Alteration of gut bacteria composition among individuals with asymptomatic Blastocystis infection: A case-control study

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Abstract:

The gut microbiota consists a diverse and complex ecosystem that is involved in beneficial functions as well as potentially harmful conditions for human. Blastocystis sp. is a common parasite of the digestive tract of animals and humans; however, limited data is available concerning the association of asymptomatic Blastocystis infection and gut bacteria composition. Hence, in this cross-sectional study, the gut bacteria composition of twenty asymptomatic Blastocystis sp. positive and twenty Blastocystis sp. negative individuals was assessed with real time PCR. The case and control groups were matched for age and sex. Both groups were negative for other gastrointestinal infections and did not have any gastrointestinal symptoms. The subtype of ten Blastocystis sp. isolates was assessed based on sequencing. Sequencing of ten Blastocystis sp. isolates revealed the ST1, ST2, and ST3 subtypes in 40%, 30%, and 30% of the isolates. The relative expression of each bacteria in the case than control group revealed that the expression level of Bifidobacterium group ($P < 0.033$), Peptostreptococcus productus ($P < 0.014$), Lactobacillus/Enterococcus group ($P < 0.001$), and Escherichia coli ($P < 0.001$) were significantly upregulate in the Blastocystis sp. carriers than the control group, while the relative amounts of Bacteroides fragilis ($P < 0.001$) and Enterococcus sp. ($P < 0.001$) were significantly downregulated in the case than the control group. Taken together, the results of this study have shown that asymptomatic Blastocystis infection could alter the composition of gut bacteria in healthy individuals.

Keywords: Blastocystis; Dysbiosis; Eubiosis; Iran; Microbiota; Protozoa