


This
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is presented to


Toetik Koesbardiati

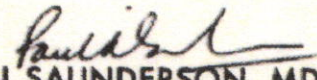
as delegate during the 20th International Leprosy Congress with the theme
*"Global Partnership in Addressing Current Challenges:
Zero Transmission. Zero Disability. Zero Discrimination."*
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at the PICC Reception Hall, Pasay City, Philippines.

Given this 13th day of September 2019.


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LEPROSY IN PREHISTORIC ERA IN INDONESIA

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abstract

Archaeological-paleoanthropological excavation in Lembata island, Flores Indonesia, yielded 5 individual human remains. Macroscopic observations based on the categories presented by Ortner and Rodriguez-Martin suggest that one of those 5, suffered leprosy i.e. LL I/5. In addition, biomolecular study continued to provide the information about the evolution of microorganisms and related diseases by using PCR. The aim of this research is to detect *Mycobacterium leprae* DNA from archaeological specimen to study leprosy infection in prehistorical era especially in Indonesia. The skeletal code LLI/5 have dating result of LL I/5 is 2990 +/- 160 BP according to Carbon14 examination method and to identify the bacteria, the 18 kDa antigen *M.leprae* in regio RLEP3 repetitive element (X17153) was chosen to amplify by nested PCR, it is also based on several recent report. Positive result was detected from the isolates using spesific primers LP-1, 2 and LP3, 4. It is mean that the archaeological speciment contain *M.leprae* DNA. It is concluded that in Indonesia, especially in the eastern part, leprosy has already infected in human since prehistoric time.

Keywords:

Prehistory, infectious disease, leprosy, Indonesia

Introduction

Monot et al. (2005) state that the spread of leprosy is related to the migration of modern humans originating from Africa around 100,000 years ago. This conclusion is based on the SNP study of 175 clinical and laboratory specimens from 21 countries. The results of the analysis of SNP indicate that there are 4 types of SNP for *Mycobacterium leprae* that are spread throughout the world. This also provides clues about the spread of humans, some of which carry *mycobacterium leprae*. SNP-type 1 spread across Asia, Pacific Region and East Africa. SNP-type 2 according to Monot et al. is the rarest type, spread in Ethiopia, Malawi, Nepal / North India and New Caledonia. SNP-Type 3 is distributed in Europe, North Africa and America. Finally, SNP-Type 4 is found in the West Africa and Caribbean regions. Furthermore, Monot et al. explained that based on the SNP pattern leprosy distribution is related to modern human mobility, which is moving from East Africa to the rest of the world. The spread of leprosy for example through infected traders, explorers, and colonialists and migrants

According to Robbins et al. (2009) leprosy development coexists with cultural development. Cultural developments affect the needs of living space. The spread of humans has become inevitable, related to colonization or finding a new place to live. The

development of culture means increasing interaction, both between individuals and between populations. In other words, the denser the living space, the more the interaction of the people increases. Interaction can be brief but also intensive and prolonged.

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In the analysis of Monot et al., Asia is dominated by SNP-Type 1. At the Balathal site, India, found the remains of human skeletons from the period of 2000 BC that proved infected with leprosy. The presence of leprosy in Asia is strengthened by the notes in the ancient South Asian manuscripts, Sushruta Samhita Arthashastra (6 century BC), Chinese Manuscript Shuihudi Qin Jia (3 century BC) (Robbins, et al., 2009) which indicates that leprosy is an ancient disease that have existed since prehistoric times.

In Southeast Asia, evidence was found that leprosy existed in prehistoric times. In the Noen U-Loke community, Thailand (2500-1700 BP) the remains of human skeletons infected with leprosy have been found (Tayles & Buckley, 2004). In Indonesia, evidence of leprosy infection found in the remains of human skeletons comes from Lewoleba, Lembata Island, in eastern Indonesia (Koesbardiati, 2011) with an antiquity based on C14 of 2990 ± 160 BP.

