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

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**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/

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## 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

# 82) Novel Detection of Leishmania RNA Virus-1 (LRV-1) in Leishmania Viannia panamensis Clinical Isolates

Ruwandi Kariyawasam1, Rachel Lau2, Braulio M. Valencia3, Alejandro Llanos-Cuentas3, Andrea K. Boggild4

1Institute of Medical Sciences, University of Toronto, Toronto, ON, Canada 2Public Health Ontario Laboratories, Toronto, ON, Canada 3Instituto de Medicina Tropical "Alexander von Humboldt", Lima, Peru 4Tropical Disease Unit, UHN-Toronto General Hospital, Toronto, ON, Canada

American tegumentary leishmaniasis (ATL) comprises a discrete set of clinical presentations of leishmaniasis endemic to Central and South America. Leishmania RNA virus-1 (LRV-1) is a double stranded RNA virus identified in 20-25% of the Leishmania (L.) Viannia (V.) braziliensis and L. V. guyanensis, and is believed to be a predictive biomarker of severe ATL. To date, LRV-1 has loosely been described in other members of the Viannia complex including L. V. peruviana and L. V. lainsoni, however not in L. V. panamensis. We describe the novel detection of LRV-1 in L. V. panamensis and its associations with clinical phenotypes of ATL. Unique surplus discard clinical isolates were identified from Public Health Ontario Laboratory (PHOL) and the Leishmania Clinic of the Instituto de Medicina Tropical “Alexander von Humboldt” between 2012 and 2018. Banked clinical isolates were species identified by PCR, RFLP analysis, and Sanger sequencing. Clinical isolates identified as L. V. panamensis were screened for LRV-1 by real-time PCR. Patient isolates were stratified according to clinical phenotype: localized cutaneous leishmaniasis (LCL) was defined as "non-severe" ATL, whereas "severe ATL" was defined as mucosal or mucocutaneous leishmaniasis (ML/MCL); erythematous, purulent, or painful ulcers and/or lymphatic involvement (inflammatory ulcers); or multifocal/disseminated ulcers ($\geq 4$ in $\geq 2$ anatomic sites). Of 22 patients with confirmed L. V. panamensis, 9 (41%), 7 (32%), 5 (23%), and 1(0.5%) had travel history to or resided in: Peru, Costa Rica, Ecuador and Panama, respectively. Nine (41%) and 13 (59%) patients had the severe and non-severe phenotypes, respectively. Three (33%) of 9 severe cases and 4 (30.8%) of 13 non-severe cases were positive for LRV-1, respectively ($p=0.90$). Median age of patients did not differ by clinical phenotype (median age 45.75 years in severe ATL vs. 31.93 years in non-severe ATL, $p=0.09$), or LRV-1 status (median age 34.14 years in LRV-1 positive patients vs. 38.27 years in LRV-1 negative patients, $p=0.64$). No differences in sex were observed for clinical phenotype ($p=0.60$) and LRV-1 status ($p=0.52$). Although an association between LRV-1 status and clinical phenotype was not demonstrated, we describe the novel detection of LRV-1 in L. V. panamensis, a species that has been documented predominantly in Central America. The role of LRV-1 in severe disease of L. V. panamensis requires further exploration to understand the dynamics of influencing host-immune responses as observed by L. V. braziliensis and L. V. guyanensis.