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CO-INFECTION OF COVID-19 WITH DENGUE AND CHIKUNGUNYA: A STUDY FROM A TERTIARY CARE HOSPITAL

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Abstract

Background: The present study is aimed to identify the co-infection of Covid-19 with Dengue and/or Chikungunya. The present study was conducted from June 2021 to August 2021. **Materials and Methods:** 125 serum samples were collected from febrile patients of all age groups suffering from cold and fever. These samples were tested for the presence of Covid-19 antibodies. The Covid-19 positive sample were tested for the Dengue and/or Chikungunya infections by using IgM ELISA. **Result:** Among 125 samples, 91 samples were tested positive for SARS-CoV-2 antibodies. In these 91 Covid-19 positive samples, 3 samples were Dengue IgM positive and 14 were positive for Chikungunya by IgM ELISA. **Conclusion:** In the present study, antibodies against CHIKV, DENV were detected in Covid-19 positive patients. 14 cases of coinfection between Covid-19 and Chikungunya and 3 cases of coinfection between Covid-19 and Dengue were reported from the present study.

INTRODUCTION

Dengue viruses (DENV) cause classic Dengue fever, Dengue Hemorrhage Fever (DHF) and Dengue Shock Syndrome (DSS) with four serotypes (DENV-1, DENV-2, DENV-3, DENV-4).^[1,2] The case fatality infection with Dengue ranges between 0.5% to 3.5%.^[3] Thrombocytopenia, hemorrhagic symptoms, hypotension, and shock are the hallmarks of Dengue Hemorrhagic Fever and Dengue Shock Syndrome, which can result in organ failure and death.^[4] Chikungunya virus (CHIKV) is a alphavirus and is responsible for acute and chronic articular manifestations.^[5] Since the 1950s, CHIKV has been observed to circulate in developing countries causing occasional outbreaks in Asia and Africa.^[6] Since 2004, CHIKV has been an emerging pathogen, causing large outbreaks in many islands in the Indian Ocean and in the Indian subcontinent. In the year 2005-06 alone, over a million cases of CHIKV infection were reported from different states.^[7] SARS-CoV-2 is a beta coronavirus belonging to the subgenus Sarbecovirus. The global spread of SARS-CoV-2 and the thousands of deaths caused by coronavirus disease (COVID-19) led the World Health Organization to declare a pandemic on 12 March 2020.^[8] SARS-CoV-2 virus primarily affects the lower respiratory tract. The most commonly reported symptoms include fever, cough,

shortness of breath, anosmia, ageusia.^[9] The main recognized route for the transmission is through droplets and aerosols in air when the infected persons coughs or sneezes.^[10] The mean incubation period is 4-5 days. The combined case fatality rate was 2.3%.^[11] The standard diagnosis is the identification of the viral genome targets by Real Time Polymerase Chain Reaction (RT-PCR) during the first week of symptoms. Laboratory tests such as complete blood count, C-Reactive Protein, CRP, Ddimer, clotting tests, lactate dehydrogenase (LDH) identify risk of disease with greater severity.^[12] Due to overlapping of symptoms of these arboviral infections and SARS-CoV-2, there is a chance of co infection which may increase the severity of disease. The purpose of this study is to identify the coinfection of SARS-CoV-2 with Dengue and Chikungunya and to show the necessity of correct diagnosis in order to reduce the risk of wrong treatment due to false positivity occurred by crossreactivity which can lead to life threatening conditions.

MATERIALS AND METHODS

Sample Collection

The study was conducted at a tertiary care centre in Hyderabad, India between June 2021 and August 2021. A questionnaire was used to record special notes regarding age, sex, symptoms, residence and febrile history. Individuals of all age groups presenting symptoms of fever, cold and cough were included. The blood samples were collected from these patients and centrifuged at 1000rpm at 3 minutes to separate the serum. The collected serum was then stored at -20°C until it was tested.

ELISA

ELISA was performed for the detection of antibodies towards SARS-CoV-2 using Wantai CoV Antibody ELISA kit (Beijing, China) according to manufacturer's instructions. Further, the positive Covid-19 samples were tested for dengue IgM (Dengue Standard E, SD Biosensor Pvt. Ltd. India) and Chikungunya IgM antibodies (NIV MAC ELISA kit, India) according to the manufacturer's instructions. Results are interpreted using absorbance value at 450nm.

