UNIVERSITY OF TORONTO

Microbiology & Infectious Diseases Research Days

Monday, June 3rd, 2019 – Trainee Day (Selected from Abstracts)
Tuesday, June 4th, 2019 – Invited Lectures & Poster Session

Talks in Medical Sciences Building, Room 2170

Posters & Lunch in Medical Sciences Building, Room 2171 (C. David Naylor Student Commons)

Website: http://microbeto.ca/mid-2019/

Monday, June 3rd, 2019

9:30 - 9:40 WELCOME ADDRESS

9:45 – 10:00: Avid Mohammadi
Characterizing the impact of penile-vaginal sex on HIV-susceptible CD4+ T cell subsets in the female genital tract

10:05 - 10:20: Erin O. Y. Wong
Developing defined microbiota to model inflammation in the mouse gut

10:25 - 10:40: Nora Mellouk
An ATG16L1-dependent pathway promotes plasma membrane repair and limits Listeria monocytogenes cell-to-cell spread

10:45 - 11:15: COFFEE BREAK

11:20 - 11:35: Jean-Paul R. Soucy
Joint modelling of resistance to six antimicrobials in urinary *Escherichia coli* isolates in Quebec, Canada

11:40 – 11:55: Sarah Birstonas
EHEC utilizes two-component systems to modulate expression of major flagellar subunit protein, FliC, in response to host intestinal cues

12:00 - 12:15: Nathaniel Winsor
NLRP6 regulates the colonic mucus layer during Tritrichomonas infection

12:35 – 1:30: LUNCH

1:35 - 12:50: Samuel Salamun
Epstein-Barr Virus Protein BMRF1 Modulates Cellular SUMO and DNA Damage Response Pathways by Binding the Cellular NuRD Complex

1:55 - 2:10: Nicola Case
Elucidating the mechanism of Candida albicans morphogenesis in response to phagocytosis by macrophages

2:15 - 2:30: Sarah Kronheim
A small molecule anti-phage defense mechanism in Streptomyces

2.30 - 3:00: COFFEE BREAK

3:05 - 3:20: Alexandra Willis
Understanding inherited immunity using a *C. elegans* model of microsporidia infection

3:25 - 3:40: Genevieve Mailhot
Differentiating between protective and pathogenic neutrophil responses during *Neisseria gonorrhoeae* infection

3:45 – 4:00: Tiffany Fitzpatrick
Successes of anti-RSV prophylaxis among infants in Ontario: results from a multi-decade, population-based controlled interrupted time series analysis using health administrative data

Poster Presentations

85) Sequence Heterogeneity in Leishmania RNA Virus-1 (LRV-1) Detected in Strains of *Leishmania Viannia* spp.

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Alexander von Humboldt", Lima, Peru 4Tropical Disease Unit, UHN-Toronto General Hospital, Toronto, ON, Canada Leishmania RNA Virus (LRV) is classified as a Group III dsRNA virus belonging to the family Totiviridae, containing a 5284 nucleotide sequence. Two main types of LRV are known to infect strains of Leishmania: LRV-1 and LRV-2. LRV-1 in the New World has 14 subtypes (LRV-1-1 – LRV-1-14) predominantly isolated from the Amazon basin. Since the detection of LRV-1 in a patient with cutaneous satellite lesions and lymphatic involvement after visiting Suriname, the notion that LRV-1 in the parasite might be causing more severe disease has been the focus of evaluation over the past few decades. We wanted to understand whether sequence heterogeneity within the LRV-1 virus could contribute to the severe phenotype observed in some patients infected by the Leishmania Viannia spp. Nucleic acid was extracted from clinical cultured cells for species identification and LRV-1 detection using quantitative real-time PCR (qPCR). Cultures positive by qPCR were confirmed by end-point PCR and Sanger Sequencing using primers targeting LRV-1-1 and LRV-1-4 subtypes primarily known to circulate in Latin America. Of 56 available clinical cultures, 18 were positive by qPCR. To date, 3/18 (16.7%) LRV-1 positive clinical cultures have been confirmed by end-point PCR with sufficient sequence product. The following species were identified: 2/3 (67%) L. V. braziliensis and 1/3 (33%) L. V. panamensis. A phylogenetic molecular analysis was performed using the Maximum Likelihood method (BioEdit version 7.2.5) post ClustalW Multiple alignment using the three previously mentioned clinical cultures, ATCC© 50126 L. V. guyanensis and NCBI reference genomes: NC002063.1 and NC00306.1. An unrooted tree was produced 2 distinct clusters whereby the 2 LRV-1 positive L. V. braziliensis and 1 ATCC© 50126 L. V. guyanensis strains were branched from the same node (length = 0.08639, $p < 0.01$) while the LRV-1 positive L. V. panamensis, NC00306.4 and NC002063.1 strains branched from an unrelated node (length = 1.23789, $p < 0.01$). Further analysis of the remaining LRV-1 positive cultures will provide more insight into the divergence of LRV-1 between species as well as implications into the severity of disease in ATL.