, sL89V, sT118A, s161L, sE164D, sI195M, sI208T PreS1 E86Q, PreS1 N91K, PreS2 P41H, sQ30K, sP120T, sL176V, sV194F or a combination thereof or an equivalent mutation.

18. The method of Claim 17 wherein said mutation is selected from sF161L, sE164D and sI195M or a combination thereof or an equivalent mutation.

19. A method for detecting an agent which exhibits inhibitory activity to an HBV, exhibiting resistance or decreased sensitivity to ETV and/or LMV wherein the HBV variant comprises a mutation in a DNA polymerase selected from spacerL97I, spacerK115R, spacerH116L, spacerL128F, spacerS137G, spacerR139G, spacerF142S, rtY54H, rtL91I, rtA97V, rtY124H, rtH126R, rtS135Y, rtI169T, rtM250V, rtV173L, rtL180M, rtM204V, rtA21S, rtA38E, rtF122L, rtT128N, rtQ130P, rtT184G, rtS202I, rtH248N, rtY252L or a combination thereof or an equivalent mutation with the *proviso* that where the HBV variant is resistant to LMV alone, then the mutation is not rtV173L, rtL180M or rtM204V, said method comprising:

generating a genetic construct comprising a replication competent-effective amount of the genome from said HBV contained in a plasmid vector and then transfecting said cells with said construct;

contacting said cells, before, during and/or after transfection, with the agent to be tested;

culturing said cells for a time and under conditions sufficient for the HBV to replicate, express genetic sequences and/or assemble and/or release virus or virus-like particles if resistant to said agent; and

subjecting the cells, cell lysates or culture supernatant fluid to viral- or viral-component-detection means to determine whether or not the virus has replicated, expressed genetic material and/or assembled and/or been released in the presence of said agent.

20. A method for detecting an agent which exhibits inhibitory activity to an HBV, exhibiting resistance or decreased sensitivity to ETV and/or LMV wherein the HBV variant comprises a mutation in a DNA polymerase selected from spacerL97I, spacerK115R, spacerH116L, spacerL128F, spacerS137G, spacerR139G, spacerF142S, rtY54H, rtL91I, rtA97V, rtY124H, rtH126R, rtS135Y, rtI169T, rtM250V, rtV173L, rtL180M, rtM204V, rtA21S, rtA38E, rtF122L, rtT128N, rtQ130P, rtT184G, rtS202I, rtH248N, rtY252L or a combination thereof or an equivalent mutation with the *proviso* that where the HBV variant is resistant to LMV alone, then the mutation is not rtV173L, rtL180M or rtM204V, said method comprising:

generating a genetic construct comprising a replication competent-effective amount of the genome from said HBV contained in or fused to an amount of a baculovirus genome effective to infect cells and then infecting said cells with said construct;

contacting said cells, before, during and/or after infection, with the agent to be tested;

culturing said cells for a time and under conditions sufficient for the HBV to replicate, express genetic sequences and/or assemble and/or release virus or virus-like particles if resistant to said agent; and

subjecting the cells, cell lysates or culture supernatant fluid to viral- or viral-component-detection means to determine whether or not the virus has replicated, expressed genetic material and/or assembled and/or been released in the presence of said agent.

21. A method for detecting an agent which exhibits inhibitory activity to an HBV, exhibiting resistance or decreased sensitivity to ETV and/or LMV wherein the HBV variant comprises a mutation in a DNA polymerase selected from spacerL97I, spacerK115R, spacerH116L, spacerL128F, spacerS137G, spacerR139G, spacerF142S, rtY54H, rtL91I, rtA97V, rtY124H, rtH126R, rtS135Y, rtI169T, rtM250V, rtV173L, rtL180M, rtM204V, rtA21S, rtA38E, rtF122L, rtT128N, rtQ130P, rtT184G, rtS202I, rtH248N, rtY252L or a combination thereof or an equivalent mutation with the *proviso* that where the HBV variant is resistant to LMV alone, then the mutation is not rtV173L, rtL180M or rtM204V, said method comprising:

generating a genetic construct comprising a replication competent-effective amount of the genome from said HBV contained in or fused to an amount of a baculovirus genome effective to infect cells and then infecting said cells with said construct;

contacting said cells, before, during and/or after infection, with the agent to be tested;

culturing said cells for a time and under conditions sufficient for the HBV to replicate, express genetic sequences and/or assemble and/or release virus or virus-like particles if resistant to said agent; and

subjecting the cells, cell lysates or culture supernatant fluid to viral- or viral-component-detection means to determine whether or not the virus has replicated, expressed genetic material and/or assembled and/or been released in the presence of said agent.

