

세미나 초록

성명	이정찬
소속	한국과학기술연구원 청정에너지연구센터
발표 주제	Spatial metagenomics and AI-enabled culturomics for mapping microbiome spatial hubs
발표 내용	<p>Microbial communities play essential roles in human and environmental health, yet many of their key functions emerge not from individual bacteria but from spatially organized consortia with complex interactions. These spatial structures influence metabolism, ecological stability, and evolutionary dynamics, but remain largely inaccessible using conventional approaches. Bulk sequencing lacks spatial resolution, while imaging-based methods are limited in throughput and taxonomic coverage. In this seminar, I will introduce SAMPL-seq (Split-And-pool Metagenomics PLOT-sampling sequencing), a spatial metagenomics approach that enables high-throughput mapping of microbial organization at micron-scale spatial resolution using DNA sequencing. By combining ecological plot sampling with split-and-pool metabarcoding, SAMPL-seq captures thousands of spatially resolved microenvironments from a single sample. When applied to human and animal gut microbiomes, as well as to complex environmental systems such as soil and biofilms, SAMPL-seq reveals conserved spatial co-localization patterns and the emergence of "microbiome spatial hubs." These hubs represent groups of microbes that repeatedly co-occur and form functionally interacting communities. To connect spatial organization with experimentally testable functions, we further integrate AI-enabled culturomics, allowing the targeted isolation and characterization of representative microbes from these spatial hubs, including previously uncultured or rare taxa. Together, this framework provides a scalable strategy to move from spatial mapping to functional understanding of microbiomes, offering new opportunities to decipher and engineer microbial communities across diverse ecosystems.</p>