

Microarray for Hepatitis B Virus Genotyping and Detection of 994 Mutations along the Genome^{∇†}

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Genome analysis of hepatitis B virus (HBV) in patient sera is helpful for monitoring treatment. We developed an improved version of a DNA microarray to identify HBV genotypes and to detect mutations of interest in the S, Pol, Core, and X genes. It includes an automated software analysis of fluorescence values for simpler, more robust data interpretation. In this version, probes were added to identify genotype H, to analyze 155 additional positions, and to detect 561 additional polymorphisms. Sequences were added to the alignments to resolve hybridization problems due to natural polymorphisms in the vicinity of important codons. The duplex PCR protocol allowed whole-genome analysis in a single tube. An alternative nested-PCR protocol allowed genotyping and mutations in S and reverse transcriptase (rt) genes in patients with low viral loads, as demonstrated in patients with less than 400 HBV genome copies/ml. Reproducibility was high, with variation coefficients lower than 3%. Only 0.57% of 20,771 codons from 253 samples could not be identified. The concordance with Sanger sequencing for the identification of codons improved from 92.8% to 95.7% with the improved version. Concordance was higher than 91% for codons associated with resistance to lamivudine, emtricitabine, telbivudine, famciclovir, entecavir, and tenofovir with vaccine escape and for pre-Core mutants. Concordance was lower for adefovir resistance mutations (68.6%) and mutations in the basal core promoter (60.3%), probably because hybridization efficiency was affected by the low GC content of the probes. A concordance of 93.7% with sequencing for genotype identification was observed in 190 specimens, lower than that obtained with the first version, possibly due to mixed virus populations.

According to the WHO, hepatitis B virus (HBV) has infected more than 2 billion people worldwide, and more than 350 million people suffer from chronic hepatitis B (<http://www.who.int/mediacentre/factsheets/fs204>). The treatment of chronic hepatitis B is difficult, and complete cure is still rare (7). Polymorphisms in the viral genome have important impacts on disease prevention, natural history, and treatment, and laboratory methods for their detection are important tools for clinicians, epidemiologists, and researchers.

Eight viral genotypes have been described, named A to H, differing by at least 8% on the whole genome or by 4% in the S gene (1). They have different geographical prevalences (13, 21). Recombinants between genotypes and coinfection with different genotypes have been described (9, 12, 29, 32). The genotype may influence the treatment response (4, 11), disease evolution, and coinfection with other parenterally transmitted viruses, i.e., HIV, hepatitis C virus (HCV), and hepatitis D virus (HDV) (12).

Mutations in the precore (pre-C) gene are more frequent in patients with persistent viremia and severe disease (3). Mutations in the basal core promoter (BCP) have been associated with fulminant hepatitis and severe disease (10, 22, 26). In a recent meta-analysis, Liu et al. (15) showed that mutations in the pre-S region, as well as in enhancer II of the core (C) gene and BCP, both overlapping with the X gene, are associated with hepatocarcinoma (HCC). These mutations may be useful biomarkers to predict the outcome of the disease and evolution toward HCC. Mutations in the X gene regulate viral infectivity and may induce hepatocarcinogenesis (19, 20, 33). Mutations in the pre-S1 and pre-S2 regions can induce inhibition of viral secretion (12), and mutations in the core gene can affect HBc antigenicity (12, 38), resulting in escape from host surveillance.

In addition to alpha interferon, antiviral molecules targeting the reverse transcriptase (rt) activity encoded by the Pol (P) gene are now available for the treatment of hepatitis B: lamivudine and, more recently, adefovir, entecavir, tenofovir, and emtricitabine. The emergence of mutant strains resistant to these drugs has been described (16, 27, 37), associated with mutations that compensate for loss of viral fitness (28). Lamivudine should not be used alone, as resistant strains are observed in 70% of patients after 4 years of treatment (6). Recent studies recommended the standardization of treatment strategies according to patient profiles and the implementation of mutant detection assays (17).

Mutations associated with vaccine escape and immunotherapy failure have been described in the S gene, especially in the region coding for the *a* determinant of HBsAg (5, 12, 36). Mutations in the gene have also been associated with

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occult hepatitis, although the mechanisms of action are not yet clear (8).

