**Antimicrobial resistance**

**PO - (8275) - HEPATITIS B VIRUS IMMUNE ESCAPE MUTANTS AMONG APPARENTLY HEALTHY INHABITANTS IN IBADAN SOUTHWESTERN NIGERIA**

Bakarey, Adeleye Solomon (Nigeria)¹; Ifeorah, Ijeoma Maryjoy (Nigeria)²; Akere, Adegboyega (Nigeria)³

1 - College of Medicine, University of Ibadan, Ibadan, Nigeria; 2 - University of Nigeria, Nsukka, Nigeria

**Background:** The documentation of circulation of immune escape mutants (IEMs) poses a risk on the continual success of HBV prevention and control. Therefore this study aimed to determine the possible circulation of IEM among asymptomatic dwellers in southwestern Nigeria.

**Methods:** Blood samples collected from consenting 133 males and 305 female participants in Ibadan were tested for HBsAg, HBeAg, HBcIgM, HBcTotal and HBsAb by ELISA technique. Samples positive for HBsAg were further analyzed for HBVDNA by amplifying and sequencing the S gene. Isolates were genotyped and subtyped based on amino acid residues at position 122, 127, 134, 160 of the S gene.

**Results:** Of the 438 subjects tested 31 (7.1%) were positive for HBsAg, 2(6.5%) of which were HBeAg positive. Ninety-nine (22.8%) had detectable HBsAb, 3(0.7%) were positive for HBcIgM and 195 (44.5%) were HBcTotal positive. HBVDNA was amplified and sequenced in 27 out of 31 and 4 could not be amplified due to low titres. After sequencing, 9(33.3%) were not exploitable due to the presence of multiple peaks. Of the 18 exploitable isolates, only 15 showed significant similarity to HBV S-gene. Eleven of the 15 isolates were subtyped as ayw4 while others could not due to substitution at s122p. Phylogram showed that the 11 isolates were genotype E. Two of the 4 isolates with R122Q/P substitutions also belonged to genotype E while the other 2 which were >11% divergent from the reference genotype E sequence clustered with an isolate previously described as an Immune Escape Mutant.

**Conclusions:** This study identified high endemicity of HBV infection, presence of markers of infection even in non detectable HBsAg levels and circulation of genotype E ayw4 and vaccine mutants in southwestern Nigeria. It therefore emphasizes the risk of development of an indigenous infected population that may not be protected by the current vaccine.