

kits. The percentage prevalence of HBV infection was calculated by using patients with positive samples as numerator and the total numbers of the voluntary blood donor among the population of the study area as denominator. The data generated from this study were presented using descriptive statistics and chi-square to determine any significant relationship infection rate, age and gender.

Results: The overall prevalence rate of HBsAg of 8.9% was recorded. Age group (20–29) years had the highest prevalence of HBsAg (4%) compared to (3.1%) of the age group (10–19) years and (1.8%) of age group (30–39) years. HBsAg seropositivity was more prevalent among males (10.5%) than their female counterparts (9.26%). Age and Sex were statistically significant (p -value<0.05) by Chi-square test. This study confirmed that HBsAg is prevalent among screened asymptomatic healthy and sexually active youths in Ishiagu community

Conclusion: Hence, general surveillance, mass immunization and public health education to stop the spread of the infection among general populace in Ishiagu community in Ivo Local Government of Ebonyi State is advocated. General surveillance through mass screening to identify those with infection and instituting appropriate treatments, mass immunization of the uninfected population against the virus and public health education to enlighten blood donors in entire Ishiagu Community of the possible risk factors and routes of infection are indeed advocated.

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Room: Hall 3 (Posters & Exhibition)

Molecular diversity of Hepatitis B virus (HBV) x gene: A preliminary report from Kerala

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Background: The HBV- x gene expresses a 154 aminoacid multifunctional protein widely associated with hepatocellular carcinoma in chronic patients. Genetic variability of the x gene may impact the differential oncogenic potential of HBV genotypes. This study attempts to investigate genetic variability of the HBV x gene in patients with chronic hepatitis B (CHBV) infection at a tertiary care hospital in Kerala, South India.

Methods & Materials: Blood samples from fifteen CHBV patients attending the gastroenterology unit of Pushpagiri Institute of Medical Science and Research Centre (PIMS & RC) were included. All samples were tested for HBsAg, HBeAg, Hbc IgM, Anti HBs titre and biochemical tests {Aspartate transaminase (AST) & Alanine transaminase (ALT)}. All samples were screened by nested PCR, using primers targeting the core gene of HBV genome. HBV x

and compared to the consensus HBV sequence to detect the mutations. Phylogenetic and mutation analyses were done using MEGA version 6.0.

Results: Of the 15 samples that were positive for HBV core gene, the HBV x gene was detected in 11 (73%) samples while four were negative. Majority of patients were infected with genotypes A (6, 54%) followed by D (5, 45%). All genotypes A strains belonged to subgenotype A1. The A1762T/G1764A double mutation in the BCP region, significantly related to HCC in earlier reported studies was found in 4 patients. Patients with genotype A1 had 50% risk of harbouring the 1762/1764 double mutation. The mutation C1485T in the x gene region were found in 10 samples. The mutation G1467A were observed in all patients with genotype A1.

Conclusion: A1 was the predominant subgenotype seen in this study. Mutations were significantly high in A1 strains. Association of these mutations with HCC/cirrhosis is unknown. Larger studies are essential for better understanding of the role of these mutations.

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Hepatitis B virus genotypes and unique recombinants circulating among outpatients in selected hospitals in Kenya



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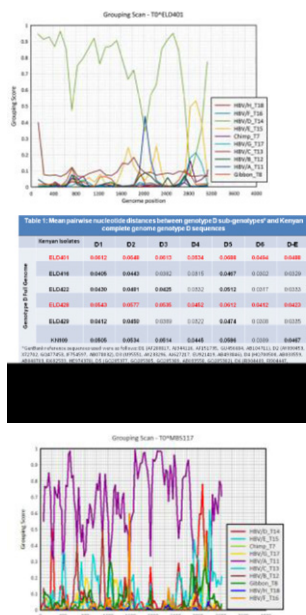
Background: HBV causes 780,000 deaths yearly worldwide. It's endemic in Africa and of the ten known genotypes (A–J), A,D and E are prominent in Africa. Kenya is geographically located at the junction of these three genotypes and there is a paucity of HBV genotyping data.

This study investigated molecular characterization of HBV circulating among outpatients of selected hospitals in Kenya.

Methods & Materials: 332 serum samples were obtained from patients with jaundice seeking medical services in four selected hospitals in Kenya. Hepatitis B surface Antigen and Antibody to the core antigen (HBsAg and HbcAb) were tested using commercial EIA (Elecys, Roche Diagnostics). The HBsAg coding region was amplified and sequenced in all HBV DNA positive samples, with 20 specimens chosen at random for full genome sequence analysis.

