Enterovirus A71 Genogroups C and E in Children with Acute Flaccid Paralysis, West Africa

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To the Editor: Human enterovirus 71 (EV-A71) of the species enterovirus A, genus Enterovirus, and family Picornaviridae is a public health threat because it can cause large outbreaks of hand, foot, and mouth disease (HFMD). In addition, EV-A71 has been associated with severe and sometimes fatal neurologic complications that affect mostly infants and children and that range from aseptic meningitis and encephalitis to poliomyelitis-like acute flaccid paralysis (AFP) (1). EV-A71 has been classified into 7 genogroups, A–G, on the basis of the identity of the nucleotide sequences of the viral protein 1 (VP1) capsid (1,2). Since 1997, increasing epidemic activity of genogroups B and C has been reported in the Asia-Pacific region and has caused large HFMD outbreaks with high rates of illness and death. Subgenogroup C2 was identified as the main cause of AFP outbreaks in 3 years before they were detected. However, we cannot exclude the possibility that these isolates originated from multiple importation events from abroad, especially from countries in Europe. The fourth isolate (from Niger) clustered within genogroup E, which, before this study, included only 2 complete VP1 sequences from isolates from Central African Republic and Cameroon and an additional partial VP1 sequence from an isolate from Nigeria. Comparison of complete VP1 amino acid sequences of all EV-A71 strains considered for the phylogenetic analysis showed that 107 (36%) of 297 aa sites were variable. None of the residues found in the variable sites of the African strains in our study corresponded to residues previously associated with genogroup C neurovirulent phenotypes (A170V, N31D, L97R, G145E and D164E) (9,10). The Niger E isolate showed specific residues (L24M, A170T) that differed from those of other genogroup E isolates.
Figure. Phylogenetic tree created with the complete VP1 nucleotide sequences (891 bp in length) of enterovirus A71 isolated from 4 patients with acute flaccid paralysis in West Africa, the most similar nucleotide sequences identified by a search in GenBank by using BLAST (http://www.ncbi.nlm.nih.gov/), and a representative global set of enterovirus A71 sequences belonging to different genogroups and subgenogroups. The coxsackievirus A16 prototype G-10 sequence was introduced as the outgroup. The tree was inferred by a neighbor-joining method that used MEGA5 software (http://www.megasoftware.net/). Distances were computed by using the Kimura 2-parameter model. The robustness of the nodes was tested by using 1,000 bootstrap replications. Bootstrap support values >80 are shown in nodes. Black triangles indicate the 4 strains from this study. Open square indicates a partial sequence. Scale bar represents nucleotide substitutions per site. Abbreviations of virus names indicate genogroups or subgenogroups/GenBank accession number/origin/year of isolation, respectively. A color version of this figure is available online (http://wwwnc.cdc.gov/EID/article/22/4/15-1588-F1.htm).
Hepatitis E Virus Prevalence among Blood Donors, Ouagadougou, Burkina Faso

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To the Editor: The safety of blood product use is continually improving, but blood transfusion remains a challenge in Africa, given the high prevalence of bloodborne pathogens (1). In Africa, the main serologic tests done to reduce blood transfusion risks are for HIV and hepatitis B and C viruses. However, unknown or emerging pathogens among the population of blood donors, such as hepatitis E virus (HEV), may also jeopardize transfusion safety.

HEV is emerging as a potential threat to blood safety. High rates of HEV IgG prevalence among blood donors have been found in studies in the United States (7.7%), England (13.5%), France (16.6%), and Spain (19.6%) (2,3). A study in Iran showed a prevalence of 14.3% (4), and a study in China showed rates of up to 22.7% (5). Cases of HEV transmission by transfusion or transplantation have been reported, and recent studies in France and England showed risk for HEV in donated blood ranging from 1/2,218 to 1/2,848 donations (5,6).

In Burkina Faso, the prevalence of HEV IgG has been reported as 11.6% among pregnant women during 2012. Prevalence is >70% among butchers, who form a population exposed to pigs, which are a reservoir for HEV (7,8). To determine whether HEV continues to circulate among human populations outside known at-risk populations, we investigated prevalence of HEV IgG and IgM in the blood donor population of Ouagadougou.

During June and July 2014, we recruited 1,497 first-time blood donors (398 women, 1,099 men) within the National Blood Transfusion Centre in Ouagadougou. Persons 17–65 years of age who weighed >50 kg were included (Figure, panel A). Candidate donors were excluded if they had previously received blood transfusions, had jaundice or clinical