

Dr. Roger Lévesque

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“Syst-OMICS of *Pseudomonas aeruginosa* and *Salmonella*: Tomorrow’s Genome the Next Day”



Wed. Oct. 19, 2016
SSC 1511 @ 10:30 am

Studies of the genetic structure of microbial populations are central in understanding the evolution, ecology, epidemiology of infectious diseases and spread of antibiotic resistance. Numerous studies describing the genetic structure of pathogen populations are based on samples drawn overwhelmingly from clinical collections. The International Pseudomonas Consortium includes collaborators from 28 institutions on 5 continents and producing an extensive collection of genomes from a single species for studying genome evolution, comparative genomics of antibiotic resistance and virulence genes. Given the potential link between environmental strains and evolution towards infection by *P. aeruginosa* in animals and in humans, we need to better understand genome evolution and how patients become infected. In addition to the identification of prognostic markers, I will discuss rapid antibiotic-resistance predictions from genome data for better and rapid evidence-based decisions on patient care.

Fall 2016 Schedule

| Fall 2016 Schedule | |
|--------------------|---|
| Oct. 19th | Dr. Roger Lévesque, IBIS, Université Laval (Co-Hosts: Dr. C. Khursigara and Dr. J. Lam) |
| Nov. 2nd | Dr. Peter Davies, CRC Protein Engineering, Queen’s University (Host: Dr. S. Graether) |
| Nov. 16th | Dr. Philip Hieter, Michael Smith Laboratories, University of British Columbia (Host: Dr. K. Yankulov) |
| Nov. 30th | Dr. Lynn Maquat, Centre for RNA Biology, Univ. of Rochester Med. Centre (Host: Dr. S. Rothstein) |

“A GREAT OPPORTUNITY TO HEAR LEADING RESEARCHERS IN THE SCIENTIFIC COMMUNITY DISCUSS THEIR WORK”

* ALL WELCOME TO ATTEND *

* COFFEE, TEA AND TIMBITS *

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