The purpose of this study is to describe Lewoleba (LLI / 5) as individuals infected with prehistoric leprosy and describe the possible pathways of modern human movement in Indonesia

Morphologically leprosy can be recognized from the face. Therefore the method applied is macroscopic according to Aufderheide and Rodriguez-Martin (1998) and Ortner (2003). Both Aufderheide and Rodriguez-Martin and Ortner state that leprosy causes changes in bone. This change can be single or in combination. Moller-Christensen begins morphological observations and explains the characteristics of human skeletons infected with leprosy (Moller-Christensen & Hughes, 1966).

In general, the most obvious changes are in the nasal cavity, alveolar process and the surface of the oral cavity. Changes to the bone include: 1. Prolonged resorption of the prosthion in the anterior and posterior parts of the maxillary incisors. This results in loosening of the incisors and ends in tooth loss due to leprosy (*paradentosis leprosa*). 2. Atrophy of the anterior nasal spine. 3. Slowly the periphery of the piriform aperture undergoes bilateral and symmetrical resorption, followed by remodeling. 4. Changes occur in the palatine process, where a bulge arises along the palatine suture that will turn into perforation on the entire surface of the palate. 5. The intranasal structure is absorbed to form a broad and empty nasal cavity. This characteristic is referred to as *facies leprosa* by Moller-Christensen & Hughes (1966).

Figures 1a, b, c, d are LLI / 5 showing the character of leprosy that appears on the bone, which is the nasal spina that has been absorbed (Figure 1a). Figure 1b is a portion of the palate showing the presence of protuberances. Perforation is not very visible, because of the attached matrix. Figure 1c shows the edges of the piriform aperture which begin to undergo remodeling to form a rounded piriform aperture. The internal cavity is not visible because it is filled with a matrix. The absorption of the alveolar portion is vague because the extracted incisors which is associated with tradition (Figure 1d). Another method applied is molecular. The 18 kDa *M.leprae* antigen in the RLEP3 repetitive element (X17153) region was chosen to amplify by nested PCR, it is also based on several recent reports. Positive results were detected from the isolates using specific primers LP-1, 2 and LP3, 4. It is the mean that the archaeological specimen contains *M.leprae* DNA. In other words, leprosy has existed in Indonesia since prehistoric times

