presented anti-Zika antibodies at the time of delivery. A total of 7 (6.8%) newborns were diagnosed with microcephaly, while 96 (93.2%) were classified as newborns without microcephaly.

Methods & Materials: In June 2017, we began a prospective follow-up of these infants without microcephaly exposed to Zika Virus *in utero* by evaluating neurodevelopment delays, performing neurological examinations and applying the Bayley Scales of Infant Development III (BSID-III), Mental Development Index (MDI) and Bayley-III cognitive and language scales. Auditory evaluations were performed by Otoacustic emissions (OAE) and Brainstem Auditory Evoked Potential (BAEP).

Results: To date we have evaluated 18 infants, mean age 1.7 years. Of these, 55.6% are male and 61% were delivered by C-section. Anti-Zika IgG serology was positive in 75% and three (16.6%) presented positivity for Zika by PCR on urine samples within 24 h of birth. Based on head circumference (HC) at time of birth, all were classified as normal by the Intergrowth scale and currently fall within normal HC percentiles. Cognitive delay was identified in five (33%) infants, language delay in four (26.6%) and motor delay in two (13.3%).

Conclusion: Our preliminary results indicate that *in utero* exposure to Zika virus could be associated with neurodevelopmental delay, even in children born without microcephaly at birth. Currently, only microcephalic infants are referred to specialized care, while normocephalic children are maintained in primary health care. We believe that all newborns exposed to Zika *in utero* should be referred to specialized centers for the early detection of neurodevelopmental delays and timely intervention.

https://doi.org/10.1016/j.ijid.2018.04.3533

Final Abstract Number: 22.004
Session: Oral Presenations: Arboviruses
Date: Friday, March 2, 2018
Time: 17:00-18:00
Room: Retiro A

Type: Oral Presentation

Neurological complications associated with arboviruses during Zika outbreak in Salvador, Bahia-Brazil

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Background: An unprecedented and concurrent outbreak of Dengue (DENV), Chikungunya (CHIKV) and Zika (ZIKV) virus happened in Brazil in 2015. Approximately 18.372 cases of an acute exanthematous illness were notified in Salvador, Bahia and several cases of Guillain-Barré Syndrome (GBS) raised.

Methods & Materials: We started a hospital surveillance for GBS and other neurological syndromes in two general hospitals in Salvador, northeastern Brazil.

Results: Twenty-seven cases were included, of which 18 (66%) were female. The mean age was 40 years and 26 (93%) of them had acute symptoms suggestive of arbovirus infection before the onset of neurological symptoms. The main symptoms were skin rash, pruritus, myalgia, and fever. The median time between onset of acute symptoms and neurological symptoms was 10.5 days. Seventeen cases (63%) were classified as GBS, 3 (11%) as acute encephalitis, 2 (7%) as opsoclonus-myoclonus ataxia syndrome (OMS), 2 (7%) as myelitis, 1(4%) as Carpal tunnel syndrome and 1 (4%) as acute disseminated encephalomyelitis (ADEM). GBS cases presented in a variety of clinical spectrum, with 8 (47%) as acute ataxic neuropathy, 5 (29%) as classic GBS, 2 (11%) as bifacial weakness with paraesthesias, 1 (5%) as paraparetic GBS and 1 (5%) as classic Miller-Fischer syndrome. Twelve (44%) patients were admitted to semi-intensive or intensive care units and none died. The arbovirus diagnosis was established in 21(77.8%) of the cases. Serological evaluation by ELISA singly detected IgM-specific DENV antibodies in 3 cases (2 SGB and 1 Myelitis), IgM-specific CHIKV antibodies in 4 cases (3 SGB and 1 myelitis) and IgM-specific ZIKV antibodies in 3 cases (SGB). Six cases had both anti-ZIKV and anti-DENV (2 SGB, 2 encephalitis, 1 ADEM, 1 OMS) with a presumptive ZIKV diagnosis. One case of OMS had a coinfection by CHIKV and DENV-4 established by RT-PCR.

Conclusion: Herein, we describe 28 cases of GBS and other neurological syndromes associated with arboviruses. Besides GBS, we also identified cases of encephalitis, ADEM and OMS, a rare syndrome characterized by chaotic eyes movement and ataxia. Thereafter, clinicians and health care providers should be aware of the potential severe neurological complications associated with arbovirus infection in epidemic areas.

https://doi.org/10.1016/j.ijid.2018.04.3534

Final Abstract Number: 22.005
Session: Oral Presenations: Arboviruses
Date: Friday, March 2, 2018
Time: 17:00-18:00
Room: Retiro A

Type: Oral Presentation

Projecting the end of the Zika epidemic in Latin America: A modelling analysis

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Background: Zika virus disease emerged in Latin America in early 2015, which had serious implications for population health. In 2016, the World Health Organization declared a cluster of neurological disorders and neonatal malformations associated with Zika cases a Public Health Emergency of International Concern. 2017 incidence has declined, and future disease incidence in Latin America remains uncertain due to gaps in our understanding of the natural history of infection, considerable variation in surveillance and a lack of a comprehensive collation of available data from affected countries.

Methods & Materials: This analysis combines publically available data on Zika virus incidence across most Latin American countries and a spatio-temporal dynamic transmission model for Zika virus infection to determine key transmission parameters and likely future incidence in 87 cities. Seasonality was determined by spatio-temporal estimates of Aedes aegypti vector capacity. Country and state-level data are used to infer key model parameters using Monte-Carlo methods, different movement models were tested against the data and the best-fitting parameter combinations were used to estimate incidence within each city.