22. The method of Claims 19 or 20 or 21 wherein the HBV genome is stably integrated into the cells' genome.

23. A vaccine comprising an antigenic component of the HBV variant of any one of Claims 1 to 14 or an antibody thereto.

24. The vaccine of Claim 23 wherein the antigenic component is an HBsAg or PreS1 or PreS2.

25. The vaccine of Claim 23 wherein the antigenic component is a defective HBV variant.

26. The vaccine of Claim 23 comprising an antibody to HBsAg or PreS1 or PreS2.

27. A computer product for assessing the likely usefulness of a viral variant or biological sample comprising same for determining an appropriate therapeutic protocol in a subject, said product comprising:

(1) code that receives as input I_{VS}:

(a) an altered DNA polymerase from wild-type HBV selected from spacerL97I, spacerK115R, spacerH116L, spacerL128F, spacerS137G, spacerR139G, spacerF142S, rtY54H, rtL91I, rtA97V, rtY124H, rtH126R, rtS135Y, rtI169T, rtM250V, rtV173L, rtL180M, rtM204V, rtA21S, rtA38E, rtF122L, rtT128N, rtQ130P, rtT184G, rtS202I, rtH248N, rtY252L or a combination thereof or an equivalent mutation and rtI169T, rtV173L, rtL180M, rtT184G, rtS202I and rtM204V or a combination thereof or an equivalent mutation; and

(b) an altered surface antigen from wild-type HBV selected from PreS1 N114D, PreS1 T115S, PreS2 F22L, PreS2 V39A, PreS2 P52L, sL89V, sT118A, s161L, sE164D, sI195M, sI208T PreS1 E86Q, PreS1 N91K, PreS2 P41H, sQ30K, sP120T, sL176V, sV194F or a combination thereof or an equivalent mutation and sF161L, sE164D and sI195M or a combination thereof or an equivalent mutation;

(2) code that adds said I_Vs to provide a sum corresponding to a P_V for said viral variants or biological samples; and

(3) a computer readable medium that stores the codes.

28. A computer for assessing the likely usefulness of a viral variant or biological sample comprising same in a subject, wherein said computer comprises:

(1) a machine-readable data storage medium comprising a data storage material encoded with machine-readable data, wherein said machine-readable data comprise I_Vs for at least two features associated with said viral variant or biological sample; wherein said features are selected from:-

(a) an altered DNA polymerase from wild-type HBV selected from spacerL97I, spacerK115R, spacerH116L, spacerL128F, spacerS137G, spacerR139G, spacerF142S, rtY54H, rtL91I, rtA97V, rtY124H, rtH126R, rtS135Y, rtI169T, rtM250V, rtV173L, rtL180M, rtM204V, rtA21S, rtA38E, rtF122L, rtT128N, rtQ130P, rtT184G, rtS202I, rtH248N, rtY252L or a combination thereof or an equivalent mutation and rtI169T, rtV173L, rtL180M, rtT184G, rtS202I and rtM204V or a combination thereof or an equivalent mutation; and

(b) an altered surface antigen from wild-type HBV selected from PreS1 N114D, PreS1 T115S, PreS2 F22L, PreS2 V39A, PreS2 P52L, sL89V, sT118A, s161L, sE164D, sI195M, sI208T PreS1 E86Q, PreS1 N91K, PreS2 P41H, sQ30K, sP120T, sL176V, sV194F or a combination thereof or an equivalent mutation and sF161L, sE164D and sI195M or a combination thereof or an equivalent mutation;

(2) a working memory for storing instructions for processing said machine-readable data;

(3) a central-processing unit coupled to said working memory and to said machine-readable data storage medium, for processing said machine readable data to provide a sum of said I_{VS} corresponding to a P_V for said compound(s); and

(4) an output hardware coupled to said central processing unit, for receiving said P_V.

29. A composition comprising an anti-HBV agent which has selective activity against an HBV exhibiting reduced sensitivity to ETV and/or LMV said anti-HBV agent identified using an HBV variant as defined in any one of Claims 1 to 14, said composition further comprising one or more pharmaceutically acceptable carriers and/or diluents.

30. The composition of Claim 29 wherein the agent is a recombinant protein from said HBV variant.

31. The composition of Claim 30 wherein the recombinant protein is HBsAg or PreS1 or PreS2.

32. The composition of Claim 29 wherein the agent is capable of inhibiting an HBV variant polymerase.

33. The composition of Claim 32 wherein the agent is identified by natural product screening or rational drug design.

34. The composition of Claim 29 wherein the agent is a defective HBV variant.

35. The composition of Claim 29 wherein the agent is an antibody directed to an HBV compound.

36. The composition of Claim 29 wherein the agent is a ribozyme, antisense molecule or sense molecule relative to an HBV gene.