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Seroprevalence of hepatitis B among HIV infected patients attending Specialist Hospital Sokoto, Nigeria

Aliyu B[1], Danlami M B[1], Manga S B[2] and **Muh'd U K[2]**
[1]Federal University, Nigeria
[2]Usmanu Danfodiyo University, Nigeria

Hepatitis B virus (HBV) is of public health importance globally. Viral hepatitis, especially B forms a considerable percentage of liver disease worldwide. This study aims to determine the seroprevalence of hepatitis B virus among HIV infected patients attending Sokoto Specialist Hospital with a view to establish prevalence rate in the state. Serum samples were collected from HIV infected patients, and analyzed to determine the presence of hepatitis B surface antigen (HBsAg) using Biorex ELISA kit (HBV). Out of 140 HIV patients tested for hepatitis B surface antigen (HBsAg) only 19 individuals were found positive given the prevalence rate of 13.6% (19/140) among HIV patients. The statistical analysis has shown that there was no observable statistical significant difference between demographic data, clinical characteristics and risk factors with respect to HBV infection. Two of the 140 HIV patients were in the chronic stage of the infection giving a prevalence of 1.43% and two of the patients were at the acute stage of the infection with a percentage prevalence of 1.43% while the remaining 15 patients were in the active stage of the infection. There was no statistically significant relationship between the mean CD4 counts (428 cells/µl of blood) in HIV mono-infected patients and the mean CD4 counts (391.1579 cells/µl of blood) in HBV/HIV co-infected individuals (t=22.1351, df=1, p-value=0.02874, 95% confidence interval: 174.435–644.5648, mean=409.5). Therefore, HIV patients should be screened for HBV during their clinical visit in order to inform clinical management, also adequate care and support programs should be organized to help people living with both infections.

bamailato67@gmail.com

Evaluation of microbiological and molecular methods for detection and quantification of Streptococcus milleri group and total bacterial load from sputa of patients with cystic fibrosis

Azad Salih Abdul
University of Sulaimani, Iraq

One of the commonest life-threatening autosomal genetic disorders among the Caucasian populations is cystic fibrosis (CF) which, among other pathologies, affects the respiratory system by providing an ideal environment for chronic bacterial colonization and super-added infections. Respiratory failure postulated to result from reiterated respiratory infection exacerbations is the leading cause of mortality in CF patients. Recently, a group of bacteria called Streptococcus milleri group (SMG) has been hypothesized as an etiological agent of pulmonary exacerbation, when these bacteria may be present at concentration of 107 CFU/m1 or more in the sputum of affected patients. However, the presence and/or the role of SMG bacteria in children with CF remain to be investigated. In the present study, 29 CF-associated sputum samples, 15 adults and 14 children, were examined for detection and quantification of SMG and total bacterial load by applying quantitative real time PCR (qPCR) assays targeting the SMG specific cpn60 gene and the bacteria-conserved 16S rDNA genes. Traditional culture-based methods using recently developed semi-selective McKay agar and supplemented brain heart infusion (sBHI) agar were also applied. Real-time PCR for total bacterial load identified as a much higher concentration of bacterial cells than sBHI culture and with a statistically significant difference ($p<0.05$), probably due to the detection of organisms not culturable by this method. The cpn60-based qPCR assay was positive 25 of the 29 samples tested, suggesting presence of SMG bacteria in the majority of sputum samples. By contrast, McKay agar based culture only detected SMG in 12 of the samples, all of which were also qPCR positive. However, none of the samples contained more than 107 CFU/ml SMG bacteria, a previously suggested cut-off for hypothesized SMG-associated exacerbations. A further 61 frozen DNA samples derived from the respiratory samples (11 BAL and 50 sputa) of children with CF were tested by qPCR alone. SMG was detected in 58 of these samples. One sample had SMG bacterial concentration of >107 CFU/ml. These findings suggest that SMG can be detected at a very high prevalence using qPCR in sputa or bronchoalveolar lavage samples obtained during periods of exacerbation from children with CF, raising the important question as to whether exacerbations were associated with an increase in the number of SMG bacteria in the lungs of children with CF, as has been proposed for a subset of adult CF patients.

azad.abdul@univsul.edu.iq