BiophysTO Lunchtime Talks

William Navarre

Department of Molecular Genetics
University of Toronto

How bacterial gene silencing proteins contribute to the evolution of pathogens

Only a vanishingly small fraction of the estimated million trillion trillion (10^30) bacterial cells on the planet are capable of causing disease in humans. Among those pathogens, most represent a narrow set of strains in a much larger group of closely-related but harmless bacterial species. While the vast majority of *E. coli* strains live harmlessly in the intestines of mammals including humans, *E. coli* O157:H7 is a major cause of deadly food poisoning. The evolution of pathogenesis is therefore an exception to the general rule. It is dictated by the fact that bacterial genomes are highly flexible and able to exchange genes between species, including genes encoding toxins. Genetic exchange can have negative impacts on the fitness of bacteria if the newly acquired genes are not properly regulated. I will discuss how bacteria silence newly acquired genetic material using an interesting DNA binding protein called H-NS and our recent efforts using single molecule studies to elucidate how this molecule helps potentiate the evolution of deadly pathogens.

Host: Dr. Anton Zilman

(Refreshments and pizza will be provided)

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Thursday, November 3, 2016 – 12:00 pm, noon
McLennan Physical Laboratories, Room MP606
(and via streaming to DV3129 at UTM)