Hepatitis B Virus:

A Longitudinal Study

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Abstract

Hepatitis B Virus (HBV) is a member of the hepadnavirus family. Viruses from this family infect primate, rodent and avian species. Wild type HBV virions consist of partially double-stranded circular DNA which is converted into covalently closed circular molecules in nuclei upon infection into host cells. The HBV genome is about 3.2kb in size and consists of four transcripts encoding the surface, core, polymerase and X proteins, in overlapping reading frames. HBV infection causes a variety of liver diseases in humans, for example, liver cirrhosis and hepatocellular carcinoma. Clinical manifestations range from asymptomatic to acute. The outcome of acute hepatitis B infection may be influenced by host factors some of which are controlled by the Major Histocompatibility Complex (MHC). In humans the MHC is known as the Human Leukocyte Antigen (HLA) region. Accordingly, the individuals involved in this study were HLA typed.

The aim of this study is to investigate HBV DNA differences in three different clinical types of hepatitis B disease over a 15 year period, and to determine if there is a correlation between specific HBV variants and particular clinical states. In 1985, 93% of the population of Kawerau (7,901) was tested for HBV, those found to be positive (519) have been monitored ever since. In 1998, individuals that fitted our requirements were invited to participate in our study. HBV DNA was extracted from blood samples and complete genomes sequenced, over 120,000 nucleotides were sequenced. Differences in HBV genomes sequenced between clinical types and HBV genotypes were compared. HLA alleles between the different clinical types were compared, as well as comparing HBV infected individuals with the general New Zealand population. The overall project is a major one and the results of this thesis get it well underway.

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