

WJG 20<sup>th</sup> Anniversary Special Issues (9): Hepatitis B virus**Molecular diagnosis and treatment of drug-resistant hepatitis B virus**

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Author contributions: All authors contributed to this work.

Supported by Konkuk University

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Received: October 27, 2013 Revised: January 29, 2014

Accepted: March 19, 2014

Published online: May 21, 2014

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**Key words:** Hepatitis B virus; Drug-resistance; Molecular diagnosis; Antiviral treatment; Chronic hepatitis B

**Core tip:** Although several antiviral agents have been developed in the last two decades for the treatment of chronic hepatitis B (CHB), antiviral resistance remains an important challenge for long-term CHB therapy. In this review, we discussed the currently available molecular diagnosis tools, *in vitro* phenotypic assays for validation of drug-resistant hepatitis B virus (HBV), and treatment options for drug-resistant HBV.

Kim JH, Park YK, Park ES, Kim KH. Molecular diagnosis and treatment of drug-resistant hepatitis B virus. *World J Gastroenterol* 2014; 20(19): 5708-5720 Available from: URL: <http://www.wjgnet.com/1007-9327/full/v20/i19/5708.htm> DOI: <http://dx.doi.org/10.3748/wjg.v20.i19.5708>

**Abstract**

Oral antiviral agents have been developed in the last two decades for the treatment of chronic hepatitis B (CHB). However, antiviral resistance remains an important challenge for long-term CHB therapy. All of the clinically available oral antiviral agents are nucleoside or nucleotide analogues that target the activity of viral reverse transcriptase (RT), and all are reported to have resistant mutations. Since the hepatitis B virus (HBV) RT, like other viral polymerases, lacks proofreading activity, the emergence of drug-resistance occurs readily under selective pressure from the administration of antiviral agents. The molecular diagnosis of drug-resistant HBV is based on sequence variations, and current diagnostic methods include sequencing, restriction fragment polymorphism analysis, and hybridization. Here, we will discuss the currently available molecular diagnosis tools,

**INTRODUCTION**

Chronic hepatitis B (CHB) affects 240 million people worldwide and is a leading cause of liver-related morbidity and mortality<sup>[1-3]</sup>. The last two decades have seen the introduction of oral antiviral agents for the treatment of hepatitis B virus (HBV) infection<sup>[4-8]</sup>. Long-term antiviral therapy is needed in the majority of patients, and incomplete viral suppression and emergence of drug resistance is a major concern<sup>[9]</sup>. All of the clinically available HBV drugs are nucleoside or nucleotide analogues that inhibit the activity of viral reverse transcriptase (RT), and all drugs approved as anti-HBV agents are reported to have viral resistance due to specific mutations in the

RT domain<sup>[10]</sup>. In treatment-naïve patients, the prevalence of such mutations is low and routine mutation analysis is not recommended<sup>[11]</sup>. The emergence of resistant strains is due to the selective pressure of the therapeutic regimen, although other factors, such as host immune response and therapy adherence, also play a role<sup>[12]</sup>. The development of antiviral resistance is one of the most important factors predicting the success or failure of CHB treatment<sup>[13]</sup>. The emergence of antiviral resistance results in the resumption of active viral replication that has been previously suppressed after the initiation of antiviral therapy, and can impair biochemical or histologic improvement<sup>[14]</sup>. Furthermore, increasing use of antiviral agents for CHB has led to a greater likelihood of antiviral resistance<sup>[12]</sup>. A recent prospective cohort study showed that antiviral drug resistance increased the risk of hepatocellular carcinoma in decompensated HBV-related cirrhotic patients, especially in those failed rescue therapy<sup>[15]</sup>. To avoid development of drug resistance, the current guidelines recommend tenofovir (TDF) and entecavir (ETV) as first-line antiviral agents<sup>[13,16-18]</sup>.

In this review, we will discuss methods of diagnosis, phenotypic assays for drug resistance, and treatments for drug-resistant HBV strains.

## MOLECULAR MECHANISM OF ANTIVIRAL RESISTANCE

The HBV RT, like other viral polymerases, lacks proof-reading activity on the newly synthesized viral genome, resulting in the introduction of random mutations into progeny HBV DNA. The error rate of HBV polymerase is approximately 1 per 10<sup>5</sup> to 10<sup>7</sup> base syntheses due to the highly error-prone nature of the HBV RT<sup>[19]</sup>. Under selective pressure from the administration of antiviral agents, HBV quasispecies converge on a dominant HBV mutant that can escape selection pressure, producing a drug-resistant HBV strain.

Since the molecular mechanisms and clinical significance of resistance to HBV nucleoside/nucleotide analogue drugs have been extensively reviewed in literature<sup>[10,20-22]</sup>, detailed explanations of the documented resistant mutants will not be reviewed here.

Lamivudine (LMV), a synthetic nucleoside analogue with activity against HBV and HIV, is sequentially phosphorylated to LMV triphosphate by cellular kinases and incorporated into the growing HBV DNA at the 3'-end by HBV polymerase, which induces premature chain termination. The primary resistance mutation to LMV is the rtM204I/V in the YMDD motif. This mutation is usually accompanied by a compensatory mutation including rtL180M, L80I/V, and V173L, which enhances the viral replication of replication-defective rtM204I/V mutants (Figure 1). LMV resistance does not confer cross-resistance to adefovir (ADV) or TDF<sup>[20,21]</sup>.

