The 47th Global and Local Infectious Diseases Research Seminar

RCGLID
OITA UNIVERSITY

June30th , 2026
１５:00-１６:00

FREE
REGISTRATION ▶
https://forms.gle/i9Az4PRCCgNLUDGS7

Presenter : Gulnur Zhunussova

Leading Researcher, Associate Professor, Laboratory of Molecular Genetics, Institute of Genetics and Physiology

Venue: OITA Univ. RCGLID Meeting Room & Teams

This seminar will be held in English.

Integrated Phenotype–Genotype Analysis of Helicobacter pylori in Kazakhstan: Mapping Population Structure Across Regions and Host Diversity and Predicting AMR

Kazakhstan faces a high burden of gastric cancer linked to chronic Helicobacter pylori infection, yet the population genetics and antimicrobial resistance (AMR) dynamics of this highly recombinogenic pathogen remain critically understudied. Our recently published single-center study in Almaty revealed alarming resistance rates (metronidazole 87.2%, clarithromycin 33.7%, and multidrug resistance 34.8%), compelling us to move toward genome-based evolutionary analyses. To address this knowledge gap, we have initiated a landmark multi-regional project expanding from our Almaty site to 16 additional regions across Kazakhstan (17 locations total), targeting ~340 culture-positive isolates. Through a joint Kazakhstan-Japan collaboration with Oita University's RCGLID, we will perform whole-genome sequencing (Illumina MiSeq and PacBio), standardized antimicrobial susceptibility testing, and recombination-aware population genetics to characterize circulating lineages, identify genomic AMR determinants, and contextualize Kazakh strains within global phylogenetic frameworks. This project will generate the first nationwide genomic map of H. pylori population structure and AMR dynamics in Kazakhstan, directly informing region-specific eradication strategies and establishing a sustainable genomic surveillance foundation for Central Asia.

Manager Yoshio Yamaoka
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Seminar Contact
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