CHAPTER 5

Conclusions

In Asia Pacific region HBV infection remains a major public health problem. Despite effective vaccines against HBV are available, perinatal HBV transmission still continues to occur. This study provides a better knowledge about the relationship between HBV genetic diversity in the context of HBV/HIV co-infection and perinatal transmission of HBV. A higher genetic diversity was observed in *preS/S* region among women who transmitted HBV to their babies but no particular mutation pattern was found associated with perinatal transmission. Pregnant women HBeAg-negative had a higher diversity in *pol, preC/C* and *preS/S* regions and this study confirmed that A1896G mutation was associated with HBeAg negativity in HBV/HIV co-infected pregnant women.

Assessment of viral factors associated with perinatal transmission of HBV may provide information useful for the design of new and highly effective vaccine to better prevent HBV infection. However, in our study, perinatal transmission of HBV was not associated with a higher genetic diversity of HBV or particular mutation pattern. Higher HBV genetic diversity in women who seroconverted HBeAg may be due more rapid evolutionary rates of HBeAg negative sequences. In addition, large-scale studies are needed to evaluate the prevalence of A1896G mutation and its impact on the result of HBeAg testing and thus, the usefulness of HBeAg testing. Were this prevalence high, HBV DNA quantification would be the appropriate approach to assess viral replication in all HBeAg negative people.