CHAPTER VI

CONCLUSION

The mycobacteria were isolated from HIV-infected patients who were admitted in 4 hospitals and their environment in Chiangmai province. The 4 hospitals are Maharaj Nakorn Chiangmai hospital, Nakornping hospital, Sanpatong hospital and Sansai hospital. The environment samples were water supply, soil and stool of livestock. The mycobacteria were classified into 2 groups including slow-growing mycobacteria and rapid-growing mycobacteria. The slow-growing mycobacteria were classified as M. tuberculosis 91 isolates, M. avium 72 isolates, M. intracellulare 40 isolates, M. scrofulaceum 38 isolates, unclassified MAC 16 isolates, M. kansasii 1 isolate and Mycobacterium spp. 27 isolates by PCR-REA technique. The M. avium were isolated from blood and any sputum of 36 patients (9.1%) only but not found in the environment. So, it was the question for the origin of infection. The DNA fingerprinting of 76 M. avium isolates from the patients were studied. Twenty isolates (26.3%) did not hybridize with IS1245 probe. The others had 2 to 31 bands. Twenty-three IS1245-hybridization patterns were found. The patterns could be divided into 4 groups including group I or a low-copy-number group had 2 to 4 bands (30.3%), group II had 8 to 9 bands (16.1%), group III had 13 to 14 bands (16.1%), and group IV had 17 to 31 bands (37.5%). The RFLP showed the very high diversity percentage (82%). This indicated the directly infection from the environmental not by the specific epidemic strain. The sex ratio of each group of the bacteria were not significantly difference (p=0.599).