

Participation Report for GSCN Travel Award- Keystone Symposia: Single Cell Biology

Place/Date: Breckenridge, Colorado USA. January 13—17, 2019

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Background:

Single cell biology is emerging as a new area which spans classical cell biology, developmental biology, genomics and computational biology. It allows us to go deeper of the cell population to study the heterogeneity of cells. This year I had the great opportunity to attend one of the prestigious meeting: Keystone Symposia Single cell biology in Colorado USA from 13th to 17th of January, 2019 with the support of GSCN travel award. There were around 450 people from all over the world in this meeting. This meeting bring people from different background together to discuss the advancement of single cell biology. It also invited many famous pioneer scientists in this field, such as Xiaowei Zhuang, Scott Fraser, Carry Nolan, Hongkui Zeng, Rahul Satija, Allon Klein and so on. They gave us very high quality of talks and unpublished data on their research.

Highlights:

Prof. Xiaowei Zhuang who is from Harvard University gave us an amazing talk. She showed that a new approach which was a combination of single-cell RNA-sequencing and MERFISH (multiplexed error-robust fluorescence in situ hybridization) to map the identity and location of specific cell types within the mouse preoptic hypothalamus. Although single cell RNA sequencing has developed a lot and many new sequencing methods has emerged in recent years, but we still need to dissociate the tissue to get single cell. However, the dissociation will lead to the loss of spatial context for the cells in the tissue which is very important for understanding brain function. In her talk, she showed us many advantages of MERFISH. It is a high input and cheap method and they can process 1.1 million cells with this method. MERFISH can also be used for major cell class spatial organization, neuronal sub-type identification. More importantly, MERFISH and scRNAseq complement each other, MERFISH clusters and scRNAseq clusters have strong correlation. The combination of MERFISH and scRNAseq would allow us to generate a molecular inventory of neuronal types while mapping their spatial and functional organization.

Another interesting talk was from Prof. Hongkui Zeng who is from Allen Institute for Brain Science. The title of her talk was Cell Type Classification in the mouse brain. As there are so many different cell types in the mouse cortex and they are segregated into layers and functionally distinct areas, so far we have identified only a few cell types. In her study, she built a unified cell type taxonomy in the mouse cortex. In the long run, it will be very important for scientists to study cell type, function and even neural circuits in the cortex. They analyzed around 24,000 cells from the primary visual cortex and the anterior lateral motor cortex with deep, single cell RNA sequencing and found 133 different cell types. Her results showed that GABA containing neurons are shared across both areas. But most types of glutamatergic neurons were found in one of the two areas. Her study establishes a combined transcriptomic and projectional taxonomy of cortical cell types from functionally distinct areas of the adult mouse cortex. It extremely expanded our knowledge on the cell type in mouse cortex.

Personal experience and interaction during the conference:

As my poster was accepted for the poster session, I had more opportunity to interact with attendees in front of my poster and I got a lot of feedback for my work which was quite valuable for the next step of my project. As this was my second time to go to USA for a conference, I met a lot of new friends who are working or studying there. I got to know a lot experience of research and life in USA, I think it was quite nice and important because it will help me to decide whether I want to choose this country as my next step career development.

In addition, during the interaction with the people in the conference, I think it would be very important for me to start to learn some bioinformatics skills for my future plan. As we have step in “Big Data Age”, I think it will be very important for researchers to get the ability to process large dataset in their research.

In summary, single cell biology field especially single cell RNA sequencing field has changed a lot in past a few years. Nowadays scientists can sequence large scale of cells, even from frozen tissue from patients. The advancement and low cost of single cell sequencing will increase the possibility to develop personalized therapy in future.