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Prevalence of *Giardia duodenalis* assemblages and sub-assemblages in symptomatic patients from Damascus city and its suburbs

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Background: *Giardia duodenalis* is one of the most important human enteric parasites worldwide and is endemic throughout the world with a vast range of mammalian hosts. However, there is limited information on the prevalent genetic variability of *G. duodenalis* in Syria.

Aim: This study aimed to evaluate the predominance of *G. duodenalis* assemblages/sub-assemblages causing humans infection in the city of Damascus and its suburbs.

Methods: 40 symptomatic giardiasis patients were recruited in this study. Fecal samples were genotyped using PCR/RFLP assay targeting the ß-giardin and glutamate dehydrogenase (gdh) genes. HaeIII, BspL1 and RsaI restriction enzymes were used to differentiate between *G. duodenalis* assemblages/sub-assemblages.

Findings: Our data showed that 65% of isolates were of assemblage A; 45% belonged to sub-assemblage AII and 20% to sub-assemblage AI. Assemblage B was detected in 27.5% of isolates; 12.5% fit in sub-assemblage BIV, 5% fit in sub-assemblage BIII and 10.5% fit in Discordant genotype BIII/BIV. Mixed genotypes (AII+BIII and AI+BIV) were identified in three isolates (7.5%). Significant correlation was found between Giardia AII sub-assemblage and weight loss symptom (P-value=0.05) as well as between contact with domestic animals (cats, P-value=0.027). Moreover, a significant correlation was found between sub-assemblage AI and livestock breeding (P-value=0.000).

Conclusion: The genotyping of human *Giardia duodenalis* isolates suggests anthroponotic transmission for the route of infection in Damascus and its suburbs. Further studies are needed to screen a wide geographic area in Syria and to estimate the prevalence of *G. duodenalis* infection in our population.

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