SPEECH INFORMATION (For Conference Program Book)	
Topic	Deciphering Ecological and Functional Complementarity of Microbiomes via Integrative Multi-Omics Approaches
Abstract	Multi-omics integration provides powerful strategies to elucidate the ecological and functional principles of microbiomes. Broadly, two complementary approaches can be employed: model-based integration, which relies on statistical or machine-learning frameworks to infer latent structures across omics layers, and knowledge-based integration, which builds upon known biological relationships and theories. As an example of the model-based strategy, we applied the Multi-Omics Factor Analysis (MOFA) framework to integrate 16S amplicons and metabolomic data in evaluating an anticoccidial vaccine in chickens. The model harmonized heterogeneous datasets and uncovered infection-induced pathogenic shifts, vaccine-associated restoration of beneficial taxa, and sphingolipid signatures as key metabolic markers. This demonstrates how model-based integration enhances biological inference and biomarker discovery. In contrast, our second study exemplifies the knowledge-based approach, using metagenomic profiling and ecological modeling to decipher a nine-species minimal gut consortium from rat cecum. Two functionally distinct sub-communities—a cellulolytic group and an *E. coli*-dominated group—exhibited metabolic complementarity, exchanging carbohydrate and amino-acid intermediates to achieve equilibrium. This division of labor aligns with the Black Queen Hypothesis, highlighting how metabolic interdependence stabilizes microbial consortia. Together, these studies illustrate how integrative multi-omics, through both model- and knowledge-driven perspectives, can reveal the ecological and functional complementarity fundamental to microbiome systems.