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Multilocus genotyping of Giardia duodenalis reveals human-to-human transmission pattern in Tehran, Iran

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Background: *Giardia duodenalis* protozoan parasite lives in the small intestine of human and a large number of domestic and wild animals. *Giardia duodenalis* is a species complex with at least eight distinct assemblages nominated as A to H. Assemblages A and B are the main cause of infection in humans, as well as a wide range of mammals. Today, multilocus genotyping (MLG) has become a useful tool for genotyping and subtyping of *G. duodenalis*. Better understanding of the genetic diversity of *Giardia* helps to further explore the taxonomy and molecular epidemiology of this parasite. The purpose of this study was to identify *G. duodenalis* assemblages, sub-assemblages, and genotypes based on multilocus analysis of triose phosphate isomerase (*tpi*), *β -giardin* (*bg*) and glutamate dehydrogenase (*gdh*) genes, in Tehran.

Material/methods: Sixty-two Giardia positive-cyst human fecal specimens were included in the study. Extracted DNA was subjected to Nested-PCR analysis of three genes and sequencing in both directions. Nucleotide sequences of isolates were aligned with the sequences in GenBank database and the phylogenetic analysis was performed to identify assemblages, sub-assemblages, and genotypes of *G. duodenalis* isolates.

Results: Of 62 *Giardia*-positive samples, the sequencing analysis of *tpi*, *bg* and *gdh* genes showed 26 (41.9%) assemblages A and 27 (43.5%) assemblages B. Nine (14.5%) samples recognized different assemblage with each locus that named as discordant assemblages. At the sub assemblage level, all A assemblages were AII. At the genotype level, A2, A3, B3 and B4 genotypes were identified.

Conclusions: The present study confirmed that the MLG was an important tool in determining the assemblages and sub assemblages for isolates of assemblage A, but less important in determining the sub assemblages for isolates of assemblage B. The finding of assemblage B and the sub assemblages AII suggested human-to-human transmission pattern in Tehran, Iran.