CSI SINGAPORE - KYOTO UNIVERSITY JOINT SYMPOSIUM 2025

PROGRAMME BOOKLET

24 - 26 Nov

CRC Auditorium
MD11 - Clinical Research Centre
10 Medical Dr, Singapore 117597

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GENERAL INFORMATION

Confidentiality & Use of Materials

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Day 1: Monday, 24 Nov

14 30 - 14 45	**Welcome & Opening Addresses by:** **Ashok VENKITARAMAN** Director, Cancer Science Institute of Singapore Distinguished Professor of Medicine, Yong Loo Lin School of Medicine, NUS Chief Scientist, Biomedical Research Council, Agency for Science, Technology and Research **Nagahiro MINATO** President, Kyoto University **Eng Chye TAN** President, National University of Singapore
Keynote Session **Moderated by: Ashok VENKITARAMAN**	
14 45 - 15 30	**Nagahiro MINATO** President, Kyoto University **Keynote Lecture - T cell Meets Cancer: Cure Within**
15 30 - 15 45	Coffee/Tea break
SESSION 1: Immuno-oncology **Moderated by: Wee Joo CHNG & Kenji CHAMOTO**	
15 45 - 16 15	**Allen YEOH** Head and Senior Consultant Division of Paediatric Haematology and Oncology, National University Cancer Institute, Singapore (NCIS) / National University Hospital (NUH) **CARing for ALL: CAR T-cell Therapy for Acute Lymphoblastic Leukaemia**
16 15 - 16 45	**Sidonia FAGARASAN** Vice Director, Center for Cancer Immunotherapy and Immunobiology Professor, Center for Cancer Immunotherapy and Immunobiology / Division of Integrated High-Order Regulatory Systems, Graduate School of Medicine, Kyoto University **Metabolic Regulatory Pathways and Anti-cancer Responses**
16 45 - 17 15	**Wee Joo CHNG** Senior Principal Investigator & Professor Cancer Science Institute of Singapore **Identification of Immunotherapeutic Target in High-risk Haematology Malignancies**
17 15 - 17 45	**Kenji CHAMOTO** Professor, Department of Immuno-oncology PDT Kyoto University **The Role of Fatty Acid Oxidation in Cancer Immunotherapy**
17 45 - 18 00	Discussion
END OF DAY 1	

Day 2: Tuesday, 25 Nov

SESSION 2: Early Cancer Initiation Moderated by: Yasuki FUJITA & Peter YEOW	
09 00 - 09 30	**Polly CHEN** Principal Investigator & Associate Professor Cancer Science Institute of Singapore **The Involvement of Endogenous dsRNA Species in the Evasion of Tumor Immune Responses**
09 30 - 10 00	**Yasuyuki FUJITA** Professor, Department of Molecular Oncology, Graduate School of Medicine, Kyoto University **Cell Competition between Normal and Transformed Epithelial Cells**
10 00 - 10 30	**Ashok VENKITARAMAN** Director, Cancer Science Institute of Singapore Distinguished Professor of Medicine, Yong Loo Lin School of Medicine, NUS Chief Scientist, Biomedical Research Council, Agency for Science, Technology and Research **Genetic and Environmental Triggers for Cancer Initiation and Progression**
10 30 – 10 45	Discussion
10 45 - 11 00	Coffee/Tea break
SESSION 3: Genome Instability Moderated by: Jason PITT & Hiroshi HARADA	
11 00 - 11 30	**Jason PITT** Principal Investigator Cancer Science Institute of Singapore **Multiview Learning of Mutational Patterns Improves Pancancer Prediction of Homologous Recombination Deficiency and Platinum Response**
11 30 - 12 00	**Hiroshi HARADA** Professor, Graduate School of Biostudies Kyoto University **Hypoxia - the Hidden Driver of Cancer Genome Instability**
12 00 - 12 30	**Marco FOIANI** Senior Principal Investigator Cancer Science Institute of Singapore **Mechanisms and Pathways Maintaining the Integrity of Replicating Chromosomes**
12 30 - 12 45	Discussion
12 45 - 13 45	Lunch

Day 2: Tuesday, 25 Nov cont'd

SESSION 4: Precision Oncology Moderated by: Akira YOKOYAMA & Boon Cher GOH	
13 45 - 14 15	**Akira YOKOYAMA** Senior Lecturer, Medical Oncology Kyoto University **Cancer Risk Evaluation using Somatic Mosaicism in the Buccal Mucosa**
14 15 - 14 45	**Boon Cher GOH** Senior Principal Investigator & Professor Cancer Science Institute of Singapore **Individualised Treatment: Dosing and Germline Genotypes Matter**
14 45 - 15 15	**Seishi OGAWA** Professor, Department of Pathology and Tumor Biology Kyoto University **Chromatin Landscape and Epigenetic Heterogeneity of Acute Myeloid Leukemia**
15 15 - 15 45	Discussion
15 45 - 16 00	Coffee/Tea Break
END OF DAY 2	

