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Hepatitis B virus (HBV) genotype distribution and lamivudine-resistant mutations in HIV/HBV co-infected patients attending a Parisian hospital

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Purpose of the study

Co-infection with HBV and HIV-1 is particularly common among patients from sub-Saharan origin, because of the high prevalence of HBV and HIV-1 infection. Differences in HBV subtypes, hepatitis B early antigenemia (HBeAg), and drug resistance mutations can influence the outcome in patients with chronic HBV. The aim of this study was to examine the HBV marker characteristics in HIV/HBV co-infected patients originating from Europe and sub-Saharan Africa attending a Parisian hospital, and to determine risk factors for liver-related morbidity.

Methods

A total of 100 consecutive HIV-1 infected patients with chronic HBV infection, followed up for at least 2 years, were included in the study. Patients were classified into two groups according to their geographical origin: Group 1 (n = 35 from Europe); Group 2 (n = 65 from sub-Saharan Africa).

Summary of results

The studied population included 39 females (14.3% of Group 1 and 52.3% of Group 2, $p < 0.001$). The predominant route of HBV and HIV transmission was homosexual in Group 1, while in Group 2, perinatal and horizontal infection early in childhood where thought to be the main routes of HBV transmission, along with heterosexual transmission of HIV-1. HBV genotypes could be determined in 63 patients (30/35 from Group 1, 33/65 from Group 2). Patients in Group 1 were infected with genotype A (21), genotype G (two), genotype D (two), genotype B (one) genotype C (one), and genotype E (three), whereas patients in Group 2 were infected with genotype E (24) and genotype A (nine). At baseline, the number of HBeAg-positive patients was significantly higher in Group 1 (60.4%) than in Group 2 (24.6%) ($p = 0.001$). Thirteen patients in Group 2 were co-infected with HDV. Lamivudine was administered to 83 patients. Of the 38 patients with available viral genotype data, 19 (14 in Group 1 and five in Group 2) were identified as harbouring mutations associated with lamivudine resistance. The predominant mutations were L180M+M204V (nine patients), V173L+L180M+M204V (eight patients), and L180M+M204I (two patients). Advanced liver disease was diagnosed in 19 patients during the follow-up.

Conclusion

The two groups of co-infected patients differed in the ratio of males to females, the route of transmission and the predominant HBV genotype. Patients in Group 2 had lower HBV viral load and were more often HBeAg-negative. Neither HBV genotype nor geographical origin were statistically associated with advanced liver disease.