Revision of Interpretation Criteria of the INNO-LiPA HBV Genotyping Assay

We read with great interest the recent article published by Mercier et al. (4) on the overestimation of mixed infections as a result of erroneous genotype H detection by use of the new version of the INNO-LiPA HBV genotyping assay. In this study, the INNO-LiPA assay identified 28 mixed infections in a population of 200 HBsAg- and anti-HBcAg-hepatitis B virus (HBV)-DNA-positive French blood donors. Nine of the 28 mixed infections included genotype H as part of a double or triple infection. Sequencing after molecular cloning did not confirm the presence of genotype H in these samples; therefore, the authors concluded that the high proportion of genotype H in these samples is restricted to South and Central America (1) and that very few coinfections with genotype H are described in the literature. Conversely, the authors concluded that the high proportion of genotype H in these samples; therefore, the authors concluded that the high proportion of genotype H in these samples is restricted to South and Central America (1) and that very few coinfections with genotype H are described in the literature. Sánchez et al. reported a G/H coinfection in 6 out of 25 HBV-positive Mexican men who have sex with men (MSM) (5). As described by the authors, they used the INNO-LiPA system according to the manufacturer’s instructions and the hybridization patterns were interpreted according to the chart provided. For cases of mixed infections, guidelines for interpretation of patterns not present on the chart are presented in the package insert. It is mentioned that a single reaction corresponding to line 11 (representing one D probe) and a single reaction corresponding to line 15 (representing one F probe) should be interpreted as representing genotype H. For cases in which reactions corresponding to lines 10, 11, and 15 are present, no conclusion regarding the presence or absence of genotype H can be taken. For such cases, we refer to the following guideline in the current kit insert: “if multiple genotype specific lines show for one genotype, together with a positive single line for a second genotype, this should be interpreted as a single genotype.” If this guideline is followed, line patterns 10, 11, and 15 should be interpreted as representing genotype D and not genotype D/H, according to the authors. When line 11, line 14, and line 15 are present, this should be interpreted as representing genotype F and not F/H, according to the authors.

To avoid this kind of interpretation error, we plan to include in the kit insert a statement indicating that genotype H should not be reported when genotype D and/or genotype F is identified by the use of INNO-LiPA. In this regard, Jardi et al. (3) and El Aziz Khaled et al. (2) reported identification of genotype D and/or genotype F by the use of the INNO-LiPA genotyping assay but never in association with genotype H. We apologize for not clearly citing this limitation.

In conclusion, we plan to revise the interpretation criteria of the INNO-LiPA HBV genotyping assay by including a statement clarifying this limitation to avoid erroneous genotype H detection in case of mixed infections.

REFERENCES

Authors’ Reply

In a recent publication (1), we reported that the new version of the INNO-LiPA HBV genotyping assay was prone to erroneous genotype H detection, leading to an overestimation of HBV mixed infections. This resulted from the absence of specific probes for genotype H and from unclear guidelines in the kit insert, leading, in some cases, to the misinterpretation of the hybridization patterns. Thus, the epidemiological studies based on the determination of HBV genotypes performed with this assay must be accurately analyzed, especially when genotype distributions are compared. We are pleased to note that, thanks to our findings, the manufacturer decided to improve the interpretation criteria. Nevertheless, the most suitable measure to prevent such misinterpretation would be to include a probe specific for genotype H. We understand that the low frequency of genotype H in HBV-infected patients may not justify the development of a new version of the Inno-LiPA assay; in addition, compared to that of other genotypes, genotype H identification is a lesser concern because of its restricted geographical distribution.

REFERENCES

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