United States — Japan Cooperative Medical Sciences Program

2024 International Conference on Emerging Infectious Diseases (EID) in the Pacific Rim

And meetings of the Acute Respiratory Panel, Cancer Panel, AIDS Panel, Hepatitis Panel, Viral Diseases Panel, Immunology Board, and the 2nd International Symposium for Infectious Diseases Research Institutes Cooperation (IDRIC)

March 5-8, 2024
Hybrid and Grand Hyatt Hotel
Incheon, South Korea

Japan Agency for Medical Research and Development

Ministry of Health, Labour, and Welfare (MHLW) of Japan

Ministry of Education, Culture, Sports, Science, and Technology (MEXT) of Japan

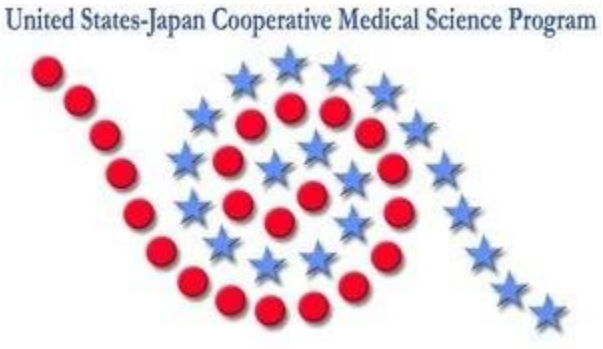
Ministry of Foreign Affairs (MOFA) of Japan

Korea Disease Control and Prevention Agency
National Institute of Health
National Institute of Infectious Diseases

International Vaccine Institute

National Institute of Allergy and Infectious Diseases

National Cancer Institute (NCI)



The Joint 24th International Conference on Emerging Infectious Diseases in the Pacific Rim of the U.S.-Japan Cooperative Medical Sciences Program (USJCMSP)

ABSTRACT E-BOOK

March 7: HIV/AIDs Panel

[in order of presentation]

SESSION ONE: Data Science / AI and Emerging Technologies

Bali Pulendran, PhD, Stanford University

Mobilizing Integrated Organ Immunity Against HIV

Hiroaki Takeuchi, PhD, Tokyo Medical and Dental University

Identification of Host Factors Regulating HIV-1 Latency and Their Potential Therapeutic Targets in HIV-1 Latency Reversal

Currently, the Human Immunodeficiency Virus (HIV) continues to be a global health concern, affecting millions of people worldwide. Despite progress in combination antiretroviral therapy (cART), a cure for diseases caused by HIV remains elusive owing to the persistence of viral reservoirs. To seek new strategies to overcome HIV-1 latency, one of the major barriers to HIV elimination, it is crucial to better understand how this state is maintained.

Although considerable progress has been made in the understanding of HIV latency in CD4+ T lymphocytes, the mechanisms underlying HIV latency in monocytes/macrophages remain unclear. To investigate the host cell factors involved in HIV latency in monocytes, we employed a genome-wide RNAi screen in a newly established latently infected model monocyte-lineage cell clone, THP-1 Nluc #225 (#225 cell), capable of expressing NanoLuc (Nluc) reporter protein in the nef region of the HIV-1 provirus.

We found that Nluc activity in several host protein-depleted #225 cells was markedly enhanced, suggesting its possible involvement in HIV-1 latency maintenance. Transcriptome analysis of one of these protein-depleted #225 cells revealed preferential reactivation of HIV-1 provirus compared with that of several typical latency-reversing agents (LRAs)-treated #225 cells. Our findings deepen our understanding of the role of host proteins in HIV latency and might lead to the development of a new class of LRA.

