



2025 Special Seminar on The IDEC Institute

From Genomics of Communities to Single Cells

Abstract



Microbial and viral diversity remains one of the largest frontiers in biology, with much of it inaccessible to traditional laboratory cultivation. This hidden diversity, sometimes referred to as microbial and viral “dark matter”, plays critical roles in ecosystem function, biogeochemical cycles, and potentially human health. Cultivation-independent genomic methods, particularly metagenomics and single-cell sequencing, have become indispensable for revealing the identities, functions, and ecological roles of these uncultivated organisms.

In this talk, I will introduce the U.S. Department of Energy National Laboratories and the Joint Genome Institute as a genome science national user facility and present a series of studies from my lab that demonstrate how we integrate bulk and single-cell approaches. Metagenomics allows us to survey complex microbiomes and, more recently, uncover new insights from giant virus genomes. In contrast, targeted single-cell sequencing enables us to isolate and characterize rare or unique taxa - the “needles in the haystack” - by using labeled probes or substrates as bait for targeted capture. Single cells also provide insight into the population structure of certain clades and allow us to link mobile genetic elements. Together, these strategies offer a powerful lens for exploring the genomic underpinnings of microbial and viral ecosystems at both scale and resolution.



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Date

2025
9/4
Thursday

15:00 ▶ 16:00

Language : English

Online

<https://00m.in/kDKmP>



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Hiroshima University, Graduate
School of Advanced Science of
Matter Build A, 6F Seminar
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