



**FAMILIAL TRICHOSTRONGYLIASIS OUTBREAK IN GUILAN PROVINCE, NORTHERN IRAN, MIS-DIAGNOSED WITH ACUTE FASCIOLIASIS**

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The suitable climatic conditions and high amounts of rainfall, accompanied with traditional herding, expose the livestock to parasitic diseases in Guilan province. These livestock then play a critical role in transmitting parasitic diseases to humans through infecting the environment by their fecal materials, containing ova and larvae. Guilan province has been recognised as the focus of human fascioliasis in Iran and the whole Asia, because of the two largest outbreaks in the world, affecting more than 15000 individuals. Local physicians consider hypereosinophilia as a marker of fascioliasis, especially when accompanied with abdominal pain, fever and allergic manifestations. So, it is frequently confused with other parasitic diseases prevalent in the area. We are reporting an interesting case of such misdiagnosis in one family. Three sisters of the same family, aged 33, 35 and 38 years old, presented at the same time for medical care with a three-week history of abdominal and epigastric pain radiating to their back, mild to severe diarrhoea, urticaria on their hands, chest and back associated with itching, poor appetite, weakness and weight loss. Blood tests revealed hypereosinophilia of 20, 56 and 60%, while anti-Fasciola and anti-Strongyloides antibodies were both negative. The patients reported regular consumption of fresh vegetables, obtained from their home garden fertilized with fresh sheep manure. Three stool samples from each person were examined using formalin-ether and Kato-Katz techniques under a liver-free diet, and were negative for any ova, cyst and larvae. The patients were diagnosed as having acute fascioliasis based on clinical and epidemiological evidence and received 10 mg/kg of Eगतen. One month later, they were readmitted without any sign of recovery. Three new stool samples were examined from each patient, under the same conditions and by the same specialist, which surprisingly were positive for *Trichostrongylus* ova. The patients were treated by combination of the usual doses of mebendazole and albendazole and their fecal materials were collected for 24 hours after therapy. Two species of *Trichostrongylus*, (*T. colubriformis* and *T. vitrinus*) were identified by morphological and molecular techniques. All other three family members, who were subsequently analyzed, also shed *Trichostrongylus* eggs. Fascioliasis and trichostrongyliasis share many epidemiological and clinical characteristics, and are both prevalent in climates and living conditions similar to those of Guilan Province. This case highlights the need to consider trichostrongyliasis in the differential diagnosis of fascioliasis patients, particularly in the acute phase when the eggs are not present in stool, and whenever there is a history of eating fresh vegetables fertilized with fresh livestock manure, or close contact with herbivorous animals.

**Keywords:** trichostrongyliasis, *Trichostrongylus colubriformis*, *T. vitrinus*, familial outbreak, Iran

**GENETIC VARIATION IN THE SEQUENCES OF THE INTERNAL TRANSCRIBED SPACERS (ITS) OF NUCLEAR RIBOSOMAL DNA (RDNA) AMONG AND WITHIN TOXOCARA NEMATODE OF DOGS AND CATS FROM DIFFERENT AREAS IN IRAN**

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*Toxocara canis* and *Toxocara cati* are ascaridoid nematodes of dogs and cats. The objectives of the present study were to identify the sequence variation of the internal transcribed spacer (ITS) region within and among isolates of *T. canis* and *T. cati* from dogs and cats in Iran. Genomic DNA was extracted from 23 isolates of *T. canis* and 35 isolates of *T. cati* collected from dogs and cats in different geographical areas of Iran. ITS region in nuclear ribosomal DNA was PCR-amplified. The PCR product of 5 isolates of *T. canis* and 9 isolates of *T. cati* were sequenced. The sequences were aligned using the BioEdit software and compared with published sequences in GenBank. Phylogenetic analysis was performed using Mega 5.0 software and Maximum likelihood method. The amplicons of about 1000 and 1100 bp were successfully produced for *T. canis* and *T. cati*, respectively. Pairwise comparison of the sequences did not show any differences in nucleotide sequences within *T. canis* isolates. Likewise, sequences of *T. cati* were identical and exhibiting 100% homology. However, 12% inter-species sequence difference was found between the isolates of *T. canis* and *T. cati*. Regarding to no intra-species variation and a significant inter-species variation in ITS region among *T. canis* and *T. cati* isolates, it is concluded that the region can be used for identification and differentiation of *Toxocara* species.

**Keywords:** genetic variation, *Toxocara canis*, *Toxocara cati*, ITS, Iran