

DIVERSITY OF  
MYCOBACTERIUM LEPRAE ON  
THE BASIS OF REPETITIVE  
SEQUENCES OF TTC FROM  
ANCIENT BONES FOUND IN  
BALI AND EAST NUSA  
TENGGARA, EAST INDONESIA

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**DIVERSITY OF MYCOBACTERIUM LEPRAE ON THE BASIS OF REPETITIVE SEQUENCES OF TTC FROM ANCIENT BONES FOUND IN BALI AND EAST NUSA TENGGARA, EAST INDONESIA**

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**Introduction:** Excavations of the genetic material of pathogenic organisms in the ancient bones provide important information for the study of certain infectious diseases in ancient populations. In addition, the identification of bacterial DNA provides direct evidence and the frequency of occurrence of infectious diseases in ancient populations and may provide information about the evolution of microorganisms and related diseases. Several recent reports have succeeded in

isolating several *Mycobacterium* by using PCR technique, because the PCR technique, although very small amount of DNA in ancient biomaterials such as bone or soft tissue but can be identified. This new approach not only of knowledge related to the evolution of different strains of *Mycobacterium*, but may also provide correlative data on the influence of environment on the development of *Mycobacterium* and biodiversity. However until now has never reported any *Mycobacterium* especially *Mycobacterium leprae* was found in a ancient bones from Indonesia, so too has not been widely reported throughout the world of *M. leprae* from ancient bones found on the old 2990 +/- 160 BP. The purpose of this study was performed diversity analysis of *M. leprae* on the basis of repetitive sequences of TTC from ancient bones found in Bali and East Nusa Tenggara, East Indonesia.

**Methods:** One of ancient bones who lived 2990 +/-160 BP from Lembata Island-Flores, Indonesia (code LL 1/5) and the one of ancient bones who lived Paleometallic period derived from Semawang-Bali, Indonesia (code SMW/III/1990). The DNA extraction was performed using a kit from Qiagen products and its TTC repeating pattern were seen with the method of direct sequencing.

**Results:** The inner part of the ancient bone from Lembata Island-Flores, Indonesia (code LL 1/5) was obtained by 13 repetitions TTC and the one derived from Semawang-Bali was obtained by 20 repetitions TTC. The different number of TTC repetitions have showed the different isolates of *M. leprae* between in the ancient bone from Lembata-Island-Flores, Indonesia and from Semawang-Bali, Indonesia

**Conclusion:** The result towards of TTC. Its commonly show that 13X TTC motif was found of ancient bone from Flores, Indonesia. Whereas 20X TTC motif was found of ancient bone from Bali, Indonesia. If it was related to leprosy spreading in Indonesia. That alot of them were found in East Indonesia. Whereas in the middle area was few relatively and it West area, it was none relatively, except in Aceh. In historical, if it was indeed so leprosy always follows in human migration from Asia continent to Indonesia. So it shouldn't empty space of leprosy in the middle area. In spite of it was estimated that also interrelated to the influences of Wallacea area, that covered Sulawesi, Maluku and Papua which have different environment like in West area excited.

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