Abstract:

Hundred and ten liver biopsy specimens from various parts of the world were examined for episomal and integrated HBV-DNA sequences. In 54 patients with HBsAg chronic liver disease episomal HBV-DNA was found in 83% of HBeAg-positive patients, compared to only 22% of patients with anti-HBe. Furthermore episomal HBV-DNA in the latter predominated among the Asians. Integrated HBV-DNA was found only in 5.5% of HBeAg-positive patients but in 16.5% of patients with anti-HBe. In 28 HBsAg-positive patients with hepatoma, episomal HBV-DNA was found in 50% of HBeAg-positive patients but in only 11% of anti-HBe patients. Conversely integrated sequences were less common (25%) in HBe-Ag-positive patients than in anti-HBe patients (50%), giving an overall incidence of integration in this group of 45%. No episomal, and only one case of integrated sequences of HBV-DNA, could be detected among 10 patients with HBsAg-negative hepatoma. In addition neither episomal nor integrated HBV-DNA could be detected in 18 patients with non-HBV-related liver disease. Our data suggests that stable integration of HBV-DNA into the host's genome is not necessarily a prerequisite for the maintenance of the state of malignant transformation but may be necessary for its initiation. Alternatively, the detection of integrated HBV-DNA may represent a 'snap shot' of a random integration event amplified by clonal expansion promoted by other factors.