

The 30th Hot Spring Harbor International Symposium
Chromatin Potential in Development and Differentiation
The 6th Symposium of the Inter-University Research Network for Trans-Omics Medicine

New technologies meet Biology
January 18 - 19, 2022
Online meeting

Tuesday, January 18, 2022

09:25-09:30 Opening Remarks:
 Hiroshi Kimura (Tokyo Institute of Technology)

Session 01: New Technologies

Chair: Hiroshi Kimura (Tokyo Institute of Technology)

09:30-10:00 S-01 : **Wu Ting** (C-ting) (Harvard Medical School, USA)
 Doubling down on pairing

10:00-10:30 S-02 : **Long Cai** (California Institute of Technology, USA)
 Spatial multi-omics: RNA and DNA seqFISH+

10:30-11:00 S-03 : **Yasuyuki Ohkawa** (Kyushu University, Japan)
 Chromatin structure in skeletal muscle regeneration

11:00-11:05 Short break

11:05-11:25 S-04 : **Hiroshi Ochiai** (Hiroshima University, Japan)
 STREAMING-tag system: A novel technology to analyze the spatio-
 temporal relationship between transcriptional regulators and transcriptional
 dynamics at the single gene level

11:25-11:45 S-05 : **Takayuki Nojima** (Kyushu University, Japan)
 POINTing towards transcription termination

11:45-12:05 Selected from poster abstract
 P-12 : **Yuki Iwashima** (Kanazawa University, Japan)
 The role of nuclear pore complex in the transcriptional regulation
 P-17 : **Hiroaki Kato** (Shimane University, Japan)
 A chimeric chemical model revealed asymmetric DNA pattern in transcribed
 nucleosomes

12:05-12:20 Meet the speakers (2 Breakout Rooms)
 Chair1: Hiroshi Kimura (Tokyo Institute of Technology)
 Chair2: Noriko Saito (The Cancer Institute of JFCR)

12:20-13:00 Lunch

Session 02: Imaging and Modeling

Chair: Yasushi Hiraoka (Osaka University)

- 13:00-13:30 S-06 : **Hiroshi Kimura** (Tokyo Institute of Technology, Japan)
Dynamics of histone modification and RNA polymerase II in living cells
- 13:30-13:50 S-07 : **Akatsuki Kimura** (National Institute of Genetics, Japan)
Quantification and formulation of the effect of nuclear size on the mobility of chromatin in the *C. elegans* embryo
- 13:50-14:20 S-08 : **Tomoko Nishiyama** (Nagoya University, Japan)
Single-molecule approaches for understanding genome architecture
- 14:20-14:40 S-09 : **Yuma Ito** (Tokyo Institute of Technology, Japan)
Live-cell single-molecule imaging of the dynamic interaction between RNA polymerase II and chromatin nanostructures
- 14:40-15:00 S-10 : **Shin Fujishiro** (Nagoya University, Japan)
The role of dynamic cohesin looping in chromatin compaction and phase separation
- 15:00-15:05 Short break
- 15:05-15:20 Meet the speakers (2 Breakout Rooms)
Chair1: Yasushi Hiraoka (Osaka University, Japan)
Chair2: Tokuko Haraguchi (Osaka University, Japan)

Poster Session 01

- 15:20-16:40 Poster Session (odd)

Session 03: Genome and Protein Structure

Chair: Jun-ichi Nakayama (National Institute for Basic Biology)

- 16:40-17:00 S-11 : **Rawin Poonperm** (RIKEN, Japan)
Establishment of the late-replicating inactive X chromosome during differentiation
- 17:00-17:30 S-12 : **Ana Pombo** (Max Delbrück Center for Molecular Medicine, Germany)
3D genome topologies distinguish pluripotent epiblast and primitive endoderm cells in the blastocyst
- 17:30-18:00 S-13 : **Patrick Cramer** (Max Planck Institute, Germany)
Recent insights into chromatin transcription
- 18:00-18:30 S-14 : **Hitoshi Kurumizaka** (The University of Tokyo, Japan)
Structural insights into the dynamics of the chromatin architecture

18:30-19:00 Meet the speakers (2 Breakout Room)
Chair1: Jun-ichi Nakayama(National Institute for Basic Biology)
Chair2: Hidetoshi Kono (National Institutes for Quantum Science and
Technology)

