RIKEN Center for Integrative Medical Sciences

SEMINAR

Tue. January 30, 2018　15:00 ~ 16:00　Koryuto Hall, 1F Main Office Bldg.

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"Epigenetic and chromatin reprogramming at the beginning of mammalian life"

Mammalian sperm and oocytes have different chromatin organization and epigenetic landscapes. Following fertilization, the protamine-packaged sperm genome is assembled into chromatin de novo, while the maternal chromatin is inherited from the egg. During preimplantation development, both genomes go through reprogramming to become largely equal with the exception of imprinted loci. After global DNA demethylation, zygotic genome activation takes place to prepare the embryos for the first cell lineage specification and later embryonic development. Despite their importance, the molecular mechanism underlying these fundamental developmental processes are not well understood due to the technical difficulties in working with limited cell numbers. In the past several years, we have developed a number of techniques which allowed us to tackle these important yet technically challenge questions. In addition to reprogramming sperm, egg can also reprogramming somatic cells into totipotency. We identified a major epigenetic barrier for somatic cell nuclear transfer (SCNT)-based reprogramming and demonstrated that we can overcome this barrier to achieve high reprogramming efficiency, which has great potential for regenerative medicine. In the seminar, I will present our major discoveries that underlying mammalian preimplantation development and SCNT reprogramming, including the first TF important for ZGA and a new mechanism of genomic imprinting.

Publications relevant to the seminar

1. Matoba, S. et al. Embryonic development following somatic cell nuclear transfer impeded by persisting histone methylation. *Cell* 159, 884-895 (2014)
2. Chung, Y.G. et al. Histone demethylase expression enhances human somatic cell nuclear transfer efficiency and promotes derivation of pluripotent stem cells. *Cell Stem Cell* 17, 758-766 (2015)
3. Inoue, A. et al. Nucleosome assembly is required for nuclear pore complex assembly in mouse zygotes. *Nature SMB* 21, 609-16 (2014)
4. Inoue, A. et al. Replication-dependent loss of 5-hydroxymethylcytosine in mouse preimplantation embryos. *Science* 334, 194 (2011)
5. Shen, L. et al. Tet3 and DNA replication mediate demethylation of both the maternal and paternal genomes in mouse zygotes. *Cell Stem Cell* 15, 459-470 (2014)
6. Lu, F. et al. Establishing chromatin regulatory landscape during mouse preimplantation development. *Cell* 165, 1375-1388 (2016)
7. Inoue, A. et al, Maternal H3K27me3 controls DNA methylation-independent genomic imprinting. *Nature* 547, 419-424 (2017)
8. Inoue, A. et al. Genomic imprinting of Xist by maternal H3K27me3. *Genes Dev*. 31, 1927-32 (2017)

Host: Haruhiko Koseki
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