ADV dipivoxil, an analogue of adenosine monophosphate, can be easily phosphorylated by cellular kinases to the active metabolite ADV diphosphate, which inhibits

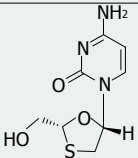
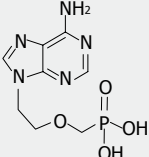
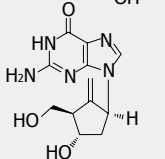
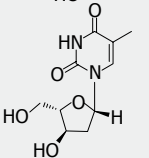
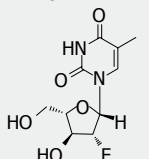
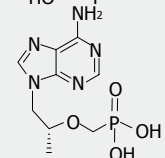
HBV DNA polymerase by competing with the natural substrate deoxyadenosine triphosphate. The incorporation of ADV diphosphate into the growing viral DNA causes premature DNA chain termination similar to LMV. Genotypic analysis has revealed that ADV resistance is conferred by the rtN236T and/or rtA181T/V mutations. *In vitro* drug susceptibility assays showed that the rtN236T mutation does not affect sensitivity to LMV, telbivudine (LdT), or ETV; however, the rtA181T mutation was shown to decrease susceptibility to LMV (< 10-fold), ADV (2- to 8-fold), and TDF (2- to 3-fold)<sup>[32]</sup>.

ETV, a guanosine nucleoside, is efficiently phosphorylated to the active triphosphate form. By competing with the natural substrate deoxyguanosine triphosphate, ETV triphosphate functionally inhibits the activities of HBV polymerase. ETV is the most potent among the currently available anti-HBV agents. The mutations associated with primary resistance to ETV are the most complex and have not been fully established in patients. Mutations associated with the emergence of ETV resistance have been mapped to the B domain (rtI169T, rtL180M, and rtS184S/A/I/L/G/C/M), C domain (rtM204I/V and rtS202G/I), and E domain (rtM250I/V). ETV resistance does not confer cross-resistance to ADV or TDF<sup>[22]</sup>.

LdT, a synthetic thymidine nucleoside, is the unmodified L-isomer of the naturally occurring nucleoside, thymidine; therefore, phosphorylation to the active LdT triphosphate form by cellular kinases is easily accomplished. The LdT 5'-triphosphate eventually inhibits HBV DNA polymerase by competing with the natural substrate, thymidine 5'-triphosphate. The rtM204I substitution confers primary resistance to LdT treatment and frequently co-occurs with the rtL80I/V and rtL180M substitutions. An *in vitro* study revealed that LdT resistance does not confer cross-resistance to ADV, TDF, or ETV<sup>[33]</sup>.

Clevudine (CLV), a pyrimidine analogue, inhibits HBV polymerase by competing with the natural substrate, thymidine. CLV inhibits the DNA-dependent DNA activity of HBV polymerase, as well as reverse transcription and priming. Since CLV is a fluorinated LdT, it has a similar resistance profile to LMV and LdT. Kwon *et al*<sup>[23]</sup> identified the rtM204I substitution as the most common mutation during viral breakthrough in four CLV-failure patients, whereas rtL229V was shown to be a compensatory mutation for the impaired replication of the rtM204I mutant. A quadruple mutant (rtL129M+rtV173L+rtM204I+rtH337N) conferred greater replicative ability and strong resistance to both CLV and LMV<sup>[23]</sup>.

TDF disoproxil fumarate is a methyl derivative of ADV with activity against retroviruses, including HIV-1/2 and HBV. TDF demonstrates a mechanism of action and antiviral resistance pattern very similar to ADV. Like ADV, TDF is rapidly metabolized by cellular kinases into the active metabolite, TDF diphosphate. In turn, TDF diphosphate inhibits HBV DNA RT by competing with the natural substrate, deoxyadenosine triphosphate, causing the termination of the growing HBV DNA. *In vitro*

Molecule	Structure	Brand name	Company	Year of FDA approval	<i>In vitro</i> IC <sub>50</sub> (μmol/L) <sup>[23]</sup>	Resistant mutations	5 yr cumulative resistance rate <sup>[25-31]</sup>
Lamivudine		Zeffix, Heptovir, Epivir, Epivir-HBV	GlaxoSmithKline	1998 (for adults) and 2000 (for children) in United States	3.3 <sup>[23]</sup>	rtL80V/I rtV173L rtL180M rtM204I/V	70%
Adefovir		Preveon, Hepsera	Gilead	2002 (United States)	6.3 <sup>[23]</sup>	rtA181T/V rtN236T	29%-65% <sup>[57]</sup>
Entecavir		Baraclude	Bristol Meyers Squibb	2005 (United States)	0.01 <sup>[23]</sup>	rtI169T rtL180M rtT184S/A/I/L rtS202G/I rtM204I/V rtM250I/V	1.2%-1.5%
Telbivudine		Sebivo (Europe), Tyzeka (United States)	Idenix, Novartis	2006 (United States)	0.19 <sup>[24]</sup>	rtA181T/V rtM204I	34% (3 yr)
Clevudine		Levovir, Revovir	Bukwang Pharm	2006 (South Korea)	0.9 <sup>[23]</sup>	rtL180M rtM204I/V	30% (3 yr)
Tenofovir		Viread	Gilead	2008 (United States)	2.5 <sup>[23]</sup>	rtA181T/V rtA194T rtN236T	0%

**Figure 1** Approved anti-hepatitis B virus drugs and their resistant mutations. IC<sub>50</sub> values are dependent on the duration of drug exposure to cells, the cells used, and the protocol used.

drug susceptibility assay demonstrated that the rtA194T, rtA181T/V, and/or rtN236T mutations are associated with TDF resistance<sup>[22]</sup>. Resistance to TDF has been proven so far in *in vitro* studies.

