International Symposium on Plasmid Biology 2024
PacBio Japan luncheon seminar
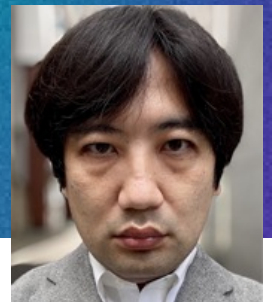# September 4th 12:30-13:30
Room #41 (4F) ※No recording

PacBio

Antimicrobial Resistance and Plasmids in Microbiome

Speaker : Dr Masato Suzuki

Antimicrobial Resistance Research Center, National Institute of Infectious Diseases, JAPAN

Dr. Masato Suzuki

Recently, infections caused by antimicrobial-resistant (AMR) bacterial pathogens, particularly ESKAPE pathogens (*Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* spp.), have become a serious global public health threat. AMR bacteria are rapidly spreading throughout the natural environment worldwide, as well as within human communities. Therefore, the One-Health approach based on international collaboration is essential to combat AMR. However, there are limitations to the information that can be obtained from genomic research based on bacterial isolation and identification. Clinically important AMR genes, such as carbapenemase genes, are often transferred among bacterial communities via mobile genetic elements, such as plasmids. Although plasmid typing methods using replicon sequences have been established for plasmids in *Enterobacterales*, including *Escherichia coli*, and some Gram-positive bacteria, they have not been established for plasmids in *Pseudomonas* spp., including *P. aeruginosa*, and many other pathogenic and environmental bacteria due to a lack of information. Here, we constructed a novel plasmid replicon sequence library, PRDB-ESKAPE, which covers over 70% of known plasmids in bacteria, including those in ESKAPE pathogens, and conducted comprehensive metagenomic analysis using PacBio HiFi sequencing and Hi-C analysis focusing on AMR-associated plasmids from the environmental samples.

Prior to Dr Suzuki's presentation, PacBio introduction session will be taken place (20 minutes)

PacBio long read sequencer: Revio System