Sequencing remains the gold standard for molecular characterization. However, its interpretation can be influenced by several biases and requires specific skills. At least three different runs are needed to get the whole 3.2-kb HBV sequence. Line probe assays (LiPA [Innogenetics, Gent, Belgium]) are easy to perform, although at least three LiPA strips are required to get information on genotypes (A to G only), 3 mutations in BCP/pre-C, and 6 mutations in rt (18).

In this work, we describe a diagnostic tool for HBV genotyping and mutation detection in a single experiment with automated software analysis. It is an improved version of an assay that was described previously (24, 34) and was designed to improve nucleotide identification and to detect an extended list of mutants and the recently identified H genotype.

MATERIALS AND METHODS

Microarray design. The Affymetrix *in situ* synthesis technology (Affymetrix) was used to design a microarray with 520,327 different probes allocated to the detection of polymorphisms/mutations in the HBV genome. Individual probes are 20-mer oligonucleotides spotted individually on 11- μ m-wide squares. An alignment of 1,454 HBV sequences was created in order to identify natural polymorphisms and to design the probes. We retrieved 986 sequences from GenBank (<http://www.ncbi.nlm.nih.gov/GenBank/>) and 586 from the private database of INSERM U871 (Lyon, France). The genotype A sequence X02763 was chosen as a reference for the alignment. The GenBank accession numbers of the other chosen reference sequences for each genotype are as follows: B, D00329; C, X01587; D, J02203; E, X75657; F, X75658; G, AF160501; and H, AY090454. A phylogenetic tree was created by combining PHYLIP, DNADIST (F84 distance), and NEIGHBOR software that identified 816 genomic positions as relevant for discriminating genotypes. A 4L tiling strategy was retained for exhaustive resequencing, using, for each position, a set of four probes differing only at position 12, where A, C, G, or T is present. To take into account the genetic variability of the virus, several sets of four probes have usually been designed to identify a single position. Each set, referred to as a tile, includes polymorphisms that have been detected in the vicinity of the position of interest. We used the standard nomenclature of Stuyver et al. (31) for codon numbering in the rt region of the Pol gene. Mutants in BCP are designated according to their genomic nucleotide positions, which start with the 4th nucleotide of the (hypothetical) EcoRI site.

Samples. Samples were provided by Azienda Ospedaliera (Pisa, Italy), the Intercollegiate Faculty of Biotechnology (Gdansk, Poland), and CEPEN-IPEP ATRO (Porto Velho, Brazil) and were characterized by Sanger sequencing covering the pre-S1, pre-S2, S, rt, BCP, pre-C, C, and X regions. Sequences were aligned for codon identification and genotype determination.

Thirty-seven plasmids encoding rare rt mutations, as well as artificial mixtures of mutants, were provided by INSERM U871, Lyon, France. These plasmids (derived from plasmid pTriEXModHBV) contain 1.1 genomes of either wild-type (WT) HBV or the same genome engineered to introduce the mutations using the Quick-Change kit (Stratagene, La Jolla, CA) (2).

DNA extraction, amplification, labeling, and hybridization. DNA was extracted from sera and amplified in a duplex PCR as previously described (34). If the two bands with expected sizes of 1.5 and 1.7 kbp were not detected by agarose gel electrophoresis, an alternative nested-PCR protocol generating a 741-bp amplicon in rt/S from the 1.7-kbp amplicon was used with the following primers: 5'-AAGGTATGTTGCCCGTTTGTC-3' and 5'-GGGTTGCGTCAGCAAACACT-3'. The amplification mixture was composed of MgCl₂ buffer, 2 mM; deoxynucleoside triphosphates (dNTPs), 0.3 mM; and Roche Fast-Start *Taq* Pol enzyme, 2 U. Amplification required 40 cycles at 93°C for 30 s, 48°C for 30 s, and 68°C for 1 min, finishing with 68°C for 7 min. Labeling and cleavage of PCR fragments were done by successively adding 5 μ l of RNase-free water, 5 μ l of PCR product, 5 μ l of M bis-biotin-phenylmethyl-diazomethyl (bis-bioPDAM) (bioMérieux, Marcy l'Etoile, France), and 5 μ l of 20 mM HCl and incubating them for 25 min at 95°C. The labeled fragments were purified, hybridized on the microarray, and stained as described previously (37). The microarrays were immediately scanned at 570 nm using the GS3000 scanner and GCOS software (Affymetrix, Santa Clara, CA).

