When Should “I” Consider a New Hepatitis B Virus Genotype?

Recently, Huy et al. described a new hepatitis B virus (HBV) strain isolated in Vietnam (3) and claimed it to be a “new genotype,” “HBV genotype I,” with a complex recombination involving genotypes C, A, and G. We refute both claims.

Using complete genome sequence analysis of their single isolate, VH24 (AB231908), the authors documented an over 98% similarity with three other Vietnamese strains (2). Earlier, Hannoun et al. provided comprehensive information regarding those strains, showing recombination between genotype C and an unknown genotype in the pre-S/S region (2). Mean genetic divergence from genotype C of <8% in the entire genome and evidence of recombination had prevented the authors from assigning the strains to a new genotype. The same conclusion for the strains was reached by a later study using a new methodological approach (10). By providing neither additional information nor a new analytical approach, Huy et al. (3) surprisingly conclude that their strain, with those previously reported, represents a new genotype.

First, phylogenetic analysis of the complete genome of the four Vietnamese HBV isolates shows them to cluster with subgenotypes of C (C1 to C5) and to differ from genotype C by a mean of 3.5% (2). As shown for the B/C recombinant, which accounts for the majority of genotype B strains in mainland Asia (12), the geographical distribution and clinical relevance have been extensively reported (5, 6). In addition to the eight currently recognized genotypes, intergenotype recombination can spread in humans and develop specific distributions and epidemiology as shown for the B/C recombinant, which accounts for the majority of genotype B strains in mainland Asia (12). Since sequencing and phylogenetic analyses are widely available, numerous further reports on HBV variation can be expected. If every new recombinant is assigned to a new genotype, we would soon be running out of alphabet letters. Principles of HBV classification must be established and accepted by the international community of experts in the field in order to ensure that genotyping is consistent, relevant, and significant.

REFERENCES


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