

Interview with Prof. Katsushi Tokunaga during the APCHG 2017

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On Nov 10th, the 12th Asia-Pacific Conference of Human Genetics (APCHG 2017) successfully ended in Bangkok, Thailand, after a dense 3-day agenda blending a scientific and educational program. The theme of the conference is “Genomic Medicine and Clinical Practice”, focusing on a wide range of topics from basic to advanced genetics. As the journal partner of the meeting, the editorial office of *Annals of Translational Medicine* is invited to attend and give reports to the conference.

During the meeting, Prof. Katsushi Tokunaga from Department of Human Genetics, Graduate School of Medicine, The University of Tokyo, gave an excellent presentation on the topic “Genetics of hepatitis B/C virus related disease” (Figure 1). After the presentation, we were honored to conduct an interview with Prof. Tokunaga (Figure 2).

Question 1. Could you briefly introduce yourself?

My name is Katsushi Tokunaga, professor and chairman of Human Genetics Department, Graduate School of Medicine in the University of Tokyo. My research interest is mainly focused on the findings of genetic factors for various complex diseases. The findings will be beneficial to prediction of individual genetic risks and our understanding on pathogenesis of diseases. And if we are lucky, the development of new therapies and drugs can be foreseen through our hard work.

Question 2. Would you like to summarize some main points of your presentation on “Genetics of hepatitis B/C virus related disease” during the APCHG?

First, for hepatitis C treatment, we have identified the genes, which are strongly associated with the outcomes and adverse reactions after the treatment; during our research for hepatitis B, we also identified important genetic factors, HLA genes, which are strongly related to the disease’s progression (from infection to chronic hepatitis, chronic hepatitis to hepatocellular carcinoma).

One of the other significant findings of our research is the discovery of the interaction between host genome

and pathogen genome variations. That is also the case in hepatitis B or C virus infection for the development of hepatitis and hepatocellular carcinoma.

We found an interesting relationship between human and hepatitis B virus variations. There is one specific combination between human genome factor, HLA gene polymorphism, and virus variation. Those specific combinations can lead to the development of a new testing for predicting the risk of hepatocellular carcinoma, and hopefully, the realization of personalized medicine or precision medicine.

Question 3. Would you like to share the recent studies that you and your team are focusing on?

First, we concentrate on the study of infectious disease. Among our research, we mainly work on the genome analysis, function analysis and clinical studies for hepatitis and tuberculosis. And to connect the whole picture of infectious disease, we study both pathogen and host genomes. I believe, the comprehensive study of both fields will give us the most important message we want to deliver. In addition, we are engaged in human genome-wide association studies (GWAS) for various kind of diseases, such as primary biliary cholangitis, Stevens-Johnson syndrome, narcolepsy, nephrotic syndrome, etc. for nation-wide collaboration teams.

Question 4. Besides research works, you also act as editorial board members for some journals, and president of Japanese Society for Histocompatibility and Immunogenetics as well as a director of Japan Society of Human Genetics. Which role you enjoy the most?

The role I enjoy the most is, of course, as a researcher. But, in my age, we have certain responsibilities to the society. I would like to encourage young scientists and support them as much as possible. Frankly, I am not a good teacher. What I can do is to help promoting young scientists to higher positions, such as a board member or a director in the academic community. And the other is to open the door



Figure 1 Snapshot of Prof. Tokunaga.



Figure 2 Interview with Prof. Tokunaga.

for them to publish their research on variety of journals, bringing their hard works to a bigger platform.

In recent years, I am actively involved in the journal, *Human Genome Variation*, as Editor-in-Chief. The journal is open-access journal for various fields in human genetics. It also provides short reports of new variants identified by genome analysis of rare diseases. Single variation report is not easily published or being seen in high-ranking journals. However, such information is very important for clinical medicine. Now, genome-based clinical medicine is rapidly increasing. The importance of sharing up-to-date variation data is getting crucial. This is why *Human Genome Variation* wants to create and provide more opportunities for researchers to spread their data to the world.

Question 5. What's the secret of balancing your work and life?

I enjoy research activities a lot. My wife and my family are my solid support. They understand my responsibility to the society. Although I can only have short-period of vacation every year, I try to enjoy such occasion and treasure every

minute with them.

Question 6. Why did you choose the medical area at the early stage?

I was a student in the Department of Biology. Although it was primary natural science, my passion in human led me to the specialty for a particular biological species, *Homo Sapiens*, which is “Physical Anthropology”. I started to cooperate with clinical doctors, especially in autoimmune diseases. Because of my studies in the field of HLA and immunogenetics, Professor Juji at Department of Blood Transfusion Medicine in Tokyo University Hospital invited me to join them. And I was appointed the head of Research Section in Japanese Red Cross Central Blood Center. Our team had published a substantial number of papers, which Medical Faculty of Tokyo University was highly interested. Here came the final turn to my present position—a professor of Department of Human Genetics, Graduate School of Medicine in University of Tokyo. That moment, my research field was mostly connected to both medical and clinical areas.

Expert's introduction

Katsushi Tokunaga, PhD, is Professor and Chairman at Department of Human Genetics, Graduate School of Medicine, The University of Tokyo, Tokyo, Japan.

He also plays important editorial roles for many journals, including the Editor-in-Chief for *Human Genome Variation*, Advisory Editor for *Journal of Human Genetics*, *HLA* (previously *Tissue Antigens*), *International Journal of Immunogenetics*, etc.

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None.

Footnote

Conflicts of Interest: The authors have no conflicts of interest to declare.

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