con was transfected into Huh 7.5 cells for production of infectious HCV particles. The culture supernatant was collected to infect naive Huh 7.5 cells. siRNAs were targeted against NS5B region of HCV genome as well as cellular factors in order to down regulate HCV in cell model. Furthermore, multiple combinations of siRNAs were used to observe the additive HCV down regulation.

Results: Down regulation of La autoantigen, PSMA-7, hVAP-A and NS5B genes resulted in inhibition of HCV replication by about 65%, 30%, 35% and 40% respectively. Combination therapies of siRNAs against La autoantigen with NS5B and La autoantigen with hVAP-A resulted in ~ 85% inhibition in HCV replication.

Conclusion: Our findings indicate that in addition to HCV-specific siRNAs, siRNAs targeted to host cellular genes have showed promising down regulation in HCV replication. We also showed that simultaneous silencing of more than one target is more effective than silencing a single target to inhibit the viral replication. Therefore, multiple combinations of siRNAs against both the virus and host genes are likely to be a potent approach in the treatment of chronic hepatitis C.

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Detection and molecular characterization of unusual rotavirus group A genotypes G12P[11] and G10P[14] in hospitalized children with acute gastroenteritis in Kolkata, India

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Background: Group A rotavirus induced acute gastroenteritis affects infants and children <5 years globally. Predominantly isolated rotavirus G types from human are G1, G2, G3 and G4 throughout the world including India. However, in recent years there has been an increased detection of G9 and G12 genotypes. Genotypes belonging to different animal origin such as G8, G10 and other rare genotypes have also been reported in humans with low frequency.

Methods & Materials: During an on-going hospital based surveillance study in 2014, stool samples were collected from patients (0-80 years) admitted with acute gastroenteritis at Infectious Disease (ID) Hospital, Kolkata. Presence of rotaviral VP6 protein was detected in stool samples using ELISA. The group A rotavirus positive samples were used for RNA extraction followed by Reverse Transcription and PCR. Cycle Sequencing and phylogenetic analysis were further used in the study.

Results: Sequence analysis of VP7 and VP4 gene segments of group A rotavirus positive samples identified two unusual genotypes namely G10P[14] and G12P[11]. The unusual nature of their G and P types led us to characterize the remaining nine gene segments for deciphering their evolutionary dynamics.

Conclusion: Our study reports the identification and characterization of unusual group A rotavirus strains i.e. G12P[11] and G10P[14] from Kolkata, India. The full genome sequencing highlighted interspecies transmission and multiple reassortment events in the origin of these strains. The G10P[14] strains possessed genomic constellation commonly found in artiodactyls and therefore probably have a zoonotic origin. The G12 strains predominantly carry Wa-like genomic backbone while P[11] type is derived from DS-1-like rotavirus strains and therefore possible reassortment events between the two genomic backbones might have led to the emergence of G12P[11] genotype. The study highlights the need for continued rotavirus surveillance and complete genetic characterization for monitoring unusual rotavirus strains and understanding their evolutionary origin.

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Co-circulation of all four dengue virus serotypes with concurrent infections in a single dengue season

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Background: Dengue is one of the notable mosquito borne viral infections of public health concern. Dengue viruses (DENV) belongs to the genus Flavivirus and family Flaviviridae and has four antigenicaly related serotypes designated as DENV 1- 4. All the four serotypes can cause clinical manifestation ranging from mild self-limiting illness to severe dengue hemorrhagic fever (DHF) and dengue shock syndrome (DSS). However, severity in dengue viral infection is known to be affected by secondary infection with heterologous antibodies or with certain dengue virus serotypes and genotypes. This necessitates the study of circulating dengue serotypes in a particular locality. The present study reports for the first time the circulation of all the four dengue serotypes along with concurrent infections in an eastern state of India.

Methods & Materials: A total of 148 samples were received from clinically suspected dengue patients during September to December, 2014.

All the 148 samples were subjected to dengue specific MAC ELISA (Pan Bio, Australia), and NS1 antigen detection by ELISA (Pan Bio, Australia) for detection of dengue IgM antibody and dengue NS1 antigen respectively. Twenty early acute samples (<3days of illness) received were subjected for detection of dengue viral RNA and serotyping using type specific nested multiplex RT-PCR.

Results: Twenty five samples were positive for dengue serology (dengue NS1 and/or dengue IgM Ab). Five samples were found to be positive for dengue viral RNA by RT-PCR. The type specific PCR revealed, Dengue type 2 (DENV-2) in 2 samples, DENV-4 was found in one and 2 samples were co-infected with DENV-1 and DENV-3. All the dengue positive patients had dengue fever and none had dengue hemorrhagic fever.

Conclusion: The present study reports for the first time the co-circulation of all the four dengue serotypes along with rarely detected DENV-4 for the first time from eastern India.

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