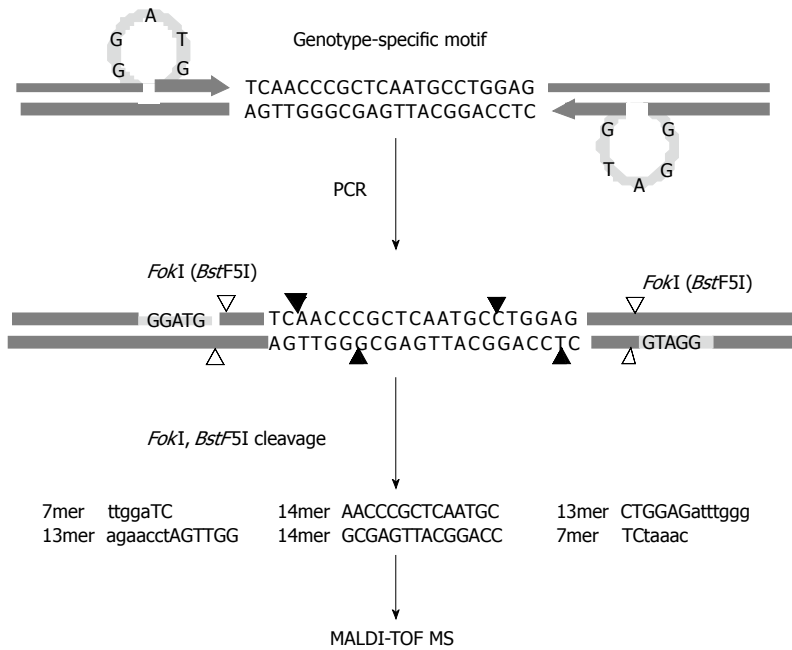
## MOLECULAR DIAGNOSIS OF DRUG-RESISTANT HBV

The molecular diagnosis of drug-resistant HBV is performed by genotypic assay, which determines the resistance-related mutations in the viral RT gene by comparing the patient-derived viral strain with wild-type. To date, several methods have been developed and clinically used to determine genotypic resistance. These methods include sequencing (PCR-based direct sequencing, cloning and sequencing, and ultra-deep pyrosequencing), restriction fragment length or mass polymorphism (RFLP or RFMP), and hybridization (DNA microarray and line-probe assay). Since the conventional methods for HBV genotyping have been extensively reviewed in literature<sup>[20,22]</sup>, only those technologies that have received lesser

attention elsewhere, such as ultra-deep pyrosequencing and RFMP, will be reviewed here in detail.

### PCR-based direct or cloning sequencing

Currently, genotypic analysis is largely performed by sequencing-based assays. Only sequencing can provide all of the information on the mutations present in a viral genome. Therefore, this assay is useful to identify novel resistant mutations responsible for the insufficiency of new antiviral drugs<sup>[23]</sup>. However, limited by sensitivity, this assay can only detect the majority species present in the total viral population and is generally capable of detecting quasispecies comprising more than 20 percent of a viral population. This limitation can be overcome by multiple rounds of cloning followed by sequencing. This method is impractical for use in large cohort studies or clinical laboratories since the process is hard to standardize, labor-intensive, and time-consuming. However, cloning-based sequencing is the only method available to analyze the colocalization of mutations within the same HBV genome.



**Figure 2 Schematic diagram of the restriction fragment mass polymorphism genotyping strategy.** Polymerase chain reaction is performed with primers designed to introduce a type II S restriction endonuclease recognition sequence (*FokI*) ahead of the genotype-specific motifs upon amplification. The enzymatic cleavage of the products leads to excision of multiple oligonucleotide fragments representing the motifs shown in capital letters, and then the masses of the resulting oligonucleotide fragments are examined by MALDI-TOF MS. Cleavage sites of *FokI* and *BstF5I*, an isoschizomer of *FokI*, are indicated by filled and blank arrows, respectively, and recognition sites for both restriction endonucleases are specified by the shaded bars.

### Ultra-deep pyrosequencing

Recently, ultra-deep pyrosequencing, a next-generation sequencing technology, was successfully applied to detect HBV quasispecies and also to identify drug-resistant mutants that present at very low concentrations in patient sera<sup>[34-37]</sup>. This is one of the most sensitive techniques capable of detecting minority virus populations that are less than 0.1% of the total, and that are typically missed by direct or cloning-based sequencing. However, application of this technology in determining drug resistance is limited by its high cost. The one advantage of this next-generation sequencing technique is the production of vast quantities of sequence data without prior information on the sequence of interest. Very recently, Rodriguez *et al.*<sup>[37]</sup> generated approximately 480000 sequences (4010 ± 843 sequences per sample) from ADV-resistant patient sera by ultra-deep pyrosequencing. They found that the dynamics of ADV-resistant viral populations are very complex and more heterogeneous than expected. More importantly, the identified ADV-resistant variants (including rtA181 and rtN236) were already present as minor populations at baseline in most of the treatment-naïve patients who subsequently developed viral DNA breakthrough to ADV therapy.

### Restriction fragment mass polymorphism

RFMP technology is based on detection of the mass difference in DNA fragments resulting from drug-resistant mutations in the RT gene<sup>[38]</sup>. Mass spectrometry generates precise information of the molecular mass of the analytes and enables quantitation of both strands of DNA in parallel using a fully automated procedure. Mass

spectrometry directly assesses the nature of the PCR products, whereas other technologies indirectly measure the PCR products either through hybridization or by sequencing reactions.

