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Introduction: Full-length intrahepatic hepatitis B virus (HBV) genome mutations and quasispecies characteristics in hepatocellular carcinoma (HCC) were investigated.

Methods: HBV DNA was extracted from the tumour and non-tumour tissues of 16 HCC patients. Overlapping DNA fragments covering the entire HBV genome were amplified and sequenced. To study HBV sequence at the quasispecies level, the preS region was amplified and clonal sequenced. HBV mutation profiles, quasispecies complexity and diversity, and phylogenetic characteristics were assessed.

Results: Overall, 14 patients had full-length HBV amplification. Hot-spot mutations at HBx aa130-131 and preS deletions were detected in 13 (93%) and 6 (43%) patients, respectively. Deletions in the X/preC/C regions were more frequently detected in the tumour than the non-tumour tissues (P=0.031). Compared to the non-tumour tissues, the tumour tissues had a lower quasispecies complexity (P=0.014 and 0.043, at the nucleotide and amino acid levels, respectively) and diversity (P=0.048 and 0.022, at the nucleotide and amino acid levels, respectively). Phylogenetic analysis showed that HBV sequences derived from tumour and non-tumour tissues were separately clustered, suggesting the occurrence of compartmentalisation, which was confirmed by the correlation coefficient testing on both the number and length of branches of viral populations (all P<0.02).

Conclusion: HBV mutation patterns in HCC tumour and non-tumour tissues were different. HBV quasispecies were compartmentalised, and tumour tissues had a lower genome complexity and diversity, suggesting that a selection of HBV mutations was involved in hepatocarcinogenesis.

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Introduction: White matter hyperintensities (WMH), best discerned on T2-weighted or fluid-attenuated inversion recovery magnetic resonance imaging (MRI), have been increasingly recognised as one of the underlying causes of insidious cognitive decline. However, there is little information in the literature concerning the cognitive profile of patients with such lesions. We aimed to identify and assess the spectrum of cognitive impairments associated with advanced WMH in a cohort of 340 otherwise healthy hypertensive elderly Chinese.

Methods: Demographical information, standard neuropsychological tests and multi-sequence MRI scans were obtained from all participants. The neuropsychological tests evaluated the following domains: attention, visuospatial ability, memory, language and related functions, executive function, information processing speed, and motor speed. Z score of every single test was generated from dividing the difference between individual test score and mean test score by the standard deviation. An overall Z score for multiple test domains was calculated from individual Z scores of all the component tests. WMH were evaluated using Fazekas white matter scale to generate the scores for both periventricular hyperintensities (PVH) and deep white matter hyperintensities (DWMH). Spearman correlation was used to evaluate any association between different degrees of WMH and cognitive performance in various domains. Finally, regression models were used to assess whether these associations were independent of age and education levels.

Results: Severe DWMH were negatively correlated with cognitive function on information processing speed, executive function, and motor speed. Furthermore, high PVH scores were correlated with worse performance in all test domains except language and related functions (P<0.01). After adjustment for age and education levels, severe PVH were associated with reduced information-processing speed and executive function (P<0.05).

Conclusion: Significant cognitive decline is associated with severe WMH especially PVH. Such associations with information-processing speed and executive function are independent of age and education levels.