samples (79.1%). The phylogram showed that the strains of one genotype divided into three subgenotypes: D1 — 1 (2.9%), D2 — 15 (44.2%) and D3 — 18 (52.9%). The genotype C was detected in 7 (16.3%) patients and four of them formed a cluster with Chinese samples that were registered in the GenBank database. Genotype A was isolated in 2 (4.6%) samples and formed a cluster with strains isolated in Poland and Belgium.

HBV genotype D comprised out of subgenotypes D1, D2, D3 and prevailed among the CHB patients living in Poland and Belgium.

The occurrence of HCV markers in the Nanaysky District of the Khabarovsk Territory.

Hepatitis C virus (HCV) infection plays an important role in liver diseases. The burden of HCV infection continues to be significant in low- and middle-income countries, especially in Asia and Africa. The global elimination of HCV by 2030 is possible with the advent of effective diagnostic methods available to the majority of the population. The aim of the study was to estimate the prevalence of serological and molecular HCV markers among the apparently healthy people in Kindia region of the Republic of Guinea and Khanh Hoa region of Viet Nam.

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