The assay is based on the amplification and mass detection of oligonucleotides excised using a type II S enzyme digestion and matrix-assisted laser desorption/ionization time of flight mass spectrometry (MALDI-TOF MS) as depicted in Figure 2. PCR is performed with primers designed to introduce a type II S restriction endonuclease recognition sequence ahead of the polymorphism site. The use of a type II S restriction enzyme means that this assay does not depend on the fortuitous occurrence of restriction sites, because these enzymes typically have cleavage sites distal to their recognition sites. The enzymatic cleavage of the reaction products leads to excision of multiple oligonucleotide fragments containing the mutated motifs, after which the masses of the resulting oligonucleotide fragments are examined by MALDI-TOF MS. Differences are observed as the presence, absence, or mass change of peaks corresponding to fragments affected by the existence of polymorphisms, including substitutions, deletions, and insertions in the RT gene<sup>[38]</sup>. In addition to its speed and high-throughput capacity, the RFMP assay is very sensitive and can detect drug-resistant mutants that constitute less than 1% of a total virus population, enabling distinctions between mixed-genotype samples<sup>[39]</sup>. A clear correlation has been observed between estimated peak heights and real proportions in mixed-genotype pools, indicating the RFMP assay enables better quantitative detection of mixed populations without the need for population-based cloning

and subsequent sequencing. By combining the merits of unique assay chemistry and the established techniques of MALDI-TOF MS, the RFMP assay is able to screen for viral mutants in a robust, high-throughput manner and is known to be capable of simultaneously analyzing 384 samples in 3 h, which is almost 10 times faster than existing methods<sup>[40]</sup>. The improved sensitivity of the RFMP assay has allowed for its application in monitoring early intervention and prevention in antiviral therapy for HBV. An RFMP analysis of YMDD motifs within 740 consecutive samples collected from 116 hepatitis B patients demonstrated that YMDD mutants occur throughout the course of LMV therapy irrespective of the occurrence of viral DNA breakthrough. This indicates that the mere detection of YMDD mutants is not sufficient to predict viral DNA breakthrough, although the presence of YMDD mutants has been associated with a high incidence of viral DNA breakthrough, and a five-fold predominance of YMDD mutant-to-wild-type virus was significantly associated with viral DNA breakthrough. Periodic testing by RFMP assay was shown to be useful in detecting the predominance of YMDD mutants for monitoring drug resistance, enabling early intervention and prevention of viral breakthrough<sup>[40]</sup>.

Multiplex RFMP methods were developed to have practical advantages over existing methods, enabling the simultaneous detection of several resistant mutations within a large number of samples, and to address the dynamics and evolution of resistance and the relationship between viral genotypes and clinical outcomes<sup>[41,42]</sup>. This assay has proven to be reliable for clinical virus genotyping in concert with regular measurements of HBV viral load, for the early detection of LMV, ADV, ETV, and MDR mutations, and for the timely introduction of new salvage agents<sup>[43-45]</sup>. However, RFMP technology cannot provide information on the colocalization of mutations within the same HBV genome and requires access to a mass spectrometer.

### Hybridization-based assays

Hybridization-based assays rely on affinity differences between amplified nucleotides harboring mutations and wild-type viral sequences. These techniques include the line-probe (LiPA) assay<sup>[46]</sup> and DNA microarray<sup>[47]</sup>. The commercially available LiPA assay (Innogenetics, Belgium) can detect single nucleotide mismatches and discriminate HBV resistance mutations within minor fractions constituting 5% or more of the total viral population<sup>[39,46]</sup>. DNA chip microarrays can simultaneously detect multiple resistant mutations with relatively low labor and cost<sup>[47]</sup>.

Although hybridization techniques are generally reliable, the main limitations of all hybridization-based assays arise largely from their relatively low specificity and from the fact that they are qualitative rather than quantitative. Moreover, the design and optimization of new sets of specific probes are required for every mutant in order to detect a single nucleotide change because mutations