Results: HBsAg positivity was 50.6% (168/332) with 66.9% showing DNA positivity among samples having sufficient volume for DNA testing (93/139). 2.0% were anti-HBc IgM positive, indicating acute infection Based on HBsAg region sequencing, genotype A was predominant (90.3%), followed by genotype D (9.7%). HBV/D-infected individuals had a mean age of 43.0±2.0 years whereas HBV/A-infected individuals had a mean age of 34.0±4.0 years (Fisher test, p =0.02). Nucleotide distance measurements of the 20 full genome HBV/D sequences demonstrated two isolates having

a distance >4% from all HBV/D subgenotypes and recombinants, suggesting a new HBV/D subgenotype. "Putative recombination between genotypes A and E was observed in a single isolate from the coastal region (Figure 3a), while putative genotype D/E recombinants were observed in 2 isolates from the western region (Figure 3b)."



Conclusion: Despite of the availability of a stable HBV vaccine, the Prevalence of the virus was high among jaundice patients seeking health care. Genotype A1 is the predominant genotype in Kenya and in the Western region there are D/E. recombinants. Finding of the novel HBV recombinant strains in Kenya indicates that further investigation is required as the morbidity and progression of infection with such strains is not known.

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Molecular detection of enteroviruses in pigs in Lagos, southwestern Nigeria

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Background: Enteroviruses infect numerous mammalian species including humans, Non-Human Primates (NHP), sheeps, cows and pigs. Infections in pigs are mostly asymptomatic but can sometimes be severe and occasionally fatal. Enteroviruses in pigs are associated with a wide array of clinical presentations such as reproductive failure, diarrhoea and neurological disorders.

Methods & Materials: This study detected the enterovirus RNA from pigs in Ikeja Local Government Area of Lagos State, Southwestern Nigeria from a total of 110 (60 nasal and 50 faecal) samples from apparently healthy pigs in a major piggery between February

and March, 2015 using reverse transcriptase polymerase chain reaction (RT-PCR). Amplification and detection were carried out to obtain enterovirus RNA specific bands of 154bp after agarose gel electrophoresis.

Results: Only 1 (0.9%) Enterovirus RNA positivity for specie and genus specific VP1 gene was detected from this study. Although the prevalence of Enteroviruses in pigs from this study is relatively low.

Conclusion: This still indicates a potential source of transmission to pig handlers, consumers and the general public at large. However, the continued surveillance of Enterovirus with the possibility of a wider coverage of the different regions within the state and the country at large is solicited.

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Diarrhea in adult patients with influenza B

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Background: During 2014-2015 season we observed 147 cases of influenza. 34% cases were patients with influenza B, 49% - patients with several strains of influenza A/H3N2 and 17% - with influenza A/H1N1pdm2009.

Methods & Materials: Diagnosis was confirmed by PCR in nasal swabs. All patients received treatment in the central municipal hospital of Rostov-on-Do., Diarrhea was not recorded in patients with influenza A. 24% of patients with influenza B (12 cases) demonstrated diarrhea in the early stage of disease.

Results: All patients were women in the 50- to 65-year-old age group with the exception of the 26 year old pregnant woman who was an intravenous drug user. In all cases, patients had no epidemiological link and were hospitalized in a different period of time. In all cases the disease started with a fever up to 38.5 – 39 degrees C, weakness, headache. After a few hours of the onset of symptoms. 1-3 times vomiting developed in 42% of cases. Also, liquid stool without pathological admixtures 4-7 times a day throughout 2-3 days was recorded in 100% of patients since the first day of disease.

Before hospitalization 83% patients were treated with antipyretics. Patients admitted to the hospital on 1-2 day of disease with the preliminary diagnosis of acute infectious diarrhea.

Within 1-2 days of treatment in hospital dyspeptic symptoms disappeared and catarrhal symptoms started to dominate in the clinical picture of the disease: nasal congestion, sore throat, dry and wet cough. All patients with diarrhea had level of WBC count between $3.0-3.5 \times 10^9/L$ observed on the 2-3 day and 7-8 day of disease, radiological signs of acute bronchitis or bronchopneumonia were detected in 92% cases. Bacteriological investigation of feces did not detect any pathogenic enterobacteria, rotavirus and norovirus rapid tests and PCR on enterovirus were also negative. Mild or moderate dysbiosis of intestinal flora was detected

