V Summary and conclusions
This study estimated the risk factors, intrafamilial spread, histological changes and molecular distribution of chronic Hepatitis B infection in Kerala. The results sheds light on many important aspects of HBV molecular epidemiology in Kerala, that are very much important for identifying the population at risk of acquiring HBV infection, developing severe disease and pose a risk of transmission through different modes.

Salient findings of the study are:

1. History of intravenous injections/infusions and history of contact with an infected person were found to be major risk factors for chronic HBV infection in Kerala. Intrafamilial transmission was seen in 16.5% of the family members screened. This poses a serious threat and can be limited by awareness among infected individuals about the need to vaccinate uninfected family members. Social factors, such as poverty and low levels of education, were positively correlated with heightened transmission.

2. Steatosis was a major finding on liver biopsy in 73%; of these 61% had severe degree of steatosis. Even though the results were inconclusive to determine the role of the virus in steatohepatitis, the high prevalence of steatosis is a cause of concern and more studies are required to elucidate the effect of HBV independent of metabolic syndrome. HAI score of >3 was seen in 76% of the patients and 35% had fibrosis score of >1.

3. Genotypes A and D were found in the study; Genotype A accounted for 76% of the infection and A1 was the predominant subgenotype.

4. A high frequency of G1862T was observed in our patients. The absence of G1896A mutation was expected among the genotype A samples. Basal Core Promoter double mutation 1762T\1764A was observed in 40% of the samples.
Practical Implications:

1. The study helps in understanding the molecular biology of the disease in Kerala. The high prevalence of genotype A, will help the clinicians in redefining management strategies in patients; Genotype A is associated with a significantly higher sustained response to Interferon therapy than HBV genotype D and showed better sustained response rates than HBV genotype C, B or E.

2. Further research would help in understanding and predicting the effect of mutations in the BCP/Pre C region on HCC development.

3. This information is essential for determining the risk factors associated with HBV infections, to formulate necessary preventive measures to lessen the burden of new infections and spread of new genotypes.

4. High transmission rates among family members is disconcerting, making vaccination of family members mandatory and the need to propagate awareness about the risks for infection.

Finally, together with contributing unique data on molecular epidemiology of HBV in India, this thesis work also opens new avenues for further studying Hepatitis B Virus at the molecular level.