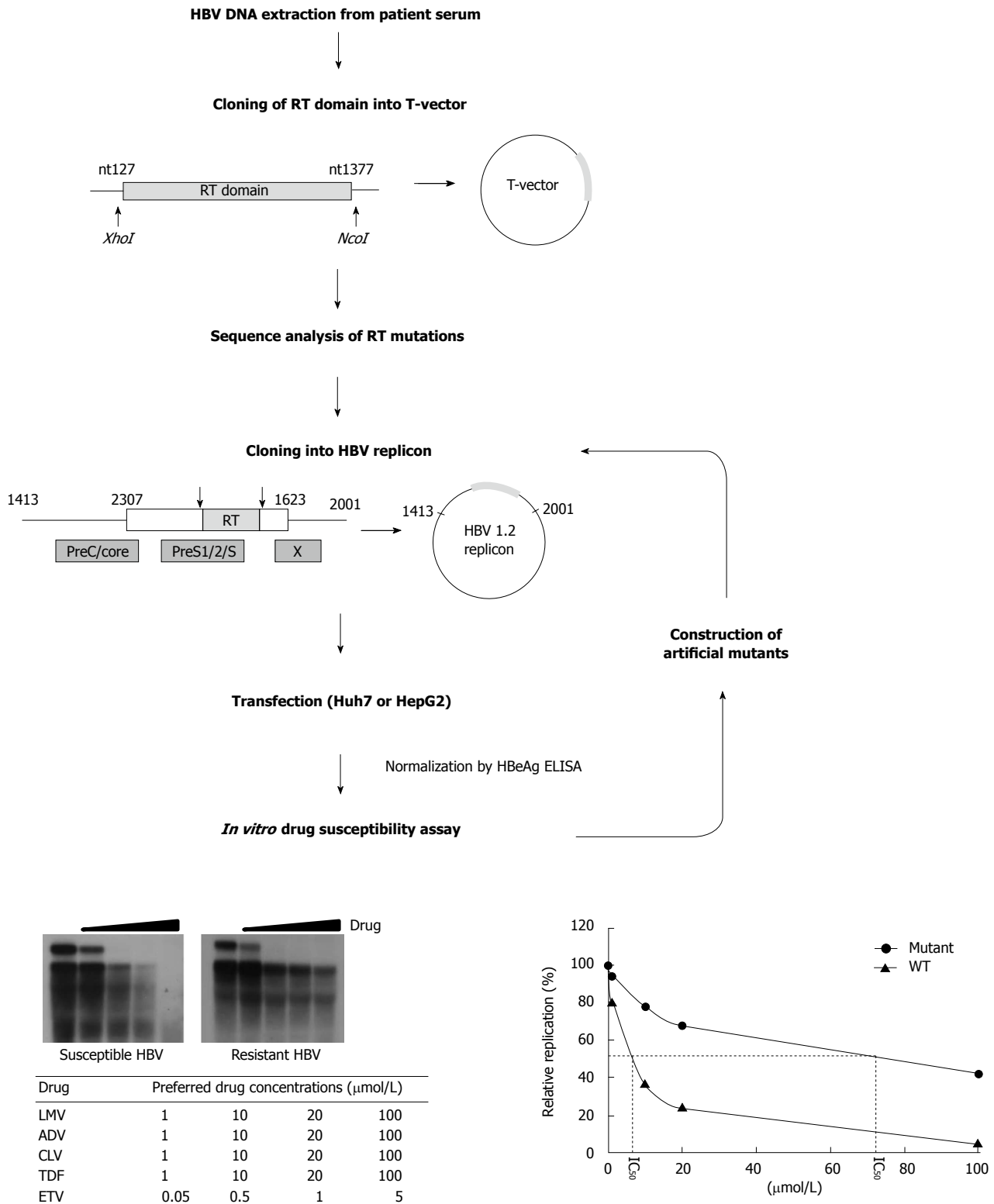
in neighboring regions affect the sensitivity of the target sequence.

## IN VITRO PHENOTYPIC ASSAY FOR VALIDATION OF DRUG-RESISTANT HBV

Only an *in vitro* phenotypic assay can confirm genotypic antiviral resistance. However, current methodology is labor-intensive and time consuming due to the need for construction of a replication-competent HBV replicon and the use of Southern blot analysis. Although the detailed methods for the validation of drug-resistant HBV may vary slightly based on approach, the basic concept is identical<sup>[48-50]</sup>. A typical approach to analyze phenotypic resistance is presented in Figure 3. The HBV genome is isolated from patient sera, and the RT mutation sequence is analyzed. To assess whether the mutations are colocalized within the same HBV genome and to select a specific RT mutant more easily, the PCR products are subcloned into a T-vector. After sequence analysis, the selected RT mutants are once again cloned into an HBV replicon such as an HBV 1.1mer, 1.2mer, 1.5mer, or dimer. For this procedure, the *XhoI* and *NcoI* restriction sites are preferentially used for insertion into both the T-vector and the replicon. The replicons are then transfected into Huh7 or HepG2 hepatocyte cell lines. Secreted HBeAg is considered to normalize transfection efficiency. Secreted HBsAg cannot be used as a control since the RT and surface genes overlap, and, thus, mutations in the RT gene can affect the antigenicity of HBsAg. Four to five days after treatment with antiviral drugs, cell lysates are subject to Southern blot analysis, which gives the most accurate result. Since drug potency varies, the preferred drug concentrations are indicated in Figure 3. After quantification of replication ability using a PhosphorImager imaging system, the IC<sub>50</sub> (μmol/L) for each drug is calculated by interpolation. Finally, the fold resistance (R factor) is determined. By doing this, it is possible to determine the presence of drug-resistant mutations in the quasispecies contained in clinical isolates. To identify the sequence elements responsible for drug-resistance, artificial replicons that harbor conserved mutations in clinical isolates need to be constructed and tested for drug susceptibility. An example of the overall characterization of drug-resistant HBV was recently reported, including detailed methods<sup>[23]</sup>. Alternatively, real-time PCR can be used to measure replication ability, an approach that is suitable for automated and large-scale testing in a hospital setting<sup>[51]</sup>.

## TREATMENT

The development of drug resistance is associated with virological breakthrough, biochemical breakthrough, and, sometimes, hepatic decompensation<sup>[52]</sup>. Furthermore, resistance may also reverse histological improvement and oppose the reduction in disease progression among patients with advanced fibrosis and early cirrhosis<sup>[53]</sup>.



**Figure 3** Scheme for *in vitro* phenotypic validation of drug-resistant hepatitis B virus. Hepatitis B virus (HBV) DNA is purified from patient serum, and the sequence of RT mutations is analyzed. After cloning into replication-competent HBV replicons, each mutant is transfected into hepatoma cell lines followed by Southern blot (or real time polymerase chain reaction) analysis. The IC<sub>50</sub> (μmol/L) value is obtained by quantification of replication ability and curve-fitting. To characterize the specific mutation(s) conferring resistance to antiviral drugs, each artificial mutant must be constructed and individually tested.

