Evaluation of the assay for hepatitis B virus (HBV) surface antigen quantification in the laboratory diagnosis of HBV infection

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INTRODUCTION AND PURPOSE

Hepatitis B virus (HBV) infection is a global public health burden, affecting around 2 billion people worldwide [1]. HBV infection is a leading cause of chronic hepatitis, liver cirrhosis, and hepatocellular carcinoma. Actually, in Italy the incidence of HBV infection is of 1 case per 100,000 inhabitants [2]. The quantitative measurement of hepatitis B surface antigen (HBsAg) monitors the progress of chronic hepatitis B, and its rapid decline may be a predictor of the efficacy of the antiviral therapy [3-5]. Although the measurement of serum HBV DNA is the gold standard method for viral load evaluation, this assay is expensive and time consuming, while HBsAg quantification (qHBsAg) is rapid and cost-effective. The aim of this study is to compare the results of qHBsAg and HBV DNA determination, referred to subjects with chronic hepatitis B, in order to advance the understanding of the applications of qHBsAg to the study of evolution of HBV infection.

METHODS

Study sample

From 2013 to 2015, 359 plasma/serum samples, belonging to 359 subjects, referred to the Unit of Virology of the Diagnostic Department of the University Hospital of Parma (Northern Italy) for qHBsAg.

Of the studied population, 219 (61%) were males (median age 53 ± 15.4 years) and 140 (39%) females (median age 53 ± 14.8 years); 229 (63.8%) were Italians and 130 (36.2%) foreigners. Of these subjects, 63 (17.5%) were outpatients from polyclinics, 285 (79.4%) inpatients from infectious diseases wards, 11 (3.1%) inpatients from medical wards.

Serological and molecular assays

The qHBsAg was carried out by means of the ARCHITECT HBsAg assay (Abbott, Germany) and HBV DNA determination with COBAS AmpliPrep/COBAS TaqMan HBV version 2.0 assay (Roche, Germany). Hepatitis B e antigen (HBeAg) and human immunodeficiency virus type 1 (HIV 1) antibodies were determined using the ARCHITECT HBeAg assay and the ARCHITECT HIV Ag/Ab Combo assay (Abbott, Germany), respectively. The HIV antibody confirmatory assay employed was the MP Diagnostics HIV BLOT 2.2 (MPD, Germany).

Statistical analysis

By means of *t*-test, the *P* values less than 0.05 were considered statistically significant.

RESULTS

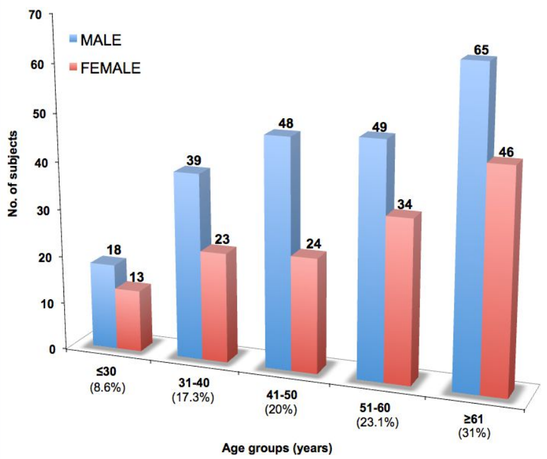

Fig. 1 Distribution by gender and age of the study population.

In the studied population (359 subjects), subjects aged 61 years or over (31%) prevailed.

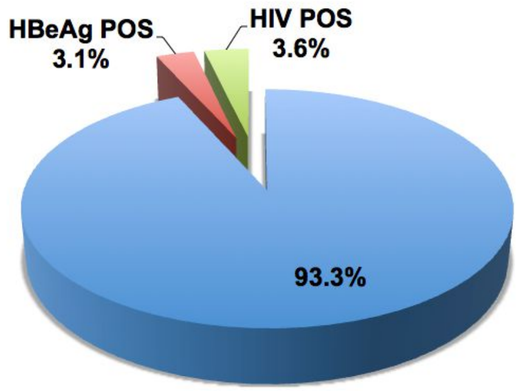

Fig. 2 Distribution of the 359 samples examined for qHBsAg in relation to HBeAg or anti-HIV 1 antibodies presence.

Of the 359 samples examined for qHBsAg, 11 (3.1%) were positive for HBeAg and 13 (3.6%) for anti-HIV 1 antibodies.

