

ORAL PRESENTATION

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# Genetic determinants of hepatitis B vaccine response

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Hepatitis B is a major public health problem. Approximately one-third of the world's population has serological evidence of infection with hepatitis B virus (HBV). 350 million of these are carriers who have chronic HBV infection, and about a million of these carriers die each year from chronic liver disease, including cirrhosis and liver cancer. Fortunately, HBV is a vaccine preventable disease, and the increasing adoption of this vaccine has led to dramatic reductions in the morbidity and mortality caused by this virus. However, as much as 10% of the population fails to mount a protective immune response after vaccination. Twin and other epidemiological studies have demonstrated an unusually high heritability to this trait, which suggests a high likelihood of identifying genetic variation influencing HBV vaccine response. In search of such variation, we performed a two stage Genome Wide Association Scan (GWAS) in participants of a vaccine efficacy trial from Batam, Indonesia. In Stage 1, we used the fixed content Illumina Infinium 550K SNP BeadChip to genotype 2000 vaccinees. Tests of association were performed to identify 7,000 SNPs to carry forward to a second stage of 2,300 vaccinees. Several independent regions attained genome-wide significance, including the HLA-DR and HLA-DP regions. Additional details on the study design and results will be discussed in the presentation.

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