Results: We predict that the highest incidence in 2018 will be observed in Colombia and some Brazilian States (Parana, Sao Paulo, Rio de Janiero and Minas Gerias), but the estimated number of

infections will be no more than a few hundred and the incidence risk ratio will be below 0.05. There was limited transmission in 2015, but for most cities 2016 and 2017 provided a sufficient opportunity for ZIKV transmission and populations have been depleted of susceptible individuals.

Conclusion: The findings suggest that much of the ZIKV-associated morbidity will be in neonates and children that are born up to the end of 2017. The findings present a challenge to planned ZIKV-specific interventions such as phase III vaccine trials, as we predict substantially lower numbers of infections in 2018.

https://doi.org/10.1016/j.ijid.2018.04.3535

Final Abstract Number: 22.006
Session: Oral Presenations: Arboviruses
Date: Friday, March 2, 2018
Time: 17:00-18:00
Room: Retiro A

Type: Oral Presentation

Seroepidemiology of Arbovirus in pregnant women participating in Cohort study in Jundiai, SP, Brazil: Preliminaries results of Cohort Zika - Jundiaí

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Background: Arboviruses are transmitted by arthropods. The most common in Brazil, are: Yellow Fever, Dengue and recently Chikungunya and Zika. Zika has emerged associated with cases of fever, arthralgia, Guillain-Barré syndrome and congenital malformation. Beyond, cases of microcephaly in newborn were associations with ZIKV infections. Further studies are needed to confirm this association.

Methods & Materials: From May 2016 to date, 757 pregnant women are being followed up in a cohort study. Blood, saliva and urine were collected from pregnant women and newborns. In the first sample of the mothers the ELISA was performed to detect IgG immunoglobulins anti ZIKV, CHIKV and DENV. The ELISA was performed in 728 (96.2%) of this women.

Results: ZIKV ELISA was performed in 350 pregnant women: 15 (4.2%) positive, 334 (95.4%) negative and one (0.3%) undetermined. Among ZIKV negative cases, 48 (14.4%) were ZIKV positive by RT-qPCR. Of the positive cases, 3 (0.9%) were also ZIKV positive by RT-qPCR. CHIKV ELISA was performed in 709 pregnant women, 63 (8.9%) positive,629 (88.7%) negative and 17 (2.4%) undetermined. DENV ELISA was performed in 253 pregnant women, 55 (21.7%) positive,195 (77.1%) negative and 2 (0.8%) undetermined. The diagnosis for three arboviruses were performed in 168 women: Four (2.4%) were ZIKV positive, 4 (2.4%) CHIVK, 31 (18.5%) DENV, 3 (1.8%) ZIKV and DENV and one (0.6%) CHIKV and DENV. Nine (5.4%) of theses mothers were ZIKV positive by RT-qPCR. Two (1.2%) mothers had children ZIKV positive by RT-qPCR. Three (1.8%) newborns with microcephaly were detected; one positive for DENV and the other two were negative for any Arboviruses studied.

Conclusion: The individually diagnosis, detected high occurrence of ZIKV (14.4%) and DENV (21.7%) and lower occurrence of CHIKV 63 (8.9%). Cases of co-infection can be detected, at lower levels. The number of patients with complete diagnosis is small, yet. But IgG ELISAs will be performed on remaining mothers and all newborns and IgM ELISA will be performed for all participants.

Financial support: FAPESP (2016 / 08578-0)

https://doi.org/10.1016/j.ijid.2018.04.3536

Final Abstract Number: 24.001
Session: Clinical Applications of Whole Genome Sequencing
Date: Friday, March 2, 2018
Time: 17:00-18:00
Room: La Pampa

Type: Invited Presentation

Whole genome sequencing for diagnosing infectious diseases

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Given the complex nature of diagnostic practices for infectious diseases, the one unifying characteristic of the agents investigated is their possession of a genome. While many molecular diagnostic tests investigate parts of the genome, whole-genome sequencing (WGS) has emerged as a cost-effective and convenient approach for answering the varied microbiological questions that arise. In that regard, four essential tasks are addressed: species identification, phenotypic characterization, e.g., antimicrobial resistance and virulence, evolutionary traits and pathogen tracking.

Some of the benefits already available include, in addition to the ability to fully characterize prospective and retrospective isolates, the ability to be applied directly to clinical samples for simultaneous identification and predicting antimicrobial susceptibilities (even in culture-negative cases); identification in polymicrobial samples; generating regional phylogenomic sublineages; correlation of genomic features with strains of clinical importance; tracking of multidrug resistant organisms in hospitals and communities. These benefits, while largely seen in reports from North America and Europe, are also being observed in Latin America and the Caribbean. Further, WGS allows for estimation of mutation rates among isolates, as well as assessment of the rates and breadth of horizontal gene flow within and between species, the evolution of new virulence traits, and the role of host genetics in host-pathogen interactions, all with the view to develop novel therapeutic interventions.

The main directions of WGS applications include diagnosis and control of local and regional infectious diseases; detection of multidrug resistance (MDR) and virulence characteristics; surveillance of pathogen evolution and transmission dynamics; development of new (portable) diagnostic tests and assays for use in clinics and outpatient facilities; and discovery of novel antimicrobial drugs and therapeutics and assessment of their prevention and control. Given that pathogens occur in complex microbial communities, further elaborations to explore the pathobiome using metagenomics and high-throughput sequencing will assist with the understanding of the forces supporting population structure, including pathogen plasticity.

https://doi.org/10.1016/j.ijid.2018.04.3537