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Spread of Chikungunya Virus East/Central/South African Genotype in Northeast Brazil

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We investigated an outbreak of exanthematous illness in Maceió by using molecular surveillance; 76% of samples tested positive for chikungunya virus. Genetic analysis of 23 newly generated genomes identified the East/Central/South African genotype, suggesting that this lineage has persisted since mid-2014 in Brazil and may spread in the Americas and beyond.

Dengue virus (DENV), Zika virus (ZIKV), and chikungunya virus (CHIKV) co-circulate in Brazil, are predominantly transmitted by *Aedes aegypti* mosquitoes, and cause similar clinical symptoms upon infection, complicating epidemiologic surveillance. Brazil harbors the highest diversity of CHIKV in the Americas; both the Asian and the East/Central/South African (ECSA) lineages circulate in the country (1). Despite high prevalence of CHIKV in Brazil (352,773 notified cases during January 2016–May 2017) and its widespread distribution (2), little is known about its transmission. We report a molecular and genomic investigation of an outbreak of CHIKV infection in Maceió, Alagoas state, Northeast Brazil.

During March 30–May 3, 2016, ≈12,000 patients visited 2 private hospitals in Maceió; roughly 70% of them had exanthematous illness symptoms compatible with DENV, CHIKV, or Zika virus infection. We analyzed 273 randomly chosen samples by using molecular diagnostics and virus discovery methods. The study was approved by the Faculty of Medicine from the University of São Paulo Review Board, and we obtained informed consent from all participants.

Analyzed samples were from patients who were on average 37 years of age (range 1–86 years); 175 (64%) were female, and 198 (73%) resided in Maceió municipality. Diagnostic tests for DENV, ZIKV, and CHIKV confirmed that 208 (76%) were positive for CHIKV RNA (online Technical Appendix, <https://wwwnc.cdc.gov/EID/article/23/10/17-0307-Techapp1.pdf>). In addition, 66 (24%) were positive for Zika virus RNA and 36 (13.2%) were co-infected with CHIKV and Zika virus, consistent with Zika virus circulation in Northeast Brazil in mid-2016 (3). We detected no DENV infections. Cycle threshold (C_t) values for CHIKV RNA-positive samples were lower (average $C_t = 24.6$) than those for ZIKV (average $C_t = 33.5$).

We applied a metagenomics next-generation sequencing protocol to 38 randomly chosen CHIKV RNA-positive samples (4) (online Technical Appendix). We recovered 23 CHIKV genomes (>4,000 bp) by using the MiSeq Sequencer (Illumina, Inc., San Diego, CA, USA); mean genome coverage was 72× and mean depth coverage 207× (online Technical Appendix Table 1). We also

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reports (8) and in contrast with the unrecognized circulation in the region of Zika virus, which typically causes milder symptoms (3). The most common clinical signs and symptoms for the sequenced CHIKV cases were fever (87%), arthralgia (70%), headache (44%), exanthema (30%), and myalgia (26%) (Technical Appendix Table 2). CHIKV infection is often characterized by prolonged periods of disability. Further investigation is needed to study potential differences in the effects of CHIKV and Zika virus infection on public health, as well in pathology and innate and adaptive immune responses to each genotype.

The unrecognized transmission of the CHIKV ECSA genotype in Northeast Brazil is unique in the Americas. The spread of this genotype in this region will be mediated by several factors, including herd immunity, vector suitability, and human mobility. Serologic and molecular surveys in human and mosquito populations are required to characterize the factors involved in transmission and the extent of cross-protection of the Asian and the ECSA genotypes in the Americas. Although CHIKV ECSA has been found only in *Ae. aegypti* mosquitoes (9), a recent study has shown that *Ae. albopictus* mosquitoes in Brazil are also highly competent in CHIKV ECSA transmission (10). Given the widespread distribution of both vectors in the Americas (1), it is possible that the ECSA lineage may spread to other regions in the Americas and beyond. A better understanding of the transmission dynamics of CHIKV, DENV, and Zika virus in the Americas is essential to fully understand the risk of arbovirus-associated congenital anomalies, Guillain-Barré, and other neurological syndromes.

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