Prevalence of HBV Infection Among Different HIV-Risk Groups in Hai Phong, Vietnam

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Hepatitis B virus (HBV) infection in Hai Phong, northern Vietnam, was characterized by analyzing the prevalence and genotype distribution of HBV as well as co-infection with human immunodeficiency virus type 1 (HIV-1) among five different risk groups for HIV infection. Plasma samples were collected from intravenous drug users (n = 760, anti-HIV-1 antibody positive rate: 35.9%), female sex workers (FSWs; n = 91, 23.1%), seafarers (n = 94, 0%), pregnant women (n = 200, 0.5%), and blood donors (n = 210, 2.9%) in 2007 [Ishizaki et al. (2009): AIDS Res Hum Retroviruses 25:175–182]. Samples were screened for the hepatitis B surface antigen (HBsAg) and anti-HBs antibody and analyzed genetically. The cumulative HBV incidence rate (HBsAg + anti-HBs) was 53.2% (10.7 + 42.5%) in intravenous drug users, 51.6% (11.0 + 40.6%) in FSWs, 54.3% (9.6 + 44.7%) in seafarers, 50.5% (12.5 + 38.0%) in pregnant women, and 51.0% (18.1 + 32.9%) in blood donors; there was no significant difference among these groups. Of 163 HBsAg-positive samples, 113 could be analyzed genetically. Phylogenetic analysis, based on the preS1 region, revealed genotype B4 was most prevalent (90/113; 79.6%), followed by C1 (17.7%), I1 (1.8%), and B2 (0.9%). There was no significant difference in HBV genotype distribution among different HIV infection-risk groups. The prevalence of HBsAg was 10.3% (31/301) in HIV-1-infected individuals and 12.5% (132/1,054) in non-HIV-1-infected individuals, which was not significant. In addition, no significant difference in HBV genotype distribution was observed between HBV/HIV-1 co-infected and HBV mono-infected groups. These results suggest that, although HBV and HIV-1 share modes of transmission, major transmission routes of HBV have been different from those of HIV-1 in Hai Phong, Vietnam.
発表会聴講

ウイルス感染症制御学（所属教室）での講義

実験

論文審査