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Genetic diversity of human *Blastocystis* isolates in Makkah, Saudi ArabiaRaafat Taha Mohamed Makhlof^{1,2}, Anhar A. Mohamed^{1,3}, Mohamed A. EL Bali¹, Mona A. Abdel-Fatah^{3,5}, Saeed A. Al-Harhi¹, Mohamed EL-Malky^{1,4}, Nawras M. E. Mowafy^{1,2}, Dina Zaghloul⁵ and Rowaida Bakri¹¹Umm AL-Qura University, Saudi Arabia²El-Minia University, Egypt³Ain Shams University, Egypt⁴Mansoura University, Egypt⁵Microbiology Laboratory, King Abdellah Medical city, Saudi Arabia⁶Assuit University, Egypt⁶Al-Noor Specialist Hospital, Saudi Arabia

Blastocystis spp. is commonly found in the feces of human worldwide. Infection has been reported as asymptomatic, acute symptomatic and chronic symptomatic. This wide range of responses to infection could be related to the genetic diversity. Since the genotype of human *Blastocystis hominis* isolates is highly polymorphic, PCR-based genotype classification using known sequence-tagged site (STS) primers would allow the identification or classification of different genotype. This study was done on 650 stool samples collected from patients referred to two major hospitals in Makkah city, Saudi Arabia in 2014-2015. All microscopically positive samples were subjected to *in vitro* culture using D-MEM media with 20% horse serum and antibiotics with incubation at 37 °C anaerobically. The screening of *Blastocystis* organisms in 3 to 4 days old cultures was done observing the typical vascular or granular forms, then sub-culturing more than 2 times and freezing for DNA extraction. PCR was done using seven kinds of STS primers. One hundred forty isolates were confirmed positive using diagnostic primers. Ninety-nine out of 140 isolates were identified as subtype-I genotype (ST1) followed by 24 isolates identified as subtype-II genotype (ST2) while 14 isolates identified as subtype-III genotype (ST3). Only two isolates were negative with all the STS primers, the phylogenetic position was inferred from the small subunit rRNA (SSU rRNA) genes with the known sequence data of 20 *Blastocystis* isolates. In conclusion, the ST1 is the predominant genotype among Saudi patients.

Biography

Raafat Taha Mohamed Makhlof has completed his PhD in 1999 at Institute of Medical Science, Tokyo University, Japan and Postdoctoral studies from 2001-2003 at Department of Molecular Immunogenetics, Institute of Tropical Medicine, Nagasaki University, Japan as a Postdoctoral Fellow. He is one of the Staff Members at Department of Medical Parasitology. He has published more than 10 papers in reputed journals.

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