

Title

**Viral Load and Genotype Study of Recent HEV
Outbreak in Chittagong, Bangladesh**

Investigators

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Introduction

- Hepatitis viruses constitute the mainstay of liver diseases in Bangladesh. Among the different viruses hepatitis B, C, and E contributing the most.

Introduction

- Hepatitis E virus is the leading cause of acute hepatitis in this country and it causes a outbreaks in different regions like recently in 2018 at Chittagong, Bangladesh.

Introduction

- Being a member of the developing world with significant poverty and poor hygienic conditions, not unexpectedly Bangladesh offers favorable conditions for nurturing hepatitis E virus (HEV) infection.

Introduction

- HEV isolates have been divided into at least four genotypes, and 24 subtypes. Genotype 1 is mostly found in isolates from Pakistan, Nepal, India and China.
- Genotype 2 was detected from an epidemic outbreak in Mexico.

Introduction

- HEV genotype 1 and 2 are said to be the reason for the waterborne hepatitis E in developing countries like Bangladesh and these genotypes are mainly restricted to humans.

Introduction

- An outbreak of hepatitis is observed in western part of Chittagong City of Bangladesh for 6-8 months in the year 2018.
- But due to lack of expertise and infrastructure detection of viral load and genotype is scarce.

Introduction

- So present study is designed to find out the HEV genotyping with viral load in collaboration with Bangladesh and USA researchers.

Methods

It was an observational study done in a tertiary care hospital(CMOSHMC), Chittagong, Bangladesh in collaboration with a research laboratory of Texas, USA.

Methods

Period of study was one year and duration of sample collection was 5 months from 1/8/18 to 31/12/18 while the outbreak of hepatitis was maximum in that region.

Methods

Patients with history suggestive of hepatitis (anorexia/nausea/vomiting/yellow eye/dark urine) with past history of short duration fever or if researchers clinically suspected the patients had acute hepatitis in their background history and examination or hospital admitted patients with clinically documented acute hepatitis biochemically or serologically were recruited in the study.

Methods

- During that period a total of 125 Ig-M HEV positive cases done by ELISA (Biolab Diagnostic Company Limited) – Germany) were recruited as study sample. 13-14 ml of venous blood were collected from those positive cases and mixed with EDTA anticoagulant.

Methods

Plasma was separated after centrifugation and preserved at -20° C. After collection of all samples, those were sent to Sliea Gen L.L.C research laboratory, Austin, Texas, USA for further analysis.

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Methods

- During shipment of the sample , dry ice were used to maintain the temperature of the sample below -20° C.

Methods

In USA HBsAg(ARCHITECT i2000SR HBsAg , Abbott Diagnostics), Anti HCV(ARCHITECT i2000SR Anti-HCV, Abbott Diagnostics), IgM Anti HAV (ARCHITECT i2000SR HAV ab-IgM, Abbott Diagnostics), HEV viral load in IU/ml and HEV viral load log (RealStar HEV RT-PCR Kit 2.0) and HEV genotype were done in all 125 samples.

Methods

- For the study ERB clearance was taken from hospital authority, informed written consent was taken from all patients for data and blood collection and FDA approval was taken to carry the sample and study in USA.
- Study was funded by Sliea Gen L. L. C. research laboratory, USA.

- Results

Table 1: Sex distribution of patients(n=125)

Gender		Frequency	Percent
	Female	35	28.0
	Male	90	72.0
	Total	125	100.0

Table 2: Age of the patients

Age group		Frequency	Percent
	<20 years	19	15.2
	20-30 years	45	36.0
	30-40 years	30	24.0
	40-50 years	16	12.8
	50-60 years	9	7.2
	>60 years	5	4.0
	Age 106 years	1	0.8
Total		125	100.0

Table 3: Virus screening by serology

Serology	Frequency	Percent
IgM Anti HEV positive	125	100
HBsAg positive	9	7.2
Anti HCV positive	1	0.8
Anti HAV positive	0	00

Table 4a: Viral load in IU/ml

Viral load(IU/ml)		Frequency	Percent
	00	11	8.8
	1-100	16	12.8
	100-1000	20	16.0
	1000-10,000	30	24.0
	10,000-1,00,000	25	20.0
	1,00,000-10,00.000	23	18.4
Total		125	100.0

Table 4b: Viral load(Log)

Viral load(Log)	Frequency	Percent
Log <2	27	21.6
Log 2-4	20	16.0
Log 4-6	55	44.0
Log >6	23	18.4
Total	125	100.0

Table 5: HEV Genotype Test Result

		Frequency	Percent
	Genotype 1F	68	54.4
	Inhibition	3	2.4
	Not available to type	21	16.8
	unable to type	33	26.4
	Total	125	100.0

- In the present study genotype 1F was found as the only genotype in this region of Bangladesh and further exploration might increase the knowledge in this ground.

- Thank you very much!