3552
Topic Category: 4181-ASIP Parasitic pathogenesis

First Author: Thibault Allain
University of Calgary
Department of Biological Sciences 2500 University Drive NW Calgary, AB T2N1N4
Canada
Phone: 4035725254
thibault.allain@ucalgary.ca

First Author is a: Postdoctoral Fellow
First Author is a member of: Not a Member of a Host EB Society
First Author Degree: PhD, DSc, or equivalent

Presentation Preference: Oral

Sponsor: Andre Buret
Sponsor Phone: 4032202817
aburet@ucalgary.ca
Sponsor's Society: Pathology - American Society for Investigative Pathology (ASIP) - Host Society
Keywords: 1. Giardia 2. metabolomic

The metabolomic signature of *Giardia* sp.

Thibault Allain, Ryan Groves, Ian A. Lewis, Andre G. Buret. Department of Biological Sciences, University of Calgary, Calgary, AB, Canada

BACKGROUND

Giardia duodenalis is a protozoan parasite responsible for giardiasis, a parasitic disease characterized by intestinal malabsorption, diarrhea, weight loss and abdominal pain. The pathophysiological processes occurring during giardiasis involve epithelial abnormalities, mucus depletion and microbiota disruption, however the mechanisms are poorly understood. Upon infection, *Giardia*, which has a minimal biosynthetic capacity, compete locally with the commensal microbiome for nutrients and ecological niches in the duodenum.

AIM

In this context, we performed a metabolomic study to characterize the nutritional requirements and the secretome of several *Giardia* strains, isolated from human patients (assemblages A and B), outbreaks, as well as a variety of mammals.

METHODS

The metabolomic profiles of *Giardia* sp. isolates were determined using mass spectrometry. Trophozoites were grown to confluence in MTYI media and supernatants were collected at different time points (3, 6, 9, 12 and 24 hours) and mixed with ice cold methanol. Methanolic extracts were analyzed by Ultra High Performance Liquid Chromatography mass spectrometry and resolved by Hydrophilic interaction liquid chromatography column.

RESULTS

We identified a multitude of produced and consumed compounds such as amino acids, nucleic acid precursors, protein catabolism precursors, as well as carbohydrates and energy metabolites. Interestingly, nutrition requirements of *Giardia* trophozoites are significantly different between isolates, both intra and inter-assemblages. For instance, isolate WB6 (assemblage A) is more auxotrophic for arginine than GSM strain (assemblage B), while GSM strain requires more inosine, uridine and asparagine than other isolates.

CONCLUSION

This study gives insight into how *Giardia* survives the host's intestinal tract and shows strain specific metabolomic signatures. A metabolomic approach may further help to understand the impact of nutritional modulation by *Giardia* trophozoites on the gut microbiome and host physiology.

Support or Funding Information
Grant support: University of Calgary Eyes High postdoctoral fellowship