

Improvement of Tuberculosis disease control through the development of diagnostic method and risk prediction system

(International Collaborative Research Program : Science and Technology Research Partnership for Sustainable Development (SATREPS))

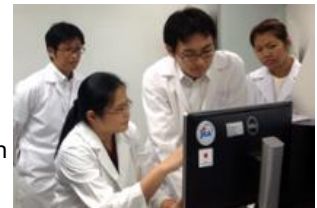
- Tuberculosis disease is one of the three major infectious diseases in the world, this project aimed to implement measures for Tuberculosis control that can be applied not only in Thailand, but also applied globally in the future, by developing a diagnostic method and a risk prediction system through the integrated use of genomic information from humans and pathogenic bacteria.
- In collaboration with Thailand, this project developed a whole-genome analysis method for *Mycobacterium tuberculosis*, and revealed a part of the molecular mechanism of Tuberculosis pathogenesis through functional analysis of genetic factors. In addition, as a prediction system for the side effects of anti-Tuberculosis drugs, this project developed a prediction method for the risk of liver injury based on NAT2*¹ genotype and age information as covariates.
- The results of the project were adopted in the Tuberculosis control guideline of Thailand (FY2018). It consists of NAT2 genetic testing, treatment policy decision based on genetic analysis of resistant strains, and whole-genome sequencing analysis of *Mycobacterium tuberculosis* for outbreak investigation, and is being used for the treatment in Thailand.
- 9 papers were published during the project, and 17 co-authored papers related to the research and development have been published in prominent scientific journals such as Cell Host Microbe, Lancet Microbe, Emerg Infect Dis, and Nat Commun since the completion of the project.

*1: NAT2 (N-acetyltransferase 2)

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- Project Title: Integrative Application of Human and Pathogen Genomic Information for Tuberculosis control
- Research period: FY 2014 – FY 2018
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A collaborative study using next-generation sequencers



National Tuberculosis Control Guidelines, Thailand

