SCIENCE AT THE EDGE

2016 SEMINAR SERIES

Quantitative Biology Graduate Program | Gene Expression in Development and Disease

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"Networks of Exchanging Antibiotic Resistance Between Commensal, Environmental, and Pathogenic Bacteria"

While the most acute effects of increasing antibiotic resistance in pathogens are observed in clinical settings, it is becoming increasingly clear that the evolution and transmission dynamics of resistance gene dissemination is an ecological problem. Indeed, steady use and abuse of antibiotics over the past century in food animals, humans, and the environment has provided substantial selective pressure for enrichment of resistance genotypes in each of their associated microbiomes. An over-reliance on culture-based methods, the standard in the study of clinical resistance, has vastly underestimated these reservoirs of resistance genes (or 'resistomes'). To address this issue, we have recently developed high-throughput metagenomic functional selections, aided by next-generation sequencing, to characterize resistomes encoded by the microbiota of healthy human adults and children as well as diverse soils. By combining these analyses with 16S amplicon sequencing and deep shotgun sequencing, we model the impact of various anthropogenic perturbations on the transmission and evolutionary dynamics of microbial communities and their resistomes across time and habitats. Hundreds of resistance genes we identify from specific taxa in these different microbial communities are identical to resistance genes found in major human pathogens, indicating recent genetic exchange between these microbes. We also find thousands of functionally validated resistance genes which are genetically novel, but flanked by genes involved in horizontal gene transfer, including transposases and integrases. Together, these findings highlight the substantial antibiotic resistome encoded by microbes from diverse environments, which is available for exchange with pathogens, with the potential to severely exacerbate the problems with clinical resistance.

References:

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Gonzales PR, Pesesky MW, Bouley R, Ballard A, Biddy BA, Suckow MA, Wolter WR, Schroeder VA, Burnham CA, Mobashery S, Chang M, Dantas G. Synergistic, collaterally sensitive β-lactam combinations suppress resistance in MRSA. **Nature Chemical Biology**. 2015 Nov;11(11):855-61. doi: 10.1038/nchembio.1911. Epub 2015 Sep 14. PubMed PMID: 26368589; PubMed Central PMCID: PMC4618095.

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11:30AM, ROOM 1400 BPS

Refreshments at 11:15

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