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Kinetics of Foxp3-expressing regulatory cells in experimental *Toxocara canis* infection

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Abstract

Foxp3-expressing cells have recently been recognized as a cornerstone for the homeostasis of the immune system, and as key cells in many infectious diseases. Moreover, they have been found to contribute to the regulation of parasite-induced immunopathology in many parasitic infections. However, their role in *Toxocara*-induced immunopathology has not yet been investigated. The aim of this study is to assess the kinetics of Foxp3-expressing regulatory cells during the course of experimental infection by *Toxocara canis* (*T. canis*). Foxp3⁺ cells were identified in the liver by immunohistochemistry, and splenic Foxp3 gene expression was evaluated. We found significantly progressive increase in Foxp3-expressing cell counts in the liver starting from 5 weeks p.i. These cells were detected within and around *Toxocara*-induced granulomas as well as in isolated inflammatory foci in the portal tracts or within the hepatic parenchyma. Likewise, expression of Foxp3 mRNA in the spleen significantly increased at 5 and 16 weeks p.i. Furthermore, immunization of mice with *Toxocara* excretory–secretory antigen prior to experimental infection caused earlier mobilization and recruitment of Foxp3⁺ cells to the liver and enhanced splenic expression of Foxp3 transcripts. These results suggest a potential role of Foxp3-expressing regulatory cells in the evolution of the immunopathological events during infection by *T. canis*.

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Identification of a novel Assemblage B subgenotype and a zoonotic Assemblage C in human isolates of *Giardia intestinalis* in Egypt

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Abstract

Giardia intestinalis (*G. intestinalis*) is a flagellate parasite which has been considered the most common protozoan infecting human. Molecular techniques are of great value in studying the taxonomy, the zoonotic potential of animal isolates and the correlation between the genetic variability of the parasite and the range of clinical symptoms observed in humans. The present work aims at genotyping *G. intestinalis* isolates from Egypt using molecular techniques. PCR targeting the β -giardin locus, RFLP and sequencing were applied to 12 microscopically positive and 3 microscopically negative samples (which were positive by real time PCR targeting SSUr DNA). Two other loci, triose phosphate isomerase (TPI) gene and glutamate dehydrogenase (GDH) gene PCR and RFLP were also applied to all study isolates. The most frequent genotype was Assemblage B (13 out of 15), while Assemblage A and C were present in one sample each. This is the first report on zoonotic transmission of Assemblage C (dog genotype) to human in Egypt. Sequencing of the Assemblage B isolates revealed new subgenotypes with consistent mutations at specific positions, some of which were not characterized previously. The results shed light on the possibility that *G. intestinalis* can infect humans through a zoonotic route and open the door to wider investigations using different genetic loci to genotype *Giardia* isolates.