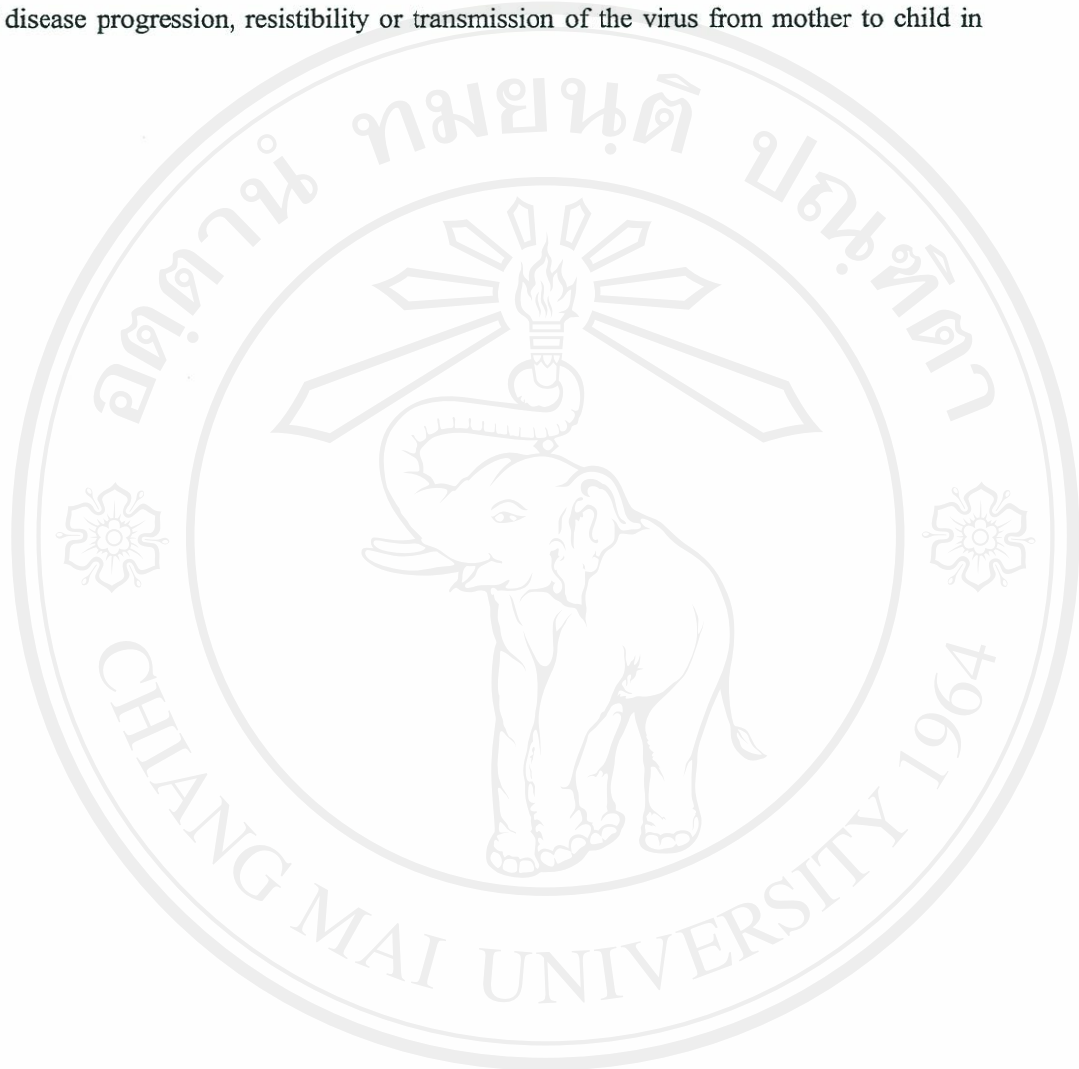


CHAPTER VI

SUMMARY

Twenty HIV-1 highly exposed persistently seronegative (HEPS) individuals and their HIV-1 seropositive spouses were enrolled at Sunpatong and Doisaket Hospital, Chiang Mai province during 2001 to 2002. They were classified as HEPS by the criteria assigned for the inclusion. The nucleotide variations on the coding region of CCR5 gene: CCR5 Δ 32 and CCR5-m303, were determined in HEPS, their HIV-1 seropositive spouses and healthy normal individuals. The CCR5 Δ 32 was determined by using the PCR technique, while CCR5-m303 was determined by the Nested-PCR technique and restriction enzyme analysis. The CCR5 Δ 32 and CCR5-m303 alleles were not detected in all subjects. The nucleotide variations on the promoter region of CCR5 gene were determined in HEPS individuals and their HIV-1 seropositive spouses by the nucleotide sequencing technique. The CCR5P4 haplotype with CCR5-59029G/G and CCR5-59353T/T were identified in both HEPS individuals and their HIV-1 seropositive spouses. One of 19 HEPS individuals was carried CCR5P2 haplotype with CCR5-59029A/A which was known to associate with HIV-1 rapid progressors. However, the effect of CCR5-59029A/A in the HEPS individuals was not associated with the increasing expression of the CCR5 molecules on the surface of the target cells. The CCR5 expression on the surface of the HIV-1 target cells was assayed in the HEPS individuals and their HIV-1 seropositive spouses when compared the healthy normal individuals by using direct immunofluorescent technique and flow cytometry. The median of CCR5 density on the surface of CD4⁺ T lymphocytes and monocytes from HEPS and healthy normal individuals had been significantly lower than those from HIV-1 seropositive individuals. The variations on the coding region (CCR5 Δ 32 and CCR5-m303) and the nucleotide polymorphisms on the promoter region of the CCR5 gene were not likely associated with the level of CCR5 expression on the surface of the HIV-1 target cells. This study provided the primary information in the study of genetic factor that influence resistibility to HIV-1 infection in the HEPS individuals. It contributed to better understanding of mechanisms

controlling HIV-1 infection in highly exposed persistently seronegative (HEPS) persons and could be primary information for further study of genetic factors that are valuable in prediction the rate of disease progression, resistibility or transmission of the virus from mother to child in the future.



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