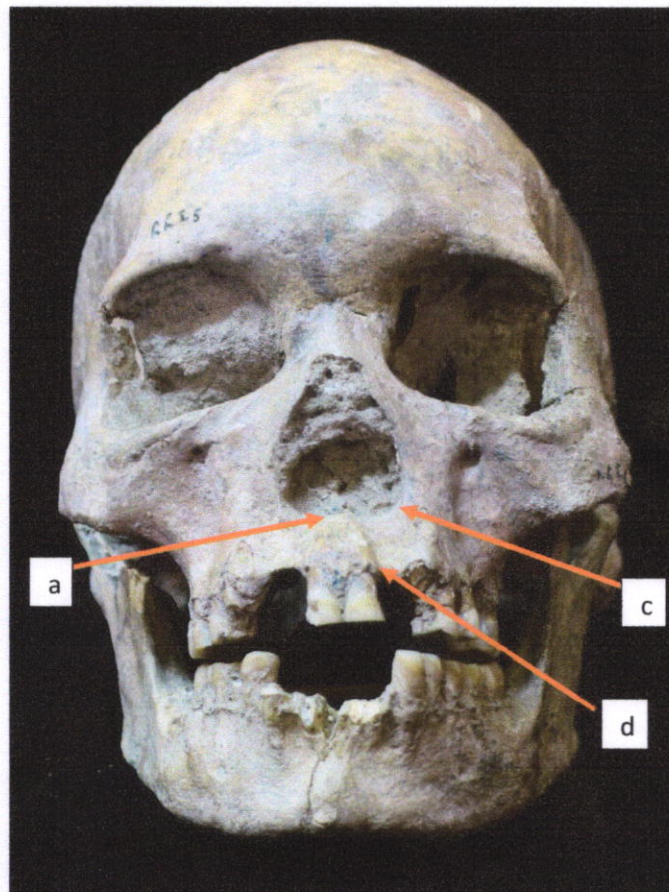


Figure 1. Characteristic of *facies leprosa*

How is the potential spread of leprosy in Indonesia if it is related to ancient migration patterns? It is stated by Monot et al. (2005) that SNP-type 1 was identified along the coast in the Middle East, India, Sri Lanka, Thailand bound for Indonesia. Evidence of archaeological findings (Balathal, India; Noen U-Loke, Thailand; and Lembata, Indonesia) shows that leprosy has spread in prehistoric societies with antiquity around the 2000s

BC. In the dispersal of modern humans, it is mentioned that the first modern humans came from Africa who migrated through the north and south. The southern route through the entire coast from the Arabian Peninsula to India, the Andamans towards east, including Indonesia. The next migration was known as migration from Austronesia at a much younger age. This route goes through mainland Asia heading south, through Thailand. It is suspected that Austronesian migration to Indonesia via Asia mainland (included Thailand). At least there are cultural similarities found between Thailand and Indonesia, for example the similarity of the tradition of dental modification. These waves of migration have the potential to spread leprosy.

One of authors (DA) analyzes LLI / 5 based on TTC repeat. TTC repeat is a genetic marker, a powerful tool to be able to see the endemic potential, variation and distribution of leprosy. Therefore, TTC Repeat can be used to track the migrants. TTC repeat results on LLI / 5 (14 copies) show closeness to Sulawesi (14 copies), Java (14 copies), and the Philippines (14 copies), and Thailand. This indicates that Indonesia was affected by several episodes of migration. Based on TTC repeats, it is suspected that leprosy was brought along with Austronesian migration originating from the southern route of Indonesia (via Thailand and / or India) and from the northern route, via Oceania, including the Philippines. Further research is highly recommended to look for possible new strains so that they can be traced not only to strains but also to track the direction of further migration.

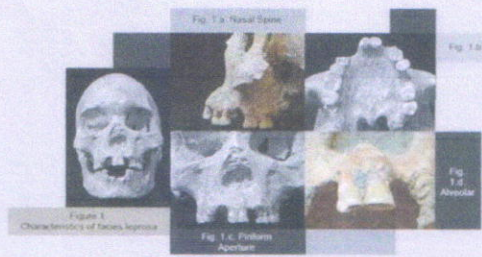
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OBJECTIVES:
The purpose of this study is to describe Lewoleba (LLI / 5) as individuals infected with prehistoric leprosy and describe the possible pathways of modern human movement in Indonesia

METHODOLOGY:
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SUMMARY:
How is the potential spread of leprosy in Indonesia if it is related to ancient migration patterns? It is stated by Monot et al. (2005) that SNP-type 1 was identified along the coast in the Middle East, India, Sri Lanka, Thailand bound for Indonesia. Evidence of archaeological findings (Balathal, India, Noen U-Loke, Thailand, and Lembata, Indonesia) shows that leprosy has spread in prehistoric societies with antiquity around the 2000s BC. In the dispersal of modern humans, it is mentioned that the first modern humans came from Africa who migrated through the north and south. The southern route through the entire coast from the Arabian Peninsula to India, the Andamans towards east including Indonesia. The next migration was known as migration from Austronesia at a much younger age. This route goes through mainland Asia heading south, through Thailand. It is suspected that Austronesian migration to Indonesia via Asia mainland (included Thailand). At least there are cultural similarities found between Thailand and Indonesia, for example the similarity of the tradition of dental modification. These waves of migration have the potential to spread leprosy.

CONCLUSION:
This study indicates that Indonesia was affected by several episodes of migration. Based on TTC repeats, it is suspected that leprosy was brought along with Austronesian migration originating from the southern route of Indonesia (via Thailand and / or India) and from the northern route, via Oceania, including the Philippines. Further research is highly recommended to look for possible new routes that have been found and not yet studied, but also to



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