UNIVERSITY of GUELPH

COLLEGE of BIOLOGICAL SCIENCE

DEPARTMENT OF MOLECULAR AND CELLULAR BIOLOGY

Announcement:

All interested members of the university community are invited to attend the Final Oral Examination for the degree of ***Doctor of Philosophy*** *of*

KAITLYN OLIPHANT

on Monday, December 17, 2018 at 9:30 a.m. in SSC 2315

Thesis Title: **Exploring the application of ecological theory to the human gut microbiota using complex defined microbial communities as models**

Examination Committee:

Dr. R. Lu, Dept. of Molecular and Cellular Biology (Exam Chair)
Dr. E. Allen-Vercoe, Dept. of Molecular and Cellular Biology
Dr. L. Mutharia, Dept. of Molecular and Cellular Biology
Dr. J. Geddes-McAlister, Dept. of Molecular and Cellular Biology
Dr. L. David, Duke Centre for Genomic and Computational Biology

Advisory Committee:
Dr. E. Allen-Vercoe (Adv)
Dr. L. Mutharia
Dr. K. Dunfield
Dr. F. Auzanneau

Abstract: The ecosystem of microorganisms that inhabit the human gastrointestinal tract, termed the gut microbiota, critically maintains host homeostasis. Alterations in the gut microbiota are thus unsurprisingly exhibited in patients of gastrointestinal disorders when compared to the healthy population. Therefore, strategies that aim to remediate such gut microbiota through microbial supplementation have been attempted, with variable clinical success. Clearly, more knowledge of how to assemble a health promoting gut microbiota is required, which could be drawn upon from the framework of ecological theory. Current theories suggest that the forces driving microbial community assembly include historical contingency, dispersal limitation, stochasticity and environmental selection. Environmental selection additionally encompasses habitat filtering, *i.e.* host-microbe interactions, and species assortment, *i.e.* microbe-microbe interactions. I propose to explore the application of this theory to the human gut microbiota, and I hypothesize that microbial ecological theory can be replicated utilizing complex defined microbial communities. To address my hypothesis, I first built upon existing methods to assess microbial community composition and behaviour, then applied such tools to human fecal-derived defined microbial communities cultured in bioreactors, for example by using marker gene sequencing and metabonomics. I determined that stochasticity is an important influencer of species structure within the gut microbiota, whereas dietary interventions greatly impacted the metabolic behaviour. Additionally, habitat filtering predominated over species assortment. Together, this work would suggest that successful modulation of the gut microbiota would involve providing microbes as coevolved guilds that can colonize niches ubiquitous amongst the human population.

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Curriculum Vitae: Kaitlyn obtained her Bachelor of Science (Honours) at the University of Guelph in February 2014. In the summer of 2014, she began her M.Sc. graduate work with advisor Dr. Emma Allen-Vercoe, and then transferred directly to the Ph.D. program in the fall of 2015.

Awards:

(2014) CIHR Canada Graduate Scholarship-Masters
(2015-2016) Ontario Graduate Scholarship
(2017-2018) NSERC Canada Graduate Scholarship-Doctoral
(2017) Michael Smith Foreign Study Supplement

Publications:

Carlucci, C., Jones, C., Oliphant, K., Yen, S., Carriero, C., Daigneault, M., Petrof, E.O., Weese, S., and Allen-Vercoe, E. (submitted) Examining the effects of defined gut microbial ecosystem components on the growth and virulence of *Clostridioides difficile*. *Scientific Reports*.

Wissenbach*, D.K., Oliphant*, K., Rolle-Kampczyk, U., Yen, S., Höke, H., Baumann, S., Haange, S.B., Verdu, E.F., Allen-Vercoe, E., and von Bergen, M. (2016) Optimization of metabolic profiling and characterization of defined *in vitro* gut microbial ecosystems. *International Journal of Medical Microbiology*, 306 (5): 280 – 289. **Authors contributed equally*

Gohari, I.M., Parreira, V.R., Nowell, V.J., Nicholson, V.M., Oliphant, K., and Prescott, J.F. (2015) A novel pore-forming toxin in type A *Clostridium perfringens* is associated with both fatal canine hemorrhagic gastroenteritis and fatal foal necrotizing enterocolitis. *PLoS One*, 10 (4): e0122684.

Yen, S., McDonald, J.A.K., Schroeter, K., Oliphant, K., Sokolenko, S., Blondeel, E.J.M., Allen-Vercoe, E., and Aucoin, M.G. (2015) Metabolomic analysis of human fecal microbiota: a comparison of feces-derived communities and defined mixed communities. *Journal of Proteome Research*, 14 (3): 1472 – 1482.