LMV is not recommended as a first-line treatment due to high resistance development. Currently, the newer and potent drugs, TDF and ETV are recommended<sup>[13,16-18]</sup>. Several practice guidelines suggest strategies for treat-

ment of CHB patients with resistance. The American Association for the Study of Liver Diseases guidelines were published in 2009<sup>[18]</sup>. The updated guidelines from the European Association for the Study of the Liver,

**Table 1 Guidelines for treatment of resistance**

Resistant drug	AASLD 2009 <sup>[18]</sup>	EASL 2012 <sup>[16]</sup>	APASL 2012 <sup>[17]</sup>	KASL 2012 <sup>[13]</sup>
LMV	Add ADV or TDF Stop LMV, switch to Truvada (TDF + FTC)	Switch to TDF Add ADV (If TDF not available)	Add ADV Switch to TDF Switch to IFN-based therapy	Add ADV or TDF Stop LMV, switch to ADV or TDF + other nucleoside analogues Switch to TDF
ADV	Add LMV Stop ADV, switch to Truvada Stop ADV, switch to or add ETV	NA-naïve; Switch to ETV or TDF Prior LMV-resistance; Switch to TDF + a nucleoside analogue	Add LMV, LdT, or ETV Switch to TDF Switch to IFN-based therapy	With prior LMV resistance, -Stop ADV, switch to TDF + other nucleoside analogues -Add ETV 1mg ADV as a first-line therapy -Stop ADV, switch to TDF + other nucleoside analogues -Add other nucleoside analogue, if rtA181T, add ETV
ETV	Switch to TDF or Truvada	Switch to TDF Add TDF Add ADV (If TDF not available)	Add TDF or ADV Switch to IFN-based therapy	Add nucleotide analogue
LdT	Same treatment as LMV	Switch to TDF Add TDF Add ADV (If TDF not available)	Same treatment as LMV	Same treatment as LMV
CLV TDF		Add ETV, LdT, LMV or FTC (LMV-naïve; Switch to ETV/ prior LMV-resistance; Add ETV)		Same treatment as LMV
Multidrug-resistance		Combination of a nucleoside and a nucleotide (preferably TDF)	ETV + TDF Switch to IFN-based therapy	TDF + ETV 1 mg ADV + ETV 1 mg
Comment	Update is required especially for multidrug-resistance	Recommendation about IFN-based therapy is limited	Recommendation about TDF resistance is limited	Recommendation about TDF resistance and IFN-based therapy is limited

KASL: Korean Association for the Study of the Liver; AASLD: American Association for the Study of Liver Diseases; APASL: Asian Pacific Association for the Study of the Liver; EASL: European Association for the Study of the Liver; LMV: Lamivudine; ADV: Adefovir; LdT: Telbivudine; CLV: Clevudine; TDF: Tenofovir; FTC: Emtricitabine; ETV: Entecavir; IFN: Interferon.

the Asian Pacific Association for the Study of the Liver, and the Korean Association for the Study of the Liver were published in 2012<sup>[13,16,17]</sup>. The main principle of these guidelines is to choose antiviral agents without cross-resistance and to begin rescue therapy as soon as possible<sup>[13,16,17]</sup>. These guidelines are compared and summarized in Table 1.

**LMV, LdT, and CLV resistance**

LMV, LdT, and CLV are L-nucleoside analogues, and mutations at rtM204 are considered the primary cause of resistance to these agents<sup>[20,54,55]</sup>. rtM204I or rtM204V, with or without rtL180M mutations, are sensitive to ADV and TDF, but exhibit cross-resistance to ETV and show an eight-fold decrease in sensitivity. The rtA181T mutation has been detected in 5% of LMV-resistant patients. These mutants exhibit cross-resistance to ADV but remain sensitive to ETV<sup>[56]</sup>.

Of the various forms of antiviral drug resistance, treatment for LMV resistance has been the most widely studied. The incidence of the rtM204I/V substitution has reportedly increased from 24% in 1 year to 70% in 5 years<sup>[23,54]</sup>. ADV monotherapy is not recommended due to the increased risk of ADV resistance, which has been shown to manifest in 18% of patients at 1 year, 25% at 2 years, and up to 65% after 5 years<sup>[57-59]</sup>. ADV add-

on therapy is accepted as a first-line rescue therapy<sup>[60]</sup>. Many studies have shown that LMV-ADV combination therapy is superior to ADV monotherapy<sup>[61-63]</sup>. However, the LMV-resistant strain rtA181T has been reported to be continuously detected even after combination therapy with LMV-ADV, so caution is necessary to avoid the possibility of multidrug-resistant HBV<sup>[32,64,65]</sup>. LdT and ADV combination therapy, or a combination of ETV and ADV, are possible treatment options<sup>[66-68]</sup>.

TDF has shown potent antiviral activity against LMV-resistant HBV and is reportedly superior to ADV monotherapy<sup>[69-71]</sup>. Therefore, treatment strategies that include TDF seem to be more effective than those involving ADV<sup>[13]</sup>. One study showed that switching to TDF is as effective as adding TDF to LMV<sup>[71]</sup>. However, there is one report of TDF resistance in an LMV-resistant CHB patient with HIV co-infection who received TDF monotherapy, so the efficacy of TDF monotherapy requires further evaluation<sup>[72]</sup>. One recent study also found that the reduction in HBV DNA levels was greater in a TDF-LMV combination therapy group than in TDF monotherapy, ADV monotherapy, or LMV-ADV combination groups<sup>[73]</sup>.

