liminary study, we planned to investigate the Ad-36 DNA in the mediastinal adipose tissue of obese adults, in order to demonstrate a possible Ad-36 relation clearly in obese adults with CD, once again for the first time in Turkey. There is a need for extended serial, particularly cohort and human-based, studies in order to have a clear understanding of the relation.

http://dx.doi.org/10.1016/j.ijid.2016.02.925

Type: Poster Presentation

Final Abstract Number: 43.190
Session: Poster Session III
Date: Saturday, March 5, 2016
Time: 12:45-14:15
Room: Hall 3 (Posters & Exhibition)

Factors leading to liver injury in acute dengue infection

S.M. Fernando[1,*], A. Wijewickrama[2], L. Gomes[1], C. Punchihewa[1], P. Madusanka[1], H. Dissanayake[1], C.K. Jeewandara[1], H. Peiris[1], G. Ogg[3], N. Malavige[1]

[1] *University of Sri Jayawardenapura, Sri Lanka, Colombo, Sri Lanka*
[2] *Infectious Diseases Hospital, Sri Lanka, Colombo, Sri Lanka*
[3] *University of Oxford, Oxford, United Kingdom*

Background: Liver damage is commonly seen in dengue infection, which can sometimes lead to acute liver failure. Although the exact causes of liver injury is unknown, direct viral injury, hypoxic injury due to vascular leakage and immune mediated liver damage are thought to contribute to liver involvement in dengue. Therefore, we proceeded to investigate the patterns of liver injury and the possible contributing factors in acute dengue infection.

Methods & Materials: 55 adult patients with confirmed acute dengue infection were recruited during day 3 -5 of the illness and serial recordings of liver function tests, viral loads, serum IL10 and IL17 levels and the extent of fluid leakage were measureddaily until discharge from hospital. According to the 2011 WHO guidelines, 19 of these patients were classified as dengue haemorrhagic fever (DHF) and 36 were classified as dengue fever (DF).

Results: Serum alanine transaminase (ALT), aspartate transaminase (AST), conjugated and unconjugated bilirubin, gamma glutamyl transaminase and alkaline phosphatase levels were highest on day 7 of illness in patients with DHF and DF. Serum albumin levels were only lower in patients with DHF. The peak in liver enzymes occurred 2 days after the peak of viraemia in patients with DHF and DF. The extent of the rise in liver enzymes did not correlate with the extent of vascular leak and there were no significant differences in any of the liver enzymes between patients with DF or DHF. In contrast, IL-17 levels were significantly associated with ALT levels ($p = 0.02$, Spearmans $r = 0.17$). IL-17 levels were significantly higher ($p = 0.008$) on day 5 of illness in patients with ALT levels > 4 times the upper limit of normal (mean 38.2 SE $\pm$ 10.1), when compared to those with lesser degree of liver involvement (10.3, SE $\pm$ 10.2). Although IL-10 were higher in patients with higher AST levels, this was not significant.

Conclusion: Dengue associated liver injury appears to peak at day 7 of illness and appears to associate with serum IL-17 levels but not with the degree of fluid leakage or viraemia. Since IL17 was also shown to cause liver injury in dengue mice models, the mechanisms by which this occurs needs to be further investigated.

http://dx.doi.org/10.1016/j.ijid.2016.02.926

Type: Poster Presentation

Final Abstract Number: 43.191
Session: Poster Session III
Date: Saturday, March 5, 2016
Time: 12:45-14:15
Room: Hall 3 (Posters & Exhibition)

Molecular diversity of rotavirus strains from hospitalized children in Central Kerala

S. George[1,*], J.O. A[1], S. Jes[1], S. Bai[2], S. Oommen[2], S. Chandy[1]

[1] *Pushpagiri Institute Of Medical Sciences And Research Centre, Tiruvalla, Kerala, India*
[2] *Pushpagiri institute of medical science and research centre, Tiruvalla, India*

Background: Group A Rotaviruses cause acute gastroenteritis (AGE) in children. In India, ~ 500,000 children are hospitalized with AGE annually, with an estimated 100,000 deaths attributed to rotaviruses. This study was aimed to characterize circulating rotavirus genotypes in a tertiary care centre in Central Kerala.

Methods & Materials: Stool samples (n = 75) were collected from hospitalized children (age < 10 years) with symptoms of acute diarrhoea at Pushpagiri Institute of Medical Sciences and Research Center (PIMS & RC), Tiruvalla, Kerala between January 2013-December 2013. Screening was done by rotavirus antigen detection ELISA (PremierTM Rotaclone,USA). Positives were confirmed by conventional Reverse Transcriptase based Polymerase Chain Reaction using published primers targeting VP6 gene. Genotyping was done by sequencing VP7 (G typing) and VP4 (P typing) genes, followed by phylogenetic analysis using MEGA.6 software.

Results: Of the 75 cases, 23 (30.6%) were positive for rotavirus by ELISA and RT- PCR. Among these positive cases, 26% required intensive care and three fourths of them were in 0 to 2 years of age . G1(n = 17, 80.95%) was the most predominant G type detected, followed by G9 (n = 4,19.04%) and few non-typeable strains (n = 2,8.6%). P types were P[8(n = 21,91.3%), P[6](n = 1,4.3%) and P[4](n = 1,4.3%).

Phylogenetic analysis revealed that majority of G1strains showed 98% homology with Indian strains and clustered in lineage 1,while few (n = 3) clustered in lineage 2 with vaccine and other reference strains with a high bootstrap support. G9 strains exhibit maximum identity with Indian reference strains and were clustered in lineage 3. These strains showed only 87-89% identity with vaccine strain.

G1P8 (n = 16,69.56%) was the most predominant strain circulating in this region. G9P[8], G1P[6], G9P[4] are the other strains encountered in this study.

Conclusion: This preliminary study helps to understand the rotavirus genotypes circulating in Central Kerala. Strains from this study clustered closely with previously reported Indian strains, indicating common ancestral strains. G9 and G1 strains showed only 87-90% homology with vaccine strains, suggesting genetic diversity to escape from vaccine-derived immune response. This epidemiological data is important to detect the emergence of potentially epidemic strains, for the formulation of rotavirus vaccines.

http://dx.doi.org/10.1016/j.ijid.2016.02.927