TP-51

Analysis of Immunological Characteristics and Screening of Bio-markers in High-risk Populations Infected with M. tuberculosis

Division of Tuberculosis and Bacterial Respiratory Infections, 1National Institute of Health, 2The Korean Institute of Tuberculosis

Seung-Eun Song1, Ji Yeon Yang1, Seong-Han Kim1, Mi-Sun Park1, Hee-Jin Kim2, Soo-Yon Oh2, Sang-Hee Park1*

Introduction: Antibody responses are typically investigated in infectious diseases where antibody production strongly affects pathogenesis and outcome. Determining what constitutes protective immunity to TB is critical for the development of improved diagnostics. The comparison of the immune system between contacts of TB patients, who later develop TB disease (progressors), versus contacts who remain healthy (non-progressors), allows for identification of predictive markers of TB disease.

Methodology: A total of 2,567 contacts from the 37 high schools were included. The mean age of the contacts was 15.3 years (range, 14-18), and 1,660 (56.1%) of the contacts were male. The 26 patients who were diagnosed through collection period. Antibody microarrays were probed with plasma from 10 patients(61.5%). Whole plasma sample were purified protein derivative from two groups(10 progressors and 10 non-progressors). The 656 of antibodies were measured in supernatants using an Explorer antibody array assay.

Result: We found differences in median responses in 18 of the 656 antibodies: 2 higher in TB patients and 5 higher in TB patients and progressors. And 2 proteins are significant different expression who later develop TB disease.

Conclusion: Our systems approach to the study of the antibody response in tuberculosis defines the boundaries of the immunologically reactive proteins. But additional experiments are required in order to understand the immune response between TB patients and progressors.

TP-52

Longitudinal Analysis of Mycobacterium Tuberculosis Antigens-specific T Cell Subsets in Relation to Change of QuantiFERON-TB Gold In-Tube Test after Anti-tuberculous Treatment

경북대학교 의학전문대학원 내과학교실
이재희, 유승수, 이신엽, 차승익, 박재용, 김창호

Background: The potential of the whole blood IFN-γ release assay (IGRA) as a surrogate for treatment response has been evaluated, but seems still challenging. To overcome this limitation, flow cytometry with intracellular cytokine staining has been investigated recently. The aim of our study was to longitudinally evaluate the change of Mycobacterium tuberculosis antigen (MTB Ag)-specific cytokine-secreting CD4+T cell subsets according to treatment.

Methods: QuantiFERON–TB Gold In–Tube (QFT–IT) test and flow cytometry were performed before and after treatment in 28 patients with active TB.

Results: 1) The frequencies of MTB Ag–specific IFN-γ +TNF-α +CD4+T cells and IFN-γ -TNF-α +CD4+T cells increased during active TB and then decreased significantly after treatment (p<0.001). 2) The frequency of MTB Ag–specific IFN-γ +TNF-α -CD4+T cell subset did not significantly change after treatment; rather, the proportion of IFN-γ +TNF-α -CD4+T cell subset increased significantly in treated TB patients (p=0.049). 3) In 8 patients with no decrease of IFN-γ concentration in QFT–IT test after treatment, the proportion of MTB Ag–specific TNF-α producing CD4+T cells decreased significantly, while the proportion of IFN-γ producing CD4+T cells increased significantly (p=0.017).

Conclusion: Dynamic change of cytokine producing CD4+T cell subsets occurs after treatment, although there was no significant change of mean IFN-γ concentration in follow-up QFT–IT test. This may indicate that flow cytometric approach can be a new biomarker for monitoring the curative response of TB.