Wednesday, January 19, 2022

Session 04: Development and Differentiation

Chair: Kazuo Yamagata (kindai University)

- 09:30-10:00 S-15 : **Hiroyuki Sasaki** (Kyushu University, Japan)
Establishment of the proper DNA methylation landscape requires the DNMT3A domains recognizing histone modifications in mouse oocytes
- 10:00-10:30 S-16 : **Wei Xie** (Tsinghua University, China)
Epigenetic inheritance and reprogramming during early animal development
- 10:30-11:00 S-17 : **Atsushi Suzuki** (Kyushu University, Japan)
Direct reprogramming technology for basic research and clinical applications
- 11:00-11:30 S-18 : **Noriko Saitoh** (The Cancer Institute of JFCR, Japan)
ELEANOR non-coding RNAs associate with chromatin and regulate the 3D genome structure in breast cancer
- 11:30-11:50 Selected from poster abstract
P-06 : **Tomoko Sunami** (National Institutes for Quantum Science and Technology, Japan)
FRET analysis of sequence dependence of nucleosomal DNA unwrapping
P-23 : **Yuichi Saito** (Kyushu University, Japan)
Variant histone H3.3 expression controls the plasma cell differentiation
- 11:50-12:05 Meet the speakers (2 Breakout Rooms)
Chair1: Kazuo Yamagata (Kindai University)
Chair2: Hiroshi Ochiai (Hiroshima University)
- 12:05-12:50 Lunch

Poster Session 02

- 12:50-14:10 Poster Session (even)

Session 05: Transcription and Mathematical science

Chair: Yoichi Shinkai (RIKEN)

- 14:10-14:40 S-19 : **Lacra Bintu** (Stanford University, USA)
The KRAB domains: high-throughput characterization, single-cell dynamics, and tool development
- 14:40-15:10 S-20 : **Keiichi Nakayama** (Kyushu University, Japan)
Life sciences in the near future: Towards an era of data-driven sciences with artificial intelligence

- 15:10-15:30 S-21 : **Tetsuya Yamamoto** (Hokkaido University, Japan)
Regulation of nuclear bodies by transcription
- 15:30-15:50 S-22 : **Chie Kikutake** (Kyushu University, Japan)
Pan-cancer analysis of mutations in open chromatin regions and their possible association with cancer pathogenesis
- 15:50-15:55 Short break
- 15:55-16:10 Meet the speakers (2Breakout Rooms)
Chair1: Yoichi Shinkai (RIKEN)
Chair2: Akatsuki Kimura (National Institute of Genetics)

Session 06: Chromatin and Epigenetics

Chair: Ichiro Hiratani (RIKEN)

- 16:10-16:30 S-23 : **Yukako Hattori** (Kyoto University, Japan)
Investigating the adaptive role of two histone methyltransferases to carbohydrate-rich diets in animal growth
- 16:30-17:00 S-24 : **Yoichi Shinkai** (RIKEN, Japan)
H3K9 and H3K27 methylation pathways exclusively and coordinately regulate heterochromatin organization
- 17:00-17:30 S-25 : **Jop Kind** (Hubrecht Institute, The Netherlands)
Single-cell multiomic epigenetic profiling in early embryogenesis
- 17:30-17:45 Meet the speakers (Breakout Room)
Chair: Ichiro Hiratani (RIKEN)

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- 17:45-17:50 Closing Remarks:
Yoshinori Fukui (Director, MIB, Kyushu University)

