【LGS Report: Self-initiative Overseas Training 2018 (Cancer Research Center of Marseille (CRCM), Marseille, France)】

Date	2018/10/30-12/3
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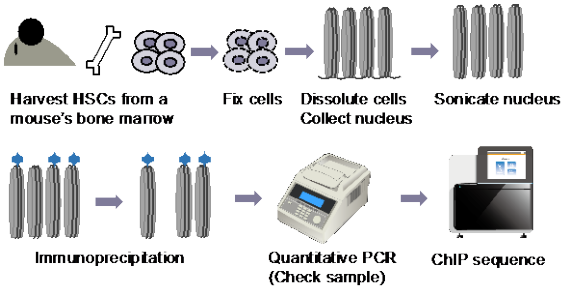
【Summary】

I visited Prof. Estelle Duprez lab in Cancer Research Center of Marseille (CRCM) from 2018/10/30 to 12/3. The purpose of my oversea training was to learn and discuss specific techniques for our epigenetic research. I learned sample preparation for ChIP sequence analysis and immunohistochemistry during the training. I also took part in the weekly meetings of her lab and discussed with the lab members. In addition, I made my presentation on my research and received constructive feedback and useful advice for writing a dissertation.

Marseille

【Important content】

Dr. Duprez lab actively perform ChIP sequence analysis of H3K27 acetylation using a small number of cells such as hematopoietic stem cells (HSCs), so I wanted to introduce their protocol to our lab. I conducted detailed condition survey with her lab members and mastered the protocol completely. I then performed ChIP sequence analysis using the HSCs samples I had prepared in Japan. Unfortunately, we failed the analysis, because those samples did not fit in the protocol of the Duprez lab. The sample purification protocol that I learned there is different from our protocol in Japan; therefore, I need to optimize Duprez's protocol for our samples. Once I succeed to develop my own protocol, I'll try to analyze our samples again.



Sample preparation for ChIP sequence analysis

【Development of your research activities】

I took part in four lab meetings, at one of which I made a presentation, and one seminar by an invited speaker. In her lab, three out of seven members are bioinformatician, so it was a great experience for me to discuss their research. Especially, Dr. Herault's study on the single-cell-RNA sequence analysis using HSCs and multipotent progenitors of aged and young mice was interesting for me, because his research was really close to mine. He performed clustering analysis by each cell type using Seurat, which is useful software for a single cell analysis. Interestingly, the significant differentiation between long-term-HSCs and short-term-HSCs, which can be observed in young mice, was not identified in aged mice. He will continue researching the relationship between the decline in a polarity of HSCs' cell division and transcriptional changes during aging. In addition, I realized that some of high expressed genes are common in my lab's sequence data, which used thousands of young and aged HSCs. Dr. Herault and I decided to compare his data with mine and analyze them altogether in near future.