Day 3: Wednesday, 26 Nov

SESSION 5: RNA Biology Moderated by: Yvonne TAY & Makoto HAYASHI	
08 30 - 09 00	Coffee/Tea Break
09 00 - 09 30	**Yilong ZHOU** Principal Investigator, Cancer Science Institute of Singapore Assistant Professor, Department of Biochemistry National University of Singapore **RNA Damage Compartmentalisation by Stress Granules**
09 30 - 10 00	**Yasuhiro MURAKAWA** Professor, Department of Pathology and Biology of Diseases, Graduate School of Medicine, Kyoto University **Decoding Human Transcriptome Architecture with Oxford Nanopore Full-length RNA Sequencing**
10 00 - 10 15	Discussion
10 15 - 11 15	Concluding Session Moderated by: **Yvonne TAY & Makoto HAYASHI**
END OF DAY 3	

SPEAKERS' PROFILES

NAGAHIRO MINATO

KEYNOTE LECTURE - 24 NOV, 14 45 - 15 30

President, Kyoto University

T cell Meets Cancer: Cure Within

One of the most striking impacts of the checkpoint-blockade cancer immunotherapy, which now serves as the first-line therapy for a wide variety of cancer types, may be that it has proved that the acquired immunity in the host does matter substantially in human cancers, after decades of arguments and frustration. This has prompted us to carefully reinvestigate every aspect of the immune responses taking place in the body in the context of cancer immunity, to improve and maximize its potential capacity in the therapy of cancer patients. In this talk, I will focus on the interplays between immune system and cancer microenvironment in the host. While it is well recognized that cancer cells may be associated with highly variable stromal cell reactions in the tissues, their significance in the development and progression of cancer has been a matter of arguments for decades. Based on our recent studies, I propose that appropriate stromal cell remodeling in the cancer microenvironment takes an important part for the effective manifestation of cancer immunity.

Biosketch

Nagahiro Minato is the president of Kyoto University. Born in 1951, he holds the degree of doctor of medicine. After graduating from Kyoto University's Faculty of Medicine in 1975, he worked as an associate researcher at the Albert Einstein College of Medicine from 1977–80. In 1992, he was appointed as professor of immunology and cell biology at Kyoto University's Graduate School of Medicine, where he served as dean from 2010–14. After serving as Kyoto University's provost and executive vice-president, Dr. Minato was appointed as the 27th president in October, 2020. His main interest is immunology, a field in which he has published approximately 220 scientific papers throughout his career. In 2002, he invented PD-1 checkpoint blockade cancer immunotherapy with Dr. Tasuku Honjo.

ALLEN ENG JUH YEOH

SESSION 1 - 24 NOV, 15 45 - 16 15

Head and Senior Consultant
Division of Paediatric Haematology and Oncology,
National University Cancer Institute, Singapore (NCIS) /
National University Hospital (NUH)

CARing for ALL: CAR T-cell Therapy for Acute Lymphoblastic Leukaemia

Chimeric antigen receptor (CAR) T-cell therapy has transformed the treatment of relapsed/refractory ALL. This transformation from fatal relapsed/refractory disease into deep molecular remission within 1 month is remarkable. Yet, about 50-70% of responders are cured. Failure to cure stem from

1. Loss of CAR T-cell persistence
2. Loss of target antigen like CD19 negative relapse
3. Toxicity from CAR T-cell therapy – Cytokine release syndrome, Neurotoxicity (ICANS) and hematotoxicy.

NUS approach is by complete antigen targeting using flow guided antigen selection. I will share NUS approach to CAR T-cell therapy.

Biosketch

Professor Allen Yeoh is the VIVA-Goh Foundation Professor in Paediatric Oncology in NUS. He is the principal investigator of the Malaysia-Singapore ALL study group and co-leader of NUS CAR T-cell therapy.

SIDONIA FAGARASAN

SESSION 1 - 24 NOV, 16 15 - 16 45

Vice Director, Center for Cancer Immunotherapy and Immunobiology
Professor, Center for Cancer Immunotherapy and Immunobiology /
Division of Integrated High-Order Regulatory Systems,
Graduate School of Medicine,
Kyoto University

Metabolic Regulatory Pathways and Anti-cancer Responses

Metabolites are emerging as critical factors of the immune system, involved in both metabolic circuits and signaling cascades. Accumulated evidence suggests that altered metabolic programs initiated by activation and maturation of immune cell subsets is accompanied by the delivery of various metabolites into the local environment. For example, GABA is mostly known for its inhibitory role in the mammalian brain. GABA was found to have inhibitory roles outside the brain, namely on the immune system. I will discuss the data showing the source of peripheral GABA and its mechanism of action particularly related to anti-tumor responses. I will also discuss a novel metabolic pathway employed by cytotoxic T cells to survive the highly oxidative stress conditions encountered within the tumor microenvironment.

