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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 assignation 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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TABLE 1. Nucleotide distance between proposed subgenotypes C6 Philippines and C6 Papua-Indonesia of HBV and other reference genotype strains from the database

Genotype/ subgenotype strain	Nucleotide distance between strains[a]																						
	A1	A2	A3	A4	B1	B2	B4	B5	C2	C3	C4	C5	C6 Papua-Indonesia	C6 Philippines	D1	E	F1	F2	F3	F4	G	H	C1	B3
A1																								
A2	0.049																							
A3	0.051	0.054																						
A4	0.046	0.046	0.040																					
B1	0.100	0.096	0.102	0.098																				
B2	0.098	0.096	0.099	0.095	0.046																			
B4	0.100	0.096	0.100	0.097	0.055	0.039																		
B5	0.102	0.098	0.103	0.097	0.065	0.048	0.046																	
C2	0.092	0.089	0.092	0.084	0.105	0.095	0.093	0.091																
C3	0.095	0.091	0.093	0.086	0.104	0.094	0.091	0.093	0.044															
C4	0.106	0.102	0.103	0.095	0.118	0.107	0.105	0.107	0.069	0.065														
C5	0.092	0.092	0.096	0.089	0.112	0.100	0.097	0.098	0.055	0.060	0.084													
C6 Papua-Indonesia	0.098	0.097	0.098	0.091	0.111	0.101	0.100	0.099	0.048	0.045	0.071	0.066												
C6 Philippines	0.092	0.091	0.093	0.084	0.106	0.096	0.094	0.090	0.041	0.047	0.072	0.059	0.051											
D1	0.106	0.103	0.106	0.102	0.119	0.112	0.111	0.112	0.107	0.106	0.113	0.108	0.118	0.103										
E	0.101	0.100	0.102	0.095	0.118	0.112	0.111	0.113	0.106	0.097	0.113	0.107	0.111	0.104	0.078									
F1	0.148	0.149	0.154	0.144	0.156	0.151	0.151	0.155	0.146	0.147	0.151	0.149	0.147	0.149	0.153	0.140								
F2	0.148	0.145	0.153	0.150	0.155	0.150	0.147	0.150	0.145	0.142	0.153	0.143	0.144	0.142	0.149	0.142	0.060							
F3	0.157	0.159	0.158	0.154	0.159	0.153	0.152	0.155	0.146	0.142	0.151	0.148	0.145	0.143	0.150	0.141	0.059	0.049						
F4	0.152	0.151	0.155	0.154	0.158	0.150	0.150	0.150	0.153	0.145	0.157	0.149	0.152	0.151	0.145	0.143	0.067	0.041	0.051					
G	0.118	0.118	0.121	0.115	0.138	0.133	0.128	0.129	0.129	0.131	0.146	0.129	0.134	0.132	0.120	0.115	0.158	0.155	0.154	0.157				
H	0.156	0.154	0.161	0.156	0.162	0.155	0.155	0.158	0.152	0.154	0.157	0.160	0.153	0.150	0.149	0.153	0.089	0.090	0.091	0.098	0.158			
C1	0.095	0.095	0.095	0.088	0.110	0.098	0.095	0.094	0.047	0.055	0.079	0.063	0.061	0.051	0.110	0.110	0.150	0.145	0.149	0.153	0.130	0.154		
B3	0.103	0.096	0.104	0.100	0.066	0.047	0.043	0.031	0.092	0.091	0.109	0.100	0.100	0.092	0.108	0.114	0.157	0.152	0.155	0.148	0.132	0.159	0.093	

[a] The comparisons were performed over the complete genome with the Kimura two-parameter model using MEGA version 4.0 (12). Between groups, the average was calculated.

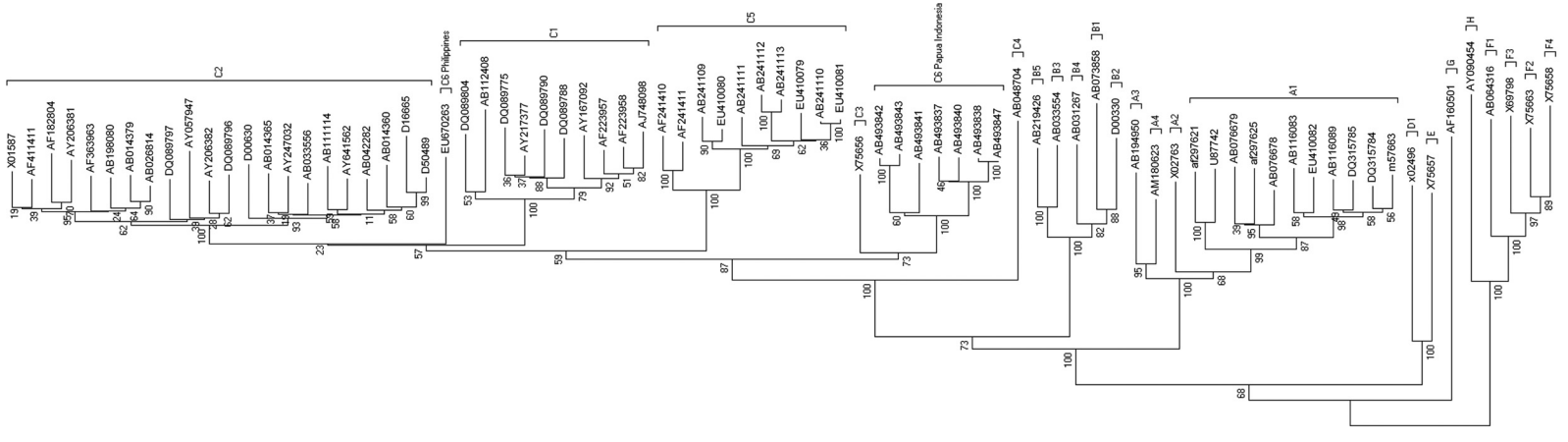

FIG. 1. Phylogenetic tree of complete HBV genomes of genotypes A to H. An alignment of complete sequences was performed with ClustalW using the program DNASTAR. The alignment was further analyzed by bootstrapping with 500 replicates, using the neighborhood-joining method contained in MEGA version 4.0 (12).