

## CDB SEMINAR

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Monday, June 27, 2016 16:00~17:00 A7F Seminar Room

## Defining the stem cell lineages in adult skin epidermis

## Summary

The inter-follicular epidermis regenerates from heterogeneous basal cell populations that divide at different rates. Infrequently dividing basal cells are identified as label retaining cells (LRCs) and are putative long-lived stem cells while non-LRCs are putative short-lived progenitor cells. Here we employ the H2B-GFP pulse-chase system in adult mouse skin and find that epidermal LRCs and non-LRCs are molecularly distinct and are preferentially marked by Dlx1 and Slc1a3, respectively. Long-term lineage tracing reveals that DIx1- and Slc1a3-marked cells act as two distinct stem cell populations, with different kinetics of not only proliferation, but also differentiation and upward cellular transport. During normal homeostasis, these two stem cell populations are spatially segregated in distinct territories and can preferentially produce unique differentiated lineages. However, upon wounding or selective killing, they can temporarily replenish each other's territory and differentiated lineages. Our work re-defines the lineage hierarchy in the epidermis and identifies two discrete stem cell populations with different cell division frequencies.

References Sada A et al., Nat Cell Biol. 2016 Defining the cellular lineage hierarchy in the interfollicular epidermis of adult skin.

Host: Mitsuru Morimoto Lung Development, CDB <u>mmorimoto@cdb.riken.jp</u> Tel: 078-306-3199 (ext:1602) Sada A et al., Science 2009 The RNA-binding protein NANOS2 is required to maintain murine spermatogonial stem cells.

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