Biosketch

Graduated from “Iuliu Hatieganu” University of Medicine and Pharmacy in Cluj-Napoca, Romania and had residency in gastroenterology and specialty in Clinical Laboratory, Microbiology, Biochemistry and Hematology at the same university. She received Ph.D. at Kyoto University. She was appointed Team leader at the Laboratory for Mucosal Immunity in RIKEN in 2002, Professor at Center for Cancer Immunotherapy and Immunobiology (CCII), Kyoto University in 2020 and Vice Director at CCII in 2024.
Her research activity includes impact of immune system on diversity, structure and resilience of gut microbiota, and the symbiotic relationships between the microbiota and the immune system. Recent works uncovered the role of immune activation in regulation of blood, brain biochemistry and behavior, and novel regulatory pathways involving secreted immune metabolites and anti-tumor responses. Received 2005 Young Scientist Award from the Ministry of Education, Culture, Sport, Science and Technology (MEXT), Japan, 2012 The 15th Japanese Society for Immunology Award, 2013 NISTEP Award from MEXT, Japan, and The Kobayashi Award 2020 from the Kobayashi Foundation, Japan. She has co-authored more than 50 research papers in international peer-reviewed journals such as Science, Immunity, Nature, Cell, and PNAS, many of which are ground breaking and highly cited.

WEE JOO CHNG

SESSION 1 - 24 NOV, 16 45 - 17 15

Senior Principal Investigator & Professor
Cancer Science Institute of Singapore

Identification of Immunotherapeutic Target in High-risk Haematology Malignancies

Despite improvement in therapeutics and outcomes, there remains some hematologic malignancies with poor outcomes such as extra nodal natural killer / T-cell lymphoma, T-cell lymphomas and extramedullary myeloma. Immunotherapeutic approaches such as CAR-T, bispecific or trispecific antibodies and antibody-drug conjugates has been game changers in cancer therapeutics. One of the current issue is that their targets are common targets based on cell types of origin meaning that effective eradication of tumor cells will also result in eradication of normal counterparts resulting in toxicity. We used a membrane proteomics approach coupled with a filtering algorithm to differentiate against normal expression and survival dependency to narrow down candidate membrane antigen that may be good targets for immunotherapy. Amongst the leading candidates, we validated several as potential targets for further development. Our results demonstrated proof of concept that our approach could yield promising targets that can be deployed against these high-risk blood cancers

Biosketch

Professor Wee Joo CHNG is the Senior Principal Investigator of the Cancer Science Institute of Singapore and the Vice President (Biomedical Sciences Research) of the National University of Singapore. He is presently the Yong Loo Lin Professor in Medical Oncology at the Yong Loo Lin School of Medicine, the Group Director of Research at the National University Health System, and the inaugural Executive Director of the Singapore Translational Cancer Consortium.

A hematologist by training, Professor Chng has been a senior consultant at the National University Cancer Institute, Singapore, for over two decades. He is a distinguished researcher in the fields of genomics, therapeutics, and hematologic malignancies, with extensive experience in clinical practice, administration, and leadership. He has produced highly translational research that has improved patient outcomes and allowed for therapy personalisation, such as the use of global genomic techniques to better identify drug resistance and enhance disease prognosis in hematological malignancies. He has received numerous national and international awards for his groundbreaking work, including the National Medical Research Council's National Outstanding Clinician Scientist Award in 2016 and the International Myeloma Foundation's Brian G.M. Durie Outstanding Achievement Award in 2020–becoming the first in Asia to achieve this honor.

Professor Chng is currently the chair of the Asian Myeloma Network, a member of various leading national and international professional committees, including the American Society of Hematology and the International Myeloma Working Group, and a former president of the Singapore Society of Hematology.

KENJI CHAMOTO

SESSION 1 - 24 NOV, 17 15 - 17 45

Professor, Department of Immuno-oncology PDT
Kyoto University

The Role of Fatty Acid Oxidation in Cancer Immunotherapy

Immune checkpoint inhibitors (ICIs) are widely used in cancer therapy, yet over half of patients fail to respond, largely due to T cell dysfunction. Our work shows that non-responsive tumors harbor $CD8^+$ T cells with impaired mitochondrial fatty acid oxidation (FAO). Pharmacological enhancement of FAO with bezafibrate or spermidine restored T cell function, increased tumor-infiltrating lymphocytes, and improved survival in mouse models. A phase I trial combining bezafibrate with nivolumab tripled median progression-free survival in EGFR mutation–negative NSCLC patients and enhanced FAO and $CD8^+$ T cell metabolic fitness. Aging-derived spermidine reduction in T cells contributes to FAO insufficiency, and exogenous spermidine or optimized analogs rejuvenate T cell cancer immunity in aged mice. In parallel, we identified acrolein, a reactive aldehyde, as a novel negative regulator of T cell mitochondrial function. Elevated acrolein levels in the tumor microenvironment suppressed FAO and accelerated T cell exhaustion, whereas acrolein scavenging rescued mitochondrial metabolism and synergized with ICIs in preclinical models. These findings highlight T cell mitochondrial metabolism, specifically FAO, as a therapeutic target and support next-generation ICI combination strategies.

