Kumamoto University

Applications of Mass Cytometry in Basic and Clinical Research

Date & Time:

17:00-18:30 (JST), 26th January 2023

＊8:30-10:00(GMT) , 26th January 2023

Venue : Online (Zoom)

Speakers:

- **Dr. Takatsugu Ishimoto** (Kumamoto University)
- **Dr. Nagesh Kalakonda** (University of Liverpool)

Organizer: Goro Sashida (IRCMS, Kumamoto University)

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Supported by JSPS Core-to-Core Program A. Advanced Research Networks
"Integrative approach for normal and leukemic stem cells"

Takatsugu Ishimoto

Gastrointestinal Cancer Biology, International Research Center of Medical Sciences (IRCMS), Kumamoto University, Japan

Single-cell proteomic profiling of malignant ascites in gastric cancer reveals the microenvironment promoting peritoneal dissemination

Abstract: Gastric cancer (GC) is a leading cause of global cancer mortality, typified by diverse disease presentations and dismal clinical outcomes. Novel immunotherapies, such as anti-PD-1 immune checkpoint inhibitors, have been developed in an attempt to update the cancer treatment paradigm; however, the clinical outcome of advanced GC patients with peritoneal dissemination remains poor. Recent studies using whole genome sequencing and transcriptome analyses of purified tumor cells from malignant ascites demonstrated that unique driver gene alterations and oncogene expression were detected in tumor cells purified from ascites. However, cellular composition in malignant ascites and the role of non-malignant cells in peritoneal dissemination have not been determined. Currently, we performed single cell proteomic analysis by mass cytometry and liquid chromatography coupled with tandem mass spectrometry (LC-MS/MS) analysis to reveal the heterogenous cell populations and extracellular components in malignant ascites.

Nagesh Kalakonda

Chair of Experimental Haematology and Honorary Consultant, Haemato-oncology, University of Liverpool and The Clatterbridge Cancer Centre NHS Foundation Trust, UK

Simultaneous and multiplexed protein and RNA profiling at single cell resolution by PLAYR-CyTOF analysis

Technological advances for single-cell transcriptional profiling are enabling characterisation of genotypic and phenotypic variations in development and disease. Traditional mass cytometry-based CyTOF analysis employs heavy-metal labelled antibodies for multi-dimensional evaluation of surface and intracellular protein expression. We have enhanced the capability of the technique by incorporating a proximal ligation assay for RNA (PLAYR) for simultaneous and multiplexed profiling of RNA (mRNAs and lncRNAs) and protein expression in individual cells. We have used the assay to better understand the pathobiology of chronic lymphocytic leukaemia (CLL), intraclonal heterogeneity, and dynamics of clonal evolution. PLAYR-CyTOF allows early prediction and prognostication of response durability in the context of B-cell receptor (BCR) inhibition in CLL patients and has great potential in other research and clinical contexts.

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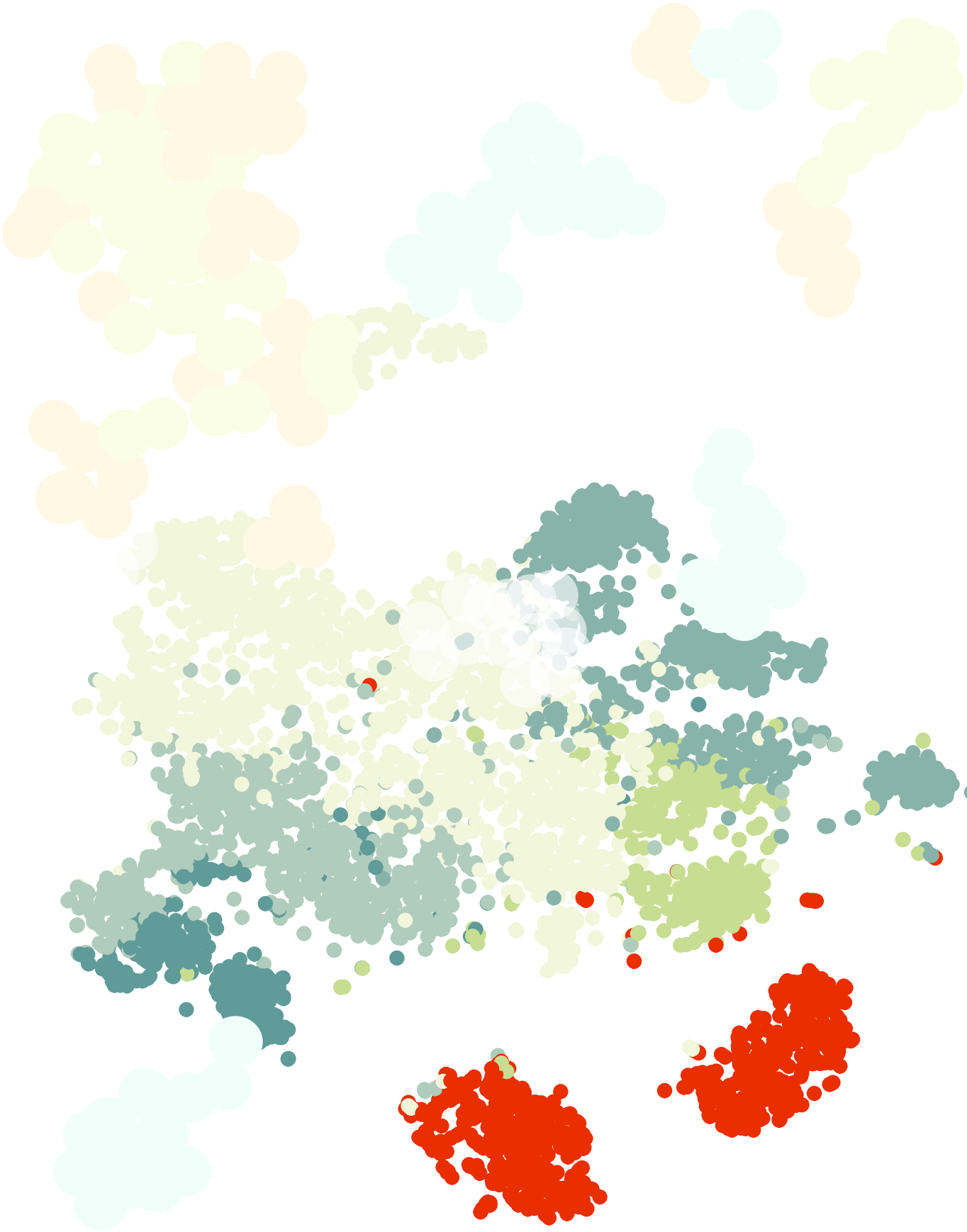

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