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

43) Validation Of A Multiplex Real-time PCR Gastrointestinal Parasites Panel

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Microscopy is the conventional method for identification of gastrointestinal parasitic pathogens in fecal samples, however, it presents numerous challenges including high technical expertise and prolonged turnaround time. Molecular methods provide higher throughput and potentially higher sensitivity and specificity. We sought to validate a commercial multiplex parasitic real time PCR panel detecting 6 protozoal pathogens: Blastocystis hominis (Bh), Cryptosporidium, Cyclospora, Dientamoeba fragilis (Df), Entamoeba histolytica (Eh) and Giardia lamblia (Gl) in unpreserved fecal specimens submitted for diagnostic parasitology. We analyzed 192 specimens, including 84 banked, frozen known positive specimens containing all of the targeted pathogens (8 Bh, 13 Crytosporidium, 13 Cyclospora, 10 Df, 15 Eh, 13 Gl and 12 mixed protozoal infections) and 108 fresh specimens randomly selected from our prospective parasitology submissions, including 4 Bh, 3 Df, 2 mixed infections, and 99 microscopy negatives. DNA extraction and PCR were setup with the Hamilton Starlet automated platform and Seegene's extraction and PCR kits. Microscopy was the reference standard for all organisms with stool ELISA as an additional reference assay for Eh. Sensitivity, specificity, positive predictive and negative predictive values of the enteric multiplex were: 96%, 90%, 60%, and 99% for Bh; 100% for Cryptosporidium; 79%, 100%, 100%, and 98% for Cyclospora; 86%, 86%, 86%, and 98% for Df; 81%, 100%, 100%, and 98% for Eh; and, finally, 94%, 85%, 85% and 99% for Gl, respectively. The platform had high sensitivity for Bh, Cryptosporidium and Gl, but suboptimal sensitivity for detection of Cyclospora, Df, and Eh. Low positive predictive value for Bh may reflect challenges to accurate microscopic identification of this organism. Negative predictive value was excellent for all targets, supporting that the platform accurately determines true negatives. Limit of detection was as follows: 8 parasites/g stool for Bh; 9 parasites/g stool for Cryptosporidium; 38 parasites/g stool for Cyclospora; 697 parasites/g stool for Df; 47 parasites/g stool for Eh; and 22 parasites/g stool for Gl. This particular enteric multiplex platform provides a useful diagnostic tool for Bh, Cryptosporidium, and Gl. Further optimization of the assay is required for Cyclospora, Df, and Eh prior to clinical use.