Biosketch

Dr. Chamoto is a Professor of the Department of Immuno-oncology PDT at Kyoto University Graduate School of Medicine. After earning a Ph.D. in Medicine from Hokkaido University in 2006, he pursued postdoctoral training at Harvard Medical School and the Ontario Cancer Institute/Princess Margaret Cancer Center. He got an assistant professor position at the Department of Immunology and Genomic Medicine, where he investigated the molecular mechanisms of immune regulation and tumor immunity. He got the current position in 2023. His research focuses on the intersection of immune metabolism, cancer immunology, and aging, exploring how metabolic pathways shape immune cell function within the tumor microenvironment and aged condition. His laboratory further investigates how metabolic dysregulation of mitochondria contributes to immune aging and autoimmune diseases, aiming to develop metabolism-based immunotherapies for cancer and immune disorders.

POLLY LEILEI CHEN

SESSION 2 - 25 NOV, 09 00 - 09 30

Principal Investigator & Associate Professor
Cancer Science Institute of Singapore

The Involvement of Endogenous dsRNA Species in the Evasion of Tumor Immune Responses

Cancer remains a major global health challenge, with one of the primary obstacles to effective treatment being the ability of tumors to evade immune detection and destruction. Although significant advances have been made in understanding the mechanisms underlying immune escape, strategies to effectively counteract this process are still limited. Recent research has highlighted the pivotal role of double-stranded RNA (dsRNA) molecules in modulating tumor immunity, positioning dsRNA as a novel and critical factor in cancer immune evasion. Elucidating which dsRNA species are involved, and how they are recognized and modified to facilitate immune escape, holds promise for the development of innovative therapies aimed at overcoming immunotherapy resistance and unresponsiveness. In this talk, I will present our latest findings, focusing on the complex interplay between RNA alterations and immune regulation, and their profound impact on immunosuppression in cancer.

Biosketch

Dr. Polly Leilei Chen received her Bachelor of Medicine and completed her medical training in China before earning her PhD in 2010 from the University of Hong Kong. In 2014, Dr. Chen joined the National University of Singapore (NUS) as a Principal Investigator at the Cancer Science Institute of Singapore, concurrently assuming the role of Assistant Professor in the Department of Anatomy. She was promoted to Associate Professor in 2021. Dr. Chen is an EMBO Young Investigator and an Asian RNA Research Ambassador. She currently places her research focus on functional and mechanistic investigation of RNA changes (particularly RNA editing, modification, and splicing) leading to cancer initiation and development; and the development of novel cancer therapies targeting these cancer-associated RNA changes.

YASUYUKI FUJITA

SESSION 2 - 25 NOV, 09 30 - 10 00

Professor, Department of Molecular Oncology,
Graduate School of Medicine
Kyoto University

Cell Competition between Normal and Transformed Epithelial Cells

At the initial step of carcinogenesis, transformation occurs in a single cell within an epithelial sheet. However, it remains elusive what happens at the boundary between normal and the newly emerging transformed cells. Using newly established cell culture and mouse model systems, we have shown that various phenomena can occur at the interface between normal and transformed epithelial cells. For example, when Ras-transformed cells are surrounded by normal epithelial cells, the transformed cells are often eliminated from the apical surface of the epithelial monolayer. This phenomenon is not observed when transformed cells alone are present, suggesting that the presence of surrounding normal cells affects the signaling pathways and fate of transformed cells. Furthermore, we have demonstrated that normal epithelial cells can recognize and actively eliminate various types of transformed cells and named this process EDAC (Epithelial Defense Against Cancer).
In this meeting, I will present our recent findings on cell competition between normal and transformed epithelial cells and discuss how this study can lead to the establishment of novel types of cancer preventive treatment.

Biosketch

1997 - 2002: Post-doc, MDC for molecular medicine, Berlin, Germany
2002 - 2011: Group leader, MRC, LMCB, University College London
2011 - 2020: Professor, Hokkaido University, Institute for Genetic Medicine, Division of Molecular Oncology
2020 - Present: Professor, Kyoto University Graduate School of Medicine

ASHOK VENKITARAMAN

SESSION 2 - 25 NOV, 10 00 - 10 30

Director, Cancer Science Institute of Singapore
Distinguished Professor of Medicine,
Yong Loo Lin School of Medicine, NUS
Chief Scientist, Biomedical Research Council, Agency for Science, Technology and Research

Genetic and Environmental Triggers for Cancer Initiation and Progression

Genetic background and environmental influences collude to trigger cancer initiation and progression through mechanisms that remain unclear. We have studied their collusion in the context of cancer susceptibility associated with germline mutations affecting the breast cancer gene, BRCA2, whose functions in the maintenance of genome stability our lab has investigated. BRCA2 has critical functions in error-free DNA repair by homologous recombination, and in the protection of stalled DNA replication forks during stress. We will present our recent analyses of the role of environmental triggers in eliciting replication stress in BRCA2-deficient cells, and its consequences for genome instability during early cancer initiation and progression.

