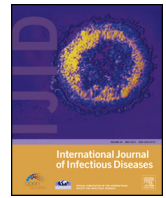




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Case Report

Zika, dengue, and chikungunya co-infection in a pregnant woman from Colombia

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SUMMARY

The clinical findings of a pregnant woman from Colombia with a triple co-infection caused by dengue, chikungunya, and Zika viruses are described. Weekly obstetric ultrasounds from 14.6 to 29 weeks of gestation were normal. She remains under follow-up and management according to the standard guidelines for the management of Zika virus-infected pregnant women.

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1. Introduction

Dengue virus (DENV), chikungunya virus (CHIKV), and Zika virus (ZIKV) are arboviruses that cause ongoing epidemics in several countries of Latin America and the Pacific.^{1,2} CHIKV, DENV, and ZIKV affect pregnancies, with a wide observed spectrum of outcomes. Adverse outcomes of CHIKV infections in pregnancy have been reported in Colombia and on the island of La Réunion, primarily encephalopathy.³ Severe dengue has been reported in pregnant women.⁴ There is a growing body of evidence suggesting that ZIKV is responsible for severe congenital complications mainly consisting of microcephaly.⁵ The extent of congenital complications related to ZIKV is, however, still a matter of debate,

principally because only a small proportion of cases have been investigated fully.⁵

Co-infections with these three viruses have been reported,⁶ but the effect of co-infections during pregnancy is unknown. In addition, in the context of the current ZIKV outbreak, which has become the focus of much attention, other pathogens with a potential impact in pregnancy may receive less attention. The case of a pregnant woman with molecular confirmation of a triple co-infection caused by DENV, CHIKV, and ZIKV is reported herein.

2. Case report

A 33-year-old woman from Sincelejo, Sucre, Colombia, an area known to have active co-circulation of DENV serotypes 1–4, CHIKV, and ZIKV,⁶ presented at 14.6 weeks of her third pregnancy with a clinical illness, that consist of non-purulent bilateral conjunctivitis, an intense pruritic maculopapular rash on the upper limbs, thorax, and abdomen, a headache, mild-to-intense bilateral metacarpophalangeal and wrist arthralgia, and limb edema, particularly of

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the ankles, 1 day before consultation. She denied myalgia, retro-orbital pain, hemorrhages, or abdominal pain. She reported that arboviral infections had not affected her or her family.

The patient had previously been referred with a provisional diagnosis of mitral valve prolapse in 2013. She had normal electrocardiogram findings, and an echocardiogram confirmed the diagnosis. She had a history of umbilical hernia in 2012 and cholecystitis in 2015, leading to a cholecystectomy. She had a single spontaneous abortion in early 2014 and had previously given birth to a healthy female infant by uncomplicated vaginal delivery in 2007. She did not report any history of blood transfusion or organ transplant.

Thick and thin blood smears for malaria were negative. Physical examination revealed cervical lymphadenopathy, non-purulent conjunctivitis, bipalpebral edema, and painful edema in the lower limbs, with an extensive maculopapular rash affecting the upper and lower limbs and abdomen, with Pastia lines (Thompson's sign). She did not have hepatomegaly or splenomegaly, either clinically or on ultrasound, either at presentation or during follow-up (Figure 1a). Her pulse rate was 88 beats/min, blood pressure was 100/60 mmHg, and temperature was 36.7 °C. A holosystolic murmur was heard on cardiac auscultation. A neurological examination was normal. Obstetric ultrasound findings were normal for gestational age, with a biparietal diameter of

