To the Editor: Dengue in the Americas is a ubiquitous and neglected problem. Surveillance for dengue virus infection is critically needed, preferably in real time, to support control measures. We recently reported results of a surveillance system that used real-time quantitative reverse transcription PCR to monitor dengue virus activity in the Americas (1).

January through December 2007, 40122 dengue virus specimens were screened by real-time reverse transcription PCR in the 11 surveillance networks of the Americas. Dengue virus was detected in 10327 (25.7%) specimens. A total of 29 strains of dengue virus type 2 were detected, resulting in a surveillance system effectiveness of 61.3%.

A DENV-2 virus with unique genomic characteristics (2) was first detected by real-time reverse transcription PCR in Colombia on 21 February 2007. The virus strain was isolated from a patient with dengue hemorrhagic fever who visited the Hospital de la Bicentenario in Medellin, Colombia (3).

The authors of the study reported that the virus strain was genetically identical to one identified in Singapore (3). However, we recently found that our sequence was not identical to the reported one (4). The difference was at the nucleotide level. This discrepancy may indicate a possible error in the sequence analysis of the reported strain of dengue virus. We recommend further analysis of this unique dengue virus strain to confirm the origin of the strain.

Dengue is the most frequent cause of severe illness in the Americas, and outbreaks continue to occur in areas where surveillance is suboptimal. Health care workers need information on dengue virus activity to design and implement appropriate control strategies.

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