Blastocystis infection and gut microbiota composition in type 2 diabetic mellitus patients and non-diabetic individuals

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ABSTRACT

Introduction: The influence of anaerobic protozoan *Blastocystis* on human gut health is not well understood. While *Blastocystis spp*. frequently inhabiting the gut, their clinical importance remains ambiguous. Therefore, a study on Blastocystis was conducted to evaluate the prevalence of *Blastocystis* and its association with gut microbiota in T2DM patients and non-diabetic individuals. **Materials and Methods:** A total of 203 participants aged 18-65 years including T2DM patients and non-diabetic individuals were recruited in the study. *Blastocystis* subtypes were identified by Polymerase Chain Reaction (PCR) and faecal microbiome was accessed by targeting V4 region of the bacterial 16S ribosomal gene. **Results:** The prevalence of *Blastocystis* in T2DM was 25.49% and 17.82% in non-diabetic individuals, with the most prevalent subtype in the total population being ST3, followed by ST1 and ST2. The older age T2DM patients (45 years old and above) had a higher prevalence rate of *Blastocystis* infections (17%) than in younger age (less than 45 years old) (9%). The composition of gut microbiota was significantly different between *Blastocystis*-positive and Blastocystis-negative groups. *Blastocystis* infection was positively associated with higher alpha diversity in T2DM patients and non-diabetic individuals. Interestingly, at the phylum level, the T2DM group had an obvious increase of Bacteroidetes and a marked increase of Actinobacteria with the presence of *Blastocystis*. **Conclusion:** The findings suggested that the presence of Blastocystis was linked to increased diversity and richness in the gut bacterial composition, signifying a potentially beneficial association between Blastocystis and the gut microbiota.

Keywords: *Blastocystis*, gut microbiota, type 2 diabetes mellitus