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Research Article

Sero-Detection of Dengue Virus in Febrile Patients Attending Nyala Teaching Hospital, Nyala, South Darfur State, Sudan

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Abstract

Dengue virus infection is one of the major global public health problems. It is caused by one of the four dengue virus (DENV) serotypes that are transmitted by Aedes mosquitoes. Following infection, an individual remains vulnerable to re-infection with a different serotype of the DENV. The infection usually occurs with clinical manifestations ranging from an asymptomatic or mild febrile illness as classical dengue fever to the potentially life-threatening illness, dengue hemorrhagic fever and dengue shock syndrome.

This study aimed to assess the previous exposure of all febrile patients attending out-patient clinics to Dengue virus in Nyala in South Darfur State.

A descriptive cross-sectional study was carried out on febrile patients attending to Nyala Teaching Hospital to Dengue virus in Nyala in South Darfur State. Sixty sera samples were collected and preserved at -20 C till analysis. An Indirect-ELISA assay was used to detect Dengue virus IgG antibodies.

Out of 60 sera samples, 46(76.6%) were reactive to Dengue virus IgG antibodies, whereas 14 (23.3%) were non-reactive.

The high percentage of previous exposure to Dengue virus in that area, this finding indicated for either successful vaccination campaigns or sporadic cases of Dengue virus infections particularly, that area are highly endemic with Aedes mosquitoes. Therefore, we are highly recommended that, a new study with larger sample size considering detection of IgM antibodies to determine the recent exposures and molecular techniques, like polymerase chain reaction to detect the actual co-existence of Dengue virus.

Keywords: *Dengue Virus; Sero-Detection; Febrile Patients; Nyala; Sudan*

Introduction

Dengue is the most common mosquito-borne infection. About 2.5 billion people are estimated to be at risk of infection. Out of 50 million infections occurring each year: 500,000 are hospitalized [1,2]. Due to many factors such as urbanization and air travel, dengue infection has become a major public health problem in the tropics [3].

Dengue fever (DF) is classified into two groups: Uncomplicated and severe [World Health Organization, 2009]. This has replaced the older classification According to WHO classification, dengue is divided into undifferentiated fever, DF, and DHF [4,5].

Dengue burden have been rising in the recent years and has become a public health problem of global importance. The World Health Organization (WHO) estimates that two-fifths of the world's population is at risk of dengue infection [6].

Immunoglobulin G is an important antibody which appears 5 - 7 days of the Dengue virus infection and reaches the highest titers three weeks post-infection. It would thereafter decrease, but without total disappearance, leaving the host body with immunological evidence of previous exposure [7]. The re-infection could however lead to abnormal increase of the IgG titer, causing severe state of the disease such as dengue haemorrhagic, or dengue shock syndrome [8].

Regionally, it is known that Dengue virus has circulated in the African continent since the early 20th century [9]. Dengue is a considerable contributor of febrile illness causes in Sudan health care facilities. Dengue serotype 3 was found in outbreak in children in Port Sudan in 2005 [10]. Moreover, presence of DENV-1, DENV-2 and DENV-3 was confirmed in the Port city of Jeddah just across the Red Sea with connections with Port Sudan [8].Lately, in 2011 an outbreak of non-specific symptoms was detected through the National surveillance system in Lagawa locality within south Kordofan [11].

Materials and Methods

Study design

A descriptive cross-sectional study.

Study area and Study population

This study area was conducted in Nyala, South Darfur State, Sudan on the febrile patients admitted to Nyala Teaching Hospital. All febrile patients diagnosed with malaria were excluded from this study. Both genders were included in this study after verbal consents have been taken from patients themselves and their guardians for patients less than 18 years old.

Sample size and study duration

A Sixty febrile individual of both sexes with different age groups were included in this study during May and March 2017.

Ethical consideration

Permission to carry out the study was taken from Nyala Teaching Hospital. The parents of febrile patients informed for the purpose of the study before collection of the specimens, and verbal consent was taken.

Laboratory analysis

A total of 60 sera sample were collected and then preserved at -20 C till analysis. The Dengue virus IgG antibodies detection was done using Indirect-ELISA technique according to EUROIMMUN, Germany protocol.

Data analysis

The data were analyzed by using Statistical Package for Social Science software (Chi-square).

Results

A total of 60 sera sample were collected from febrile illness Patients for screening of IgG antibodies of DENV. Out of 60 sera samples, 46(76.6%) were reactive to Dengue virus IgG antibodies, whereas 14 (23.3%) were non-reactive. Both genders and different age groups were showed equal opportunities for previous exposure to Dengue virus during their life with P-value (0.29) and (0.13), table 1 and 2 respectively.

Gender	Reactive	Non-reactive	Total	P-value
Female	19 (31.6%)	8 (13.3%)	27 (45%)	0.29
Male	27 (45%)	6 (10%)	33 (55%)	

Table 1: *Prevalence of Dengue virus IgG antibodies among gender.*

Age group	Reactive	Non-reactive	Total	P-value
≤ 20 years	16(26.9%)	9 (14.9%)	15 (41.8%)	0.13
21 - 40 years	26 (43.3%)	4 (6.6%)	30 (49.9%)	
≥ 41 years	4 (6.6%)	1 (1.6%)	5 (8.3%)	

Table 2: *Prevalence of Dengue virus IgG antibodies among age groups.*

Discussion

The current study was aimed to assess the prevalence of Dengue virus IgG antibodies that circulated in febrile patients attending to Nyala Teaching Hospital in Nyala, South Darfur State, Sudan. Dengue virus IgG antibodies are generally considered as an indicator for cumulative infection [12]. Our study showed higher prevalence of Dengue virus IgG antibodies among study population (76.6%) when compared with similar study was conducted in the Eastern parts of Sudan which found that the prevalence of Dengue virus IgG antibodies ranging between 6 to 9.4%, and in some neighboring countries as high as 14 to 31.33% [8]. This study also demonstrated that there was no statistical association between gender, age and Dengue virus exposure. The circulation of dengue infection in the study area could have been ongoing for long period of time, although, with little attention since most of the febrile conditions in Sudan are presumptively diagnosed as malaria. The wide distribution of dengue fever across the world has been premised on several factors which include among many others: the proliferation in breeding of Aedes mosquitoes, and movement of travelers from endemic countries [13].

In spite of the small sample size of this study, the results of the present study have significant epidemiological implications; most importantly that dengue fever is probably alien to the study area where all febrile conditions are presumptively diagnosed as malaria [14].

Most of the health facilities in the study area lack diagnostic tools for the detection of dengue viruses. Many patients presumptively diagnosed for malaria could have been misdiagnosed, while those with co-infection with dengue fever would have been mishandled; as the feverish conditions likely to persist after successful malaria treatment due to the presence of an 'undetected infection'. In most cases, these unresolved treatments are considered as 'fever of unknown origin' or malaria treatment failure. This could culminate in drug resistance by malaria parasite due to the drug abuse/ pressure or fatal casualties in patients' sequel to misdiagnosis.

Conclusion

The high percentage of previous exposure to Dengue virus in that area, this finding indicated for either successful vaccination campaigns or sporadic cases of Dengue virus infections particularly, that area are highly endemic with Aedes mosquitoes. Therefore, we are highly recommended that, a new study with larger sample size considering detection of IgM antibodies to determine the recent exposures and molecular techniques, like polymerase chain reaction to detect the actual co-existence of Dengue virus.

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