Biosketch

Ashok Venkitaraman is a Distinguished Professor of Medicine at the National University of Singapore, the Director of the Cancer Science Institute of Singapore, and Chief Scientist for biomedical research at the Agency for Science, Technology and Research (A*STAR). He learnt and practiced medicine at the Christian Medical College, Vellore, India before his Ph.D. with Sir Marc Feldmann at the University of London. After his postdoctoral work with Michael Neuberger, Ashok established his research group at the Medical Research Council (MRC) Laboratory of Molecular Biology, Cambridge, prior to his election as the inaugural holder of the Ursula Zoellner Professorship of Cancer Research at the University of Cambridge from 1998-2020. He was the Director of the MRC Cancer Unit in Cambridge from 2006-2019. Ashok's research has contributed fundamentally to our understanding of how human cancer is suppressed by genes that maintain the integrity of the genome. He has also pioneered new technologies that enable the precise identification and validation of therapeutic targets, leading to the serial spin-out by Cambridge University of biotechnology firms based on his research. Ashok's work has been recognized by international awards, and appointments to the advisory boards of leading academic and commercial organizations. He was inducted to the UK Academy of Medical Sciences in 2001, the EMBO academy, in 2004, the Academia Europaea, in 2025, and the Academy of the American Association for Cancer Research, in 2025.

JASON J. PITT

SESSION 3 - 25 NOV, 11 00 - 11 30

Principal Investigator
Cancer Science Institute of Singapore

Multiview Learning of Mutational Patterns Improves Pancancer Prediction of Homologous Recombination Deficiency and Platinum Response

Predicting homologous recombination deficiency (HRD) is vital for precision cancer therapy. Existing methods have limited accuracy as they utilize pre-selected features and overlook complex mutational relationships. Here, we develop HRD-Fuse, a multiview artificial intelligence (AI) model that uniquely integrates ("fuses") single base substitutions, small insertions/deletions, structural variants, and copy number alterations to capture HRD-relevant mutational relationships through attention-based fusion and contrastive learning. Trained with pancancer whole genome sequences (n = 3,170) enriched for BRCA1/2 biallelic loss (n = 305), HRD-Fuse consistently outperformed conventional tools like CHORD and HRDetect across many HRD prediction tasks. Its utilization of multiview mutational patterns and non-reliance on microhomology deletions explains this performance advantage. Fine-tuning of HRD-Fuse's adaptable architecture to predict platinum therapy response pancancer achieved an F1 score (0.79) nearly double that of existing response predictors. Our approach to unbiased modeling of mutational relationships represents a key advance for therapy response prediction from genomic data.

Biosketch

Dr. Jason J. Pitt is a Principal Investigator at the Cancer Science Institute of Singapore (CSI Singapore), National University of Singapore (NUS), where he also serves as a Member of the NUS Artificial Intelligence Institute and the Founding Head of CSI's Genomics and Data Analytics Core (GeDaC).

His research focuses on combining large-scale cancer genomics data, artificial intelligence (AI), and data-intensive computing to understand how genome instability (GI) patterns arise and fuel cancer evolution. Specifically, he studies the causes and consequences of GI in cancer and develops AI methods for cancer genome analytics and precision oncology. A key goal of his work is to leverage these patterns to guide cancer treatment and prevention.

Dr. Pitt earned his Ph.D. in Genetics, Genomics, & Systems Biology from the University of Chicago in 2017. His significant scientific contributions include studies on homologous recombination deficiency and aggressive molecular features in breast cancer across different ancestries, with his work appearing in journals like Cell, Nature Communications, and Cancer Cell. He has also been a finalist for the ASHG/Charles J. Epstein Trainee Award for Excellence in Human Genetics Research.

HIROSHI HARADA

SESSION 3 - 25 NOV, 11 30 - 12 00

Professor, Graduate School of Biostudies
Kyoto University

Hypoxia - the Hidden Driver of Cancer Genome Instability

It is well established that a single tumor often consists of multiple cancer cell clones with distinct genetic and phenotypic profiles, driven by genomic instability. This intratumoral heterogeneity fosters the emergence of aggressive and resistant clones, thereby contributing to disease progression, treatment resistance, and tumor recurrence. However, it is still unclear whether genomic instability arises in a stochastic or deterministic manner; and, in the deterministic case, the underlying molecular mechanisms remain largely unidentified. Here, we show that hypoxic stress reduces the activity of error-free homologous recombination (HR), thereby promoting the accumulation of gene mutations. Mechanistic analyses revealed that the initial step of HR, CtIP-mediated DNA end resection, is significantly suppressed under hypoxic conditions due to diminished interactions of CtIP with the nucleases DNA2 and Exol. This, in turn, markedly impairs the recruitment of RPA2 and RAD51 to DNA double-strand break sites. Analysis of TCGA datasets further demonstrates that tumors with high hypoxia signatures harbor significantly more insertion/deletion mutations, supporting a causal link between hypoxia and genomic instability. In this presentation, I will present our latest findings on how tumor hypoxia drives cancer genome instability in a deterministic manner, providing new insights into its role in therapeutic resistance and disease progression.

