## BDR SEMINAR (Kobe/online hybrid)

### Takashi Nagasawa

Immunology Frontier Research Center (WPI-IFReC), Osaka University

### Tuesday, April 26, 2022

16:30-17:30 1F Auditorium, DB Building C, Kobe / Broadcast online via Zoom Zoom meeting URL will be announced on the event day by e-mail. \*This seminar is open only to BDR members.

# Microenvironmental niches for hematopoietic stem cells and hematopoiesis in the bone marrow

#### Summary

Adult tissue stem cells, which play a critical role in the tissue maintenance and regeneration, are in contact with and maintained by microenvironments, termed niches. Most blood cells are generated from hematopoietic stem cells (HSCs) in the bone marrow and the identity of HSC niches has been a subject of longstanding debate. We found that the chemokine CXCL12 is essential for the maintenance of HSCs and development of B cells, and identified a population of cells having long processes and expressing high amounts of CXCL12, termed CXCL12-abundant reticular (CAR) cells in the marrow (1). We revealed that most HSCs adjoined CAR cells and that ablation of CAR cells in vivo severely impaired the production of CXCL12 and SCF, and led to a marked reduction in the numbers of HSCs and B cells (1, 2). Furthermore, we found that the transcription factors Foxc1 and Ebf3 were preferentially expressed in CAR cells and essential for the maintenance of HSCs and hematopoietic progenitors in the marrow. On the other hand, we revealed that CAR cells were self-renewing mesenchymal stem cells, which give rise to osteoblasts and adipocytes in adult bone marrow, using lineage-tracing and that Foxc1 and Ebf3 were essential for inhibiting differentiation of CAR cells into adipocytes and osteoblasts, respectively (3, 4). Furthermore, we show the presence of human counterpart of CAR cells (5). Together, the bone marrow specific population of mesenchymal stem cells, CAR cells and their long processes are the major cellular component of niches for HSCs and hematopoiesis.

(1)Sugiyama et al., Immunity 25;977, 2006 (2)Omatsu et al., Immunity 33;387, 2010 (3)Omatsu et al., Nature 508; 536, 2014 (4)Seike et al., Genes Dev 32; 359, 2018(5)Aoki et al., Br J Haematol 193; 659, 2021.



Host: Mitsuru Morimoto Laboratory for Lung Development and Regeneration, BDR Contact: mitsuru.morimoto@riken.jp

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