

From: "ROOT" <root@sctimst.ac.in>
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Date: 10/22/2024 08:48 AM
Subject: Invitation for CGR

From: "RRC Rishikesh (rrcrishikesh@aiimsrishikesh.edu.in)" <rrcrishikesh@aiimsrishikesh.edu.in>
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Cc: Meenu Singh <meenusingh4@gmail.com>
Date: Mon, 21 Oct 2024 18:09:45 +0530
Subject: [EXTERNAL MAIL] Invitation for CGR

Greetings from AIIMS, Rishikesh !!

The CGR will be held on the **Oct 22, 2024** in **CPD Hall**, AIIMS Rishikesh from **8:00 AM to 9:00 AM**.
You can join online through the following link:

Meeting link:
<https://aiimsrishikesh.webex.com/j.php?MTID=md7010ad381b0ca5128a19bc8715e4fc3> Tuesday,
Oct 22, 2024, 8:00 AM | (UTC+05:30) Chennai, Kolkata, Mumbai, New Delhi

Meeting number: 2518 747 6043
Meeting password: 221024

Thanks & Regards
Regional Resource Centre
Dept of Telemedicine
AIIMS Rishikesh

DEPARTMENT OF MICROBIOLOGY

(JOURNAL CLUB – 22ND OCTOBER 2024

Name of article	Outbreak of Oropouche virus in frontier regions in western Amazon
Journal	Microbiology Spectrum, American Society for Microbiology.
Impact Factor of Journal	3.9
Presenter	Dr. Pratiksha Kamboj
Moderator	Dr. Sukriti Yadav

Abstract

Background – Oropouche virus (OROV) is characterized as a re-emerging arbovirus of great concern for public health, being responsible for several outbreaks of acute fever identified in Latin American countries. The incidence of reports of this virus is intrinsically favoured by environmental conditions, in which such characteristics are related to the increase and distribution of the vector population to areas of human traffic. Moreover, there is a problem regarding the lack of diagnosis that aggregates the success of the etiologic agent.

Methodology & Results –The researchers utilized molecular techniques – PCR, sequencing followed by phylogenetic analysis. They identified 27 positive cases of the OROV circulating in border locations in western Amazon, with 44.44% (12/27) of the cohort characterized as infected individuals with reported symptoms, mainly ranging from fever, myalgia, and back pain. Among the positive samples, it was possible to obtain a total of 48.14% (13/27) samples to analyze the S and M segments of OROV, which showed similarities among the Brazilian sequences. Thus, it was possible to verify the circulation of the OROV in the region areas, in which the tracking of neglected arboviruses is necessary for the genomic surveillance of emerging and re-emerging viruses.

Relevance in the present scenario – The clinical presentation of OROV significantly overlaps with dengue & Zika virus infections. Thus, there is an overall delayed clinical diagnosis in the endemic regions. OROV also shares its vectors with other arbovirus which can potentially be responsible for outbreaks and dual infection. With increasing urbanization & climate changes reemergence of uncommon infection has taken a spotlight with OROV being one of them. Hence there is an acute need to understand this virus.