Biosketch

Dr. Hiroshi Harada is Professor of Laboratory of Cancer Cell Biology at the Graduate School of Biostudies and Director of the Radiation Biology Center, GSB, Kyoto University.

He received his Ph.D. in Science from the Graduate School of Science, Nagoya University, in 2002. Following a position as Research Scientist at the Pharmaceutical Division of POLA Cosmetics & Pharmaceuticals Inc., he was appointed Assistant Professor in the Department of Radiation Oncology, Graduate School of Medicine, Kyoto University in 2003. In 2009, he became Principal Investigator and Group Leader at the Career-Path Promotion Unit for Young Life Scientists, Kyoto University, serving as Senior Lecturer. He was appointed Associate Professor at the Hakubi Center, Kyoto University in 2015, promoted to Professor at the Radiation Biology Center in 2016, and subsequently assumed his current professorship at the Graduate School of Biostudies in 2018.

Prof. Harada's research focuses on the molecular networks that drive malignant progression and therapy resistance of cancer cells within the tumor microenvironment, particularly under hypoxia. His laboratory employs genetic, biochemical, and in vivo imaging approaches to elucidate how oxygen homeostasis and hypoxia-induced genome instability impact cancer development and treatment response.

MARCO FOIANI

SESSION 3 - 25 NOV, 12 00 - 12 30

Senior Principal Investigator
Cancer Science Institute of Singapore

Mechanisms and Pathways Maintaining the Integrity of Replicating Chromosomes

We study the topological mechanisms coordinating chromosome replication with transcription and those ones promoting genome condensation. We characterized the topological landscape of the eukaryotic genome by combining genomic, genetic and imaging approaches and identified positive and negative supercoiled genomic clusters and the genome-wide chirality of nucleosomes. We detected genomic elements involved in the formation of intra-chromosomal looping, in the establishment of intra and inter-chomosomal catenation events and in mediating chromosome bendability. Using electron microscopy we found evidence for intra and inter molecular hemicatenation and catenation events. I will describe the topological architecture of RNA polymerase I, II and III transcribed regions within the context of S phase and discuss the contribution of topoisomerases and condensins in coordinating S phase transcription and chromatin condensation.

Biosketch

Prof. Marco Foiani is professor at the Yong Loo Lin School of Medicine at the National University of Singapore (NUS), senior principal investigator at the Cancer Science Institute of Singapore (CSI Singapore).

Foiani obtained his Ph.D in molecular and cell biology from University of Milan in 1988. In 1989, he moved to the National Institute of Health (NICHD) in Bethesda, USA for his post-doctoral studies. In 1991, he returned to Italy as an assistant professor at the University of Milan, professor of molecular biology at the University of Milan in 1995. He joined IFOM in Milan in 1999 and became the Scientific Director of IFOM (since January 2009 to May 2022). He has been a member of the editorial board of Cell (2009-2019). He is a member of the Academia Europea, EMBO and Accademia dei Lincei (Italian Academy of Science). His major contributions are within the fields of chromosome dynamics and genome integrity. In recent years, focus of his research has geared more towards the connections between cell metabolism and genome integrity pathways and between chromosome dynamics and mechano-transduction circuits controlling cell and nuclear plasticity.

AKIRA YOKOYAMA

SESSION 4 - 25 NOV, 13 45 - 14 15

Senior Lecturer, Medical Oncology
Kyoto University

Cancer Risk Evaluation using Somatic Mosaicism in the Buccal Mucosa

Clones harboring cancer driver mutations can expand even in histologically normal tissues, a phenomenon known as somatic mosaicism, which is influenced by age, environmental exposures, and germline factors. While somatic mosaicism in blood is predictive of hematologic malignancies, its role in solid organs remains unclear due to limited access to appropriate samples. Lifestyle factors, such as alcohol consumption and smoking, along with germline variants, are known to increase the risk of esophageal squamous cell carcinoma (ESCC). Given the anatomical and histological continuity of squamous epithelium from the esophagus to the oral cavity, we non-invasively collected buccal mucosa samples from individuals with and without ESCC using swabs and performed deep error-corrected sequencing to characterize tissue remodeling by mutant clones. The effect of alcohol consumption on driver-mutant clones differed depending on germline risk status, whereas smoking and aging affected clone expansion regardless of germline background. Our findings demonstrate that clonal remodeling in the buccal mucosa reflects lifestyle factors, germline risk, and age, and may serve as a non-invasive biomarker for ESCC risk stratification.