ETV exhibits some cross-resistance with LMV, which has prompted the administration of 1.0 mg doses to LMV-resistant CHB patients<sup>[74]</sup>. However, ETV resis-

tance was reportedly more frequent than in treatment-naïve patients. A 5-year cumulative genotypic resistance rate of 51% was reported, along with an accompanying virologic breakthrough of 43%<sup>[27]</sup>. A recent study found that LMV-ADV combination therapy showed superior antiviral efficacy over ETV 1.0 mg monotherapy in LMV-resistant CHB patients<sup>[75]</sup>. For these reasons, ETV 1.0 mg monotherapy is not recommended.

Peginterferon (PegIFN) is another option for the treatment of LMV-resistant CHB patients. A randomized control trial showed that 48 wk of PegIFN alfa-2a treatment for LMV-resistant CHB patients achieved undetectable HBV DNA levels in 10.6% of patients<sup>[76]</sup>. Another study showed similar efficacy of PegIFN alfa-2a in a comparison between treatment-naïve patients and LMV-resistant patients with HBeAg-positive CHB<sup>[77]</sup>.

Few data related to LdT and CLV resistance are available. The 2-year risk of LdT resistance was shown to be 25.1% in HBeAg-positive patients and 10.8% in HBeAg-negative patients<sup>[78]</sup>. In the subgroup that had no genotypic resistance at year 2 and received LdT until year 3, an incremental 1.0% of HBeAg-positive, and 2.1% of HBeAg-negative patients developed genotypic resistance to LdT<sup>[79]</sup>. The cumulative resistance rate of LdT is 34% after 3 years<sup>[29]</sup>. In the case of LdT resistance, a switch to, or addition of TDF may be the preferred option<sup>[20]</sup>. The CLV resistance rate is approximately 20% and 30% in the 2<sup>nd</sup> and 3<sup>rd</sup> years of treatment, respectively<sup>[30,80]</sup>. According to clinical experience with LMV-resistant CHB patients, the general principles for treating LdT or CLV resistance are similar to those of LMV-resistance<sup>[13,17]</sup>.

### ADV and TDF resistance

ADV and TDF are nucleotide analogues. rtN236T and rtA181T/V are the primary mutations giving rise to ADV resistance<sup>[26,81]</sup>. The cumulative incidence of genotypic resistance to ADV is reported to be 0%, 3%, 11%, 18%, and 29% at the end of each successive year of therapy in HBeAg-negative patients<sup>[26]</sup>. As previously mentioned, ADV monotherapy in LMV-resistant patients leads to a 5-year cumulative ADV resistance of 65.6%<sup>[57]</sup>. No TDF resistance has been reported during treatment periods up to 3 years in length<sup>[82]</sup>. However, rtA181T/V and rtN236T mutations confer intermediate resistance to TDF<sup>[9]</sup>. Among patients who have the rtA181T/V and/or rtN236T substitutions, viral suppression by TDF is reduced<sup>[71,83]</sup>. rtA194T can decrease susceptibility to TDF by 10-fold in the presence of rtL180M+rtM204V mutations, according to a case study of a patient with HBV and HIV co-infection<sup>[72]</sup>.

TDF significantly suppresses HBV replication in patients exhibiting LMV resistance who have failed to respond adequately to ADV, and in patients who are resistant to both LMV and ADV<sup>[83]</sup>. TDF alone or TDF plus emtricitabine (FTC) are similarly effective in ADV-treated CHB patients<sup>[84,85]</sup>. However, reduced sensitivity to TDF has been demonstrated in ADV-resistant HBV infections, indicating potential cross-resistance<sup>[71]</sup>. The addition of

FTC led to a further decrease in serum HBV DNA levels in patients exhibiting ADV resistance and a suboptimal response to TDF therapy<sup>[86]</sup>. When LMV-TDF combination therapy was given to CHB patients who had previously failed to respond to LMV and subsequent ADV therapy, 64% achieved an undetectable level of HBV DNA after 96 wk of treatment<sup>[83]</sup>.

ETV does not share cross resistance with ADV<sup>[56]</sup>. ETV has been shown to be effective against both rtA181T/V and rtN236T mutant HBV strains<sup>[32,43,87,88]</sup>. Switching to ETV monotherapy (1 mg daily) is initially effective in LMV-resistant patients (rtM204I/V), but the subsequent risk of ETV resistance is high<sup>[27]</sup>. Another study also showed increased ETV resistance risk with ETV monotherapy switching for ADV resistance<sup>[89]</sup>. In contrast, ADV-ETV combination therapy has been shown to be a better option<sup>[13,90]</sup>. The ETV-TDF combination can also be considered for multidrug-resistant HBV infections that include ADV resistance<sup>[13]</sup>.

Although rtN236T mutants remain sensitive to LMV, the rtA181T/V mutant exhibits reduced susceptibility to LMV<sup>[56]</sup>. Therefore, LMV-ADV combination therapy is recommended. For similar reasons, LdT or CLV monotherapy is not recommended for the rtA181T/V mutant in order to avoid cross-resistance<sup>[13,56]</sup>, and add-on therapy is preferred<sup>[13,17]</sup>. One study showed that the LdT and ADV combination can be a good option for ADV resistance<sup>[91]</sup>.

To date, there are no reports of resistance to TDF among patients with CHB mono-infection<sup>[31,92-94]</sup>. An *in vitro* study found that replication of the rtA194T mutant was suppressed effectively by ETV and intermediately by LdT<sup>[95]</sup>. The clinical impact of the rtA194T mutation is still unknown<sup>[92,96]</sup>. One recent report suggested that rtP177G and rtF249A mutants also reduce susceptibility to TDF<sup>[97]</sup>. In cases of confirmed TDF resistance, an add-on combination with a nucleoside analogue is preferred, while a switch to ETV may be sufficient if the patient had no prior LMV resistance<sup>[16]</sup>.

