JCA
JAPANESE CANCER ASSOCIATION

The 74th Annual Meeting of the Japanese Cancer Association in NAGOYA

患者に繋ぐがん研究

連携から融合へ

From collaboration to integration:
Cancer research for patients' benefit

第74回 日本癌学会学術総会

PROGRAM

Date October 8 (Thu.) - 10 (Sat.), 2015

Venue NAGOYA CONGRESS CENTER
Nagoya

President Tomoki Naoe
Nagoya Medical Center
直江 知樹
独立行政法人国立病院機構
名古屋医療センター 院長

http://www.congre.co.jp/jca2015/

International Session

Room D Oct. 10 (Sat.) 13:30-16:00 E

IS11 Regulation of tumor angiogenesis
腫瘍血管新生の制御

Chairpersons: Nobuyuki Takakura (Dept of Signal Trasduction, RIMD, Osaka Univ.)
Gou Young Koh (Korea Advanced Inst. of Sci. & Tech.)
座長：高倉 伸幸（阪大・微生物病研究所・情報伝達分野）
Gou Young Koh (Korea Advanced Inst. of Sci. & Tech.)

Blood vessel formation in tumor microenvironment is induced mainly by sprouting angiogenesis from preexisting vasculature. The molecular mechanism of sprouting angiogenesis has been gradually elucidated by the analysis of physiological blood vessel formation especially during embryogenesis. Although many molecular cues involved in this process have been identified, how those molecules affect tumor blood vessel and lymphatic vessel formation has not been fully understood. To regulate tumor angiogenesis and lymphangiogenesis, we need to integrate the knowledge achieved by individual scientists. In this session, we assembled outstanding investigators in the field of vascular biology to discuss update of studies including angiogenesis and lymphangiogenesis. We hope that the hint or concept of the new angiogenic control technology is emerged triggered by this meeting.

IS11-1 Tumor endothelial cells and cancer progression
Kyoko Hida (Vascular Biol., Inst. for Genetic Med., Hokkaido Univ.)
腫瘍血管内皮とがんの進展
樋田 京子（北大・遺制研・血管生物）

IS11-2 SoxF-mediated Transcriptional Regulation of Tumor Angiogenesis
Injune Kim (Grad. Sch. of Med. Sci. and Engineering, KAIST)

IS11-3 Receptor tyrosine kinase TIEs mediated signaling in vascular formation and tumor progression
Yulong He (Cyrus Tang Hematology Ctr., Soochow Univ.)

IS11-4 Tumor endothelial cells counteract with TGF-beta-induced endothelial-to-mesenchymal transition by endogenous FGF signals
Tetsuro Watabe (Dept. of Hard Tissue Engineering, Tokyo Med. Dent. Univ.)
腫瘍血管内皮細胞は内因性FGFシグナルによりTGF-βによる内皮間葉移行(EndMT)を抑制する
渡部 徹郎（東医歯大・歯・硬組織病態生化学）

IS11-5 Role of Tie2 Activation in Tumor Vasculatures
Gou Young Koh (Dept. of MSE., KAIST)

International Session

Room E Oct. 10 (Sat.) 13:30-16:00 E

IS12 Single cell analysis for cancer research
単一細胞解析のがん研究への応用

Chairpersons: Fumio Arai (Stem Cell Biol. Med., Grad. Sch. Med. Sci., Kyushu Univ.)
Shyam Prabhakar (Genome Inst. of Singapore)
座長：新井 文用（九大・院医・幹細胞再生修復医学分野）
Shyam Prabhakar (Genome Inst. of Singapore)

Most cancers as well as normal tissue are composed of heterogeneous cells that have phenotypic and functional variations. Heterogeneity of tumor cells contributes to the disease progression and resistance to anti-cancer therapy. This heterogeneity might be caused by the variation of cancer stem cells (CSCs) or tumor-initiating cells (TICs). Recent advances in cancer research suggest that the detailed understanding of CSCs/TICs is crucial for the establishment of the effective treatment of cancers. However, such cells seem to show genetic and epigenetic differences on a cell-to-cell level. Therefore, analyzing for multiple individual cells could be key for understanding the unique characteristics of individual CSCs and for clarifying the complicated mechanisms controlling their function. In addition, it is likely that functional heterogeneity within stromal cells contributes to cancer phenotypes. Recent advances of the single-cell genomics and proteomics techniques allow for analyzing the differences between individual cells. In addition, the single-cell analysis is useful for the identification of specific sub-populations in heterogeneous cell populations and clarifies the complex networks controlling the function of stem cells in normal and tumor tissues.
In this international session, we will discuss the recent progress of single-cell analysis in the fields of normal and tumor cells.

IS12-1 Asymmetric cell division of hematopoietic stem cells
Fumio Arai (Stem Cell Biol. Med., Grad. Sch. Med. Sci., Kyushu Univ.)
造血幹細胞の非対称分裂
新井 文用（九大・医学研究院・幹細胞再生修復医学）

IS12-2 Establishment of three-dimensional culture of cholangiocarcinoma cells
Siriwat Sukphokkit[1], Tavan Janvilisri[1], Supeecha Kumkate[2], Pichamon Kiatwuthinon[3] ([1]Dept. of Biochem., Mahidol Univ., [2]Dept. of Bio., Mahidol Univ., [3]Dept. of Biochem., Kasetsart Univ.)

IS12-3 Single-cell analysis of lung adenocarcinoma cell lines; diverse expression patterns of individual cells
Yutaka Suzuki (Dept. of CBMS, the Univ. of Tokyo)
肺腺がん細胞株のシングルセル解析：遺伝子発現の多様性の解明に向けて
鈴木 穣（東大・新領域）

IS12-4 Reconstructing the Genetic Histories of Cancers with Single-Cell Sequencing
Charles Gawad (Dept. of Oncology, St. Jude Children's Res. Hosp.)

IS12-5 Molecular Characterization of Circulating Tumor Cells in Colorectal Cancer
Min-Han Tan[1,3], Igor Cima[1], Say Li Kong[2], Debarka Sengupta[2], Poh Koon Koh[1,2], Iain Tan[2,4], Jackie Y. Ying[1], Paul Robson[2], Bing Lim[2], Shyam Prabhakar[2], Axel M. Hillmer[2] ([1]Inst. of Bioengineering and Nanotechnology, [2]Genome Inst. of Singapore, [3]Fortis Surgical Hosp., [4]Natl. Cancer Ctr. Singapore)

IS12-6 Single-Cell Transcriptomics of Lung and Colon Tumors
Shyam Prabhakar[1], Huipeng Li[1], Elise Courtois[2], Debarka Sengupta[1], Say Li Kong[1], Charlene Kang[1], Yongli Hu[2], Lawrence Wee[2], Axel M. Hillmer[1], Iain Tan[1,3], Daniel Tan[1,3], Paul Robson[4] ([1]Genome Inst. of Singapore, [2]Inst. for Infocomm Res., [3]Natl. Cancer Ctr. Singapore, [4]Jackson Lab. for Genomic Med.)