Biosketch

Dr. Akira Yokoyama is a lecturer in the Department of Medical Oncology at Kyoto University. He is engaged in clinical practice involving chemotherapy and endoscopic diagnosis and treatment, while also conducting research on somatic mosaicism in the upper gastrointestinal (GI) tract.

In 2019, he received his Ph.D. in medicine from Kyoto University for his work on somatic mosaicism in the normal esophagus. His current research extends beyond the esophagus to include the entire upper GI tract, focusing on field cancerization. He also developed a simple and accurate model to predict esophageal cancer risk using somatic mosaicism in normal buccal mucosa, which was published in Science Translational Medicine in 2025.

This approach not only holds promise for esophageal cancer but also has potential applications in alcohol-related cancers. It may contribute to early cancer detection, risk stratification, and cancer prevention. Furthermore, it offers the novel possibility of visualizing the benefits of alcohol cessation. His work continues to explore these possibilities.

BOON CHER GOH

SESSION 4 - 25 NOV, 14 15 - 14 45

Senior Principal Investigator & Professor
Cancer Science Institute of Singapore

Individualised Treatment: Dosing and Germline Genotypes Matter

Precision oncology aims to deliver the right drug, at the right dose, and in the right regimen for each individual patient. This principle is especially critical in cancer treatment, where both the risk of suboptimal response and the likelihood of serious adverse events are substantially higher than with most other medications. Yet, most anticancer drugs are developed and approved based on population averages rather than individual variability. Even the labelled doses are often inadequately optimized, contributing to unnecessary toxicity.
Current approaches to precision oncology primarily rely on identifying somatic mutations through targeted next-generation sequencing (NGS) panels encompassing selected cancer-related genes. However, beyond somatic alterations, germline genetic polymorphisms can also influence treatment efficacy, toxicity, and optimal drug selection. This talk will discuss how integrating germline pharmacogenomic insights can refine therapeutic choices, enhance safety, and move precision oncology closer to true individualization of cancer care.

Biosketch

Professor Goh Boon Cher is a Provost Chair Professor at the National University of Singapore (NUS) and Senior Consultant at the Department of Haematology-Oncology, National University Hospital. He serves as Deputy Director of the Cancer Science Institute of Singapore, Deputy Director (Research) at the National University Cancer Institute, and Co-Director of the N2CR Cancer Programme at NUS. Trained in internal medicine and medical oncology, he is a Fellow of both the Academy of Medicine, Singapore and the Royal College of Physicians (Edinburgh).

Professor Goh's research bridges clinical pharmacology, translational oncology, and precision medicine. His work focuses on the pharmacogenomics of anticancer drugs, phase I/II clinical trials, and functional genomics to elucidate mechanisms of resistance in head-and-neck and lung cancers. His group integrates multi-omics approaches—including single-cell and extracellular vesicle analyses—to identify biomarkers and therapeutic strategies that overcome drug resistance and improve immunotherapy outcomes.

He has led multiple investigator-initiated clinical trials, contributed to landmark publications in Nature Communications, Clinical Cancer Research, and Lancet Oncology, and received national awards including the NMRC Singapore Translational Research Investigator Award and the Ministry of Health Distinguished Senior Clinician Award.

SEISHI OGAWA

SESSION 4 - 25 NOV, 14 45 - 15 15

Professor, Department of Pathology and Tumor Biology
Kyoto University

Chromatin Landscape and Epigenetic Heterogeneity of Acute Myeloid Leukemia

AML is a heterogeneous disease where dysregulation of transcription factors (TFs) has been implicated in leukemogenesis and differentiation arrest. Recently, we revealed AML is classified into several distinct epigenetic subtypes showing unique TF profiles. In this study, we investigated critical TFs in each epigenetic subtype by integrating bulk (n>1500) and single-cell RNA/ATAC-seq analyses, (n=35) along with ChIP-seq (n=240) for H3K27ac in a large cohort of AML patients. Integrated bulk RNA- and ATAC-seq analysis revealed that each AML subtype was characterized by a unique gene regulatory network (GRN) defined by distinct combinations of activated TFs, many of which were regulated by subgroup-specific super-enhancers and formed autoregulatory circuits, as evidenced by H3K27ac ChIP-seq. Single-cell GRN analysis, combined with pseudotime trajectory analysis, further demonstrated that activity of these critical TFs peaked at distinct stages of differentiation in a subgroup-specific manner. Notably, HOXA6 was consistently activated throughout the myeloid differentiation trajectory in NPM1-mutated AML subtypes, but its peak timing varied across epigenetic subgroups. In contrast, MYB showed an activation peak synchronized with differentiation arrest at the GMP stage in acute promyelocytic leukemia. These results suggest that aberrant activation of lineage-defining TFs at critical developmental windows underlies subgroup-specific leukemogenic mechanisms. In summary, integrative epigenomic profiling defines TF dysregulation across AML subtypes and differentiation hierarchies.

