



The 2nd International Symposium on REPLICATION of NON GENOME

Cutting Edge of Epigenetics

共催: 東京大学医科学研究所 国際共同利用・共同研究拠点

Date & Time : June 21 (Wed) 10:00 – 18:00 - June 22 (Thu) 9:30 – 15:00, 2023

Venue: Tsuki-no-Sumika, Atami Juraku Hotel, Shizuoka, Japan

Language: English

Organizer: [Makoto Nakanishi](#) (The University of Tokyo, Japan)

June 21 (Wed) 10:00 – 18:00

10:00 – 10:05

[Makoto Nakanishi](#) (The University of Tokyo, Japan) Opening remarks

Session 1 Epigenetics in Gametogenesis & Development

Chair: Shihori Yokobayashi, Hitomi Matsuzaki

10:05 – 10:35

[Masato Ikawa](#) (Osaka University, Japan)

Testis-enriched genes and their functions for spermatogenesis and fertilization

10:35 – 11:00

[Akihiko Sakashita](#) (Keio University, Japan)

The role of retrotransposon MERVL in regulating host gene expression and ontogeny

11:00 – 11:15: Coffee Break

Session 2 Epigenetics in Chromatin Regulation PartI

Chair: Hiroshi Ochiai, Takayuki Hoshii

11:15 – 11:45

[Takashi Fukaya](#) (The University of Tokyo, Japan)

Visualization of transcription hubs in living Drosophila embryos

11:45 – 12:20

[Huck Hui Ng](#) (Genome Institute of Singapore, Singapore)

Dissecting the genetic and epigenetic pathways for non-alcoholic fatty liver diseases

12:20 – 13:35

Lunch

Session 3 Epigenetics in Chromatin Regulation PartII

Chair: Atsushi Iwama, Yota Murakami

13:35 – 14:10

[Anja Groth](#) (University of Copenhagen, Denmark)

Chromatin Replication and Epigenome Maintenance

14:10 – 14:40

[Katsuhiko Shirahige](#) (The University of Tokyo, Japan)

Is Cohesin Really Necessary for Transcription? Molecular Entities of Transcriptional Dysregulation in the absence of Cohesin

14:40 – 15:00 Coffee Break

15:00 – 15:30

[Yoichi Shinkai](#) (RIKEN, Japan)

Epigenetic plasticity safeguards heterochromatin configuration

15:30 – 16:05

[William J. Greenleaf](#) (Stanford University, USA)

Exploring the physical genome

16:05 – 16:10

Comments from the Advisory Board

Group photo

16:10 – 18:00

Poster session

19:00 –

Dinner & Reception

June 22 (Thu) 9:30 - 15:00

Session 4 Epigenetics in Transcriptional Regulation

Chair: Hiroyuki Aburatani, Mitsuhiro Endoh

9:30 – 9:55

[Haruhiko Koseki](#) (RIKEN, Japan)
Polycomb in DNA damage response

9:55 – 10:30

[Kristian Helin](#) (The institute of Cancer Research, UK)
Interrogating the functional roles of histone methylation in transcription

10:30 – 11:00 Coffee Break

Session 5 Epigenetics in DNA Methylation

Chair: Motoko Unoki, Taiko To

11:00 – 11:25

[Atsushi Iwama](#) (The University of Tokyo, Japan)
TOPORS ubiquitin ligase promotes DNMT1 degradation upon DNA hypomethylating agents

11:25 – 11:50

[Kyohei Arita](#) (Yokohama City University, Japan)
Structural basis for activation mechanism of DNMT1

11:50 – 12:15

[Makoto Nakanishi](#) (The University of Tokyo, Japan)
Molecular mechanism of replication-uncoupled maintenance DNA methylation

12:15 – 13:45

Lunch

Session 6 Epigenetics in Germ Line Stem Cell Biology

Chair: Akihiko Sakashita, Naoko Hattori

13:45 – 14:10

[Kei-ichiro Ishiguro](#) (Kumamoto University, Japan)
Mechanism of cell cycle switch from mitosis to meiosis in mouse germ cells

14:10 – 14:45

[Xin Chen](#) (Johns Hopkins University, USA)
Breaking Symmetry: Asymmetric Histone Inheritance

14:45 – 14:55

Comments from the Advisory Board

14:55 – 15:00

[Hiroyuki Aburatani](#) (The University of Tokyo, Japan) Closing remarks

June 21 (Wed) 16:10 – 18:00

Poster session

1. **Tomohiko Akiyama** (Yokohama City University)
Mechanism for regulating pluripotency by a limited number of enhancers
2. **Kazumasa Aoyama** (The University of Tokyo)
The regulatory mechanism of EZH1 essential for the maintenance of EZH2-deficient myelodysplastic syndromes (MDS)
3. **Mitsuhiro Endoh** (Kumamoto University)
Dppa2/4-Pcgf6 axis epigenetically primes de novo DNA methylation target genes in naïve pluripotency for developmental fidelity
4. **Naoko Hattori** (Hoshi University)
Chromodomain Y-like 2 (Cdy12) is involved in the precise H3K9me3 patterning in mouse embryonic stem cells
5. **Takayuki Hoshii** (Chiba University)
BOD1L facilitates chromatin binding of SETD1A and promotes leukemia cell growth
6. **Junko Kanoh** (The University of Tokyo)
Evolution of telomere-adjacent regions in primates
7. **Kazumitsu Maehara** (Kyushu University)
Stability analysis of high-dimensional dynamics using single-cell data
8. **Hitomi Matsuzaki** (Tsukuba University)
Investigation of asymmetric DNA methylation formation ability of the ICR sequences using transgenic mice
9. **Yota Murakami** (Hokkaido University)
Anti-silencing factor promotes heterochromatin formation on repeated sequences
10. **Yosuke Nagahata** (Kyoto University)
Evolutionary reversion to eukaryotic unicellular ancestors in tumorigenesis
11. **Mariko Sasaki** (National Institute of Genetics)
Understanding mechanisms by which CAF-1 functions to maintain the copy number of rDNA repeats in budding yeast
12. **Michiaki Sato** (The University of Tokyo)
Analysis of the mechanism of acute myeloid leukemia maintenance by DNMT3A mutation
13. **Hiroaki Tachiwana** (Cancer Institute)
An HDAC inhibitor suppresses transcription of breast cancer specific genes
14. **Tatsuro Takahashi** (Kyushu University)
MutS α and Smarcd1 form a mispair-activated nucleosome remodeling complex that catalyzes unidirectional nucleosome sliding
15. **Junichiro Takano** (RIKEN)
The role of PRC1 in the vicinity of replication fork

16. **Shouta Tanimoto** (The University of Tokyo)
Analysis of SUMO signaling in regulating DNMT1-DNA crosslink repair
17. **Ichiro Taniuchi** (RIKEN)
Chemical inducible protein degradation in mice
18. **Taiko To** (Tokyo Institute of Technology)
Crosstalk between CG and non-CG DNA methylation drives plant epigenomic pattern formation
19. **Motoko Unoki** (The University of Tokyo)
Maintenance DNA methylation and chromosome stability: Insights from ICF syndrome studies
20. **Shihori Yokobayashi** (Kyoto University)
Understanding epigenome reprogramming in human germ cell fate using an in vitro reconstitution system
21. **Saori Yoshimura** (Kumamoto University)
HSF5 plays an essential role in transcriptional regulation at the mid-late pachytene stage transition in male meiotic prophase I