Data interpretation. In a set of 4 probes designed for a given nucleotide, the signal of a single probe is considered significant and is retained if it is at least 1.2 times higher than the other three after subtraction of the background signal. There is no need for a specific internal calibrator. Data interpretation is made using the average fluorescence intensity of all retained probes, identified by their names and the corresponding position of the interrogated base on the genome. The DNAEM software (bioMérieux, Marcy-l'Etoile, France) was used to run a computer engine to translate fluorescence intensities into sequence information by automatically selecting the most probable nucleotide at each interrogated position. The parameters of the computer engine were optimized to provide the highest global concordance with Sanger sequencing on a panel of samples. The software performs two distinct analyses: mutation identification and genotype determination. For mutation detection in coding regions, the retained amino acid is the one with the highest score after assembly of the 3 bases of a given codon. Genotype identification scores (Id scores) were obtained by comparing the experimental data obtained with a sample to the reference sequence of each genotype (from A to H) at 816 positions selected in the genome alignments because they allowed the highest discrimination between genotypes. The Id score for each genotype was the percentage of concordant bases between the reference sequence and the test sequence. The retained genotype was the one with the highest Id score. A synthetic report was generated containing sample information, genotyping results, and mutations detected for the sample. The whole process from DNA extraction to interpretation report can be done within a single working day.

RESULTS

Probes were designed to detect 994 mutants located at 298 genomic positions along the genome in the S, C, P, and X genes (Table 1). The complete list of mutations is available at <http://www.gabriel-network.org/?-publications->. Compared to the previous version of the assay (34), this version contains probes for the analysis of 155 new positions and the detection of 561 additional polymorphisms. Insertions and deletions that were included in the old version were removed because their reliable detection is not possible using the current software version. In addition, sequences of the newly described genotype H were introduced into the alignment, and corresponding probes were added to the array.

Analytical and reproducibility performance. The average signal-to-background ratio of a typical experiment at 66 positions in the rt region was estimated to be approximately 50. As shown by agarose gel electrophoresis, the duplex PCR protocol generated the expected bands from 62% of the samples (118 out of the 190 samples used to evaluate genotyping performances; see below). When this was not the case, especially in samples with less than 5,000 copies of the HBV genome/ml, we used an alternative nested-PCR protocol that allowed genotyping when the viral load was low, including in 6 samples with fewer than 400 copies/ml (Fig. 1). Furthermore, this protocol allows the identification of the most important mutations in the rt and S regions.

Reproducibility was evaluated by testing two samples (one genotype A and one genotype D). Each specimen was tested 16 times by two operators using two batches of reagents. The coefficients of variation on the fluorescent signals obtained with all probes varied between 9 and 10% (data not shown). The coefficients of variation were not higher than 3% for genotype Id scores. We observed an impact of the operator within the series obtained with the genotype A sample, resulting in a significantly higher coefficient of variation (2.6%) than was obtained with the other sample. Gel electrophoresis showed that this impact was due to lower amplification efficiency in one series by one operator (data not shown).

TABLE 1. Numbers of analyzed positions and polymorphisms

ORF ^a	Coded protein or promoter	No. of analyzed codons		No. of probed polymorphisms	
		Previous version	Improved version	Previous version	Improved version
P	Polymerase terminal protein (tp)	2	0	2 (deletions)	0
	Polymerase spacer (sp)	2	2	10	10
	Polymerase reverse transcriptase (rt)	26	66	70	197
S	Envelope (PreS1)	1	3	4	6
	Envelope (PreS2)	2	6	6	16
	Envelope (S)	54	98	150 (+3 deletions)	339
	Basal core promoter (BCP nucleotides)	15	33	38 (+16 deletions and insertions)	112
	PreCore (preC)	12	14	35 (+4 deletions)	55
	Core (C)	11	21	27 (+1 insertion and 1 deletion)	115
X	X	18	55	81 (+1 deletion)	144
Total		143	298	433	994

^a ORF, open reading frame.