RESULTS

A total of 125 samples were tested for SARS-CoV2 antibodies, among which, 91 (33 males and 58 females) were seropositive. Of 91 SARS-CoV2 antibody positive samples, 3 were positive for Dengue IgM antibodies (all males) and 14 were positive for Chikungunya IgM antibodies (10 females and 4 males) (Fig 1). Among the 3 Dengue positive samples, 2 has showed equivocal for Chikungunya. Age wise distribution of the DENV infected and CHIKV infected samples revealed that majority of the patients were in the age group of 21-40 years. Fever was seen in all the cases. The patients positive for Dengue has sore throat, running nose, high grade fever, headache, arthalgia, myalgia and low platelet count. Among the positive samples, it was observed that a higher percentage of monoinfected patients with DENV were males (100%) compared to mono-infected patients with CHIKV where females (71.4%) outnumbered males (28.5%). However, there was no gender-based difference of infections among males and females of co-infected patients.

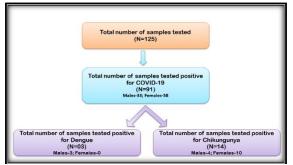


Figure 1: Flow diagram for the identification of coinfection between SARS-CoV-2 and Arboviral infections.

DISCUSSION

In the current study, we analyzed 125 samples from febrile patients for SARS-CoV2 antibodies. 91 samples were reactive for SARS-CoV2. Among these 91 patients there were 33 males and 58 females. Three samples were positive for Dengue IgM antibodies and 14 were positive for Chikungunya IgM antibodies. The 3 positives for Dengue antibodies, OD values for 2 samples fell in between the positive and negative cutoff and thus were reported equivocal for Chikungunya. All the 3 samples tested positive for Dengue IgM were males. Out of 14 samples which tested positive for Chikungunya, 10 were females and 4 were males. Co-infection with SARS-CoV-2 and Dengue resulted in worse fatality rates.^[13] Patients with SARS-CoV-2 had the same clinical symptoms as those with Dengue.^[14] Both Dengue fever and SARS-CoV-2 have similar symptoms and laboratory findings, paving way to potentially dangerous scenarios such as incorrect or delayed initial treatment.^[15] Hilmy et al. described two reports of dengue and SARS-CoV-2 coinfection in a recent study, depicting symptoms of dengue fever in the first case and further showing symptoms of Covid-19 after 5 days.^[16] Further Niraj N Mahajan et.al reported a coinfection of Malaria and Dengue in pregnant women with SARS-CoV-2.^[17] Recently, the coinfection of SARS-CoV-2 and Dengue was reported from Pakistan, and the study's findings revealed that the mortality rate in SARS-CoV-2 patients coinfected with Dengue is comparatively higher than in SARS-CoV-2 patients only.^[18] Infections with SARS-CoV-2, DENV, and CHIKV have all been linked to an increase in inflammatory cytokines.^[19] Our data also suggested the possible co infection between SARS-CoV2 and arboviral infections. Co infection between SARS-CoV-2 and dengue virus could be due to similarities in the structures of these two viruses' outer proteins, a study done by Lustig et al.^[20] The study done by Fien Vanroye et al confirmed that cross-reactivity in SARS-CoV-2 Ab RDTs can be caused by current malaria, recent malaria, and the presence of malaria antibodies.^[21] There has been increase in the cases of coinfection between covid19 and arbovirus.^[22,23] In the current study we emphasis on the co infection between covid19 and arboviral infections, a total of 125 samples with acute febrile illness were collected. Females were more infected to Chikungunya than males. Possible co infection of Dengue-Chikungunya IgM antibodies developed after infection with SARS-CoV-2. When suspecting co infections with other arboviruses, it is important to perform the molecular testing to eliminate serological overlap. Though it is not clear how substantial is this co infection and its magnitude it is recommended to perform molecular testing along serological testing.

CONCLUSION

The detection of co-infection between arboviral infections and SARS-CoV-2 by only serological test data, leads to uncertainty regarding epidemiological data. The overlapping of the symptoms and misdiagnosis also hinders clinical management, which in the absence of adequate medication, worsens the transmission and clinical picture of both the diseases. Co infection of SARS-CoV-2 and arboviral infections are possible where it can be confirmed by serological screening tests supported with molecular testing. If the results of both serology and molecular tests conducted and interpreted properly, that may help to correctly identify most (but not all) of those who have had a recent co-infection.

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