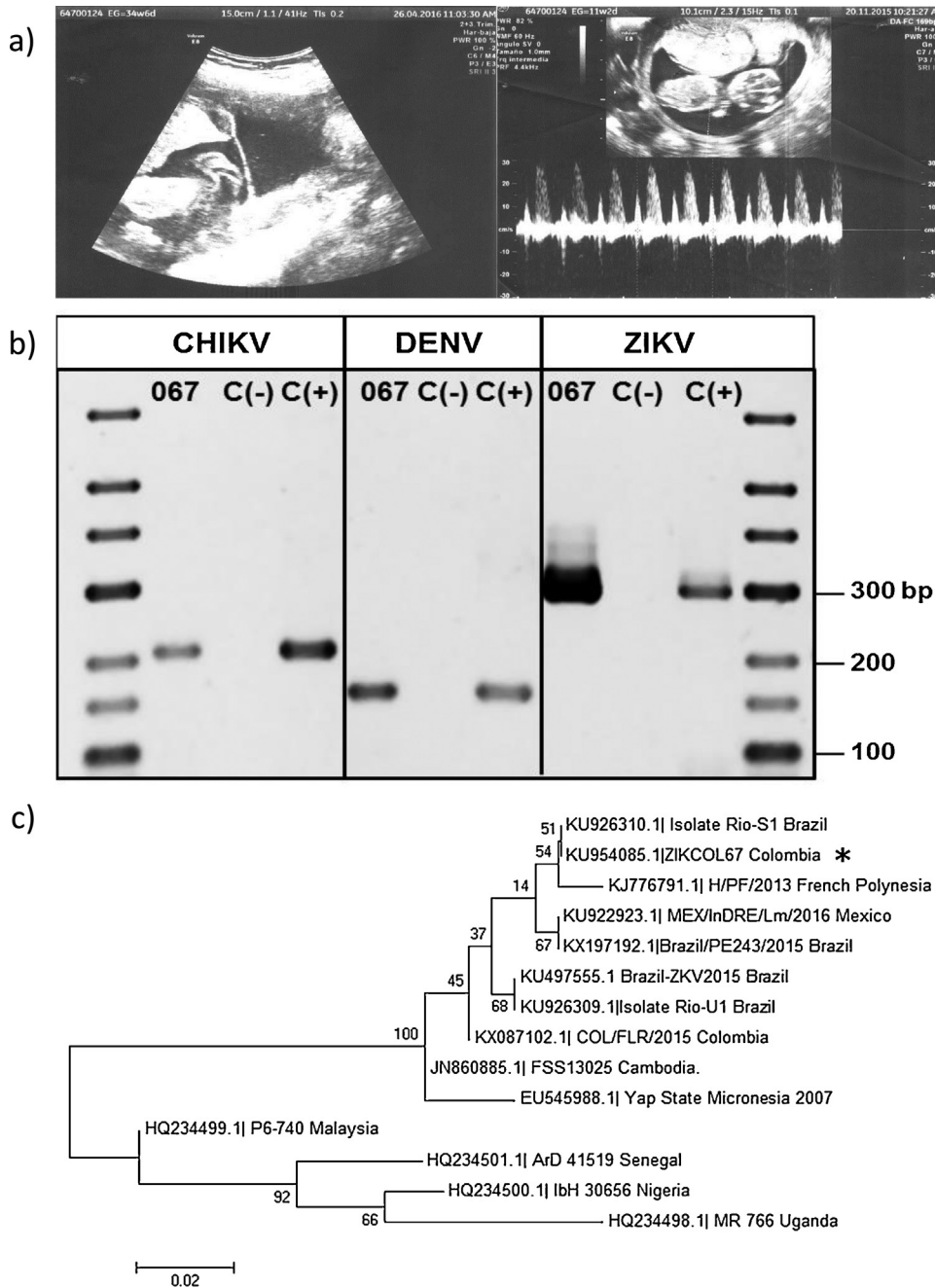


Figure 1. Findings in the pregnant woman from Colombia co-infected with Zika (ZIKV), dengue (DENV), and chikungunya (CHIKV). (a) Ultrasounds at 29 weeks of gestation, showing no alterations. (b) Agarose gel analysis of PCR products for DENV, CHIKV, and ZIKV (067, patient samples; C(-), negative control; C(+), positive control, supernatants of infected cultures). (c) Phylogenetic analysis of nucleic acid sequences was performed using 250 nucleotides of the ZIKV envelope protein. GenBank accession numbers for the complete genomes are given. The tree was inferred using the maximum likelihood algorithm based on the Tamura-parameter model as implemented in MEGA 6. The numbers shown to the left of the nodes represent bootstrap support values (1000 replicates). The asterisk indicates the sample isolated and reported in this article.

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