



The College of Graduate Studies and the College of Medicine and Health sciences  
Cordially Invite You to a

**Master Thesis Defense**

**Entitled**

ASSOCIATED RISK OF BLASTOCYSTIS INFECTION IN COLORECTAL CANCER

by

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**Date & Venue**

01:00pm

Tuesday, 11<sup>th</sup> of October 2022

Online: Microsoft Team [Click here to join the meeting](#)

Venue: Yanah Theater

\* **Location:** 2C010 located on 2<sup>nd</sup> floor 'C' block male side.

**Abstract:**

**Background:** *Blastocystis species* is an anaerobic intestinal protozoan seen in humans and a wide range of animals. Only nine *Blastocystis* subtypes are seen in humans. The pathogenicity of *Blastocystis spp.* has long been controversial. Recently, a subtype-dependent association between *Blastocystis spp.* and colorectal cancer (CRC) is being debated. Thus, this thesis aims to assess the possible association between *Blastocystis spp.* infection and CRC condition compared to cancer outside the gastrointestinal tract (COGT) and a cancer-free control (CF) group. This study is the first in its kind in the UAE.

**Methods:** Participants are divided into two groups; Cancer patients and CF participants. The Cancer group is further sub-grouped into the CRC patients' group and COGT group. Written consents for fresh stool sample collection were given by all participants. Formalin-Ethyl

Acetate concentration technique, modified Ziehl-Neelsen and Wheatley Trichrome permanent stains were used to identify any present intestinal parasites in stool samples. Furthermore, Molecular analysis was conducted to identify *Blastocystis spp.* and its sub-types in addition to *Cryptosporidium spp.* and gut mycobiome. Phylogenetic analysis for *Blastocystis spp.* was also performed for further subtype confirmation.

**Results:** We collected 104 matched samples equally divided between cancer and CF samples (n=52). Of the 52 cancer patients' samples, 15 are from CRC patients, while the remaining (n=37) are from patients with COGT. The prevalence of *Blastocystis* was significantly higher among cancer patients (n=21, 40.4%,  $p$ -value=0.009; OR=2.98, 95% CI; 1.169-7.577,  $p$ -value=0.022) compared to CF participants (n=9, 17.3%). Furthermore, this study revealed that the prevalence of *Blastocystis spp.* is significant in CRC patients (n=9, 60%,  $p$ -value=0.002; OR=5.66, 95% CI; 1.531-20.895,  $p$ -value=0.009) compared to the CF group. Contrarily, *Blastocystis spp.* prevalence in COGT patients was insignificant compared to the CF group (n=12, 32.4%,  $p$ -value=0.161). Interestingly, no significant difference in *Blastocystis* infection was seen between the two cancer groups ( $p$ -value=0.209). Gut mycobiome was found in 60 samples (57.7%), divided into equal parts between CF and cancer groups (n=30, 50%). Out of the 30 samples in the cancer group, 22 samples (73.3%) were from the COGT group, while the remaining 8 (26.7%) were from the CRC group. *Cryptosporidium spp.* was only found in 4 samples (3 CF and 1 COGT). No significant association or correlation was seen between the detection of gut mycobiome and *Blastocystis* infection ( $p$ -value=0.311) nor the two main groups (CF and cancer groups) ( $p$ -value=1). Similarly, *Cryptosporidium spp.* was not significantly associated with *Blastocystis spp.* ( $p$ -value=1) nor with cancer ( $p$ -value=0.168). The predominant *Blastocystis* subtype in all sequenced samples is ST3. ST2 is the most common in the cancer group (n=4), while ST3 is the most common in the control group (n=4).

**Conclusion:** CRC is one of the most common and fatal cancers in the UAE with no definite symptoms. Thus, studying the association and pathogenicity of *Blastocystis spp.* (a frequently encountered, potentially pathogenic protozoa) in CRC is crucial in limiting or potentially preventing the development and progression of CRC. Also, the highest *Blastocystis spp.* prevalence was among CRC patients compared to the other two groups (CF and COGT), further supporting previous literature findings.

**Keywords:** *Blastocystis spp.*, Colorectal Cancer, ST Subtypes, *Cryptosporidium spp.*, Gut Mycobiome, Phylogenetic Analysis