

## CHAPTER I

### INTRODUCTION

In the 21<sup>st</sup> century, Tuberculosis (TB) remains a major public health problem worldwide, although there has been an attention and action toward TB control and elimination. In 1997, the World Health Organization (WHO) Global Surveillance and Monitoring Project had conducted a project, "Global Burden of Tuberculosis". It aims to estimate the risk and prevalence of *Mycobacterium tuberculosis* (MTB) infection and tuberculosis (TB) incidence, prevalence, and mortality, including disease attributable to human immunodeficiency virus (HIV), for 212 countries. It was found that 1.86 billion people worldwide have latent TB infection, prevalence of MTB/HIV coinfection was 10.7 million people (0.18% of the world population) and 640,000 incident TB cases (8%) had HIV infection (Dye *et al*, 1999). In Thailand, the number of tuberculosis was 43,708 cases (78.7 per 100,000 populations) in 1998 (MOPH, 1998). HIV-infected patients were increased up to 156,309 cases (43,069 cases died), while MTB/HIV coinfection were 42,855 cases (27.4%).

Not only the number of *Mycobacterium tuberculosis* is highly increased but also the number of non-tuberculous mycobacteria (NTM). *Mycobacterium avium* complex (MAC), including *Mycobacterium avium*, *Mycobacterium intracellulare* and *Mycobacterium* sp. X or unclassified MAC (Aronson *et al*, 1999), has been reported to be a major opportunistic infection in advanced AIDS patients in the developed countries. The incidence of MAC in AIDS patients can be as high as 40% (Horsburgh, 1991) and *M. avium* was predominately isolated in the percentage of 87 to 98 of MAC (Falkinham, 1994). In Thailand, the mycobacterial hemocultures were positive for MAC in 58 (17.4%) from 334 HIV-infected patients (Chuchottaworn *et al*, 1999). MAC is a common NTM in natural environment, especially waters, are the reservoir for most human infections. Studies of DNA fingerprinting of disseminated *M. avium* in AIDS patients demonstrated that some cases are likely acquired from water. *M. avium* isolates recovered from portable water in three homes, two commercial buildings, one reservoir and eight hospitals had various degrees of genetic relatedness to 19 clinical isolates recovered from 17 patients. The large number of isolates found in hospital water suggested the possibility of the

nosocomial spread of *M. avium* to immunocompromised patients and to AIDS patients in particular (Aronson *et al*, 1999). The other sources are soil, dust (Ichiyama *et al*, 1988) and animals (Grange *et al*, 1990 and Leao *et al*, 1999). There is a high number (28.8%) of HIV-infected patients in the northern Thailand (MOPH, 1998) but there is no study conducted to identify strains of *M. avium* causing diseases in AIDS patients as well as sources of infection. Therefore, this research is conducted to study infection rate and epidemic strains of *M. avium* in AIDS patients. Both molecular genetic method and standard culture method are used.

An important factor in controlling *M. avium* infection is the ability to identify outbreaks and trace the transmission of a particular strain of *M. avium*. The more sophisticated technique employing restriction fragment length polymorphism (RFLP) analysis have detected genotypic variations among members of *M. avium*. This technique showed that RFLP analysis could be used to obtain “fingerprints” to differentiate isolates of *M. avium*. In this method, the insertion sequence, IS1245, is widely used as the standard probe in differentiating *M. avium* strains (van Solingen *et al*, 1998). So, this study, chromosomal DNA of *M. avium*, which were isolated from AIDS patients in Sanpatong Hospital, Sansai Hospital, Nakornping Hospital, Maharaj Nakorn Chiangmai Hospital were studied by using Southern hybridization technique with IS1245 as a probe.

#### **Aims of the study**

1. To study the infection rates of *M. avium* among HIV-infected patients with prolong fever of unknown origin for at least 2 weeks or diagnosed as tuberculosis from the hospitals in Chiang Mai province.
2. To study the RFLP of those *M. avium* strains prevalently found in HIV-infected patients.
3. To study sources of infection of *M. avium*.