"The 84th of Stem Cell Biology and Regenerative Medicine Forum"

Date：Sep 15th (Tue) 2015
Time : 13:00 ～ 14:30
Place：Auditorium in 1st Building at Institute of Medical Science in Univ. of Tokyo

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（Internal Speaker）

13:00-13:30 Yosuke Tanaka (Division of Cellular Therapy, IMSUT)
Identification of Runx1-direct targets important for definitive hematopoiesis

（External Speaker）

13:30-14:30 Bertie Gottgens (Professor of Molecular Haematology,
University of Cambridge)
Transcriptional Network Control of Blood Cell Development

Hosted by Center for Stem Cell Biology and Regenerative Medicine

---Information---

* Please register attendance at the reception desk.
* Next forum (the85th) will be held on Sep. 16th (Wed) 18:00～ at Auditorium
* Please contact tatsu-m@ims.u-tokyo.ac.jp, for Forum speaker recommendations

Identification of Runx1-direct targets important for definitive hematopoiesis

Yosuke Tanaka (Division of Cellular Therapy, IMSUT)

Runx1 is an indispensable transcription factor for definitive hematopoiesis, not primitive hematopoiesis. We previously showed that Runx1+Gata1+ cells are primitive erythrocyte progenitor cells and Runx1+Gata1- cells contain definitive hematopoietic progenitor cells at embryonic day 7.5-8.0 (E7.5-8.0) in Runx1-GFP/Gata1-mCherry double reporter mouse embryos. The data suggest that lineage choice/commitment toward definitive hematopoiesis has already occurred and could be monitored using these two reporters. In order to look for Runx1-direct targets important for definitive hematopoiesis, we decided to compare gene expression and Runx1-binding between two Runx1+ populations in ES cell differentiation. To this end, we established Runx1-GFP/Gata1-mCherry double reporter ES cell lines and performed RNA-Seq and Runx1-Chip-Seq analysis using two Runx1+ populations collected from Embryonic Bodies(EBs). Integration analysis gave us several candidate factors that are preferentially expressed in Runx1+Gata1- populations and have nice Runx1 peaks with well-conserved Runx1-binding motif between several species. We are characterizing function of these candidate factors for definitive hematopoiesis in ES cell differentiation system. Here we will present our new findings in this attempt.

Transcriptional Network Control of Blood Cell Development

Bertie Gottgens (Professor of Molecular Haematology, University of Cambridge)

The first rigorous assays capable of identifying stem cell activity at the level of individual cells were established for blood stem cells in the previous century. More recent technological innovations now make it possible to also perform comprehensive genome-scale molecular analysis at the single cell level. Such analysis holds great promise in our efforts to understand the molecular mechanisms that underlie key stem cell properties such as self-renewal and differentiation, and likely will play a major role in unravelling the molecular causes of stem cell heterogeneity.

Work in the Gottgens lab has recently utilised single cell expression profiling technology to study the emergence of the first wave of haematopoiesis in the developing embryo, and used the expression data from nearly 4,000 single cells to construct a transcriptional regulatory network model that captures key aspects of early blood development. In parallel work, the group has used single cell expression profiling to study the cellular heterogeneity of the adult blood stem/progenitor compartment, gaining new insights into the likely nature of long-term repopulating haematopoietic stem cells (HSCs).

Taken together, this work highlights (i) that single cell genomics is a promising technology to advance our knowledge of blood cell development, and (ii) that advanced computational analysis is essential to optimise extraction of new biological knowledge from such data.