Biosketch

Seishi Ogawa, MD, PhD, is Professor and Chair of the Department of Pathology and Tumor Biology at Kyoto University. He has led pioneering genomic and epigenomic studies of human cancers using next-generation and single-cell sequencing. His work has elucidated the mutational landscapes and clonal evolution of myelodysplastic syndromes, acute myeloid leukemia (AML), and other malignancies, defining new disease entities and molecular classifications. More recently, his research has expanded to the integrative analysis of chromatin accessibility, transcriptional regulation, and enhancer architecture across thousands of AML genomes, uncovering distinct epigenetic subtypes with characteristic transcription factor networks and differentiation hierarchies. Through bulk and single-cell RNA/ATAC-seq combined with ChIP-seq profiling, his group has revealed how aberrant activation of lineage-defining transcription factors drives subtype-specific leukemogenic programs. In this lecture, he will focus on how these epigenetic and transcriptional programs shape the chromatin landscape and define the heterogeneity of AML.

YILONG ZHOU

SESSION 5 - 26 NOV, 09 00 - 09 30

Principal Investigator
Cancer Science Institute of Singapore

RNA Damage Compartmentalisation by Stress Granules

Biomolecules incur damage during stress conditions, and damage partitioning represents a vital survival strategy for cells. Here, we identified a distinct stress granule (SG), marked by dsRNA helicase DHX9, which compartmentalizes ultraviolet (UV)-induced RNA, but not DNA, damage. Our FANCI technology revealed that DHX9 SGs are enriched in damaged intron RNA, in contrast to classical SGs that are composed of mature mRNA. UV exposure causes RNA crosslinking damage, impedes intron splicing and decay, and triggers DHX9 SGs within daughter cells. DHX9 SGs promote cell survival and induce dsRNA-related immune response and translation shutdown, differentiating them from classical SGs that assemble downstream of translation arrest. DHX9 modulates dsRNA abundance in the DHX9 SGs and promotes cell viability. Autophagy receptor p62 is activated and important for DHX9 SG disassembly. Our findings establish non-canonical DHX9 SGs as a dedicated non-membrane-bound cytoplasmic compartment that safeguards daughter cells from parental RNA damage.

Biosketch

Dr. Yilong Zhou is an Assistant Professor in the Department of Biochemistry at NUS and a Principal Investigator at the Cancer Science Institute of Singapore. He completed his postdoctoral training in Asifa Akhtar's lab at the Max Planck Institute in Germany, where he discovered DHX9 stress granules as a novel RNA damage response. His current research focuses on RNA damage signalling, RNA-protein interactions, and RNA-protein condensates in cancer. His work has been published in prestigious journals including Cell, Nature Immunology and Nature Communications. He is a recipient of the EMBO Long-Term Fellowship and the NUS Presidential Young Professorship.

YASUHIRO MURAKAWA

SESSION 5 - 26 NOV, 09 30 - 10 00

Professor, Department of Pathology and Biology of Diseases,
Graduate School of Medicine
Kyoto University

Decoding Human Transcriptome Architecture with Oxford Nanopore Full-length RNA Sequencing

Gene expression is regulated by transcriptional and post-transcriptional processes, playing key roles in human development and disease. However, challenges remain in identifying full-length sequences of structurally diverse RNAs and their modifications, which occur in a cell-type-specific manner. To address this, we prepared hundreds of high-quality RNA samples across human cells and tissues, and performed cDNA and Direct RNA Nanopore sequencing. Conventional cDNA sequencing often fails to accurately reflect full-length RNAs, making it difficult to determine complete sequences from transcription start to termination sites. Here we developed an improved cDNA preparation method, achieving an average read length of around 3,000 bases in full-length cDNA sequencing. Applying this method to hundreds of human RNA samples, we identified tens of thousands of unannotated isoforms from known loci and thousands of cell-type-specific unannotated loci from intergenic regions, significantly expanding gene annotations. Many of these newly identified elements were specific to primates or humans. Furthermore, we used Direct RNA Nanopore sequencing to comprehensively analyze RNA base modifications in various human cell types. This technique enabled the direct, high-resolution detection of RNA modifications, revealing previously unknown modifications. The resulting transcriptome and epitranscriptome atlas across human cell types provides novel insights into human biology, evolution, and disease.

Biosketch

Yasuhiro Murakawa graduated from Kyoto University School of Medicine in 2008. Following his residency at Kyoto University Hospital, he moved to the Max Delbrück Center for Molecular Medicine in Berlin, Germany, and received his PhD from Free University of Berlin in 2014. He has led a laboratory at RIKEN since 2016. In 2020, he was appointed Professor at the Institute for the Advanced Study of Human Biology (ASHBi), Kyoto University, and in 2025 he also became Professor of Pathology in the Graduate School of Medicine at Kyoto University. His research focuses on transcriptional enhancers and the development of transcriptomics methods.

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