Genotyping performance. One hundred ninety samples were used to evaluate genotyping performance. The viral loads were available for 142 of them. Figure 1 shows that samples containing less than 400 genome copies/ml could be analyzed and provided concordant results between the microarray and the reference technique. The whole duplex PCR protocol could amplify 118 samples, and the rt/S PCR protocol was used to amplify the other 72. A genotype was identified for all samples. Table 2 shows that mean Id scores varied between 89.3 (genotype A) and 55.2 (genotype F). The mean ratio between the highest Id score and the one immediately following was at least 1.17, confirming the discrimination capacity of the assay. Sequencing and the microarray gave concordant results for 172 of the 183 samples with a single expected genotype (94.0%). Although the genotyping algorithm is currently not optimized to identify multiple genotypes, in 6 out of 7 samples with a mixture of genotypes, the assay detected one of the two expected genotypes. The overall concordance was 93.7%. Discrepant results were observed for 12 samples, including one sample with a mixture of genotypes, most of them identified as genotype A by sequencing. In 4 out of these 12 samples, the Id score was low (below 60). Nine out of 12 discrepancies were observed with the whole-genome PCR protocol and 3/12 with the rt/S 740-bp nested-PCR protocol, suggesting that reducing the size of the segment used for genotyping had no significant impact on the quality of results. The initial microarray result was confirmed upon retesting of all 12 samples. For 9/12 dis-

crepant samples, a PCR product was available for retesting by sequencing, alignment, and BLAST on the NCBI website in rt/S. The initial sequencing result was confirmed in 7 out of 9 samples. In the other two samples, retesting did not confirm the initial sequencing result or the microarray result.

Mutant detection in mixed populations. To evaluate the capacity of the reagent to detect mixed populations of viruses and emergence of resistance mutations, we tested noninfected plasma spiked with different ratios of 2 plasmids with either a wild-type HBV genome or mutant codons at positions rt180 and rt204 (2). The total plasmid concentrations in these samples varied from 10e3 to 10e6 copies/ml. Table 3 shows that the results were different according to the position. Depending on the viral load, the highest identification score was obtained for the mutant rtL180M when it represented 50 to 70% of the mixture. At position rt204, the assay detected the valine mutant when it represented as little as 20% of the mixture, whatever the viral load. In the latter case, the microarray had a bias to select viruses with a valine at position rt204.

TABLE 2. Genotyping performance

Genotype (sequencing)	No. of samples	Mean Id score	Highest/second-highest Id score ratio	Sensitivity (%) ^a	Specificity (%) ^b
A	54	89.3	1.2	87	99.3
B	17	72.1	1.24	94.1	100
C	15	70.2	1.17	93.3	96
D	54	70.3	1.26	96.3	98.5
E	23	61.5	1.23	100	99.4
F	12	55.2	1.26	100	100
G	1	70.2	1.63	100	99.5
H	7	55.2	1.28	100	100
A+C	3	84.6 ^c	1.13	66.7	100
A+G	4	48.9 ^d	1.25	100	100

^a Sensitivity was calculated as the percentage of samples referenced as a given genotype by sequencing that were identified as the same genotype by the array.

^b Specificity was calculated as the percentage of samples identified as a given genotype by the array and a different genotype by sequencing.

^c Detected as A or C.

^d Detected as A or G.

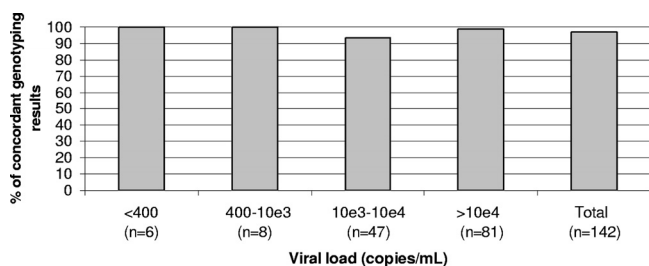


FIG. 1. Concordance between sequencing and the microarray for genotyping according to viral load.

