

Presentation 2:

Resistome of gut microbiota and modulation in healthy Hong Kong population

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Summary:

The administration of antibiotics can disrupt the gut microbiota and alter the resistome, where the magnitude of disruption varies upon population and the type of antibiotics prescribed. While probiotics have been proposed as a possible supplement to promote the recovery of gut microbiome, their efficacy remains controversial. We conducted a randomized open-labelled controlled trial in healthy subjects to examine the changes in microbiome and resistome profiles across a 3-month period. Subjects were randomly assigned to four arms, receiving one of three types of probiotics or spontaneous recovery without probiotic after antibiotic use.

Amoxicillin/clavulanate was administered orally twice per day for one week, while probiotics were given concomitantly for two weeks. Stool samples were collected at five timepoints and subjected to shotgun metagenomic sequencing to observe the dynamics of the microbiome and resistome across this period. An enrichment of the resistome at Day 7 on completion of antibiotics was observed in all subjects, with an increased carriage rate of antimicrobial resistant genes (ARGs) such as blaCTX-M and qnrS, and in association with Enterobacterales (*Escherichia* and *Klebsiella* spp.). In the probiotic(s) arms, an accelerated recovery of gut microbiota characterized by significantly reduced dissimilarity of microbiome and resistome at Day 14. However, we did not observe a complete recovery of the gut microbiota from all groups even at 3 months (Day 104). The study highlights the prolonged disturbance of gut microbiome after one course of antibiotics. Probiotics show promise as a supplement for microbiome restoration although further longitudinal follow-up and a larger sample is warranted.