To determine the causes of viral meningitis, we analyzed 22 cerebrospinal fluid samples collected during the 2014–2015 dengue epidemics in Brazil. We identified 3 serotypes of dengue virus (DENV-1, -2, and -3), as well as co-infection with 2 or 3 serotypes. We also detected the Asian II genotype of DENV-2.

Dengue is a disease of high incidence and a major public health problem worldwide (1). Approximately 2.5 billion persons live in dengue transmission risk areas, and 50 million dengue virus (DENV) infections occur annually. This disease is endemic in Brazil, with 4 DENV serotypes circulating; >1.6 million clinical cases were reported in 2015 (2).

DENV belongs to the family Flaviviridae, genus Flavivirus, and has 4 serotypes (DENV-1–4). These viruses are usually associated with a systemic and dynamic disease; the clinical conditions range from a nonspecific viral syndrome to severe disease. The most common symptoms are fever, rash, headache, nausea, vomiting, retro-orbital pain, and weakness (3). Neurologic manifestations have been increasingly reported; DENV could be considered an emergent etiologic agent of central nervous system (CNS) infection that causes encephalopathy, encephalitis, and meningitis (1). DENV infections of the CNS may or may not be associated with the classical systemic manifestations of dengue (4).

In dengue-endemic areas, co-circulation of different serotypes has been reported (5). Co-infection by different DENV serotypes has already been reported in patients and arthropods, but the effects on the disease and on the virus cycle has not been well established (6,7). The molecular diversity of DENV serotypes has been linked to different patterns of virulence. DENV-3 genotypes I and III, which circulate in Brazil, demonstrate distinct biological characteristics in mouse models (8). In 2014, the number of suspected dengue cases in Brazil was 589,107, with 58,177 in the state of Minas Gerais; in 2015, the number of cases increased to 1,649,008 in Brazil and 189,378 in Minas Gerais, with DENV-1 being the most frequently detected serotype (2). We report the detection of DENV-1, -2, and -3 co-infections in the CNS by reverse transcription PCR (RT-PCR) from cerebrospinal fluid (CSF) samples that tested negative for other classic neurotropic pathogens.

**The Study**

During the 2014–15 DENV epidemic in Minas Gerais, 22 CSF samples were collected from children suspected of having viral CNS infection who were hospitalized at the Hospital Infantil João Paulo II, Belo Horizonte, Minas Gerais, a reference children’s hospital for all counties of the state. A presumptive diagnosis of CNS viral infection was given when the CSF of patients with clinical signs and symptoms of CNS infection had normal or slightly altered cytochemical parameters and tested negative for bacterial pathogens (9). The protocol for this study was approved by the hospital’s scientific and ethical committee (no. 132/2009), and consent was obtained from parents or accompanying relatives.

The CSF samples tested negative for typical neurotropic viruses such as enteroviruses and human herpesviruses 1, 2, and 3. For DENV detection, RNA isolation and RT-PCR from 140 μL of CSF targeting the NS5 region was performed as described (10). The analyses showed that 7 samples (32%) were DENV positive. DENV-1 was detected in 1 sample (14.2% of positive samples); DENV-2 was detected in 3 samples (42.9%); DENV-3 was detected in 1 sample (14.2%); and DENV-4 was not detected in any samples. Co-infection with >1 DENV serotype was found in 2 CSF samples (28.6%); 1 sample was co-infected with DENV-2 and DENV-3 (sample from patient 571), and the other sample was...
The DENV-2 isolates from samples from patients 557 and 571 grouped with isolates of Asian II, which is a genotype that consists of viruses circulating in China, the Philippines, Sri Lanka, Taiwan, and Vietnam (13). The American/Asian genotype has been the only genotype previously identified in Brazil, although some variations have occurred within this genotype (12) (Figure, panel B). Singh et al. demonstrated that the Asian II and Cosmopolitan DENV-2 genotypes co-circulated in Nepal, with no differences in their replication rate in mosquito cells (14,15).

The DENV-3 nucleotide sequences of samples from patients 577 and 571 showed a close phylogenetic relationship with genotype III when compared with the non-structural-5 gene sequences of other DENV-3 viruses circulating in different parts of the world (Figure, panel C). Previous studies have reported circulation of DENV-3 genotypes I and III in Brazil, and differences in the course of the infection between these 2 genotypes in a mouse model have been described. This study relates DENV-3 genotype III to CNS infection (8). DENV serotype co-infection has already been described in the literature from human blood samples and in Aedes mosquitoes (5–7). However, to our knowledge, DENV serotype co-infections have not previously been detected in the CNS.

Conclusions
DENV co-infection with other flaviviruses has been described, but not in relation to the different DENV serotypes involved in CNS infection. We identified 2 patients with meningitis: 1 was infected with 2 DENV serotypes and the other with 3 DENV serotypes. We also report the circulation of the DENV-2 genotype Asian II in Brazil, where the DENV-2 genotype American/Asian has been the most prevalent genotype since 1990 (13). When and where genotype Asian II started to circulate in Brazil is unclear.
Our results also suggest that CNS DENV infection can be preceded by classic dengue fever symptoms or can occur without any classic symptoms. Because the evolution of DENV infection and DENV serotype co-infection into a CNS infection is underreported, attempts to identify the serotypes and genotypes involved in this severe clinical manifestation should be undertaken to clarify the clinical relevance of cases of DENV serotype co-infections.

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References
heteroserotypes of dengue viruses in field populations of *Aedes aegypti* and *Aedes albopictus* (Diptera: Culicidae) and serological features of dengue viruses found in patients in southern Thailand. Southeast Asian J Trop Med Public Health. 2006;37:468–76.


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