SESSION 1: AI/Data Science-based Prediction of Emerging Infection

Eli Boritz, PhD, National Institute of Allergy and Infectious Diseases, NIH (virtual)

Distinctive Attributes of HIV-Infected CD4 T Cells under ART Revealed by Microfluidics-Assisted Sorting and Whole Transcriptome Sequencing

Rare CD4 T cells that contain HIV under antiretroviral therapy represent an important barrier to HIV cure, but the infeasibility of isolating and characterizing these cells in their natural state has led to uncertainty about whether they possess distinctive attributes that HIV cure-directed therapies might exploit. We addressed this challenge using a microfluidic droplet technology that isolates the transcriptomes of HIV-infected cells based solely on the detection of HIV DNA. HIV-DNA+ memory CD4 T cells in the blood from people receiving antiretroviral therapy showed inhibition of six transcriptomic pathways, including death receptor signaling, necroptosis signaling and antiproliferative Gα12/13 signaling. Moreover, two groups of genes identified by network co-expression analysis were significantly associated with HIV DNA+ cells. These genes (n = 145) accounted for just 0.81% of the measured transcriptome and included negative regulators of HIV transcription that were higher in HIV-DNA+ cells, positive regulators of HIV transcription that were lower in HIV-DNA+ cells, and other genes involved in RNA processing, negative regulation of mRNA translation, and regulation of cell state and fate. These findings reveal that HIV-infected memory CD4 T cells under antiretroviral therapy are a distinctive population with host gene expression patterns that favor HIV silencing, cell survival and cell proliferation. This presentation will review emerging droplet-based technologies that can characterize cells harboring latent HIV. Implications for HIV cure research of early findings made using these technologies will be discussed, and future directions will be considered.

SESSION 1: AI/Data Science-based Prediction of Emerging Infection

Ramon Lorenzo-Redondo, PhD, Northwestern University

Molecular profiling of the SIV tissue reservoirs microenvironment at a single focus level during ART and post-ATI

SESSION 1: AI/Data Science-based Prediction of Emerging Infection

Nadia Roan, PhD, Gladstone Institutes; University of California, San Francisco (UCSF)

Characterization of the active HIV reservoir from ART-suppressed people with HIV

SESSION TWO: Viral Eradication and Control

Kenji Maeda, MD, PhD, Kagoshima University

In vitro Studies for the Development of Drug-based Therapies for HIV Reservoirs

SESSION 1: AI/Data Science-based Prediction of Emerging Infection

Takuya Yamamoto, PhD, National Institutes of Biomedical Innovation, Health and Nutrition

The Role of SIV-specific follicular CD8 T Cells during Chronic SIV Infection

SESSION THREE: HIV Prevention Science

Hiroyuki Yamamoto, MD, PhD, National Institute of Infectious Diseases

Targeting Specificity of SIV-specific B-cell Responses

SESSION 1: AI/Data Science-based Prediction of Emerging Infection

Jerome Kim, MD, International Vaccine Initiative, Seoul, South Korea

Beyond the Science: Going from Need to Impact with an HIV Vaccine

SESSION FOUR: Clinical Virology and Pathogenesis

Bette Korber, PhD, Los Alamos National Laboratories (virtual)

Inspiration for HIV vaccine design from within-host HIV and antibody co-evolution

SESSION 1: AI/Data Science-based Prediction of Emerging Infection

Molly Ohainle, PhD, University of California, Berkeley

Defining Cellular Barriers to HIV infection through HIV-CRISPR Knockout Screening

SESSION 1: AI/Data Science-based Prediction of Emerging Infection

Yuta Hikichi, PhD, National Cancer Institute, NIH

High-level resistance to Integrase inhibitors conferred by mutations outside of Integrase

SESSION 1: AI/Data Science-based Prediction of Emerging Infection

Yorifumi Satou, MD, PhD, Kumamoto University

HIV-Tocky System to Visualize Proviral Expression Dynamics

SESSION 1: AI/Data Science-based Prediction of Emerging Infection

Akatsuki Saito, PhD, Miyazaki University

Host ZCCHC3 Blocks HIV-1 Infection and Production by a Dual Mechanism