

Results report

1. Title of Research and Development :

International study on pulmonary disease infected with influenza virus and mycobacterium tuberculosis

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4. Results of Research and Development:

[Influenza Research Team]

Japan group: Japan group: We analyzed a role of Non-structural protein 1 (NS1) for severe pneumoniae induction using modeling simulation in gene mutation in influenza virus. Mutation at 42th amino acid which has RNA binding domain shows a virulence of H5N1 with cytokine storm (Kato et al. 2016). PL site of NS1 gene mutation associates with cytokine storm. When influenza virus infects epithelial cells in lung tight junction, the cell junction's function decreases by NS1, then inflammatory cells and plasma may pass through the junction. H5N1 viral infection increases the risk. This study was performed by all project members in addition to PhD Students Ms. Nguyen T. and Dr. Tran HD. supported by MEXT-Monka-sho in Japan.

Vietnam and Philippines group: Vietnam and Philippines group: Swab specimen have been stored for analysis of viral mutations in both countries. In Vietnam 50 specimen of influenza virus and 194 specimen for respiratory viruses from patients with severe pneumoniae have been stored. It has collection of 200 specimen of pediatrics patients, detected 50 patients positive with H1N1pdm2009, 3 patients positive with flu B and 1 patient positive with H3N1. Using Luminex system 194 nasal specimen were analyzed, 73.7% positive with respiratory virus: RSV 36.5%, Rhinovirus 31.5%, Parainfluenza 14% and Adenovirus 7%. On the other hand, in Philippines this protocol has been approval by the Philippines FDA in this February, then spacemen can be isolated from patients with severe pneumoniae. Furthermore, they started preparation of protocols for a clinical trial to intervention with Leucomycin-Josamycin for patients with severe pneumoniae.

[Tuberculosis Research Team]

Mycobacterium tuberculosis (MTB) strains that belong to seven major lineages are now spreading locally in the world. We pay attention to EAI strains, the Indo-Oceanic lineage, in Southeast Asia, because young students or workers from Southeast Asian countries including Vietnam and the Philippines often develop active tuberculosis (TB) in Japan nowadays. Using the next generation sequencing technique, we demonstrated that a particular genome structure of the EAI strains may cause genotyping error and a pitfall of the conventional MTB classification method. In Da Nang city, Vietnam, 176 sputum-smear positive active pulmonary TB patients have been recruited so far; 80% of the patients were male, the peak age at onset was around 40 years old, and a majority of the clinical isolates were EAI4_VNM or EAI5 strains. Prevalence of EAI strains in such a major city in the southern part of Vietnam is much higher than in the northern capital city, where Beijing genotype strains are predominant. In San Juan, Batangas, the Philippines, 213 of 1,505 TB suspected patients were sputum smear-positive pulmonary TB patients, and 192 were culture-proven further. According to a previous report, EAI2_Manilla strains account for 90% of the Philippine MTB strains. We are thus trying to characterize these MTB strains, which will facilitate effective control of TB in the Southeast Asian region.