TABLE 3. Detection of wild-type and mutant mixtures by the microarray

Ratio of <i>rt180/rt204mt</i> vs <i>rt180/rt204wt</i>	Amino acid identified at a total plasmid concentration (copies/ml) of: ^a							
	1×10^3		1×10^4		1×10^6			
0	rt180L	rt204M	rt180L	rt204M	rt180L	rt204M	rt180L	rt204M
0.1	rt180L	rt204M	rt180L	rt204M	rt180L	rt204M	rt180L	rt204M
0.2	rt180L	rt204V	rt180L	rt204V	rt180L	rt204V	rt180L	rt204V
0.3	rt180L	rt204V	rt180L	rt204V	rt180L	rt204V	rt180L	rt204V
0.4	rt180L	rt204V	rt180L	rt204V	rt180L	rt204V	rt180L	rt204V
0.5	rt180M	rt204V	rt180L	rt204V	rt180L	rt204V	rt180L	rt204V
0.6	rt180M	rt204V	rt180L	rt204V	rt180L	rt204V	rt180M	rt204V
0.7	rt180M	rt204V	rt180M	rt204V	rt180M	rt204V	rt180M	rt204V
0.8	rt180M	rt204V	rt180M	rt204V	rt180M	rt204V	rt180M	rt204V
0.9	rt180M	rt204V	rt180M	rt204V	rt180M	rt204V	rt180M	rt204V
1	rt180M	rt204V	rt180M	rt204V	rt180M	rt204V	rt180M	rt204V

^a Two plasmids with the whole HBV genome were constructed: *rt180/rt204wt*, with leucine and methionine at positions rt180 and rt204, respectively, and *rt180/rt204mt*, with methionine and valine at positions rt180 and rt204, respectively. Mixtures of the two plasmids were assembled at different total plasmid concentrations and ratios of *rt180/rt204mt* versus *rt180/rt204wt*. The italicized letters indicate the amino acids that were identified by the microarray.

Mutation detection. A panel of 253 samples was used to analyze the performance of the microarray for the identification of nucleotide and amino acid changes in HBV genomes. A total of 20,771 codons were resequenced with the microarray in the sample panel. Considering that 298 codons are resequenced by the microarray for each sample, this assay can potentially detect changes at an additional 54,623 positions. Results were considered indeterminate by the microarray when no amino acid could be identified, i.e., when no probe in the set designed to identify each nucleotide of a codon generated a fluorescent signal significantly higher than the other three (0.57% of 20,771 codons, including 63 indeterminate results at position rt236) or when a sample sequence contained an unexpected polymorphism that was not included in the design of the probes. The observed indeterminate rates were 1.2 and 7.1%, respectively, for sequencing and the microarray.

The percentage of concordant results between the two techniques was 95.7%. This percentage was 92.8% for the previous version of the array (34). For the rt (66 positions), S (98 positions), and pre-C (14 positions) regions, the concordances were, respectively, 96.5%, 97.9%, and 93.6%. These percentages were 94.1%, 92.0%, and 94.6% with the previous version. The concordance percentages were 98.6% for X (55 positions), 95.4% for C (21 positions), and 70.8% for pre-S2 (6 positions). No reference results were available for pre-S1. BCP positions were not included in this analysis, since, although it overlaps the X reading frame, by itself it is noncoding. Due to the large number of codons analyzed for mutations, every sample tested produced at least one discrepancy. Since it was not feasible to retest every sample, we opted not to retest samples producing discrepant results. As the assay is able to identify 994 mutations, it was not possible to assemble a panel of samples covering all of them. We established a short list of positions with the highest relevance for HBV biology and disease monitoring (10, 23, 37). The results obtained at these positions are presented in Table 4 and detailed below.

Lamivudine, emtricitabine, telbivudine, and famciclovir resistance. At positions rt169, rt173, rt180, and rt204, sequencing and the microarray agreed on 596 codons (519 wildtype and 77 mutants) out of 656 (90.9%). The indeterminate rates were 5.3 and 1.7% for the microarray and sequencing, respectively. The microarray detected 10 additional mutants, 8 of them identi-

fied as wild type and 2 as indeterminate by sequencing. Sequencing detected 21 additional mutants, 4 of them identified as wild type and 17 as indeterminate by the microarray (most of them at position rt180). For codon rt173, which was also analyzed by Tran et al., (34), the concordance percentage increased from 96.1 to 96.3%. For position rt204, which was found to be difficult in the previous test, this percentage increased from 60.8 to 82.3%. Conversely, the concordance was higher with the previous version at position rt180 (93.5% versus 81.7%), reflecting the higher number of indeterminate results for this codon with the improved version.