		HBV DNA		
	Result	*Detected*	*Not detected*	Total
qHBsAg	*Detected*	227	100	327
	Not detected	0	0	0
	Total	227	100	327

Table 1 Comparison of the results of qHBsAg and HBV DNA determination obtained in 327 samples.

Of the 359 samples analysed for qHBsAg, 327 (91.1%) were subjected in parallel to HBV DNA determination. Of those, 227 samples (69.4%) were positive for both qHBsAg and HBV DNA determination; conversely, 100 samples (30.6%) were positive for qHBsAg and negative for HBV DNA.

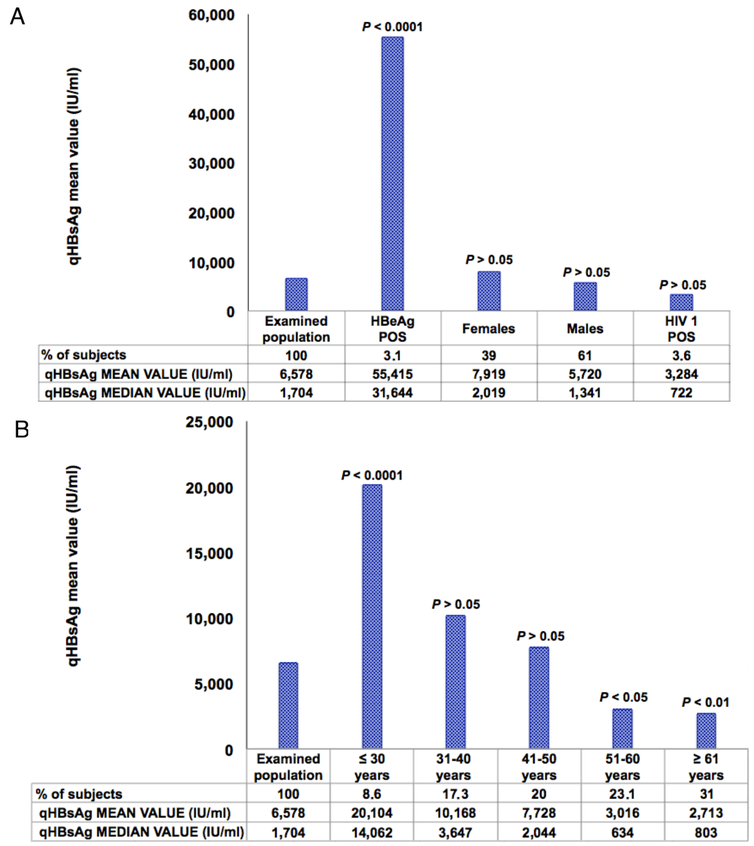

Fig. 3 Analysis of the mean qHBsAg values assessed in different subpopulations (A) and age groups (B) of the studied population.

The highest qHBsAg mean values were assessed for HBeAg-positive subjects. Females, males and HIV 1-positive subjects pointed out lower qHBsAg mean values. Furthermore, qHBsAg mean values decreased with age, being the highest values observed in subjects aged 30 years or less.

CONCLUSIONS

The present study assesses that the levels of HBsAg are different, depending on sex, age, HIV 1 co-infection and HBeAg positivity. Moreover, of the 327 samples subjected to both qHBsAg and HBV DNA assays, 100 samples (30.6%) were positive for qHBsAg and negative for HBV DNA. This latter finding may deal with the fact that, being HBsAg produced as a result of messenger RNA generated from transcriptionally active covalently closed circular HBV DNA or integrated HBV DNA sequences in the host genome, its level decreases less rapidly than HBV DNA, when replication is controlled, either spontaneously or by antiviral therapy [6].

In conclusion, this study contributes to acquire new knowledge on qHBsAg application to the study of evolution of HBV infection, evidencing that the qHBsAg assay cannot be considered a reliable substitute of HBV DNA determination, but a complementary assay, which allows better chronic hepatitis B monitoring.

References: 1 [World Health Organization (2015) Hepatitis B Fact Sheet No 204]; 2 [Zanetti A.R. et al., 2005. Lancet 336(9494):1379-1384]; 3 [Liaw Y.F., 2011. Hepatology 54(2):E1-E9]; 4 [Martinot-Peignoux M. et al., 2013. Liver Int. 33(Suppl 1):125-132]; 5 [Sonneveld M.J. et al., 2011. J Viral Hepat. 18(7):449-457]; 6 [Chevaliez S., 2013. Clin Res Hepatol Gastroenterol. 37:559-563].