



Channing Microbiome Seminar

July 27th (Friday), 2018, 11am @ 5th-floor conference room



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Comprehensive analysis of mobile genetic elements in the gut microbiome reveals phylum-level niche-adaptive gene pools

Abstract: Mobile genetic elements (MGEs) drive extensive horizontal transfer in the gut microbiome. This transfer could benefit human health by conferring new metabolic capabilities to commensal microbes, or it could threaten human health by spreading antibiotic resistance genes to pathogens. Despite their biological importance and medical relevance, MGEs from the gut microbiome have not been systematically characterized. Here, we present a comprehensive analysis of chromosomal MGEs in the gut microbiome using a method called Split Read Insertion Detection (SRID) that enables the identification of the exact mobilizable unit of MGEs. Leveraging the SRID method, we curated a database of putative MGEs encompassing seven MGE classes called ImmeDB (Intestinal microbiome mobile element database). We observed that many MGEs carry genes that confer an adaptive advantage to the gut environment including gene families involved in antibiotic resistance, bile salt detoxification, mucus degradation, capsular polysaccharide biosynthesis, polysaccharide utilization, and sporulation. We find that antibiotic resistance genes are more likely to be spread by conjugation via integrative conjugative elements or integrative mobilizable elements than transduction via prophages. Additionally, we observed that horizontal transfer of MGEs is extensive within phyla but rare across phyla. Taken together, our findings support a phylum level niche-adaptive gene pools in the gut microbiome.

Biography: Xiaofang Jiang is a postdoc at MIT. She obtained her PhD in Genetics, Bioinformatics, and Computational Biology from Virginia Tech at 2016. Since then, she has worked at the Center for Microbiome Informatics and Therapeutics of MIT and is co-advised by Dr. Eric Alm and Dr. Ramnik Xavier. She studies the genetic variations of gut microbes and how these variations are beneficial for their effective colonization and successful survival. She is developing tools to mine genetic variations from both isolate genomes and metagenomes.

Hosted by Yang-Yu Liu