Adefovir resistance. At positions rt181 and rt236, the two techniques agreed on 197 codons (181 wild type and 16 mutants) out of 287 (68.6%). The indeterminate rates were 30.3 and 0.3% for the microarray and sequencing, respectively. The microarray detected 2 additional mutants identified as wild type by sequencing, whereas sequencing detected 9 additional mutants, all of them indeterminate with the microarray. At position rt236, we observed that the microarray-based assay correctly detected codons with a C at the third position (either the wild-type AAC [Asn] or the mutant ACC [Thr]) but was unable to differentiate between the codons with a T at the third position (wild-type AAT [Asn] and mutant ACT [Thr]). This resulted in 64 indeterminate results (no amino acid identified) and may be related to the low GC content in this region of the HBV genome, which may lower hybridization efficiency (see Discussion).

Entecavir resistance. At positions rt184, rt202, and rt250, the two techniques agreed on 416 codons (414 wild type and 2 mutants) out of 441 (93.9%). The indeterminate rates were 2.3 and 0.7%, respectively, for the microarray and sequencing. The microarray detected 14 additional mutants (12 wild type and 2 indeterminate by sequencing). Sequencing detected 4 additional mutants (2 wild type and 2 indeterminate by microarray).

Tenofovir resistance. At position rt194, the concordance between the two techniques was 100% for the detection of the Ala wild-type amino acid.

Globally, in the rt region, microarray and sequencing together detected 109 mutants. The microarray detected 26 additional mutants (85% of them wild type by sequencing),

efficacy. It will also be useful to rapidly detect a source of contamination or the spread of viral strains that resist treatment or vaccination. Finally, it will help researchers to gain insights into pathology mechanisms. The microarray combines a PCR approach that allows the amplification of the whole virus genome in a single tube with a high multidetection capacity, providing significant advantages over alternative techniques. Classical Sanger sequencing requires at least 5 amplification reactions to cover the same number of genome positions. Line probe assays can detect only a limited number of mutations. Finally, the improved version includes new software and computer engine versions that allow an automated analysis of mutations. This improvement avoids human errors during the selection of tiles in a list, as in the first version of the assay. It is also an improvement over Sanger sequencing, which requires human reading and interpretation of electropherograms.

Tran et al., (34) have reported that natural polymorphisms, perhaps underrepresented in the sequence alignments, in the vicinity of interrogated codons may have an impact on the identification capacity of the microarray assay. This was especially the case at positions rt204 and s145. Probes with the variant sequences were added to solve this problem, and they improved performance significantly at both positions. On the other hand, the improved assay performed less well for the detection of polymorphisms at position rt180: the observed concordance with sequencing was reduced from 93.5% to 82.3%. At rt180, the array often detects an arginine, whereas sequencing identifies the expected wild-type (Leu) or mutant (Met) codon. This is probably due to the fact that Arg and Leu can be encoded by an unusually large number of codons (CGN and AGR for Arg; CTN and TTR for Leu). Residue rt180L is usually encoded by a CTC codon. Through G/T wobble base pairing, the CGC codon for Arg can stably hybridize to the CTC codon for Leu. Similarly, the AGG codon for Arg can hybridize to the ATG codon for Met. This problem can probably be overcome by analyzing the fluorescence values for probes containing the Arg CGC and AGG codons.

Overall, the concordance between sequencing and the microarray improved from 92.8% (tested on 11,335 codons) to 95.7% (tested on 20,771 codons) between the two versions of the assay.

Although the indeterminate rate was lower for sequencing on our panel, it may be underestimated, as we included mostly specimens with available reference sequence data. We do not know how many samples had an indeterminate or wrong result among all those initially analyzed by sequencing. The Sanger sequencing method has significant error rates. For example, an error rate of approximately 7% has been reported for Sanger sequencing of human diploid DNA (25, 30).

