

Lianne Bianca P. Cagalingan
Outcome Report for Grant Category A:
Grant for Research Presentation at Academic Conference

Revisiting the taxonomic distribution and phylogenetic relationships of the membrane-associated guanylate kinase (MAGUK) family of scaffolding proteins
International Symposium for Plasmid Biology 2024

I attended the International Symposium for Plasmid Biology, a scientific conference focused on plasmid biology, specifically the role of mobile genetic elements (MGEs) in bacterial evolution and antimicrobial resistance. This conference was instrumental in broadening my understanding of microbial population dynamics and the intricate relationships between bacteria and MGEs.

Key takeaways included the complexity of co-infection dynamics, as discussed in Claudia Igler's presentation. She highlighted how interactions between different MGEs, including conjugative plasmids and temperate phages, affect bacterial evolution in non-linear ways. These findings have broadened my perspective on the unpredictability of plasmid spread and the need for advanced mathematical models to understand these processes. This learning is particularly relevant to my own research, where understanding bacterial population responses to genetic variability plays a central role.

Allison Lopatkin's presentation on plasmid acquisition and selection expanded my knowledge of the transient metabolic costs associated with plasmid acquisition. Her work highlighted how these costs influence microbial population growth and resistance dissemination. This insight is crucial for developing new strategies to predict microbial behavior and could inform experimental design in studies on genetic transfer and bacterial adaptation.

Finally, Mikkel Meyn Liljegren's discussion of plasmids promoting microindel mutations through a novel mutation mechanism provided a deeper understanding of how plasmid acquisition influences genetic variability. His findings on the Short-Patch Double Illegitimate Recombination (SPDIR) mechanism were particularly compelling as they introduced a new dimension to the role of plasmids in bacterial adaptation beyond gene transfer.

Attending this conference has deepened my comprehension of how plasmids and MGEs contribute to bacterial evolution and resistance. It provided valuable insights into emerging methodologies and novel findings, which I aim to integrate into my ongoing research on a protein scaffolding family. This experience also reinforced the importance of interdisciplinary approaches in addressing complex scientific challenges, enhancing my research trajectory and informing future experimental designs.

I am grateful for the funding support that enabled my participation in this conference.