

(Abroad • Domestic) Official trip report form (Student)

2014/09/05 (Year/Month/Day)

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|-----------------|-----------------------------------------------------------------|
| Name            | Kiyeon KIM                                                      |
| Laboratory      | Division of Bioinformatics                                      |
| Year (Grade)    | 2                                                               |
| Destination     | Montreal, Canada                                                |
| Period of trip  | July 26 <sup>th</sup> – August 3 <sup>rd</sup>                  |
| Purpose of trip | Attending IUMS 2014 and do poster presentation for my research. |

## Summary of Activities

IUMS is acronym, which stands for International Union of Microbiological Societies. These societies have three divisions, Bacteriology & Applied Microbiology Division, Mycology Division, and Virology division. Among these three divisions, I submitted my poster to Virology division and presented my previous and present ongoing research titled with “Inferring the population structure of viruses with Tajima’s D and its application to global surveillance.” In our division totally four members joined this congress—professor ITO, Nipawit Kanbunchop, Iew Borthong and me. This year IUMS held in Montreal, Canada, from July 27<sup>th</sup> to August 1<sup>st</sup> for six days. Our daily schedule started from attending 8:30 session to 4:30 talks. Although IUMS is union of three different divisions, there are so many similarities among approaching methods for different targets. For example, I could easily find titles concerning “meta-genomics” for every day in every division.

Here, I want to briefly introduce interesting topics that I had heard and read. The most interesting talk for Monday was “Dynamics of influenza diversity” by Dr. Ghedin from New York University. She has been studied about influenza virus evolution, which had been adjusted to human environment. Especially, she focused on mutations on HA and NA gene segment and vaccine development. Viral evolution is one of my most interesting topics and I also used here previous large-scale surveillance study dataset. Tuesday, the most impressive presentation was “Influenza virus transmission” by Dr. Yoshihiro Kawaoka. He is one of the most active scientists in influenza fields. His presentation was about mutations that make H5N1 influenza virus transmit between mammals and the experimental proof that H5N1 could be influenza pandemic naturally in the future. The other thing that is interesting was an “antigenic cartography” to predict the antigenicity of influenza A virus experimentally. Though this method introduced in 1997, it was brand new to me. It was totally convergence of two different fields, cartography and epidemiology. And last ten minutes of his presentation

was focused on explanation about the role of science and ethics. Till now his research had two points of view, one is showing the possibility of H5N1 pandemic in nature in future. The other side is danger of being used for bioterrorism or danger of being spilled out from lab to nature. But, somehow, this kind of research is necessary and helpful to prepare the future pandemic risk if all experimental procedure is conducted with perfect inspection. Wednesday, I attended talk titled by “Comparative analyses of the human- and animal- adapted strains of the Mycobacterium tuberculosis of complex” by Stephen Gordon, who is one professor in GI-CoRE. He introduced several strains from human and bovine and introduced his understanding on host adaptation of each Mycobacterium species. In same day, I had a poster presentation from 12:00 to 13:00. The title was “Inferring the population structure of avian influenza with Tajima’s D and its application to global surveillance”. Even there was only one hour; I had a chance to introduce my study several times. I also had a some comment how to show my result in figures and some advise how to extend my research topics. It was very important moment for me. Friday, interesting presentation was “The skin mycobiome in human health and disease” by Julia Oh, which is concerning biomes on various parts of human skin using metagenomic technique. The researcher showed different composition of bacteria and fungi in various part of healthy human and also showed different proportion in healthy and diseased person. I had heard of this kind of study several years ago and was interested in this topic but I did not find any results of it but luckily I had a chance to attend this talk. By knowing the composition of bacteria or fungi, we could detect abnormality and also by recovering the composition back to normal environmental composition we might another approach to control disease.

IUMS was extremely huge conference that I have ever attended. And I could have a chance to attend various and interesting topics. Frankly, I prefer to attend conference, which have narrow topics for my case, “Prediction using nucleotide”. But, thanks to this conference I totally change my mind that such a big conference is also meaningful to widen my topic by listening to other researcher from different field. Though I had some problem with jet-lag, I will memorize this conference as a middle stone of my research life in Hokkaido.

## Photos

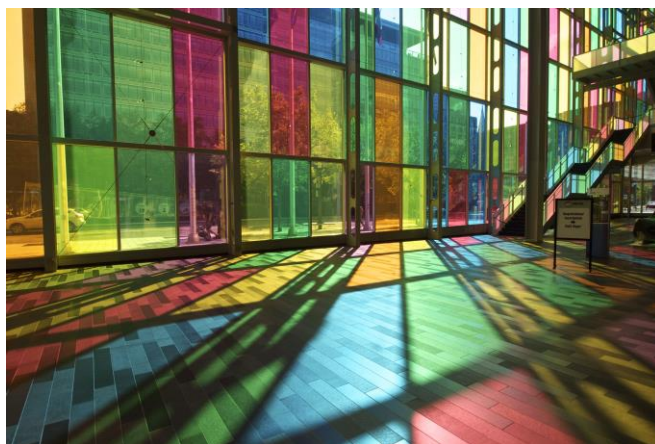


photo 1. Entrance of IUMS conference

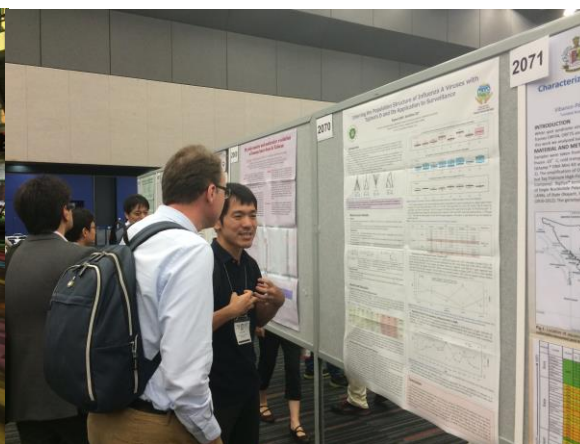


photo 2. Poster presentation

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|------------------------|----------------------------------------------------------------------------------------------------------|
| Approval of supervisor | Institution • Official title • Name :<br>Research Center for Zoonosis Control • professor • Kimihito ITO |
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