Indeterminate microarray results are more frequent at some positions (rt180, rt181, rt236, BCP1762, BCP1764, and s120), probably resulting from a weak hybridization efficiency that does not allow one probe to be distinguished among the four or generates an unexpected result. A low GC content is known to reduce hybridization efficiency. This is the case at positions rt236, BCP1762, and BCP1764, where the percentage of guanine and cytosine bases (%GC;

Chargaff coefficient) is around 30% in more than two-thirds of the designed probes whereas this percentage is close to 50% in the rest of the genome. G/T wobble base pairing may also affect the results. To reduce the possibility of wrong results, we established a cutoff fluorescence value below which results are automatically marked as indeterminate. A possible solution to overcome this difficulty and improve performance at these positions in a future version of the microarray would be to synthesize longer probes (25-mer), at least in areas with low GC content. Although not sensitive to hybridization problems, sequencing also has technical problems linked to the enzymes, which are especially affected by single-nucleotide stretches. Cross-hybridizations generating an indeterminate or a false result due to secondary structures, palindromes, or nonspecific binding to probes with similar sequences may also occur. However, looking for such sequences by BLAST was not successful (data not shown).

Multiple viruses with different sequences may also be the origin of discrepant results between sequencing and the microarray. Sequencing may preferentially detect one virus of the mixture while the microarray detects another. We observed that the microarray preferentially detected Val compared to Met at position rt204 in a mixture of plasmids designed to simulate a mixture of viruses (Table 2). This is probably due to the fact that the Val mutation usually creates a GTG codon, and hybridization to this probe is intrinsically superior to hybridization with a probe containing the Met ATG codon. However, we have no explanation as to why 12 samples of our panel have a Val (codons GTN) at that position whereas sequencing detects an isoleucine (codons ATY) (Table 4).

A major obstacle to the use of this tool for routine clinical diagnosis applications is the difficulty of assembling specimen panels to validate its sensitivity and specificity for the detection of all claimed mutations. However, this is also the case for sequencing, for which performance also varies according to the codons. Repeated sequences (35) and insertions and deletions longer than 5 bp (36) were not encountered in the panel used for our study.

A limitation of our study regarding genotyping determination is that only a few specimens have been tested for genotypes G and H. However, this is representative of the prevalence of these subtypes worldwide (13, 21).

The concordance between sequencing and the microarray observed in this study for genotyping (94% on a panel of 183 samples) is lower than that reported by Tran et al. (34) and Pas et al. (24) using the previous version of the microarray (98% and 97.5%, respectively). This slight variation may simply be due to sampling.

There is no explanation for the 12 discrepant results observed between sequencing and the microarray in this study.

The existence of viruses that are recombinant between different genotypes has been reported (9, 12, 29, 32). Sequencing usually targets only one genomic region (rt/S or pre-C/BCP/C) and may miss recombinant viruses that include sequences corresponding to another genotype in other genomic regions. On the other hand, the microarray uses 816 positions along the whole HBV genome and theoretically may be able to detect

recombinant viruses, although we did not use specimens containing such viruses in our evaluation.

The presence of several viruses with different genotypes, due to multiple HBV infections, may also explain differences between the two techniques. Sequencing and the microarray may preferentially identify only one of the viruses.

We believe that the algorithm we propose for genome amplification makes the assay valuable for the intended clinical use. It allows full analysis of most specimens with more than 5,000 genome copies/ml. For those with lower viral loads, down to approximately 400 genome copies/ml, genotype determination and detection of most resistance mutations is still possible. Notably, all specimens with a viral load below 1,000 copies/ml could be genotyped, whereas 2/3 of those specimens could not be with the previous version of the assay (34). Recent recommendations of the European Association for the Study of the Liver state that under interferon therapy, virological response is effective below 2,000 IU/ml (approximately 10,000 copies of the HBV genome/ml), and under nucleotide therapy, virological breakthrough is considered to have occurred if the viral load increases by more than 1,000 IU/ml (or 5,000 copies/ml) above the nadir (7).

Another limitation of this study is the lack of clinical information on the patients from whom samples were taken. However, it was a comparison of the microarray assay and sequencing on a panel of stored samples, and validation of the clinical utility of the assay requires additional work.

Our work shows that the microarray technology has characteristics and performance that make it a valuable tool for clinical, epidemiological, and research applications regarding hepatitis B virus. This technology has been used to analyze the genome of the virus in cohorts of patients with dual HIV-HBV infections (14) and in patients from sub-Saharan Africa (35). The present version of the assay implements several improvements, and although problems linked to the low GC content observed at some positions reduce the performance for the diagnosis of resistance to adefovir, as well as mutations in the BCP, its main advantage compared to Sanger sequencing is that it can provide exhaustive information at multiple positions along the whole 3.2-kb genome in a single reaction.

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