公開版

平成 30 年 6 月 26 日

医療分野国際科学技術共同研究開発推進事業
戦略的国際共同研究プログラム (SICORP カナダ)
事後評価コメント

研究開発課題名　正常造血及び白血病における幹細胞性とエピジェネティクス
研究開発機関名　東京大学
研究開発代表者名　中内　啓光

Final Review Report (Dick-Nakauchi team)

Project's Name	Epigenetics and stemness in human hematopoiesis and leukemia: a new generation of stem cell targeted regenerative and leukemia therapeutics
Comments	This group has tried to link hematopoietic and leukemic stem cells with epigenetics. They investigated the transcriptional and epigenetic networks underlying stemness and differentiation of hematopoietic lineages as well as leukemia and utilized the knowledge to develop therapeutics for related diseases. They have performed various omics analyses and obtained valuable resource data with a high level of quality that would promote our understanding of stem cells and leukemia, although most of the data have not yet been publicly available. Among various projects, Dick's lab collected CB samples, pooled into three groups, and flow sorted each with their advanced methods into 6 multipotent and 7 differentiated cells. To understand the changes in chromatin accessibility during HSC differentiation, they performed ATAC-seq and done detailed data analysis and validation. They also performed similar analyses using leukemic stem cells from AML samples. Furthermore, other group members collected various stem cell samples for epigenetic analyses, such as hemogenic endothelial cells (HECs) and teratoma-derived human HSCs, although the molecular and epigenetic analyses of them are behind schedule. These datasets should provide an important resource to the stem cell community. However, in spite of these comprehensive data, most important point is whether these big data can create a new concept of HSC biology. In this regard, the Dick-Ogawa group's study on the chromatin accessibility showed some of the newly defined LSC signature involving CTCF. This work will reveal a novel epigenetic regulation of HSCs as an achievement of a successful collaborative work between Canada and Japan. Compared to the other groups, collaborations among members, particularly between Canada and Japan, were initially limited. However, interactive collaborations and networking are obviously in progress. Since some of the collaborative projects are behind schedule, these collaborations should be continued, and are expected to generate several publications. In conclusion, focusing on human hematopoietic stem cells and leukemia, this

	team has made a great progress. They have developed valuable epigenomic datasets with high-quality and provided several novel regulators of HSCs. To finish up this joint research program, it would be very important to complete the epigenomic profiling in progress and provide the data to the community.

以上