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## **SeqHepB: A SEQUENCE ANALYSIS PROGRAM AND RELATIONAL DATABASE SYSTEM FOR HEPATITIS B VIRUS MUTATIONS IN HBV MONO- AND HIV-HBV CO-INFECTED PATIENTS**

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SeqHepB is a system designed to correlate large numbers of patient clinical, routine pathology and viral mutational data as well as *in vitro* phenotypic data in order to further understand the natural history of hepatitis B in mono- and HIV co-infected patients. This system is composed of a hepatitis B virus (HBV) genome sequence analysis program and a relational database to house the data obtained from these multiple sources.

The SeqHepB database currently contains routine pathology and specialist virology data for over 1500 patients, and is one of the largest database for HBV genomics in the world. Associated with these patients, there are 326 clinical histories, 1,450 treatment histories, 171 biopsy results, and 18,549 specimen records. In terms of pathology tests performed on the samples, there are 25,538 records in the database, and these include HBV, hepatitis C virus (HCV), hepatitis D virus (HDV) related pathology test results, HIV coinfection status, as well as liver function and haematology test results. Drug histories are also included. Samples within the database are associated with 3,252 HBV sequence information corresponding to 100,639 nucleotide or amino acid variation data points. The mutation data is correlated to in-house and published *in vitro* phenotype data on antiviral sensitivity.

Integration of clinical, pathology and viral molecular biology data using different artificial intelligence techniques facilitates the analysis of pathogenesis and natural history studies of hepatitis B in mono- and HIV co-infected patients. The initial correlation of these multi-disciplinary data has identified novel mutations associated with antiviral resistance and cross-resistance to lamivudine, adefovir, tenofovir, entecavir and abacavir. A linkage that exists between a 3-dimensional (3D) structure viewing program

and the database enables these mutations to be further analysed within a 3D model of the polymerase [1].

Chronic hepatitis B is a disease with a complex natural history, and this complexity increases with the use of antiviral agents and also in co-infection with HIV[2,3]. The SeqHepB system is an important tool that will enable the physician to individualize patient management, to cope with the explosion of antiviral drug-resistant associated HBV mutations, and should prove to be a useful therapeutic guide in clinical settings as new antiviral agents and combinations thereof, are implemented into patient care.

## References

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