A33 Using serological and surveillance data to infer the introduction date and unobserved transmission dynamics of Zika virus in Fiji 2013–7

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Zika virus (ZIKV) has been circulating in the South Pacific since 2007, and transmission in Fiji was first confirmed in 2015. To better understand the history and transmission dynamics of ZIKV in Fiji, we combined a transmission dynamic model with serological and surveillance data from Central Division, Fiji. A longitudinal population representative of seroepidemiological data were available from participants sampled in 2013, 2015, and 2017. In addition, ZIKV case reports were available from 2015 and 2016. Using a Bayesian approach, we fitted a transmission dynamic model with a seasonally varying transmission to these data. We also estimated the virus introduction date, given the effect this has on transmission dynamics as it interacts with the observed seasonal pattern of transmission. We found evidence that the virus was introduced in October 2013 (95% credible interval: April 2013–April 2014) and that the strong seasonal transmission pattern meant the virus persisted for several years with multiple waves of infection in consecutive years. It is important to corroborate this evidence against other work done in the same area. A phylogenetic analysis was performed on 5 ZIKV strains obtained from Fiji in 2015 and 2016, which were aligned with 33 E gene sequences from the Pacific, Americas, and Africa. This analysis showed evidence of virus persistence over multiple years in Central Division, Fiji. The estimated most recent common ancestor of the group isolated from Central Division was November 2013 (95% credible interval: March 2013–July 2015). Our modeling estimate is consistent with these results despite the very different methods being used. The availability of detailed case and serology data in an island outbreak setting, combined with mathematical models, presented a unique opportunity to gain crucial insights into these infections. Our analysis provides evidence that seasonal variation in transmission, combined with other co-circulating flaviviruses, means the timing of ZIKV introduction can have a major impact on outbreak transmission dynamics.

A34 Molecular characterization of Zika virus in Cuba

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Until now, three genotypes of Zika virus (ZIKV) have been detected (two African lineages and one Asian lineage). After the declaration of Public Health Emergency of International Concern issued by The Pan American Health Organization and the World Health Organization authors from some Latin American countries have identified the Asian genotype as the lineage responsible for the Zika epidemic in the western hemisphere. However, data from the Caribbean are sparse, and there is no published data regarding the genotypes that produced isolated outbreaks in Cuba. Aiming to realize the molecular characterization of ZIKV in Cuba, we will sequence by next-generation sequencing the full genome of the ZIKV identified in samples from Cuban patients of different provinces in which ZIKV produced outbreaks. All samples required for this study have been collected during the molecular surveillance of Arboviral diseases conducted at the National Reference Laboratory at Pedro Kourí Tropical Medicine Institute. Viral RNA will be purified from urine and serum samples collected from patients with confirmed ZIKV infection by real time PCR. Using evolutionary dynamics studies, we will map the spread of a virus or of particular variants in time and space in order to understand how frequently ZIKV has been introduced into Cuba. Moreover, we will evaluate the amino acid diversity of each ZIKV proteins. Further, we will evaluate the population dynamics of ZIKV in samples from patients with varying clinical outcomes. The results will allow us to characterize the ZIKV genome and its evolution into the Cuban population that would also have impact for vaccine development, diagnosis, and pathogenesis studies.

A35 The first laboratory confirmation of chikungunya outbreak in Ethiopia

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Chikungunya is a viral disease (genus Alphavirus) which is transmitted to humans by infected mosquitoes—including *Aedes aegypti* and *A. albopictus*. An outbreak of febrile illness, suspected to have been caused by chikungunya, was reported in June 2016 from Dolloado district, Suuf Kebele, in the Somalia regional state of Ethiopia that borders the Mandera county of Kenya where a confirmed chikungunya outbreak was ongoing. Laboratory investigation was carried out to confirm if the outbreak in Ethiopia was caused by Chikungunya virus. Ten serum samples were collected from suspected patients visiting a health center in Suuf Kebel, who were then sent to the Nation laboratory in Ethiopian Public Health Institute. RNA was extracted from the serum samples using QIAgene RNA Mini kit, and PCR detection of dengue, chikungunya, and Zika virus nucleic acid was done using Trioplex Real-time RT-PCR Assay following the protocol from the Center for Disease Control (CDC). The Trioplex Real-time RT-PCR assay, for detection and differentiation of RNA from dengue, Chikungunya and Zika, was provided by CDC as part of the zika emergency preparedness effort. Of the nine samples tested, eight (88.88%) were found to be positive for chikungunya virus nucleic acid but negative for dengue and Zika virus nucleic acids. The median age of the affected sampled patients was 40 years, and males appear to be more affected (66.6% of sampled patients). The laboratory investigation confirmed that the outbreak was caused by chikungunya virus. Even though further molecular characterization of the positive isolates will provide more information as to the circulating genotypes and elucidate the origin of the outbreak virus, it is also possible to assume that the outbreak was an extension of the outbreak in neighboring countries in Kenya and, therefore, warrants that cross-border integration efforts to control chikungunya should be implemented by the concerned countries.

A36 Analysis of CHIKV evolution during the Caribbean outbreak, 2013–5, using complete genome sequences

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Chikungunya virus (CHIKV) is a re-emerging, mosquito-borne alphavirus that causes chikungunya fever, a febrile illness characterized by severe acute and persistent arthralgia. At the end of 2013, autochthonous CHIKV transmission was detected for the first time in the Americas, on the Caribbean island of Saint Martin. Subsequently, CHIKV rapidly spread through the Caribbean Islands and onto the American mainland, causing millions of cases of chikungunya fever. During the outbreak, the Dutch National Institute of Health performed diagnostics on patient samples originating from the six Caribbean islands that belong to the Kingdom of the Netherlands. Using a subset of PCR-positive patient samples, we aimed to retrospectively analyze the 2013–5 CHIKV outbreak on the Dutch Caribbean islands using whole-genome sequences. Twenty-five CHIKV-positive sera were selected for next-generation sequencing based on viral load, location, and date of sampling. Sera were subjected to high speed centrifugation, filtration, and nuclease treatment to reduce the amount of background sequences from human and bacterial origin. Total RNA was extracted, primed with random nanomers for reverse transcription, after which dsDNA was produced and purified. Libraries were created using Nextera XT library preparation kit, and samples were run on a MiSeq desktop sequencer. Reads were trimmed and mapped to a reference sequence using the CLC Genomics workbench. To date, eight