

京都大学若手人材海外派遣事業 スーパージョン万プログラム
研究者派遣プログラム

英文報告書

提出日：平成 27 年 4 月 28 日

1. 渡航者 (日本語)			
氏名	寺尾 知可史	採択年度	平成 26 年
部局	医学研究科附属ゲノム 医学センター	電話	
職名	特定助教	メール	
研究課題名	大規模ゲノム関連解析データを用いた難治性免疫疾患病態解明と治療標的の同定		
海外渡航期間	平成 26 年 12 月 7 日～平成 27 年 3 月 31 日		
渡航先 (英語表記)	国名：アメリカ合衆国 大学等研究機関名：ハーバード大学 研究室名等： Departments of Genetics and Rheumatology 受入研究者名： Soumya Raychaudhuri		
2. 渡航の報告 (英文)			
<p>渡航先の研究環境、研究者との交流、研究発表の状況等、渡航中の滞在経験について英語(500～1000語)で記述して下さい。受入研究者と撮影した写真や研究発表で用いた図等について、可能な範囲で別添として提出して下さい。ページ数については増加してもかまいません。</p>			
<p>Under support of The John Mung Program, I had joined for about four months the laboratory at Departments of Rheumatology and Genetics, Brigham and Women's hospital, Harvard Medical School managed by Dr. Soumya Raychaudhuri, famous for genetics of RA especially analyses of HLA. The Raychaudhuri lab had a total of 8 core members. They had a regular lab meeting and many group meetings as well as meetings with collaborators. I got surprised at the abundance of genetic and clinical data in the lab. The GWAS data of rheumatoid arthritis (RA), type 1 diabetes, celiac disease and inflammatory bowel disease are available. As for clinical data, data of more than 45 autoantibodies from more than 6000 patients with RA were available. In addition to get acquainted with other post-doctoral fellows and members all of whom were talented and well-experienced, I had many chances to get acquainted with famous PIs or researchers through meetings and seminars.</p>			
<p>In the Raychaudhuri lab, I had learned the detailed techniques and basic concepts underlying the analyses of HLA they adopted. Based on which, I could write several scripts to perform HLA analyses by myself. Through weekly meetings with Soumya, I could confirm my understandings and solve questions I had.</p>			
<p>My main projects were meta-analysis of genome-wide association studies (GWAS) of systemic sclerosis (SSc) and Takayasu arteritis (TAK). I obtained GWAS data from France and performed a meta-analysis using the French data and Japanese data in Kyoto University. Collaborators and I</p>			

performed replication studies in France and Japan. As a result, we identified a novel susceptibility gene to SSc as well as potential candidates of SSc susceptibility genes. The gene showing a significant association express in skin tissue, suggesting functional relevance of the involvement of the gene with SSc pathology. We started to recruit another set of samples for the 2nd replication study. Canadian and US teams agreed to join us. We are now taking procedures to move the replication study forward. Furthermore, I analyzed HLA data of meta-analysis of GWAS data and found that there would be different associations between Japanese and French populations. Now we are looking for a possibility to expand this HLA analysis in SSc.

As for TAK, I'd like to combine GWAS data from India with our Japanese GWAS data published in 2013. Since they did not have GWAS data, I offered Indian teams to ship GWAS chips to India. The first GWAS was completed and I ordered the additional chips to ship to India. Based on the first GWAS data, I found strong genetic heterogeneity among the Indian population according to geographical origins of samples. Since origin information was available for all of the subjects, I asked Indian collaborators to pick up candidates of GWAS. Now I'm waiting for the results of India. In addition to the first Japanese GWAS data, I'm planning to increase GWAS data. Now, additional genome-scanning of Japanese samples is going on.

In addition to projects about SSc and TAK, I completed and submitted a manuscript about the association between rheumatoid factor and distribution of joint destruction in patients with rheumatoid arthritis (RA). Since Soumya is a rheumatologist, I could discuss with Soumya how I could refine the manuscript. We could show that the distribution of joint destruction of hand should make two clusters, namely, finger joint destruction and non-finger joint destruction. We also showed that rheumatoid factor was associated with finger joint destruction. This association pattern could be observed in the European population as well as the Japanese population.

In conclusion, I could learn lab management and analytic techniques, make many acquaintances, submit a manuscript and make big progresses of the two main projects. I'd like to feedback to Japan what I learned when I come back to Japan.