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Viral variability study in follow-up sera from HIV-HBV-HCV coninfected patients

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Background

The genetic variability of hepatitis B virus in sera from HBV-DNA positive patients, HBsAg negative and antiHBc positive, coinfected with both HIV and HCV, was studied, to describe the natural history of HBV occult infections.

Methods

The follow-up sera, encompassing a six to nine years period, from eight patients with triple coinfection (HIV, HBV, HCV) were tested by a real time PCR HBV-DNA assay. Four patients that were HBsAg negative and HBV-DNA positive were classified as affected by occult infection. The remaining four that were HBsAg positive were used as controls. HBV-DNA was amplified by PCR and the sequence of the whole HBV genome was characterized by phylogenetic analysis (Neighbor Joining method, implemented by MEGA 3.1 software) and for the presence of specific mutations.

Results

Three out of four HBV patients with occult infection, showed reactivation phases of HBV viremia. Different mutations were observed, with differences between pre- and post-reactivation sera. HBV-DNA remained at low levels during the entire study period also in absence of specific anti-HBV therapy. The phylogenetic analysis showed that, for each patient with HBV reactivation, all the isolates were originated from a unique parental virus. Specific mutations of PreS/S, Core and X regions were observed.

Discussion

Mutations in the "a" determinant of the S protein could be responsible for the absence of HBsAg detection. The presence of stop codon in the pre-core region and of mutations in the X region could, in part, explain the reactivation of HBV viremia.

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