

A Study on clinical profile of severe dengue fever in children

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Abstract

Dengue virus, a mosquito-borne flavivirus, is the causative agent, currently one of the most significant emerging disease challenges to global health. The dengue virus are single-stranded positive-sense RNA viruses with a genome of about 11000 bases that codes for three structural proteins, C (core protein), M (membrane protein), E (envelope protein); 7 nonstructural proteins, NS1, NS2a, NS2b, NS3, NS4a, NS4b, NS5; and short non-coding regions on the 5' and 3' ends. This was a case control study design in which 201 cases of dengue fever admitted in the pediatric emergency ward, were enrolled. After taking written informed consent, data were collected in a predesigned semi structured questionnaire regarding Socio-Demographic profile, medical history, clinical and hematological profile and outcome. 8(4%) of cases had positive family h/o dengue fever, 3(1.5%) cases had positive past h/o dengue fever and 8(4%) cases had positive h/o travel to dengue endemic areas. 201(100%) cases had fever, 94(46.8%) had persistent vomiting, 91(45.3%) had anorexia, 78(38.8%) had abdominal pain, 59(29.4%) had headache, 30(14.9%) had rashes, 16(8%) had facial puffiness, 14(7%) had convulsions and 12(6%) had abdominal distension.

Keyword: clinical profile, severe dengue fever, children

Introduction

The first epidemic of dengue occurred in 1635 in the French west Indies. Prior to 1970, only 9 countries have experienced dengue hemorrhagic fever; since then the number has increased to more than 4 fold. The disease is now endemic in many countries. An estimated 2.5 billion people in about 100 countries are at risk of acquiring dengue viral infection with more than 50 million new infections, 20000 to 25000 deaths, mainly in children^[1, 2].

Since 2000, epidemic dengue has spread to new areas and has increased in already affected regions. In 2003 eight countries-India, Bangladesh, Maldives, Indonesia, Myanmar, Sri Lanka, Timor-Leste and Thailand reported Dengue cases. Reported case fatality rate in these regions is approximately 1%. But due to focal outbreaks away from urban areas, India, Indonesia, and Myanmar have reported case fatality rates of 3-5%^[3].

Dengue virus, a mosquito-borne flavivirus, is the causative agent, currently one of the most significant emerging disease challenges to global health. The dengue virus are single-stranded positive-sense RNA viruses with a genome of about 11000 bases that codes for three structural proteins, C (core protein), M (membrane protein), E (envelope protein); 7

nonstructural proteins, NS1, NS2a, NS2b, NS3, NS4a, NS4b, NS5; and short non-coding regions on the 5' and 3' ends. The 4 serotypes are DEN 1, DEN 2, DEN 3, DEN 4. All these 4 serotypes cause dengue epidemics. Asian serotypes DEN-2 and DEN-3 are associated with severe dengue^[4].

Aedes aegypti is a mosquito that can spread Dengue, Chikungunya yellow fever and other diseases. The mosquito is a small, dark of approximately 4 to 7 mm with typical white markings on the legs and thorax. Females are larger than males. *Aedes aegypti* is a day biting mosquito. The mosquito is most active during daylight, for 2 to 3 hours after sunrise and several hours before sunset. The mosquito rests indoors, in dark places. Outside, they rest in cool shaded areas. The males do not bite humans or animals and they live on fruit. The females feed on fruit and also on blood. When seen under a microscope, male mouth parts are modified for nectar feeding, and female mouth parts are modified for blood feeding. Feeding on humans generally occurs at one to two hour intervals^[5, 6].

Methodology

This was a case control study design in which 201 cases of dengue fever admitted in the pediatric emergency ward, were enrolled. After taking written informed consent, data were collected in a predesigned semi structured questionnaire regarding Socio-Demographic profile, medical history, clinical and hematological profile and outcome. Investigations such as Complete blood count, Blood test (Serology) for Dengue fever, urine routine, serum electrolytes, random blood sugar, WIDAL/Blood culture, Liver enzymes, Chest x ray, Ultrasound abdomen, PT, aPTT, INR were done based on the clinical scenario and if necessary, blood urea, serum creatinine, CSF analysis, 2D echo, CT scan brain/MRI was also done. Non randomized purposive sampling technique will be adopted to select both cases and controls.

Since this study is a time bound study, where a series of dengue cases (as per inclusion criteria) were enrolled during a study period of one year i.e., from November 2017 to October 2018. During this study period, we were able to enroll a total of 201 cases, out of which 142 were only dengue fever, 32 were dengue fever with warning signs and 27 were severe dengue fever.

Inclusion criteria

- I) **For cases:** Any child, between age 1 month to 12 years, having tested positive for dengue NS1 antigen in serum or tested positive for antibodies (IgM) in serum against dengue fever virus along with complications such as shock or fluid accumulation with respiratory distress or severe bleeding or severe organ involvement such as liver, CNS, heart and other organs.
- II) **For controls:** Any child, between age 1 month to 12 years, having tested positive for dengue NS1 antigen in serum or tested positive for antibodies (IgM) in serum against dengue fever virus without any complications.

