

Description of a New Hepatitis B Virus C6 Subgenotype Found in the Papua Province of Indonesia and Suggested Renaming of a Tentative C6 Subgenotype Found in the Philippines as Subgenotype C7

Hepatitis B virus (HBV) genotypes (2, 4, 5, 7–9) and subgenotypes (11, 13, 14, 16–18) are important factors that influence the course of the disease and the outcome of treatment. Because of the clinical importance of the HBV classification, an accurate assignment of newly found subgenotypes to their respective clades and an unambiguous nomenclature are needed. A new HBV subgenotype should differ from previously established by at least 4%, and the segregation into a new clade should be supported by robust bootstrapping data (3).

In the June 2009 issue of the *Journal of Clinical Microbiology*, a new C6 subgenotype of HBV found in the Papua province of Indonesia (C6 Papua-Indonesia) is described (15). However, a tentative C6 subgenotype found in the Philippines (C6 Philippines) has already been published contemporaneously (1). To keep up with an unambiguous system of HBV subgenotypes, it is important to analyze if C6 Papua-Indonesia and C6 Philippines are identical or map to different clades.

Using methods described by Cavinta et al. (1) and published sequences from Utsumi et al. (15), we made a phylogenetic analysis using whole genomes that clearly showed that both C6 groups mapped to different clades (Fig. 1).

C6 Papua-Indonesia and C6 Philippines differed by 5.1% from each other and diverged by at least 4.1% from the other HBV subgenotypes (Table 1).

Thus, both contemporaneously described subgenotypes (1, 15) fulfill all criteria for having new and separate subgenotypes. Because the designation C6 has been claimed for partial sequences found in the Papua province of Indonesia already (6), we suggest that the subgenotype C6 found in the Papua province of Indonesia shall keep the designation C6, whereas the tentative subgenotype from the Philippines shall be called C7. To avoid similar confusion in the future, we have suggested a procedure that would involve the International Committee for Taxonomy of Viruses to allot new genotype/subgenotype designations (10).

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Lolita Cavinta

Department of Medical Microbiology
 College of Public Health
 University of the Philippines Manila
 Pedro Gil St.
 Manila, Philippines

Guangwen Cao

Department of Epidemiology
 Second Military Medical University
 800 Xiangyin Rd.
 Shanghai 200433, People's Republic of China

Stephan Schaefer*

Universität Rostock
 Medizinische Fakultät
 Institut für Medizinische Mikrobiologie, Virologie und Hygiene
 Abteilung für Virologie
 Schillingallee 70
 D-18057 Rostock, Germany

*Phone: 0381-494-5920

Fax: 0381-494-5925

E-mail: stephan.schaefer@med.uni-rostock.de

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