

Aspects of the interaction between probiotics and the gut microbiota

Speaker: Niv Zmora

Chairs: Marla Cunningham & Kelly Swanson

Abstract

Probiotics are commonly consumed by healthy individuals, however many aspects of their interactions with the autochthonous microbiota are unknown or controversial. In a series of experiments, we provided a metagenomic characterization of the murine and human stool and mucosa-associated gastrointestinal microbiome before, during and after the consumption of an 11-strain probiotic mixture or placebo. We showed that in colonized, but not in germ-free mice, probiotics encountered a marked mucosal colonization resistance. In contrast, humans featured varying probiotics colonization patterns that were predictable from baseline host and microbiome features. Consequently, probiotics induced a transient, individualized impact on mucosal community structure and gut transcriptome. We then examined the impact of probiotics on the gut microbiome after a week-long administration of broad-spectrum enteral antibiotics and compared this intervention with autologous fecal microbiome transplantation (aFMT) or spontaneous microbiome reconstitution. We found that while aFMT induced a rapid and near-complete recovery within days of administration, probiotics induced a markedly delayed and persistently incomplete reconstitution of the stool and mucosal microbiome and the host gut transcriptome. Finally, we reanalyzed the metagenomes for antibiotic resistance genes and found that in mice and humans a course of antibiotics resulted in expansion of the lower gastrointestinal tract resistome, which was mitigated by aFMT or during spontaneous recovery, but exacerbated after probiotics administration by supporting the bloom of strains carrying vancomycin resistance genes, but not resistance genes encoded by the probiotic strains.