### ETV resistance

ETV is cyclopentene, a type of nucleoside analogue. ETV resistance develops *via* a two-hit mechanism, as previously described. Since this presents a high genetic barrier to ETV resistance, the resistance rate in treatment-naïve subjects is very low. In studies of the long-term follow-up of ETV treatment in CHB patients, the cumulative probability of ETV resistance was reportedly 1.2%-1.5% after 5 years of ETV treatment. However, a resistance rate as high as 51% has been reported after 5 years of treatment in LMV-refractory subjects<sup>[27,28,88]</sup>.

ETV-resistant HBV maintains susceptibility to ADV, which could be considered an initial treatment option, and a clinical case has indicated that ADV can be effective in suppressing the ETV-resistant mutant<sup>[98,99]</sup>. Adding ADV to ETV would be more reasonable for reducing ADV resistance and improving antiviral efficacy<sup>[13,90,100]</sup>. Combination therapy of ADV plus LMV could be con-



sidered as another option, since a small study showed that the short-term efficacy of this combination was similar to that of combination therapy of ADV plus ETV<sup>[13]</sup>. Although TDF has not been fully evaluated in the treatment of ETV resistance, it is expected to be very effective since TDF does not show cross-resistance to ETV *in vitro* and has excellent potency<sup>[71]</sup>. Therefore, switching to or adding TDF may be preferred for addressing ETV resistance<sup>[20]</sup>.

### Multidrug resistance

Multidrug resistance (MDR) is defined as resistance to two or more classes of antiviral drugs<sup>[13]</sup>. The emergence of MDR is increasing and has raised serious concerns regarding antiviral therapy because it limits the selection of appropriate therapy<sup>[45]</sup>. Sequential monotherapy is associated with the development of MDR<sup>[22,98,101,102]</sup>. In these situations, pre-existing antiviral resistant mutations may reappear and become co-localized with newly developed resistant mutations in the same viral genome<sup>[98]</sup>. The development of a triple-drug resistant (LMV, ADV, and ETV) HBV strain has been reported in LMV- and ADV-resistant patients after sequential ETV administration<sup>[103]</sup>.

In patients with MDR, genotypic resistance testing is very useful, and a combination of a nucleoside and a nucleotide should be employed<sup>[16]</sup>. TDF-ETV combination therapy can be considered in case of resistance to both LMV and ADV<sup>[17,20]</sup>. A recent study showed that rescue therapy with TDF plus ETV achieved undetectable HBV DNA after a median of 6 mo in 51 (89.5%) of 57 patients, in whom nucleoside/nucleotide analogue therapy (LMV+ADV, ETV+ADV, or TDF+LMV) had failed and who had multidrug-resistant rtA181T/V or other MDR mutations<sup>[104]</sup>.

If TDF is not available, combination therapy with ADV plus ETV is another option<sup>[13,90,100,105]</sup>. A recently published study showed that the ADV plus ETV combination is superior to the LMV-ADV combination or to ETV monotherapy for multidrug-resistant CHB patients<sup>[106]</sup>. On the other hand, the LMV plus ADV combination is usually insufficient for treatment due to low antiviral potency<sup>[45]</sup>.

If resistant mutations to LMV, ETV, and ADV are detected in the same patient, combination therapy with TDF plus ETV may be the best option<sup>[13]</sup>.

### CONCLUSION AND PERSPECTIVES

Although ETV and TDF are powerful antiviral drugs with a high barrier to resistance, treatment failure due to resistance remains possible, especially among treatment-experienced CHB patients. The mechanisms of drug resistance have been evaluated, and many relevant diagnostic tools have been developed. Current CHB treatment guidelines suggest practical and effective strategies for resistance. However, there are still several treatment-related issues that need further evaluation. First, new diagnostic tools and *in vitro* phenotypic validation methods

for drug-resistant HBV need to be developed that can identify mutations more efficiently, with greater accuracy, and with reduced cost. Second, the role of IFN must be evaluated further. A few studies suggest the possibility of PegIFN as a treatment option for LMV-resistant CHB patients. The efficacy of PegIFN in patients with resistance to other agents such as LdT, CLV, ADV, ETV, TDF, and MDR is not yet known. New IFN agents are also under development for hepatitis C virus treatment. These must also be studied for use in drug-resistant HBV infection. Third, the efficacy of new HBV agents in resistance treatment should be evaluated. For example, LB80830 is a new acyclic nucleotide phosphonate with chemistry similar to ADV and TDF. In a phase II, open-label, multicenter study among 65 LMV-resistant patients, a dose-dependent reduction in HBV DNA of up to -3.92 log copies/mL was observed at week 12 at the optimal dose of 150 mg daily<sup>[107]</sup>. These findings clearly need further evaluation. Finally, treatment strategies for MDR should be established. Most guidelines suggest combination therapies of nucleoside and nucleotide analogues, and the ETV plus TDF combination is preferred. However, clinical data on long-term efficacy is still lacking. Furthermore, there are patients who have experienced treatment failure without a known or confirmed genotypic resistance. No treatment guidelines have been suggested for these patients. If more sensitive diagnostic tools are developed, the novel combinations of drug-resistant mutations may be diagnosed in these patients, which can give more treatment options for these patients.

### ACKNOWLEDGMENTS

We appreciate the valuable comments of Dr. SP Hong (GeneMatrix, South Korea).

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**P- Reviewers:** Abenavoli L, Al Olaby R, Ampuero J, Gatselis NK, Ikura Y, Komatsu H, Liula J, Tijera MFH, Wong GLH, Yonem O  
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ISSN 1007-9327



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