

Results report

1. Title of Research and Development : Integrative Application of Human and Pathogen Genomic Information for Tuberculosis Control
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4. Results of Research and Development:

Tuberculosis is an infectious disease and its burden for global health is well-known as HIV and malaria. Thailand is one of the 22 high burden countries of tuberculosis, and effective measures are required to control this disease urgently. Genome variation in both humans and TB bacteria may affect different phenotype and treatment. Our SATREPS project aims to analyze the variation of both host and pathogen genomes among TB patients, patients who suffered side effects 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 side effects of the drug treatment. From the results of the genomic analysis, this project will identify genetic factors associated with tuberculosis and establish highly effective and less side-effect causative treatment method. The research findings intend to improve the tuberculosis control strategies currently called DOTS to reduce TB patients and provide better quality of life to the patients globally.

The Project started on April 1, 2015. We had 1st JCC meeting in Thailand at the end of April and academic meetings in Japan from the end of June to the beginning of July. We also had investigators meeting and 2nd JCC meeting in Thailand in December 2015 in order to build mutual understanding and share each research interest between Thai and Japanese researchers. Further, procurement for 9 machines to research and develop capacity for integrative application of human and genomic information has progressed in cooperation with JICA Thailand Office. Next generation sequencing machine (NGS), digital PCR, and other 5 machines had been installed by the end of September 2015, and LC/MS/MS and vacuum centrifuge were delivered by the end of this fiscal year. Thai researchers conducted test run for digital PCR. Knowledge Co-Creation programs were conducted at The University of Tokyo (UT) and RIKEN, respectively to transfer and enhance skills for Thai researchers for NGS and LC/MS/MS. Four researchers participated in this training program. Skill transfer and test run for NGS and LC/MS/MS was conducted in October 2015 and January 2016, respectively. Concerning reaching out of this Project, we were interviewed by NHK entitled with “Fighting Tuberculosis in Thailand” and the contents were broadcasted in Japan and other countries including Thailand in December 2015.

Our output from research activities in this term is as follows. One paper from Output 2 entitled “Mutations in *rrs*, *rpsL* and *gidB* in streptomycin-resistant *Mycobacterium tuberculosis* isolates from Thailand” was published by Journal of Global Antimicrobial Resistance, and two papers entitled “Identification of ITPA on Chromosome 20 as a susceptibility gene to young-onset Tuberculosis” from Output 1 and “Development of a prediction system for anti-tuberculosis drug-induced liver injury in Japanese patients” from Output 4 were accepted by Human Genome Variation. In addition to this, a result from Output 3 “HLA association analysis and haplotype analysis identify susceptible alleles of HLA class II to tuberculosis (Abstract 820F)” was presented in American Society of Human Genetics (ASHG) and Asia-Pacific Histocompatibility and Immunogenetics Association (APHIA) in October 2015. The other four results from Output 3 and 4 including “Pathogen lineage based analysis of host genetic risk factor in young onset tuberculosis (Abstract Thu(5)-O45-1)” will be presented in International Congress of Human Genetics (ICHG) 2016 in April 2016. We will write a manuscript for each result.