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The efficacy and particular side effects of therapy peginterferon alpha-2a acute hepatitis C hemodialysed patients

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Background: Peginterferon alpha-2a is a known standard therapy for patients with acute HCV infection. Our experience with peginterferon in hemodialised patients with hepatitis C started with a million question and uncertainties. This because of the:

- acute phase of infection,which we encountered due to repetitive serological tests the patients underwent because of hemodialysis protocols.

- fragile,immunodepressed patients which had a lifetime with serious underlying diseases,primary related to nephropathies or not.

However efficacy and safety of this treatment is still unclear in regional settings. This study tends to evidence the efficacy and safety of peg-interferon therapy in Albanian hemodialysed patients.

Methods & Materials: In a one-year period (from November 2013- November 2014), we enrolled consecutive patients with detectable anti-HCV antibody and HCV-RNA in the serum, who had elevated serum alanine aminotransferase (ALT). Written informed consent was taken from them. Patients with decompensated cirrhosis were excluded and in women of fertility age,pregnancy tests were done 24 hours prior to the first dose of peginterferon alpha-2a. Underlying diseases in our hemodialysed patients included Chronic renal failure -55 cases, Acute pyelonephritis - 1 case, Renal policystosis – 6 cases,Congenital renal atrophy – 1 case, nephrolythiasis -2 cases, renal transplant- 2 cases, nephroectomy- 3 cases, Arterial hypertension- 2 cases, spondyloarthrosis – 1 case.

Results: Early virologic response and sustained virologic response rates were 84.8% (47/55) 78.2% (42/55) respectively. The most common adverse effects in descending order were flue-like symptoms (83%), hair loss 36.3%, anorexia 54.5%, weight loss 25.4%, mood changes 40%, sleep disorders 29%, hematomas 41%, epistaxis 21.8% Laboratory data evidenced anemia 96.3%, leucopenia 78.1%, thrombocytopenia 83.6%.

Conclusion: Our 55 patients manifested several adverse effects, during therapy with peginterferon alpha-2a. Despite their particular immune status, these adverse affects appeared minimal compared to the efficacy of treatment in our patients

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The role of adenovirus 36 induced obesity in obese adults with cardiovascular disorders: The first clinical study investigating ad-36 antibody in sera and DNA in mediastinal adipose tissues of cases with cardiovascular disorders from Turkey (A preliminary study)

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Background: Recently, it has been showed that obesity strongly increase risk of morbidity and mortality caused by cardiovascular complications including atherosclerosis, cardiovascular disorders (CD), coronary heart disease. Obesity which developes due to multifactorial reasons, was associated with human Adenovirus-36(Ad-36). In this study, we aimed to investigate the role of adenovirus 36 induced obesity in CD.

Methods & Materials: In this cross-sectional and case-control based study, 75 obese(BMI $\geq$ 30 kg/m^2) adults with cardiovascular problems, 28 non-obese(BMI $\leq$ 25 kg/m^2) with cardiovascular problems, and also 48 people non-obese(BMI $\leq$ 25 kg/m^2) without cardiovascular problem were included in this study as patient group(PG), patient control groups(PCG) and healthy control groups(HCG), respectively. For this purpose, mediastinal adipose tissue samples obtained PG and PCG from anterior mediastinum situated on the outer surface of pericardium during routine cardiovascular surgical procedures. Besides, the blood samples collected from the each groups(PG, PCG and HCG). In this preliminary study, the peresence of Ad-36 antibodies, leptin, adiponectin levels were assessed by serum neutralization assay(SNA) and ELISA, respectively. Mediastinal adipose tissue samples will be examined for the presence of the Ad-36 DNA by PCR.

Results: Ad-36 antibody was detected in 10(13.3%) of 75 patients by SNA. We detected significantly difference Ad-36 antibody levels in the PG compared to the PCG and HCG($p<0.05$). Mean BMI, leptin, LDL, triglyceride levels were higher in the PG, while adiponectin, levels were found to be lower in the PG. Significant differences were detected between the PG and PCG for the parametres($p<0.05$), but there was no significant differences for total cholesterol .

Conclusion: In the light of our international literature review, although we detected a significant presence of Ad-36 antibodies related with obesity in adults with CD for the first time in this pre-

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.

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Factors leading to liver injury in acute dengue infection

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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.

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Molecular diversity of rotavirus strains from hospitalized children in Central Kerala

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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.

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