Exclusion criteria

- 1) Children having other co-infections like malaria, typhoid or infective hepatitis, interfering with interpretation of the laboratory data.
- 2) Immunocompromised subjects.
- 3) Children less than 1 month.
- 4) Patients discharged against medical advice.

Results

Table 1: Age wise distribution of the study subjects

Age group	Frequency	Percent
< 1 yr	19	9.5
1-5 yrs	65	32.3
5-10 yrs	85	42.3
10-15 yrs	32	15.9
Total	201	100
Mean \pm SD	6.59 \pm 3.96	

Among the 201 cases included in the study, 19(9.5%) were less than 1 yr, 65(32.3%) cases were 1-5 yrs, 85(42.3%) were between 5-10 yrs and 32(15.9%) were between 10-15 yrs of age.

Table 2: Sex wise distribution of the study subjects

Sex	Frequency	Percent
Female	78	38.8
Male	123	61.2
Total	201	100

78(38.8%) cases were females and 123(61.2%) cases were males.

Table 3: History of dengue among the study subjects (n=201)

History of dengue	Frequency	Percentage
Family history		
Yes	8	4.0
No	193	96.0
Past history		
Yes	3	1.5
No	198	98.5
Travel history		
Yes	8	4.0
No	193	96.0

8(4%) of cases had positive family h/o dengue fever, 3(1.5%) cases had positive past h/o dengue fever and 8(4%) cases had positive h/o travel to dengue endemic areas.

Table 4: Symptomatology among the study subjects (n=201)

Symptoms	Frequency	Percentage
Fever	201	100
Abdominal pain	78	38.8
Persisting vomiting	94	46.8
Anorexia	91	45.3
Headache	59	29.4
Rashes	30	14.9
Convulsions	14	7.0
Abdominal distension	12	6.0
Facial puffiness	16	8.0

201(100%) cases had fever, 94(46.8%) had persistent vomiting, 91(45.3%) had anorexia, 78(38.8%) had abdominal pain, 59(29.4%) had headache, 30(14.9%) had rashes, 16

(8%) had facial puffiness, 14(7%) had convulsions and 12(6%) had abdominal distension.

Table 5: Distribution of study subjects based on bleeding manifestation

Bleeding MF	Frequency	Percent
Yes	31	15.4
No	170	84.6
Total	201	100

Table 6: Bleeding manifestations among the study subjects (n=201)

Bleeding MF	Frequency	Percentage
Malena	19	9.5
Epistaxis	9	4.5
Hematemesis	7	3.5
Hematuria	2	1
Bleeding gums	2	1

Bleeding manifestations were seen in 31(15.4%) of cases with 19(9.5%) had melena, 9(4.5%) had epistaxis, 7(3.5%) had hematemesis and 2(1%) had hematuria and bleeding gums. 170(84.6%) cases had no bleeding manifestations.

Table 7: Clinical type of dengue among the study subjects

Type	Frequency	Percent
Dengue fever	142	70.6
Dengue with warning signs	32	15.9
Severe Dengue	27	13.4
Total	201	100.0

142(70.6%) had dengue fever, 32(15.9%) had dengue fever with warning signs, 27(13.4%) had severe dengue fever.

Discussion

We conducted this study based on the new WHO classification 2012 of dengue fever, to know which factors can predict severity so as to facilitate timely intervention. In our study out of 201 patients with dengue, 142 were classified as dengue fever, 32 as DF with warning signs and 27 children as severe dengue. However Prasad D *et al.* found 82.1% as severe dengue and Sahana *et al.* found 24.7%^[7].

This variance in the subject distribution may be attributable to the timing of admission, the awareness in the draining community, timely intervention.

The mean age of presentation in our study was 6.59±3.96 years with 42.3% of the children in the 5-10 year age group, a finding similar to that by Gomber S *et al.* and Rasul *et al.*^[8,9].

This could be due to this age group prone for frequent mosquito bites due to their outdoor activities, but our study does not prove any significant association between age and the severity of dengue fever. Studies done by Shah I *et al.* and Rachel C *et al.* found younger age as one of the predictive markers for Dengue shock syndrome and dengue hemorrhagic fever^[10].

The male:female ratio in our study was 1.57:1 similar to study by Rasul *et al.* Though studies by Anders KL *et al.* and Phuong CX *et al.* found increased risk of shock and death among females, our study did not have a significant statistical association similar to studies by Pongpan S and Ahmed FU *et al.*^[11].

There was no significant association was found between nutritional status and the severity of dengue fever. Pichainarong stated that severe dengue is rarely seen in children with protein energy malnutrition^[12].

Many studies has been done previously to find out the risk factors significantly associated

with severity of dengue fever like bleeding manifestations, leucopenia, raising hematocrit, hypotension, narrow pulse pressure, elevated SGOT/SGPT levels, deranged PT/APTT/INR etc. which are similar to our study.

Conclusion

The presence of bleeding manifestations was having a statistically significant association with the severity of dengue fever like many other studies. The most common bleeding manifestations found in our study was melena and epistaxis followed by others.

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