Poster Presentation

※odd number : Poster Session 01 January 18

※even number : Poster Session 02 January 19

- P-01 Histone H3K36me2 and H3K36me3 form a chromatin platform essential for DNMT3A-dependent DNA methylation in mouse oocytes
Seiichi Yano (Kyushu University)
- P-02 Discovery of a novel aminocyclopropenone compound that inhibits BRD4-driven nucleoporin NUP210 expression and attenuates colorectal cancer growth
Hiroya Kondo (Kanazawa university)
- P-03 High Precise Solution Scattering
Masaaki Sugiyama (Kyoto University)
- P-04 Unravelling the dynamics and conformational states of multi-domain chromatin binding protein HP1
Amarjeet Kumar (National Institutes for Quantum and Radiological Science and Technology (QST))
- P-05 Identification of novel regulators of primitive endoderm differentiation through genome-scale CRISPR library screening
Hitoshi Owada (Hiroshima University)
- P-06 FRET analysis of sequence dependence of nucleosomal DNA unwrapping
Tomoko Sunami (National Institutes for Quantum Science and Technology)
- P-07 Heterochromatin eraser promotes heterochromatin formation at target gene cluster
Takahiro Asanuma (Hokkaido university)
- P-08 Time-lapse tracking of single-cell transcriptomes reveals a role for histone H3 upon dormancy breaking in fission yeast
Yuki Shogaki (Waseda University)
- P-09 A genome-wide survey of regulatory variants associated with immune system diseases
Naoto Kubota (Kyushu University)
- P-10 MyoD Binding in Proliferative Myoblasts during the Cell Cycle
QIANMEI WU (Kyushu University)
- P-11 MLL3/MLL4 Histone Methyltransferase Activity Dependent Chromatin Organization at Enhancers during Embryonic Stem Cell Differentiation
Naoki Kubo (Kyushu University)
- P-12 The role of nuclear pore complex in the transcriptional regulation
Yuki Iwashima (Kanazawa University)
- P-13 Development of CRISPR-Based Rainbow/Barcode Dual Labeling System
Masaki Kawamata (Kyushu University)
- P-14 Mechanisms regulating Clr4 histone methyltransferase activity

- Rinko Nakamura (National Institute for Basic Biology)
- P-15 Spatiotemporal Imaging of Histone H2A-DNA Dynamics using HS-AFM
Goro Nishide (Kanazawa University)
- P-16 Targeted inhibition of EPAS1-driven IL-31 production by a small-molecule compound
Kazufumi Kunimura (Kyushu University)
- P-17 A chimeric chemical model revealed asymmetric DNA pattern in transcribed nucleosomes
Hiroaki Kato (Shimane University)
- P-18 HDAC inhibitors induce H2A.Z accumulations to gene bodies in specific genes and their transcription suppression
Hiroaki Tachiwana (The Cancer Institute of JFCR)
- P-19 Building a Coarse-grained Model of Chromatin for Disentangling the Effects of Histone Post-Translational Modifications on Nucleosome Packing and Chromatin Structure.
Justin Chan (Institute for Quantum and Life Science (iQLS), QST)
- P-20 Discriminative feature of cells characterizes cell populations of interest by a small subset of genes
Takeru Fujii (Kyushu University)
- P-21 Pervasive occurrence of splice-site-creating mutations in genetic disorders
Narumi Sakaguchi (Kyushu University)
- P-22 Live imaging of the initiation and elongation forms of RNA polymerase II using phosphorylation-specific probes
Satoshi Uchino (Tokyo Institute of Technology)
- P-23 Variant histone H3.3 expression controls the plasma cell differentiation
Yuichi Saito (Kyushu University)
- P-24 Chromatin mobility of X-linked loci and its transcription regulation
Yuko Sato (Tokyo Institute of Technology)
- P-25 Epigenomic and genetic approaches to identify Rorc enhancers indispensable for LT_i cell development
Satoshi Kojo (Kyushu University)
- P-26 Fission yeast nuclear membrane protein Bqt4 is important for the regulation of nucleolus movement in the nucleus
Masaru Ueno (Hiroshima University)
- P-27 Transcriptomic landscape of whole lung cells after influenza virus infection in mouse
Shin-ichi Koizumi (Kyushu University)
- P-28 An analytical system for comprehensive quantitative profiling of bioactive lipids by solid phase extraction combined with LC/MS/MS
Kohta Nakatani (Kyushu University)
- P-29 Cryo-EM structure of the nucleosome containing human parasitic *Giardia lamblia*

histones

Shoko Sato (The University of Tokyo)

P-30 Cryo-EM structures of chromatin units from nucleus

Yoshimasa Takizawa (The University of Tokyo)

P-31 Establishment of CTCF looping during medaka embryogenesis

Ryohei Nakamura (The University of Tokyo)

P-32 SmcHD1 underlies the formation of H3K9me3 blocks on the inactive X chromosome in mice

Saya Ichihara (Kindai University)

P-33 Mechanisms of mismatch-induced nucleosome remodeling during eukaryotic DNA mismatch repair

Eiichiro Kanatsu (Kyushu University)