MAHIDOL UNIVERSITY
Wisdom of the Land

東京大学
THE UNIVERSITY OF TOKYO

MINISTRY OF PUBLIC HEALTH

RIKEN

公益財団法人結核予防会
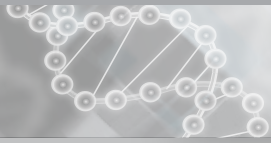Japan Anti-Tuberculosis Association

"Integrative Application of Human and Pathogen Genomic Information for Tuberculosis Control"

Tuberculosis (TB) is an infectious disease and its burden for global health. In 2015, World Health Organization reported that Thailand is one of 22 high burden countries of tuberculosis with complicated problem of drug resistant tuberculosis and HIV/TB co-epidemics and effective measures are required to control this disease urgently.

Beat TB by Strengthening TB Control Strategies through Genomic Analysis.

The project of "Integrative Application of Human and Pathogen Genomic Information for Tuberculosis Control" is conducted under the Science and Technology Research Partnership for Sustainable Development program (SATREPS) in the field of Infectious Disease Control as a collaboration between the Japan Agency for Medical Research and Development (AMED)* and the Japan International Cooperation Agency (JICA).

Genome variation in both humans and TB bacteria may affect disease development and responsiveness to treatment. This large-scale study will analyze the genetic variation of both human and pathogen genomes among TB patients, patients who suffered adverse drug reactions from the medication, and individuals who have not developed TB, in order to reveal how genomic DNA variants are associated with the development of TB and the adverse drug reactions to the anti-tuberculosis drugs treatment.

*SATREPS projects in the field of Infectious Diseases Control have been transferred to AMED. (The transfer took place on April 1, 2015. Projects that terminated before that date were not transferred.)

Collaborative Research Institutes

Research institutes in Thailand: Department of Medical Sciences, Ministry of Public Health and Mahidol University, Central Chest Institute of Thailand and Bureau of Tuberculosis.

Research institutes in Japan: The University of Tokyo, RIKEN Center of Integrative Medical Sciences, Japan Anti-Tuberculosis Association / Research Institute of Tuberculosis and Fukujuji Hospital

Research activities

I. Identification of human genetic risks associated with tuberculosis based on human genomic information.
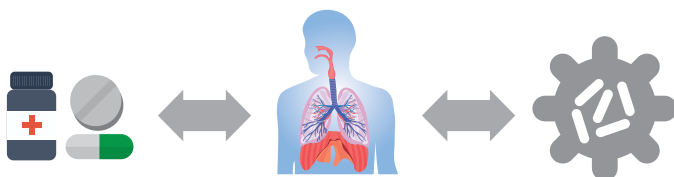
II. Establishment of data analysis pipeline for pathogen genomic information through the whole genome sequence analysis

III. Study of interactions between human genome variation and pathogen genome variation through the integrative application of human and pathogen genomic information

IV. Development of prediction system of treatment response and adverse effects from anti-tuberculosis drugs based on human and MTB genomic information

Supported by

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