PATHOGENESIS

Hepatitis E virus infection may be transmitted through blood transfusions in an endemic area

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AIM: To address the issue of whether or not hepatitis E virus (HEV) is transmitted parenterally.

METHODS: We conducted a retrospective study which involved 145 multiple transfused patients and 250 healthy controls. A prospective study was also undertaken involving 50 hospitalized patients, 25 of whom were transfused with 107 blood units, while the other 25 did not receive any transfusions.

RESULTS: In our retrospective study, markers of acute HEV infection (IgM anti-HEV and HEV RNA) were detected in a significantly higher number of multiple transfused patients (13 of 145) compared to controls (two of 250) ($P < 0.001$; OR = 12.21 [95% confidence interval: 2.71-54.70]). All 13 HEV-infected patients had been transfused at least once in a 3-month period before testing. Overall, patients positive for any of the HEV markers (IgG, IgM or HEV RNA) had received more blood transfusions, had higher occurrence of icteric disease and higher serum alanine aminotransferase levels. In our prospective study, IgG anti-HEV was detected in 11 of 107 donor samples, three of 25 patients in their pretransfusion samples (one sample was positive for IgM anti-HEV as well) and two of 25 control patients. Post-transfusion HEV infection developed in three of 22 susceptible (IgG anti-HEV negative) transfused patients; the infection was traced to their four respective donors who were asymptomatic, HEV RNA positive (4/4) and IgM anti-HEV positive (3/4). In contrast, none of the non-transfused patients developed HEV infection during the follow-up period.

CONCLUSION: Frequent transmission of HEV by blood transfusion places recipients at risk and warrants redefining of the donor screening policy by blood banks, especially in endemic areas.

Ethnic and cultural determinants influence risk assessment for hepatitis C acquisition

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BACKGROUND AND AIM: In the developed world hepatitis C virus (HCV) infection is predominantly associated with sharing contaminated equipment between injecting drug users (IDU). In developing countries inadequately sterilized medical equipment, transmission of infected blood and cultural practices have been implicated. Accurate risk factor assessment is essential for education targeted at risk reduction in culturally diverse populations.

METHODS: Ninety Australian-born Caucasians and 72 South-east Asian (SEA) HCV patients attending a Melbourne hospital liver clinic completed a questionnaire which assessed risk factor profile, perceived risk factors, knowledge of risk factors and methods to minimize transmission. Medical records were audited to identify doctor assessment of risk factors.

RESULTS: Risk factors in Caucasians were IDU, body piercing and tattooing (89%, 47% and 32%, respectively). Risk factors in SEA patients were injection therapy, dental therapy and surgery (89%, 70% and 38%, respectively). Most Caucasian patients (94%) correctly identified their mode of acquisition compared with 33% of SEA patients ($P < 0.0001$). Accurate risk factor documentation in medical records was more common in Caucasians (96 vs 32%; $P < 0.0001$). The majority of patients identified blood-to-blood and sexual/vertical transmission as important modes of acquisition. However, 33% of SEA patients believed transmission occurred through food, water and poor hygiene and 80% did not identify therapeutic injection or traditional medical practices as risk factors. Education provided to SEA patients did not address less well established routes of transmission.

CONCLUSION:thnicity influences perception and knowledge of risk factors. Improved assessment of risk factors in high-risk ethnic groups is needed. Education should be culturally appropriate and address the concerns of all populations with HCV.

Origin of serum hepatitis B virus in acute exacerbation: Comparison with HBV in the liver and from other exacerbation

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Acute exacerbation (AE) of chronic hepatitis B is usually preceded by reemergence or increase of hepatitis B virus (HBV) in the serum. To investigate the origin of the reemergence or increase, we compared the identity of the serum viral genome to that in the liver and in previous AE by full-length sequencing. The full-length viral genome and extent of quasispecies were obtained from serum and liver biopsy specimens at the same time from 9 subjects with hepatitis B exacerbation (group I). Composition of viral quasispecies was compared by the genetic diversity and the average number of nucleotide substitutions within and between different viral sources. Another 2 patients with repeated AEs (group II) were also enrolled, and their serial serum alanine aminotransferase, HBV DNA levels and full-length sequences were determined. In all group I patients, serum viral genome was identical to that in the liver. The genetic diversity and the average number of nucleotide difference were also comparable between serum and liver tissue. In 2 group II patients, the viral variant that emerged after previous AE was not identical to that caused by the subsequent AE. Dominant viral strains for serial AEs in a single patient did not show a sequential evolution, but presented as a horizontal selection of a minor population from the original viral pool. In conclusion, the findings suggest that viral strain in serum reflects the intrahepatic strain of the AE. Random reactivation of the original HBV pool, rather than a sequential evolution of one strain, also contributes to the onset of repeated AE.

Rapid steroid withdrawal in hepatitis C virus-positive kidney transplant recipients

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The effects of rapid steroid withdrawal (SW) on kidney transplantation (KT) outcome were investigated in 12 HCV+ patients in a prospective cohort study. These results were compared with 17 HCV+ patients who received KT in the prior 2 yr and treated with a standard prednisone taper protocol. SW patients received only 6 d of steroid treatment after transplantation. Eleven received Thymoglobulin and one Basiliximab induction treatment along with a calcineurin inhibitor and mycophenolate mofetil. Patient and graft survival was 92% in SW group (median follow-up 12 months, range 6-17), and 92 and 82% in the historic control group respectively (median follow-up 21 months, range 11-27). In the SW and control group, acute rejection rates were 9 and and mean creatinine levels at last follow-up 1.30 +/- 0.3618%, and 1.68 +/- 0.58 mg/dL respectively. Only two SW patients had an increase in liver function tests during follow-up (18%), compared with six patients in the control group (43%). This study demonstrates that rapid SW is safe for HCV+ KT recipients, without an increase in acute rejection episodes or liver function abnormalities in the short term.

Tumour necrosis factor alpha polymorphisms are not involved in the development of steatosis in chronic hepatitis C

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AIM: To determine whether the different tumour necrosis factor alpha (TNF-alpha) promoter gene polymorphisms are involved in the development of steatosis in chronic hepatitis C.

PATIENTS AND METHODS: One hundred and thirty patients (89 men and 41 women; mean age 42.5 +/- 12.3 years) with chronic hepatitis C were included.

Insulin resistance was measured according to the Homeostasis model assessment (HOMA IR). Serum leptin levels were also obtained and the body mass index and fat mass were calculated. Liver biopsy was carried out in all the patients, and steatosis was measured as one of four stages (0 to 3): stage 0, no steatosis; stage 1, < 25% of hepatocytes with steatosis; stage 2, 25-50%; and stage 3, > 50%. DNA samples were obtained in order to describe the polymorphisms at the TNF-alpha promoter gene position.

RESULTS: Fifty-nine of the 130 (45.38%) patients had different degrees of steatosis, while 71/130 (54.62%) were not steatosic. Six of the 59 (10.2%) patients with steatosis presented mutations at the -238 position of the TNF-alpha promoter region, while 5/71 (7.0%) patients without steatosis also showed mutations at this position (P = NS). Seventeen of the 59 (28.8%) steatosic patients showed a mutation at the -308 position, while 16/71 (22.5%) without steatosis also had this mutation (P = NS). Insulin resistance, beta cells reserve, insulin and leptin levels showed no differences between patients with or without mutations at the promoter region of the TNF-alpha gene.

CONCLUSIONS: TNF-alpha mutations do not seem to play any role in the development of steatosis in chronic hepatitis C.